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In vivo and in vitro studies of MUC1 regulation in sheep endometrium

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1 Abstract

2	In this study, we investigated the expression of MUC1 mRNA and protein in sheep endometrium at				
3	different time-points during follicular and luteal phases of estrous cycle, and also determined the				
4	effect of steroid hormone treatments and interferon tau (IFN τ) on <i>MUC1</i> mRNA expression in				
5	endometrial cell culture in vitro. In experiment 1, fifteen Welsh mountain ewes were synchronised to a				
6	common estrus and killed at precise stages of estrous cycle corresponding to i) pre-LH peak, ii) LH				
7	peak, iii) post-LH peak, iv) early luteal, and v) mid-luteal. Reproductive tracts were harvested and				
8	mRNA was extracted from the endometrial tissues. Parts of the uterine horns were fixed for				
9	immunohistochemistry. In experiment 2, mixed populations of ovine endometrial cells (from				
10	slaughterhouse material collected at the post-ovulatory stage of the estrous cycle) were cultured to				
11	70% confluence before treatment with i) progesterone (P ₄ , 10 ng/mL, for 48 h), ii) oestradiol (E ₂ , 100				
12	pg/mL, for 48 h), or with iii) E_2 priming for 12 h (100 pg/mL) followed by P_4 (10 ng/mL) for 36 h.				
13	These were compared to; iv) IFN τ (10 ng/mL, for 48 h), and v) basic medium (DMEM/F12) as				
14	control. The results showed that MUC1 mRNA and protein expression in sheep endometrium was				
15	highest during the mid-luteal stage and very low during the post-LH period compared with other				
16	stages (P<0.05). MUC1 immunostaining in the LE was apically restricted and was not significantly				
17	different across all stages of estrous cycle except at the post-LH peak where it was significantly low.				
18	In cell culture, MUC1 mRNA expression was significantly up-regulated by both steroids either singly				
19	or in combination (P<0.05), and down-regulated in the presence of IFNT. In conclusion, endometrial				
20	MUC1 expression is cyclically regulated by both E_2 and P_4 in vivo and in vitro, and directly down-				
21	regulated by IFN τ treatment <i>in vitro</i> .				

22 Key words: MUC1, endometrium, progesterone, estrogen, interferon tau

23 1. Introduction

24	Mucin 1 (MUC1) is a membrane-bound O-glycosylated protein that is a member of the mucin family.
25	It is expressed on the apical surface of mucosal epithelial cells and plays an essential role in forming
26	protective mucous barriers on epithelial surfaces and is also involved in intracellular signalling. In the
27	reproductive system, MUC1 is expressed in the uterus [1] and in the testes [2]. MUC1 has been linked
28	to numerous functions [3] including antimicrobial effects by inhibiting microbial access to the cell
29	surface as well as inhibition of cell-cell adhesion.
30	In the uterus, successful implantation requires complex interaction between trophoblast and maternal
31	endometrium. Available evidence suggests that the burden of implantation lies more on the
32	endometrium rather than the embryo [4]. It has been shown that embryos are capable to attach to
33	endometrial stromal cell culture and others tissues in vitro [5,6] however, embryos cannot attach to
34	uterine endometrium outside the short period of window of receptivity [7]. Non-receptivity of
35	endometrium has been partly attributable to features characteristic of luminal epithelia expressing
36	glycocalyx, of which trans-membrane mucin 1 glycoprotein encoded by MUC1 gene is the most
37	widely expressed and distributed in the reproductive tract [3].
38	MUC1 protein is expressed mainly in luminal epithelium (LE) and glandular epithelium (GE) of the
39	endometrium in many mammalian species including mice, rat, pig, sheep, horse and human during
40	various stages of a menstrual or estrous cycles [1, 8-11]. MUC1 is proposed to protect the
41	reproductive system by preventing entrance of pathogens through the LE into endometrium [12]. It
42	also constitutes an impediment to implantation by hindering interaction between families of
43	conformationally smaller adhesion molecules such as integrins expressed on both the trophectoderm
44	and LE [13]. In another perspective, this hindrance to implantation may be perceived as a
45	physiological barrier that ensures only a potentially viable embryo successfully modulates
46	endometrial receptivity and successfully implants. This hypothesis is supported by reduction of cell
47	surface MUC1 in endometrium of women that experienced recurrent spontaneous abortion [14].

