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Associations between foetal size and ovarian development in the pig

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- 1 **Running Title:** Porcine fetal size and ovarian development
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- 3 Associations between foetal size and ovarian development in the pig
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13 **ABSTRACT**

14 It is estimated that intra-uterine growth restricted piglets 15 represent 25% of the total number of piglets born. Growth 16 restricted female piglets have impaired reproductive 17 performance postnatally, however, when during gestation 18 this phenotype arises is not known. With this study, the aim 19 was to improve the understanding of foetal ovarian 20 development in normal and small foetuses throughout 21 gestation. Female Large White X Landrace foetuses were 22 obtained at gestational day (GD) 45, 60 and 90 (n = 5-6litters/GD). Histological analysis of GATA4 stained foetal 23 24 ovaries at GD60 and 90 indicated there were fewer primary 25 follicles ($P \le 0.05$) in the foetuses weighing the least 26 compared to those with a weight similar to the mean for the 27 litter (CTMLW) at GD90. Plasma oestradiol concentrations 28 were less in the foetuses with lesser weights compared 29 with greater weight foetuses at GD90 ($P \le 0.05$). The RNA 30 was extracted from ovaries of the lesser weight and 31 CTMLW foetuses at GD45, 60 and 90 and qPCR was 32 performed to quantify relative abundance of 12 candidate 33 mRNAs for which encoded proteins modulate ovarian 34 function and development. Gestational changes in relative 35 abundances of CD31, PTGFR, SPP1 and VEGFA mRNA transcripts were observed. Relative abundance of KI67 (P 36 37 = 0.066) and P53 ($P \le 0.05$) was less in ovaries of the

38 lesser weight compared to CTMLW foetuses at GD60. 39 There was a lesser relative abundance of *PTGFR* mRNA 40 transcript in ovaries from the foetuses with lesser weight 41 compared to CTMLW foetuses at GD45 and 60 ($P \le 0.05$). 42 These findings indicate that postnatal differences in 43 reproductive potential of growth restricted females are 44 programmed early in gestation. It is hoped that further 45 investigation will improve the understanding of the 46 relationship between prenatal reproductive development 47 and postnatal reproductive performance.

48

49 Keywords: Foetal Growth; Intrauterine Growth Restriction
50 (IUGR); Porcine; Ovary.

51 1. Introduction

52 The number of primordial follicles present in the 53 ovary at birth is considered to define a female's 54 reproductive potential, a hypothesis first suggested in the 55 19th century (Waldeyer, 1870). Numerous processes must 56 occur in the ovary during foetal development for there to 57 be adequate formation of the pool of primordial follicles 58 including proliferation and apoptosis of the germ cells, 59 formation of oogonial nests followed by follicular formation 60 and growth, accompanied by initiation of meiosis.

61 Impaired foetal growth is associated with impaired 62 reproductive potential post-puberty, in both sexes and in 63 multiple species. In an experimentally induced model of 64 intrauterine growth restriction (IUGR), there were less 65 ovarian follicles during the late gestation period in sheep 66 foetuses (Da Silva et al., 2002). The lesser follicle numbers 67 in ewes with a lesser foetal body weight included mainly 68 the primordial follicle pool, suggesting that the impaired 69 ovarian function observed postnatally may be associated 70 with defects in foetal ovarian development.

Significant variation in birth weight is observed in
piglets, with small outliers being a problem to the industry.
It is estimated that IUGR piglets contribute to 25% of the
total number of piglets born (Wu et al., 2010). Many
definitions for IUGR exist including piglets weighing less

76 than 1.1 kg at birth, weighing less than two standard 77 deviations of the mean body weight for age, the smallest 78 of each litter or a small weight statistical outlier from the 79 population, or weighing less than two-thirds of the mean 80 litter weight (Ashworth et al., 2001; Royston et al., 1982; van der Lende et al., 1990; Wu et al., 2010). It has been 81 82 suggested that IUGR in the piglet may be programmed 83 from an early stage of gestation, with marked within-litter 84 variation in foetal size observed from as early as 85 gestational day 30 to 35 (Finch et al., 2002; Foxcroft et al., 86 2006; Foxcroft and Town, 2004; Pettigrew et al., 1986; 87 Wise et al., 1997).

