

**278 Awardee Talk: Progesterone Regulates the Abundance of Mrnas and Proteins Involved in Polyamine Metabolism in the Sheep Endometrium.**

Katherine M. Halloran<sup>1</sup>, Emily Hoskins<sup>1</sup>, Claire Stenhouse<sup>1</sup>, Robyn Moses<sup>1</sup>, Michael C. Satterfield<sup>1</sup>, Kathrin Dunlap<sup>1</sup>, Heewon Seo<sup>2</sup>, Gregory A. Johnson<sup>2</sup>, Guoyao Wu<sup>1</sup>, Fuller W. Bazer<sup>3</sup>, <sup>1</sup>Texas A&M University, <sup>2</sup>Department of Veterinary Integrative Biosciences, Texas A&M University, <sup>3</sup>Department of Animal Science, Texas A&M University and Texas A&M AgriLife Research

**Abstract:** Agmatine and polyamines (putrescine, spermidine, and spermine), metabolites of L-arginine, are important for development of mammalian conceptuses. The objective of this study was to determine if exogenous progesterone administered during the pre-implantation period, which accelerates conceptus development, alters the expression of mRNAs and proteins involved in the metabolism of agmatine and polyamines in the sheep uterus during pregnancy. Mature Suffolk ewes were bred to fertile rams and assigned randomly to be treated with daily i.m. injections of either 1ml corn oil (CO;n=28) or 25mg progesterone in corn oil (P4;n=20) from Day 1.5 through Day 8 after breeding (Day 0). Ewes were hysterectomized on Day 9, 12, or 125 of gestation and endometrial samples were collected. The expression of candidate mRNAs was quantified using qPCR and proteins localized using immunohistochemistry. On Day 9 of pregnancy, the expression of mRNAs for AMD1 (P < 0.01), ASL (P < 0.01), and SLC12A8 (P < 0.05) was greater in endometria of P4-treated compared to CO-treated ewes. The expression for MAT2B mRNA was greater (P < 0.001) for P4-treated compared to CO-treated ewes on both Days 9 and 12. On Day 125 of gestation, endometria from P4-treated ewes tended to have greater expression of SAT1 (P < 0.10) mRNA compared to CO-treated ewes. In contrast, the expression of AMD1(P < 0.01), MAT2B (P < 0.05), OAT (P < 0.05), SMOX (P < 0.05), and SLC12A8 (P < 0.05) mRNAs was lower in endometria from P4-treated compared to CO-treated ewes on Day 125. Exogenous P4 appeared to increase the relative abundance of SAT1 and SMOX proteins in the uterine luminal and glandular epithelia on Day 125 of pregnancy. These results suggest that early administration of progesterone may alter the biosynthesis of agmatine and polyamines in

the sheep uterus during the pre-implantation period of pregnancy with potential 'programming' effects manifested in late pregnancy.

**Keywords:** sheep, pregnancy, polyamines

**279 Identification of Potential Biomarkers of Reproductive Development in Vaginal Gene Expression Associated with Serum Concentrations of Reproductive Hormones at key Periods in Gilt Development.**

Shannon L. Dierking<sup>1</sup>, Jodi Morton<sup>2</sup>, Juan Carlos Pinilla<sup>3</sup>, Michael Gonda<sup>1</sup>, Hossein Rekabdarkolaei<sup>1</sup>, Jeffrey A. Clapper<sup>1</sup>, Crystal L. Levesque<sup>1</sup>, <sup>1</sup>South Dakota State University, <sup>2</sup>Southern University & A&M College, <sup>3</sup>PIC: Pig Improvement Company

**Abstract:** Early puberty in gilts is associated with long-term reproductive performance. The ability to predict who will achieve early puberty is limited to intensive and invasive collection of serial blood samples to assess reproductive hormones, which is not practical for on-farm use. The objective of this pilot study was to characterize changes in gene expression in the vaginal epithelium related to reproduction during key periods in pubertal development. Pre-pubertal gilts (n =13) in 2 cohorts were followed from 70 d of age until first estrus or 213-215 d of age. Blood and vaginal epithelia were collected at five key timepoints during reproductive development (d70/77, d100/110, d130, d160 and first estrus or end of trial). Total RNA were isolated from vaginal epithelia and relative gene expression of two toll-like receptors (TLR-4 and TLR-5), tacykinin precursor-3 (TAC-3), insulin-like growth factor-1 (IGF-1), and estrogen receptor (ER)-alpha was quantified by real time RT-PCR, relative to the expression of RPLP0. Of the 13 gilts, 3 exhibited estrus early (d169 to 174), 3 were average (d194 to 195), 2 were late (d203 to 213), 3 were deemed anestrus and 2 had a silent estrus (one prior to d160 and one after d200). Statistical analysis of relative expression of each gene relative to 70 d was performed using the PCR package in RStudio (version 1.2.5025). Analysis of gene expression utilized Fisher's exact t-test for genes TLR-4, TLR-5 and TAC-3, and ANOVA for genes ER-alpha, IGF-1. Expression of IGF-1 and TAC-3 were up-regulated 9-fold and 7-fold, at the start of boar exposure (d 160; P < 0.05). Expression of ER-alpha tended to be upregulated 3-fold at 100 d of age (P = 0.08). Expression of TLR-4 and TLR-5 was not detected for most samples until standing estrus. These transcripts may be putative biomarkers for early estrus detection.

**Keywords:** gilt, puberty, biomarkers