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48 During implantation of the blastocyst to the endometrial epithelia, MUC-1 glycoforms in the 49 endometrium which have been shown to carry selectin ligands [15] might mediate initial interaction 50 with the L-selectin that is expressed on the trophectodermal surface of the blastocyst [16]. 51 Subsequently it is essential that the MUC1 barrier is eliminated to create embryonic access to the 52 uterine epithelium. In most mammalian species including sheep, this appears to be accomplished by 53 down-regulation of MUC1 gene expression, at least locally. 54 Ovarian steroids; progesterone and oestrogen, as well as the presence of embryo have been implicated 55 in MUC1 regulation [1, 13] however MUC1 regulation seems not to follow a general pattern across 56 all mammalian species and its regulation in the endometrium is therefore, species specific. 57 MUC1 is down-regulated before implantation in the receptive endometrium of mice [17], rats [18], 58 pigs [19] and sheep [10]. In contrast, MUC1 is upregulated in human endometrial at implantation [15] 59 however human embryos seems to locally down-regulate MUC1 as shown in maternal primary 60 endometrial cell culture in the region beneath embryo attachment points [1] suggesting regulatory 61 roles of embryo-produced factors. 62 In addition to steroid regulation of endometrial receptivity, INFt which is secreted by trophoblast 63 cells in ruminants is responsible for maternal recognition as it acts on uterine epithelium to down-64 regulate estrogen and oxytocin receptors thus blocking the development of the uterine luteolytic 65 mechanism [20]. Similar molecule is also produced by human embryos [21]. A progressive effort has 66 been made towards understanding transcriptional regulation of MUC1 in reproductive tract [3], 67 however, the mechanism remains to be completely understood. Besides, a direct effect of $INF\tau$ on 68 MUC1 expression in sheep endometrium has not been tested. 69 In the present study, we have investigated the temporal variation of MUC1 mRNA and protein

70 expression in sheep endometrium during different stages of estrous cycle. To evaluate specific

71 regulations, *MUC1* mRNA expression was analysed in primary culture of ovine endometrial cells

72 treated with steroid hormones or interferon-tau (IFN τ).

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74	2. Material and Methods
75	
76	2.1. Experimental design
77	
78	All experimental procedures complied with regulations in the UK Animal (Scientific Procedures) Act,
79	1986 and were conducted under a project licence which was approved by The Royal Veterinary
80	College's Ethics and Welfare Committee. In experiment 1, Mules ewes (n=15) of similar age (about 2
81	years) were synchronised to a common estrus according to the method described earlier [22]. The
82	animals were killed at precise time-points (n=3 each) as described below and reproductive tracts were
83	harvested for mRNA extraction and immunohistochemistry for protein detection.
84	In experiment 2, mixed endometrial cells were isolated from uteri obtained from abattoir as described
85	in earlier study. The cells were seeded into 24-well plates at a concentration of 5×10^5 cells/well in
86	DMEM.F12 media. At 70% confluence, they were supplemented with serum-free media for 24 h
87	before treatment with one of the following: (i) P_4 (10 ng/mL for 48 h), (ii) E_2 (100 pg/mL for 48 h),
88	(iii) E_2 (100 pg/mL) for the first 12 h followed by P_4 (10 ng/mL) for 36 h. This was compared to iv)
89	Control media or v) IFNt treatment (10 ng/mL for 48 h, Genway, Oxfordshire, UK). IFNt treatment
90	was used as a reference group since it is known to down-regulate MUC1 at the time of implantation
91	[20], hence it was used to validate our culture system. At the end of each culture, media was removed.
92	The cells were rinsed with cold PBS twice and total RNA was extracted. The treatments were done in

93 three independent replicates.