88 At birth, IUGR gilts have delayed initiation of 89 follicular development, with more primordial follicles, 90 accompanied by fewer primary and secondary follicles 91 compared to normally developing littermates (Da Silva-92 Buttkus et al., 2003). Gilts with lesser growth rates are 93 older when first mating occurs (Tummaruk et al., 2000), 94 which results in fewer litters produced by sows in pork 95 production enterprises. It has been suggested that in 96 addition to having an effect on reproductive performance 97 during their first pregnancy, gilts which have lesser birth 98 weights will also have impaired first parity reproductive 99 performance (lesser pregnancy rates and litter sizes) and 100 also at their second parity (Hoving et al., 2010).

101 Dysregulation of the foetal hypothalamic-pituitary-102 gonadal axis can alter the production of androgens and 103 oestrogens, in turn causing defective reproductive 104 organogenesis and altered development of the foetus 105 (Brooks and Thomas, 1995). In mammals, an aberrant 106 oestrogen milieu during foetal development can have 107 marked effects on postnatal ovarian function (Abbott et al., 108 2006). Considering the functions of oestrogens in the 109 regulation of oestrous cycles, oestradiol concentrations in 110 gilts during the prepubertal period can be used as a 111 biomarker for reproductive efficiency (Steel et al., 2018).

112 Impaired reproductive performance is one of the 113 primary reasons for the removal of sows from commercial 114 herds (Sasaki and Koketsu, 2011). Considering the 115 prevalence of small birthweight piglets, and the severity of 116 this reproductive phenotype, it is important that there be 117 improvement in understanding of the mechanisms 118 regulating foetal ovarian development to improve 119 reproductive efficiency. Whilst in previous studies the 120 temporal changes in follicle types during gestation have 121 been elucidated (Oxender et al., 1979; Pontelo et al., 122 2018), there is a limited understanding of the expression 123 profiles of genes, as indicated by relative abundance of 124 mRNA transcripts, associated with ovarian development 125 and function.

126 There are marked changes in the structure of the 127 foetal ovary during gestation that affect female fertility 128 postnatally. In the present study, the temporal relative 129 abundance profiles of mRNA transcripts with central 130 functions in apoptosis, proliferation and the ovarian 131 extracellular matrix was determined. Even though it is 132 widely recognized that angiogenesis is essential for organ 133 development and growth, and that angiogenesis has 134 important effects in the postnatal ovary, little is known 135 regarding vascularisation of the foetal ovary. Considering 136 this, the encoded proteins of several of the candidate 137 genes investigated in the present study have central 138 functions in the regulation of angiogenesis.

139 In the present study, the aim was to improve 140 understanding of temporal changes in ovarian gene 141 expression, as indicated by relative abundances of mRNA 142 transcripts, and histology in foetuses with relatively 143 average and lesser than average birth weights as 144 compared with the entire litter. It was hypothesised that the 145 developmental trajectory of ovarian development of the foetuses with lesser weights deviates from that of ovaries 146 147 from average-sized female foetuses.

148

149 2. Materials and methods

150 All procedures were performed with approval from 151 The Roslin Institute (University of Edinburgh) Animal 152 Welfare and Ethical Review Board and in accordance with 153 the U.K. Animals (Scientific Procedures) Act, 1986.

154 2.1. Experimental animals and sample collection

155 Large White X Landrace gilts (age 11 - 14 months) 156 were observed daily for signs of oestrus and were housed 157 in groups of 6 to 8 animals per pen. Oestrous cyclicity and 158 ovarian function were controlled in accordance with routine 159 normal practice at The Roslin Institute Large Animal Unit. 160 All gilts were inseminated twice daily for the duration of 161 oestrus with semen from one of four Large White sires. The 162 sires used were equally distributed between gilts at the 163 different gestational days (GD) of interest to minimize any 164 effect of sire. The first day of insemination was assigned 165 GD0. Gilts were humanely killed with sodium as 166 pentobarbitone 20% w/v (Henry Schein Animal Health) at 167 a dose of 0.4 ml/kg by intravenous injection via a cannula 168 inserted in the ear vein at GD45, GD60 and GD90 (*n* = five 169 - eight gilts/GD). Immediately before euthanasia, cardiac 170 puncture was performed using an EDTA coated syringe to 171 collect maternal blood from five gilts of the GD90 group.

Following confirmation of death, mid-ventralincisions were made so that there was access to the

174 reproductive tract. The tract was removed from the body 175 cavity and placed in a dissecting tray. Ovaries were 176 removed from the uterus and the number of corpora lutea 177 was quantified. The percentage prenatal survival was 178 calculated by dividing the number of live foetuses by the 179 number of corpora lutea and multiplying this value by 100. 180 Both uterine horns were dissected, from the ovary towards 181 the cervix. Foetal sex was determined morphologically. 182 Cardiac puncture was performed using an EDTA coated 183 syringe to collect blood samples from the female foetuses 184 with the relatively lesser, average (CTMLW) and relatively 185 greater weights when there was consideration of the 186 individual foetal weights for the entire litter at GD90 (n =187 five litters; Supplementary Table 1). Plasma was obtained 188 from the maternal and foetal blood samples by 189 centrifugation and samples were stored at -20 °C until 190 required. At GD45, GD60 and GD90 (n = five or six 191 litters/GD), ovaries from the foetuses that had relatively 192 lesser, CTMLW and relatively greater weights were 193 dissected, weighed (GD60 and GD90), and one ovary from 194 each foetus was snap frozen in liquid nitrogen and stored 195 at -80 °C until relevant evaluations occurred. The other 196 ovary was fixed in Bouin's for histological analysis.

197 Comparisons were made between the female198 foetuses that had relatively lesser, CTMLW and relatively

199 greater weights for plasma oestradiol concentrations and 200 ovarian weight. Considering that the majority of litters have 201 a negatively skewed distribution of birth weights (Milligan 202 et al., 2002; Quesnel et al., 2008), and considering the 203 greater prevalence of the lesser birth weight outliers, the 204 focus for the remainder of the analyses was the lighter and 205 CTMLW foetal comparisons.

206 2.2. Histological analysis

207 Ovarian samples from GD60 (n = seven CTMLW 208 foetuses; eight lesser weight foetuses) and GD90 (n = six209 from both the CTMLW and lesser weight foetuses) were 210 used. Whole ovaries were fixed with Bouin's overnight at 211 room temperature and changed daily for approximately 1 212 week in 70% ethanol (Genta Medical). The ovaries were 213 then transferred into labelled tissue processing cassettes 214 (Simport) and processed using a tissue processor 215 (ASP3005, Leica) by passing through graded ethanol 216 (70%, 95%, and 99%; Genta Medical) and xylene (Genta 217 Medical). The samples were embedded in paraffin wax 218 (Fisher Scientific), and 5 µm sections were cut and placed 219 on polysine microscope slides (Fisher Scientific).

Following dewaxing and heat-induced epitope retrieval in 0.01 M sodium citrate (Vector Laboratories), endogenous peroxidase activity was blocked by incubating slides with 0.3% hydrogen peroxide (Sigma Aldrich) in 224 methanol. Non-specific binding sites were blocked by 225 incubation with normal goat serum (Vectastain Elite ABC 226 kit; Vector Laboratories). Sections were incubated with a 227 primary antibody for GATA binding protein 4 (GATA4; sc-228 9053; Santa Cruz) at a 1:200 dilution, anti-CD31 antibody 229 (ab28364; Abcam) at a 1:100 dilution (GD90 ovaries only) 230 with rabbit immunoglobulin G (RIgG; Vector or 231 Laboratories; equivalent total protein concentration) as a 232 negative control. Sections were stained with GATA4 as 233 this protein is exclusively expressed by somatic cells, and 234 not by germ cells (Mccoard et al., 2001). The slides were 235 incubated in a humidified chamber at 4°C overnight, 236 washed in phosphate buffered saline (PBS), and incubated 237 for 30 min at room temperature with a biotinylated anti-238 rabbit IgG secondary antibody (Vectastain Elite ABC kit; 239 Vector Laboratories) at a dilution of 1:200 in PBS 240 containing 1.5% normal goat serum. Sections were 241 incubated with Vectastain Elite ABC reagent (Vectastain 242 Elite ABC kit; Vector Laboratories) for 30 min, before 243 incubation with the Novared peroxidase substrate (Vector 244 Laboratories) for 5 min. Sections were counterstained with 245 haematoxylin and dehydrated in a graded series of ethanol 246 and xylene (70%, 95%, and 99% ethanol; 99% ethanol 1:1 247 with xylene, and absolute xylene; Genta Medical). The 248 sections were imaged using the NanoZoomer slide249 scanner (Hamamatsu).

250 2.2.1. Image analysis

251 All image analyses were performed using ImageJ. 252 Six non-overlapping images from both the GATA4 and 253 CD31 stained sections were taken at x 20 magnification. 254 For each ovary, two GATA4 stained sections were 255 analysed which were a minimum of 15 serial sections apart 256 from one another from the middle of the ovary. Using the 257 GATA4 stained sections, the number of oogonia (GD60 258 and GD90), primordial (GD60 and GD90), and primary 259 (GD90) follicles were quantified within each image. The 260 data were then expressed as number of oogonial 261 nest/follicles per 100000μ M². The number of oogonia per 262 germ cell nest was counted. Only a few primary and 263 secondary follicles were observed at GD60 and GD90, 264 respectively, so further analyses on these follicle types at 265 these gestational days could not be performed.