2.2. Experimental animals and synchronisation

All 15 ewes received intravaginal Chronogest® sponges (Intervet UK ltd., Cambridge, UK) for 11
days and treated with 300 IU of PMSG (Intervet UK Ltd, Buckinghamshire, UK) i.m. at the time of
sponge removal. Estrus was observed 24 h after sponge removal. Blood samples were collected via
jugular vein into 10 ml heparinized tubes at sponge removal and every 2 days until day 6, then every

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day until the day of final slaughter. The animals were killed in a step-wise manner based on a

previous study in our laboratory [23] at time-points corresponded to the following five stages of

- 101 estrous cycle (i) pre-LH peak, (ii) LH peak, (iii) post-LH peak, (iv) early luteal and (v) mid-luteal,
- 102 with three animals in each group as shown in Figure 1. Mid-luteal ewes were killed on day 8 of estrus
- 103 (day 0 = estrus). The other 12 ewes received PGF_{2a} injection (Estrumate; 125µg i.m) on day 11 of
- 104 estrus at mid-night. Pre-LH ewes were killed at 32 h post $PGF_{2\alpha}$ injection. The remaining 9 animals
- 105 received GnRH (Receptal 1ml) at 36 h post $PGF_{2\alpha}$. LH-peak ewes were killed at 3 h post GnRH (39 h
- 106 post PGF_{2 α}). Post-LH ewes were killed at 46 h post PGF_{2 α} (10 h post GnRH). Early luteal ewes were
- 107 killed on 84 h post $PGF_{2\alpha}$ administration.
- 108 Blood samples were collected after $PGF_{2\alpha}$ injection at the following time points; 0, 28, 30, 32, 34, 36,
- 109 38, 39, 40, 42, 44, 46, 60, 72 and 84 h. They were centrifuged within few hours after collection and
- 110 plasma were transferred to 7ml tubes and kept at -20° C until the time for LH determination. The

111 reproductive tracts were harvested. Small pieces of the endometrium were carefully dissected from

the uterine horns and snap frozen for mRNA extraction and were used to determine MUC1 mRNA

113 expression using conventional PCR. Sections of uterine horns were also fixed in 4%

114 paraformaldehyde for immunohistochemistry.

115 **2.3. LH determination**

116

117 After 28 hours of $PGF_{2\alpha}$ injection, blood was collected from all animals via the jugular vein at the 118 hours 28, 30, 32, 34, 36, 38, 39, 40, 60 and 84 from the time of $PGF_{2\alpha}$ injection. The time for each 119 group was speculated prior to hormonal determination based on previuos works with the same drugs 120 in sheep in our laboratory [24]. Plasma LH was determined (at the School of Human Development, 121 University of Nottingham, Queen's Medical Centre, Nottingham NG7 2UH, UK) using radio-122 immunoassay technique according to the method described in previous study [25]. The sensitivity of 123 the assay was 0.15 ng/mL.

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2.4. Endometrial cell isolation and culture

125

126	The co-culture of both LE and ST where the two cells communicate and interact simulates the <i>in vivo</i>
127	condition better than a monoculture of either LE or ST [26]. In addition, paracrine action of the ST
128	cells supports growth of LE cells [27]. Primary endometrial cells containing both uterine LE and
129	Stromal (ST) cells were isolated and cultured following our previously optimized procedure [28].
130	Briefly, sheep endometrial luminal epithelia and stromal cells were isolated in a single digestion of 90
131	min in 50 mL of digestive solution consisting of 25 mg of trypsin III (Roche, Welyn, UK), 25 mg of
132	collagenase II (Roche), 50 mg of bovine serum albumin (BSA, Sigma). The isolated cells were plated
133	at a concentration of 5×10^5 cells/mL and 1 mL of the cell suspension was added per well in a 24-well
134	microplate (Iwaki, Scitech Div., Asahi Techno Glass) with Dulbecco Modified Eagle medium
135	(DMEM/F12, Sigma) containing 10% foetal bovine serum. The plates were then incubated in a humid
136	atmosphere at 37 $^{\circ}$ C with 5% CO ₂ . The culture media was changed every 48 h for 5-6 days until 70%
137	confluence was achieved. This was followed by a 24 h incubation in serum-free media before
138	treatment supplementation. The cell population was identified using cell morphology [29] and
139	cytoskeletal markers, cytokeratin and vimentin for LE and ST respectively as was described in
140	previous study [27]. The results showed a monolayer of a mixed population of epithelial and stromal
141	cells in the ratio of 6:4.