266 2.3. Plasma oestradiol quantification

267 Oestradiol concentrations were determined in 268 maternal plasma samples at GD90 (n = 5) and in foetal 269 plasma samples from the relatively lesser, CTMLW and 270 relative greater weight female foetuses at GD90 (n = 5271 litters) in a single ELISA validated for use with samples of 272 pigs (Abscitech; EK0373), as per the manufacturer's instructions. The detection range of the assay was 20pg/ml to 1,600 pg/ml, with a sensitivity of 25 pg/ml.

275 2.4. Analysis of relative abundances of mRNA transcripts

276 for candidate genes using qPCR

The relative abundance of mRNA transcripts for candidate genes was investigated using qPCR in ovarian samples from the foetuses that were of relatively lesser weights and CTMLW at GD45, GD60 and GD90 (n = five – six litters/GD).

282 2.4.1. Total RNA extraction and cDNA synthesis

283 The RNA was extracted from 20 to 50 µg of snap-284 frozen ovarian samples as described previously 285 (Stenhouse et al., 2019, 2018a, 2018b). The RNA was 286 quantified, and the quality assessed 287 spectrophotometrically using a Nanodrop ND-1000 288 (Labtech International Ltd.) and electrophoretically using a 289 Tapestation 2200 (Agilent Technologies; RNA Integrity 290 Number Equivalent - RINe; 9.209 ± 0.009). Extracted RNA 291 was stored at -80°C until required.

292 Complementary DNA (cDNA) was prepared from 293 0.3 µg of RNA with SuperScript III reverse transcriptase 294 Technologies) following the manufacturer's (Life 295 instructions. Each reaction contained 250 ng random 296 primers (Promega) and 40 units RNaseIn (Promega). 297 Negative controls without reverse transcriptase were included to assess for genomic contamination and allcDNA was stored at -20°C until required.

300 2.4.2. Quantification of relative abundance of mRNA transcripts301 for candidate genes in ovarian samples

302 Quantitative PCR was performed using а 303 Stratagene MX3000 instrument using SensiFAST[®] SYBR 304 Lo-ROX (Bioline) utilising cDNA from foetal ovaries at 305 GD45, GD60 and GD90. All qPCRs were conducted at an 306 annealing temperature of 60°C and dissociation curves 307 consisting of single peaks were generated. The relative 308 abundance of mRNA transcripts for candidate genes was 309 quantified: BCL-2-associated X protein (BAX) (Zhao et al., 310 2014), B-cell lymphoma 2 (BCL2), platelet endothelial cell 311 adhesion molecule (CD31), Doublesex and Mab-3 Related 312 Transcription Factor 1 (DMRT1), GATA Binding Protein 4 313 (GATA4), hypoxia inducible factor 1 alpha subunit (HIF1A) 314 (Oliver et al., 2011), insulin like protein 3 (INSL3), KI67, 315 tumour suppressor protein 53 (P53), prostaglandin F2 α 316 receptor (PTGFR) (Kaczynski and Waclawik, 2013), 317 secreted phosphoprotein 1 (SPP1) (Hernández et al., 318 2013), and vascular endothelial growth factor A (VEGFA) 319 (Oliver et al., 2011). Two reference genes were used: 320 TATA box binding protein 1 (*TBP1*) (Nygard et al., 2007) 321 and Topoisomerase II Beta (TOP2B) (Erkens et al., 2006). 322 These reference genes were identified as having stable

323 mRNA in ovarian samples by geNORM V3.5 (Ghent
324 University Hospital, Centre for Medical Genetics). The
325 primer sequences for all genes investigated are detailed in
326 Supplementary Table 2.

327 Serial dilutions of pooled cDNA ranging from 1:5 to 328 1:640 in nuclease-free water were used as standards. 329 Sample cDNA was diluted 1:25 and 2 µl of sample, 330 standard or control were added per well. Each plate 331 contained duplicate wells of a no template control, 332 standards, sample cDNA and reverse transcriptase 333 blanks. SensiFAST® SYBR Lo-ROX supermix (5 µl), 10 334 μ M forward and reverse primer stock (0.4 μ I each) and 335 water (2.2 µl).

Data were analysed using qbase+ software V3.0 Data were analysed using qbase+ software V3.0 (Biogazelle). A target and procedural specific strategy was utilised and the results, normalised to the geometric mean of two reference genes using the $2^{-\Delta\Delta CT}$, were scaled to the minimum sample. The mean slope, intercept, PCR efficiency and R^2 values are detailed in Supplementary Table 3.

343 2.5. Statistical analysis

All statistical analyses were performed using GenStat 13.1 (VSN International Ltd.). Mean values were calculated for each individual sample for each variable investigated and the normality of the distribution of the data

348 was assessed using an Anderson-Darling test. If there was 349 a *P* value of <0.05, the data were not considered to have 350 а normal distribution. Log10 and square root 351 transformations were conducted to achieve normality of 352 the distribution of the data where required. Outlier data 353 points identified using a ROUT outlier test were excluded.

354 Where data had a normal distribution, ANOVA for 355 GD or foetal size was conducted, with a block for gilt to 356 account for the common maternal environment. When 357 results with use of an ANOVA indicated there was 358 significance, a *post-hoc* Tukey test was performed. Where 359 data were not normally distributed, the Kruskal-Wallis and 360 Mann Whitney tests were performed where appropriate. 361 Analyses for foetal size were performed overall and within 362 GD of interest. A two-way ANOVA with a block for gilt to 363 account for the common maternal environment was 364 performed to assess the presence of GD by foetal size 365 interactions. To determine associations between litter size, 366 percentage prenatal survival and percentage of males in 367 the litter, and plasma oestradiol, Pearson's correlations 368 were performed. Pearson's correlations were also 369 performed for the comparison of foetal and ovarian weight. 370 In all cases, significance was considered when there were 371 mean differences with a P<0.05, with there being

372 considered to be a trending towards differences when the 373 P was > 0.05 < 0.1 and not significant when P>0.1.

374 **3. Results**

375 3.1. Ovarian weight associations with foetal size at GD60376 or GD90

377 Paired ovarian weight (Fig. 1A) and paired ovarian 378 weight as a percentage of foetal weight (Fig. 1B) were not 379 different between the female foetuses with the relatively 380 lesser, CTMLW and relatively greater weights at GD60 or 381 GD90. Paired ovarian weight (P<0.001; Fig. 1A) was 382 greater at GD90 compared to GD60. In contrast, paired 383 ovarian weight as a percentage of foetal weight (P < 0.01) 384 was less at GD90 compared to GD60. Results from 385 regression analyses indicated there was a positive 386 association between paired ovarian and foetal weight at 387 GD60 (*P*<0.05; *R*2 = 0.370; Fig. 1C), but not GD90 (Fig. 388 1D). There were no associations between ovarian weight 389 as a percentage of body and foetal weights at GD60 or 390 GD90 (data not presented).

391 3.2. Composition of follicular pool in ovaries from the
392 foetuses with lesser weight compared to the CTMLW at
393 GD90

394 The GATA4 stained ovaries were used for 395 quantification of oogonia and follicles in ovaries collected

at GD60 and GD90 ovaries (Supplementary Fig. 1). Numbers of oogonial nests (Fig. 1E), primordial follicles (Fig. 1F) and oogonia per germ cell nest (Fig. 1H) were affected by gestational day (P<0.05) but not by foetal size. In contrast, there were fewer primary follicles in the foetuses with lesser weight compared to those that were CTMLW at GD90 (Fig. 1G; P<0.05).

403 3.3. Foetal plasma oestradiol concentration associations404 with foetal size at GD90

405 There were no associations between maternal 406 plasma oestradiol concentrations and number of live 407 foetuses (Fig. 2A). There was a trend towards an inverse 408 plasma association between maternal oestradiol 409 concentration and percentage prenatal survival at GD90 410 $(R^2 = 0.6702; P = 0.09; Fig. 2B)$. Plasma oestradiol 411 concentrations were less in the lesser compared to the 412 greater weight female foetuses at GD90 ($P \le 0.05$; Fig. 413 2C).

414 3.4. Temporal changes in relative abundances of ovarian
415 CD31, PTGFR, SPP1 and VEGFA mRNA transcripts

416 There were temporal changes in relative 417 abundance of mRNA transcripts of several candidate 418 genes investigated in ovaries collected at GD45, GD60 419 and GD90 (Table 1). There was a lesser relative 420 abundance of *CD31* mRNA transcript in ovaries between 421 GD60 and GD90 (P ≤ 0.05; Table 1). 422 Immunohistochemical evaluations for CD31 protein in 423 ovaries at GD90 confirmed that CD31 is exclusively 424 present in endothelial cells in the foetal ovary 425 (Supplementary Fig. 2). Greater relative abundances of 426 ovarian PTGFR mRNA at GD90 than GD60 (P≤0.001; 427 Table 1). In contrast, there was a lesser relative 428 abundance of ovarian SPP1 mRNA transcript at GD60 429 than GD90 ($P \le 0.01$; Table 1). There was a trend towards 430 a gestational day effect on the relative abundance of 431 VEGFA mRNA (P = 0.086; Table 1). There were no 432 temporal changes in the relative abundance of BAX, BCL2, 433 DMRT1, GATA4, HIF1A, INSL3, KI67 or P53 mRNA 434 transcripts (Table 1).