- 142 **2.5. Primer design and RT-PCR**
- 143

144 The primers for MUC1 and a reference gene; GAPDH were designed using 'primer 3' web based

software using ovine nucleotide coding sequences published in the National Centre for Biotechnology

146 Information database (http://www.ncbi. nlm.nih.gov/Database/index.html). Primer alignment and

- specificity was checked using the BLAST search tool at the NCBI website (http://www.idtdna.com/
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148	analyzer/Applications/OligoAnalyzer/Default.aspx). Sequence information, accession numbers and				
149	expected product lengths as well as the running conditions of these primers are provided in Table 1.				
150	For the endometrial cell culture, total RNA was extracted using a column method (RNeasy Mini Kits;				
151	QIAGEN Ltd, West Sussex, UK) according to the manufacturer's instruction (www.qiagen.com/goto/				
152	microRNAprotocols). The procedures have been described in an earlier study [30]. The concentration				
153	and purity of the isolated RNA samples was determined with a NanoDrop ND-1000				
154	spectrophotometer (NanoDrop Technologies Inc., Wilmington, DE). All samples had an A260/280				
155	ratio of absorbance (A) between 1.8 and 2.1. The integrity of the RNA was confirmed by running it on				
156	a 1% formaldehyde gel to visualize the 18S and 28S rRNA bands. To eliminate potential genomic				
157	DNA carry over, 1 μ g mRNA from each sample was treated in a single reaction with DNAse in				
158	accordance with manufacturer's guideline (Promega Corporation, Madison, WI). DNase-treated RNA				
159	$(1 \ \mu g)$ was reverse transcribed using Reverse Transcription System Kit (Promega) in a 20 μ l reaction				
160	solution as was described in a previous study [31].				
161	The primers were used to run a conventional PCR using a Multiplex kit (Qiagen) according to				
162	manufacturer's instruction in a 50 µl reaction containing the following; 25 µl Multiplex master mix,				
163	10 μ l Q-solution, 5 μ l primer (2 uM), 5 μ l RNase-free water and 5 μ l cDNA of the test sample. In the				
164	negative and positive control templates, the sample cDNA was replaced with nuclease-free water and				
165	cDNA from endometrial strips respectively. The reaction was run for 35 cycles on a thermal cycler				
166	(Techne PCR Machine TC312; Scientific Laboratory Supplies, Yorkshire, UK). The amplicons were				
167	visualized by electrophoresis on 1% agarose gels. The amplicon bands for MUC1 were quantified				
168	with AlfaEase software as reported in earlier study [32] and expressed as fold change compared to the				
169	control after initial normalisation with GAPDH.				

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170 **2.6. MUC1 immunostaining and quantification**

171

172	MUC1 immunostaining was performed according to a standard IHC technique as previously			
173	described [31]. Briefly, the uterine sections of 5 μ m in thickness were mounted on superfrost slides			
174	(VWR international Co., Leicestershire, UK) and rehydrated in a gradient of ethanol following			
175	dewaxing in clearing agent; Histoclear (Fisher Scientific, Loughborough, UK). Rabbit polyclonal			
176	Anti-MUC1 (Abcam, Cambridge) was used at a concentration of $2 \mu g/mL$ and incubated in a			
177	humidified chamber at 4°C overnight. A biotinylated anti-rabbit secondary antibody (Dako, Denmark,			
178	at 1:100) was then applied followed by Vectorstain ABC kit according to the manufacturer's			
179	instructions (Vector Laboratories, Peterborough, UK). In the negative controls, the primary antibody			
180	was replaced with normal rabbit IgGs (Santa Cruz Biotechnology, Inc., Heidelberg, Germany) at the			
181	same concentration.			
182	The intensity of staining in the endometrial luminal epithelia was scored with the aid of a user-defined			
183	digital quantitative image analysis system (Volocity 5.5; PerkinElmer, Inc., MA, USA) as described			
184	and validated in an earlier study [33] and classified on a scale of 0 to 3, where $0 =$ negative staining, 1			
185	= weak staining, $2 =$ moderate staining, and $3 =$ strong staining. For statistical analysis, the expression			
186	level of MUC1 was evaluated using a Histology score (H-SCORE), from the intensity and area			
187	proportion scores using the following equation: H-score = $[(1 \times \% \text{ area expression of score } 1) + (2 \times (2 \times \%))]$			
188	% area expression of score 2) + $(3 \times \%$ area expression of score 3), giving a possible range of 0-300			
189	[34]. Each region was assessed based on at least 10 fields of digital format image taken at 400 \times			
190	magnification with a light microscope.			