435 3.5. Foetal size associations with relative abundance of 436 KI67, P53 and PTGFR mRNA transcripts

437 The relative abundance of mRNA transcripts for the 438 candidate genes were quantified and compared between 439 ovaries from the foetuses that had relatively lesser 440 weights, and CTMLW foetuses within GD (Fig. 3). At 441 GD60, there was a trend towards a lesser relative 442 abundance of KI67 mRNA transcript in ovarian samples 443 from the foetuses that had relatively lesser weights as 444 compared with CTMLW (P = 0.066; Fig. 31). Similarly, there 445 was a lesser relative abundance of P53 mRNA transcript 446 in ovarian samples from foetuses that had relatively lesser 447 weights than CTMLW at GD60 ($P \le 0.05$; Fig. 3J). The 448 relative abundance of *PTGFR* mRNA transcript was less 449 in ovaries of foetuses that had relatively lesser weights 450 than the foetuses with CTMLW at both GD45 and GD60 451 ($P \le 0.05$; Fig. 3K). There were GD by foetal size 452 interactions for DMRT1 (P< .05; Fig. 3E) and PTGFR 453 (P=0.01; Fig. 3K) mRNA transcripts. There were no other 454 GD x foetal size interactions. There were associations 455 between foetal size and relative abundances of ovarian 456 BAX (Fig. 3A), BCL2 (Fig. 3B), CD31 (Fig. 3D), GATA4 457 (Fig. 3F), *HIF1A* (Fig. 3G), *INSL3* (Fig. 3H), *SPP1* (Fig. 3L) 458 or VEGFA (Fig. 3M) mRNA transcripts.

459 **4. Discussion**

460 Improved understanding of the mechanisms and 461 timing of developmental changes in the foetal ovary is 462 important for improving knowledge of how female pigs 463 reach their reproductive potential postnatally. This study 464 was conducted to determine whether there were 465 differences in foetal ovarian gene expression, as evaluated 466 by determination of relative abundances of mRNA 467 transcripts for genes of interest, between littermate 468 foetuses of different size from as early as GD45.

469 Dysregulation of the hypothalamic-pituitary-gonadal 470 axis can alter the production of androgens and oestrogens, 471 in turn causing defective reproductive organogenesis and 472 altered development of the foetus (Brooks and Thomas, 473 1995). The lesser circulating oestradiol concentrations on 474 GD90 in the lesser compared to greater weight foetuses 475 indicates there needs to be further investigation into the 476 prenatal development of the hypothalamus and pituitary in 477 growth-restricted pig foetuses at multiple stages of 478 gestation.

479 Primordial germ cells have been observed in the 480 foetal pig ovary from as early as GD18. By GD30, germ 481 cells are undergoing proliferation (Black and Erickson, 482 1968) which allows for an increase to maximal numbers by 483 GD50 (Black and Erickson, 1968). Considering the marked 484 differences that have been reported regarding variation in 485 foetal size of pigs from this early stage of gestation (Finch 486 et al., 2002; Foxcroft et al., 2006; Foxcroft and Town, 2004; 487 Pettigrew et al., 1986; Wise et al., 1997), and the marked 488 developmental changes of the ovary during early and mid-489 gestation, it was hypothesized that that there would be 490 differences in relative abundances of mRNA transcripts in 491 ovaries for candidate genes involved in extracellular-matrix 492 remodelling, proliferation and apoptosis as gestational 493 stages advanced and between littermates of different 494 weight.

495 The SPP1 protein, also known as osteopontin, is an 496 extra-cellular matrix (ECM) protein which functions by 497 binding to integrin receptors present on the cell surface to 498 promote cellular adhesion and communication 499 (Humphries, 2006). As indicated by the follicular counts in 500 the present study (Figure 1) and evaluations of GATA4 501 stained sections (Supplementary Figure 1), there were 502 marked changes in the structure of the ovary during 503 gestation. There are these developmental changes in the 504 ovary so that essential functions can occur that are related 505 to female fertility postnatally. Considering the important 506 functions of this extracellular matrix protein in other tissues 507 (Fisher et al., 2001; Johnson et al., 2014, 2003), the 508 gestational changes in relative abundance of SPP1 mRNA 509 transcript were expected. Further studies should be 510 performed to characterise the functions of SPP1, integrins, 511 and other ligands of the integrin receptors such as 512 fibronectin, in the foetal ovary, improving the 513 understanding of the mechanisms involved in foetal 514 ovarian development.

515 In the current study, there was a marked decrease 516 in relative abundance of *KI67* mRNA transcript in ovaries 517 of the foetuses with lesser weights compared to the 518 CTMLW at GD60. There was a similar pattern at GD45 519 although there was not statistical significance. Growth-

520 restricted gilts at birth have delayed initiation of follicular 521 development, with more primordial follicles, and fewer 522 primary and secondary follicles compared to foetuses from 523 gilts fed a diet meeting nutritional requirements for growth 524 (Da Silva-Buttkus et al., 2003). Although not statistically 525 significant, Da Silva-Buttkus et al. reported that there was 526 a larger number of oogonial nests at birth in ovaries of 527 foetuses from growth restricted animals. In the present 528 study, there was a lesser number of primary follicles in the 529 ovary of the foetuses of lesser weight compared with those 530 with CTMLW at GD90, indicating there were differences in 531 follicle number at this stage of gestation that were also 532 present at the time of birth. Together, the histological and 533 mRNA transcript abundance data warrant further 534 examination into germ and somatic cell proliferation and 535 degeneration throughout gestation, with a particular focus 536 between days 45 and 90 of gestation.

537 Even though it is recognised that angiogenesis is 538 essential for organ development and growth, and the 539 processes of angiogenesis are integral for postnatal 540 little ovarian development, is known regarding 541 vascularisation of the foetal ovary. In the present study 542 there was a decrease in the relative abundance of CD31 543 mRNA transcript between GD60 and GD90. The CD31 544 protein is an endothelial cell marker, present at the 545 junctions between endothelial cells (Kim et al., 2013; 546 Mamdouh et al., 2003). Furthermore, the CD31 protein is 547 thought to be involved in angiogenesis by regulating 548 endothelial cell migration (Cao et al., 2009, 2002; DeLisser 549 et al., 1997; Matsumura et al., 1997; Yang et al., 1999; 550 Zhou et al., 1999). Results from immunohistochemical 551 evaluations for CD31 in the foetal ovaries at GD90 552 confirmed that CD31 is present in endothelial cells of the 553 foetal ovary and there are indications that the foetal ovary 554 has undergone marked vascularisation prior to this stage 555 of development. It is hoped that further studies will be 556 conducted to elucidate the timing and pattern of 557 vascularisation in the foetal ovary.

558 The function of PGF2 α in the development and 559 maintenance of the corpora lutea (CL) is well 560 characterised. There is no question as to whether PGF2a 561 is essential for luteolysis and the establishment of 562 pregnancy (Geisert and Bazer, 2015; McCracken et al., 563 1999; Moeljono et al., 1977; Przygrodzka et al., 2016, 564 2015; Waclawik et al., 2017; Ziecik et al., 2017). The 565 function of the PTGFR in foetal ovarian development is not 566 known. One hypothesis could be that the increase in 567 abundance of PTGFR mRNA in the foetal ovary with 568 advancing gestational day is indicative that there are 569 ovarian developmental changes occurring in preparation

570 for postnatal ovarian functions. Binding of PGF2 α to the 571 PTGFR results in increased production of VEGFA by the 572 endometrium, increasing angiogenesis (Kaczynski et al., 573 2016). Considering the functions of PGF2α in 574 angiogenesis, it could also be hypothesized that this 575 increase in abundance of PTGFR in late gestation may be 576 a mechanism to further increase vascularization of the 577 foetal ovary during this period of marked remodelling and 578 growth. Because there was a decrease in the relative 579 abundance of *PTGFR* mRNA transcript in the foetuses that 580 were of a lesser weight compared to those of average 581 weight at GD45 and GD60, this may warrant further 582 investigation into angiogenesis in growth-restricted foetal 583 ovaries during these stages of development. This study, to 584 our knowledge, is the first in which there is evaluation of 585 an association between foetal size and the relative 586 abundance of *PTGFR* mRNA transcript in the foetal ovary 587 of pigs. There should be further investigation of the protein 588 to identify which cell types produce PTGFR and to 589 elucidate the functions of PGF2 α in gonadal development. 590 Growth restriction leads to a phenotype where pig 591 foetuses are of a lesser weight, with impaired adaptation

to extra-uterine conditions, lesser rates of pre-weaning
survival, altered postnatal growth trajectories, undesirable
carcass qualities and impaired reproductive performance