191 **2.7. Statistical analysis**

192

193	Data are presented as mean	± SEM. All data were test	sted for homogeneity by I	Levene's test and were
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normally distributed. Analysis was done using ANOVA with SPSS 18.0 for Windows (Chicago, IL, 9

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- 195 USA). One way ANOVA was used to analyse the effect of stages of estrous cycle or treatment on
- 196 MUC1 expression. If the treatment effect was significant, Bonferroni post hoc tests were performed
- 197 for pairwise comparisons. Significance was established at P<0.05.

198

199 **3. Results**

3.1. LH profile

- The mean plasma LH profiles of all animals at different time points are presented in Fig. 2. The LH peak was evident at 39h after PGF_{2 α} injection which confirms successful synchronisation schedule and precise timing of sample collection. At the time of slaughter, the plasma LH concentrations were 0.7 ± 0.07 , 28.5 ± 4.5, 2.9 ± 0.8 and 0.6 ± 0.07 ng/mL for the Pre-LH peak, LH peak, Post-LH peak and Early-luteal groups respectively.
- 207 Fig. 2
- 3.2. MUC1 mRNA expression in sheep endometrium during different stages of estrous cycle
- *MUC1* mRNA was expressed in the endometrial tissue in the pre-LH and LH peak stages at similar
 level (P>0.05). This was followed by a significant (P<0.01) transient reduction at the post-LH stage
 (Fig. 3). As the cycle entered into early luteal stage, there was a significant increase in the MUC1
 transcripts expression compared to the post-LH samples and similar to those at pre-LH and LH peak.
 Expression of MUC1 mRNA in the endometrium was maximum in the mid-luteal phase compared
 with other stages.
- 216 Fig. 3

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217	3.3. MUC1 protein expression in sheep endometrium during different stages of oestrous cycle			
218				
219	MUC1 immunostaining in the LE was detected during all stages of estrous cycle at the apical surface			
220	of the LE and glandular epithelium (GE) cells. It was also observed that MUC1 protein protruded well			
221	above the cell surface of the LE. It was strongly present in the uterus at Pre-LH and LH stages as well			
222	as early and mid-luteal stages. In contrast, a significantly (P<0.05) lower staining intensity was			
223	observed in the post-LH group (Fig. 4). The negative control sections had no background staining.			
224	Fig. 4			
225				
226	3.4. MUC1 expression in endometrial cells treated with steroids			
227				
228	Supplementation with P ₄ and/or E ₂ increased MUC1 mRNA expression in the endometrial cell culture			
229	compared to the hormone-free control and IFNt treatment (P<0.05, Fig. 5). A relative increment			
230	observed in the E_2+P_4 group was not significantly higher (P>0.05) than either P_4 or E_2 alone.			
231	Treatment with IFN τ resulted in a significant (P<0.05) reduction in MUC1 mRNA compared to the			
232	control and steroid treatments.			
222	Fig. 5			
200				
234	4. Discussion			
235				
236	In the present study, we evaluated the expression of MUC1 mRNA and protein in sheep endometrium			
237	at precise time-points during follicular and luteal phases of estrous cycle. This was further			
238	complemented with studying the effect of steroid hormones and INF τ on MUC1 mRNA expression in			
239	endometrial cell cultures in vitro. The results showed that MUC1 mRNA and protein expression in			
240	sheep endometrium were variably highly expressed during all stages of estrous cycle except a			
241	transient down-regulation at the post-LH peak stage. MUC1 expression in vitro was up-regulated in 11			

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the presence of one or both steroid hormones, and down-regulated by INFτ.