595 post-puberty (Wu et al., 2006). Male piglets are often 596 considered to be at a disadvantage from a product 597 productivity perspective postnatally (Baxter et al., 2012), 598 and results from recent investigations assessing IUGR 599 pigs have indicated female piglets are more likely to 600 undergo compensatory growth than male IUGR piglets 601 (Gonzalez-Bulnes et al., 2012). In the current study, 602 several differences in gene expression, as evidenced by 603 relative abundances of mRNA transcripts, were observed 604 at GD45 or GD60 but not GD90. This could be interpreted 605 either that there are changes that occur in the early foetal 606 ovary which program the postnatal impaired reproductive 607 phenotype in small gilts or that whilst there are marked 608 changes in the foetal ovary early in development, there 609 appears to be compensation in ovarian development as 610 gestational stage advances.

611

612 **5. Conclusions**

These findings indicate there are differences in reproductive potential of lesser birthweight females postnatally that are programmed early in gestation. It is hoped that further investigation will improve the understanding of the association between prenatal reproductive development and postnatal reproductive performance.

620

621 Acknowledgements

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625 Author contribution statement

626 CS, CJA, and FXD devised the experiment. CS, CJA and
627 COH collected samples. CS and YCA performed the
628 experiments. CS, YCA and CJA analysed the data. COH
629 provided technical support. CS and CJA prepared the final

630 manuscript. All authors approved the manuscript.

631

632 Competing interest statement

The authors declare that there is no conflict of interest that
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636

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914

915 Figure Legends

916 Fig. 1. Foetal ovarian weights and histological analyses at 917 GD60 and GD90; Foetal paired ovarian weight (A) and 918 paired ovarian weight as a percentage of body weight (B), 919 number of oogonia (E), number of primordial follicles (F), 920 number of primary follicles (G), and number of nuclei per 921 oogonia (H) were compared between foetuses of different 922 size; Mean values presented. n = 4-7 foetuses per group; 923 Error bars represent S.E.M.; The association between 924 foetal weight and paired ovarian weight at GD60 (C) and 925 GD90 (D) was assessed.

926

927 Fig. 2. Maternal and foetal plasma oestradiol
928 concentrations on GD90; Maternal plasma oestradiol
929 concentrations were correlated with (A) number of live

930 foetuses and (B) percentage prenatal survival; Foetal 931 plasma oestradiol concentrations were compared between 932 foetuses of different size (C); Letters indicate that group 933 means differ from one another (P<0.05); n = 4-5 foetuses 934 per group; Error bars represent S.E.M.

935

936 Fig. 3. Candidate relative abundances of ovarian mRNA 937 transcripts in foetuses of different sizes at days 45, 60 and 938 90 of pregnancy; Relative abundance mRNA transcripts 939 for BAX (A), BCL2 (B) BAX:BCL2 Ratio (C), CD31 (D), 940 DMRT1 (E), GATA4 (F), HIF1A (G), INSL3 (H), KI67 (I), 941 P53 (J), PTGFR (K), SPP1 (L) and VEGFA (M) in the 942 lesser weight to mean litter weight (CTMLW) foetal ovaries 943 at gestational days 45, 60 and 90; n = 3-6 foetuses per 944 group; Error bars represent S.E.M.; *P < 0.05.

945

946 Supplementary Fig. 1. Representative Images of GATA4 947 immunohistochemistry in foetal ovaries; 948 Immunohistochemistry results indicated that GATA4 949 protein is present in the somatic cells in both the foetuses 950 of lesser weight (D and F) and those closest to mean litter 951 weight (CTMLW) (C and E) at both gestational day (GD) 952 60 (C and D) and 90 (E and F); Rabbit IgG controls at an 953 equivalent protein concentration were utilised as a 954 negative control (A and B); Scale bars represent 100 µm.

955

956 Supplementary Fig. 2. Representative Images of CD31 957 Immunohistochemistry foetal in ovaries; 958 Immunohistochemistry confirmed that CD31 protein is 959 present in endothelial cells in the ovary of both the lesser 960 (C) and closest to mean litter weight (CTMLW) (B) foetuses 961 at gestational day (GD) 90; Rabbit IgG controls at an 962 equivalent protein concentration were utilised as a 963 negative control (A); Scale bars represent 100 µm.