243	Highest expression of MUC1 mRNA was seen during the luteal phase especially at the mid-luteal
244	stage compared to other stages of estrous cycle. These stages correspond to the period of high plasma
245	progesterone and its associated dominance in the endometrial LE. These results agree with previous
246	reports of increased MUC1 expression under progesterone-dominated endometrial epithelium in
247	rabbit [35] and human [1]. Interestingly, we could detect a significant drop in MUC1 mRNA
248	expression at post LH peak stage which was also confirmed by immunostaining. This may be
249	explained by low steroid concentrations at this time point. During post-LH peak, transition from
250	follicular to luteal phases involves decreasing estrogen level to basal while progesterone level is still
251	low. This is also consistent with our observation that the control endometrial cell cultures had lower
252	MUC1 expression compared to those treated with P ₄ and/or E ₂ . During the luteal phase, high
253	MUC1immunostaining was previously reported at the apical surface of the uterine LE at Days 1, 3, 5,
254	and 7 of the estrous cycle which was then decreased until Day 15 [10]. MUC1 expression after day
255	15 and during the follicular phase of oestrous cycle was not examined in the later study [10]. We
256	observed protrusion of MUC1 from the apical surface of the LE which is in agreement with earlier
257	report of its being a trans-membrane protein with a large mucin-like extracellular domain, projecting
258	so high above the cell surface beyond the region most common receptors are located [3].
259	The apical expression of MUC1 protein in the endometrial LE and GE observed in the present study is
260	at par with the results of Johnson et al. [10]. In addition, our data has revealed a transient decline in
261	MUC1 mRNA and protein expression at the post-LH in both regions providing further evidence for
262	MUC1 dependency on steroid hormones [1]. This period coincides with the optimum insemination
263	time in sheep. Therefore it is reasonable to conceptualise that the reduction in MUC1 may allow
264	sperm interaction with endometrial epithelium during transport in the uterus and facilitate sperm
265	capacitation or transport as was earlier suggested [36]. After copulation/insemination, sperm-
266	endometrial interactions are evident [37,38] and it is hypothesised in a recent review [39] that these
267	interactions may play regulatory roles in induction of immunologic tolerance against paternal
268	antigens, preparation of the endometrium for implantation and maintenance of pregnancy.

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In the cell culture, both steroids caused a significant increase in *MUC1* transcript expression. The relative increase in expression of *MUC1* after initial priming of the endometrial cell with E_2 prior to P_4 treatment is understandable because E_2 is known to up-regulate progesterone receptors (PR) [40] such that treatment with progesterone later produced a higher effect than individual steroids. This concurs with the finding of earlier study in human Ishikawa cell line [41]. In a related study, *MUC1* mRNA expression was higher in infertile women with ovulatory polycystic ovarian syndrome than fertile women [42].

276 In the present study, we found that exposure of endometrial cell culture to $INF\tau$ in the absence of 277 steroids directly induce a reduction in MUC1 mRNA expression IFNt concentration (1130 ng/mL) 278 used here mimics the amount produced by day-8 harvested ovine embryo (11 ng/mL) after in vitro 279 culture for 24 h [43]. Since IFN τ is the embryo signal of pregnancy in sheep [20], this result is at par 280 with down-regulation of MUC1 by the human blastocyst through a paracrine signal especially at the 281 region of implantation in human endometrial epithelial cells [1]. Similarly, the same observation (loss 282 of MUC1) due to embryo signal was also observed in rabbit epithelia co-culture with blastocyst [35]. 283 In the later study, loss of MUC1 from the epithelial surface was confined only to implantation sites 284 (region directly beneath the blastocyst) while high level of MUC1 expression continued in non-285 implantation regions. We did not study the interactions between $INF\tau$ and steroid hormones on MUC1 286 expression in cell culture. It has been postulated that, in sheep, extended exposure of LE and GE cells 287 to elevated progesterone levels result in down-regulation of progesterone receptors in LE and GE but 288 not in stromal cells and was associated with a reduction in MUC1 expression [44]. Simulating these 289 changes in vitro is difficult due to the complexity of the interaction between different cells types, cell 290 differentiation and loss of specific functions during prolonged culture conditions. Nevertheless, our 291 results simply suggest that ovine blastocysts can directly reduce MUC1 expression in endometrial 292 cells which may play a novel regulatory role during embryo adhesion in sheep.

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293 **5.** Conclusion

294

295	We show evidence that MUC1 mRNA and protein expression in sheep endometrium are variably				
296	highly expressed both during the progesterone dominant luteal phase and the estrogen dominant				
297	follicular phase. We have also demonstrated that in vitro using endometrial cell cultures where either				
298	estrogen or progesterone supplementation up-regulated MUC1. The transition at post-LH peak stage				
299	was an exception where a transient down-regulation of MUC1 was observed both at mRNA and				
300	protein levels. The physiological role of this transient down-regulation during this period is yet to be				
301	investigated.				
302					
303	Acknowledgement				
304					
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307	and Michael Okpara University of Agriculture, Umudike, Nigeria.				

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308 **Figure Captions**

309

- 310 Fig. 1. Estrus synchronization and hormonal treatments of ewes and timing of sample
- 311 collections. Blood samples were collected at all time-points after PGF2 α injection. A total of 15 ewes
- 312 were used. Three ewes were sacrificed in each group
- 313 Fig. 2. LH concentration in blood samples collected at different time points during the
- 314 experiment. Values are presented as Mean ± SEM. From 0-32h, n=12; 36-39h, n=9; 40-46h, n=6; 60-315 84h, n=3.
- 316 Fig. 3. Representative gel images of RT-PCR products for MUC1 and GAPDH in sheep
- 317 endometrium during different stages of estrous cycle. Bands were quantified with Alpha EaseFC
- 318 software and presented in the bar chart as mean±SEM. Legends: Lut; luteal, MUC1; mucin 1,
- 319 GAPDH; glyceraldehyde 3-phosphate dehydrogenase. Estrous Bars with different superscripts are
- significantly different at ^{a vs b or c} P<0.01 or ^{b vs c} P<0.05 320
- 321 Fig. 4. (A) Photomicrograph of MUC1 protein expression and (B) bar chart presentation of H-
- 322 Score with Volocity software. Data are shown as mean \pm SEM from ten different scored regions

323 from each stage of estrous cycle (n=3 each). Significant difference is established at x vs y or z P

- 324 <0.05; y vs z P <0.1.
- 325 Fig. 5. (A) Representative gel image of MUC1 (upper panel) and GAPDH (lower panel) PCR
- 326 products from endometrial cell culture treated with progesterone (P_4), oestradiol (E_2), $E_2 + P_4$
- 327 or interferon tau (IFN τ) and (B) bar chart presentation of band quantification with AlfaEase
- 328 software. Expression of MUC1 mRNA was compared to the control after normalisation with GAPDH
- 329 as the reference gene. Data are shown as mean \pm SEM from three independent replicates. Different
- 330 superscripts indicate significant difference at P < 0.05.

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332

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Table 1. Oliqonucleotide primer sequence information. Legend: MUC1; mucin 1, GAPDH;

glyceraldehyde 3-phosphate dehydrogenase, A; adenine, C; cysteine. G; guanine, T; thiamine, Rev; reverse, FOR; forward

Gene	Primer Sequence (5'- 3')	Size (bp)	Accession no.	Annealing Temp.
MUC1	FOR: CTCAGTCCCAGCTCTGAAA REV: GAGGCCCAGAAAATCCCTCT	252	NM_174115.2	60.0°C
GAPDH	FOR: CACTGTCCACGCCATCACT REV: GCCTGCTTCACCACCTTCT	267	NM_001190390	.1 63.3°C
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- We studied regulation of MUC1 expression in endometrium during estrous and *in vitro*.
- MUC1 was highly expressed at pre-LH peak, LH-peak and luteal phases
- MUC1 expression was reduced only at the post-LH peak period
- Estrogen and/or progesterone augmented MUC1 expression in endometrial cell culture
- *MUC1* expression was low in the absence of steroids as in the presence of IFN-tau