PHYSIOLOGY AND ENDOCRINOLOGY: INTERRELATIONSHIPS BETWEEN ENVIRONMENTAL, METABOLIC AND PHYSIOLOGICAL PROCESSES I

1963 Non-targeted plasma metabolomic profile at early and late lactation in parity 1 dams with diverging body composition at weaning. L. A. Rempel* and J. R. Miles, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Following Lactation is an extremely energy demanding event, impacting naïve dams to a greater extent as they are still physiologically immature. The objective of the current study was to determine if a unique plasma metabolome exists at early and late lactation from first parity gilts having similar body measurements and litter sizes post-farrow (PF) with divergent body condition measurements at weaning. Farrowing data, body composition traits (bodyweight, backfat thickness, and loin eye area), and a plasma sample were collected PF (2.7 ± 1.45 d) and 1d prior to weaning (WN) from composite Landrace-Duroc-Yorkshire gilts bred with Yorkshire semen. Twenty-seven gilts were identified from 68 first parity farrowings with similar farrowing ages (P = 0.9442), PF body weight (P = 0.6789), PF backfat thickness (P = 0.8549), and litter size ($P \geq 0.2263$). Dams were fed to appetite from d3 PF through WN. Of the 27 dams, 10 with the greatest (Hi) and 10 with the least (Lo) body weight loss ($P < 0.0001$; 26.1 ± 1.90 kg and 8.6 ± 1.48 kg, respectively) and backfat thickness loss (P = 0.0094; 4.7 ± 0.86 mm and 1.3 ± 0.67 mm, respectively) had plasma samples submitted for non-targeted profiling by UPLC-MS and GC-MS techniques. Raw spectral data was processed using XCMS package in R to generate feature detection and alignment followed by grouping of features into compounds. Samples were blocked by time of collection (PF and WN) and body condition loss (Hi and Lo) and ANOVA was performed on each compound in R with a Benjamini-Hochburg false discovery rate adjustment. Several compound changes ($P \leq 0.05$) in the metabolome occurred from PF to WN under both detection techniques (UPLC-MS, 112; GC-MS, 59). While changes ($P \leq 0.05$) in compounds between Hi loss and Lo loss also occurred, the prevalence was much less (UPLC-MS, 21; GC-MS, 11). Interestingly, the interaction of time by body condition loss yielded unique compound profiles for both detection techniques (UPLC-MS, 16; GC-MS, 20). Of the 36 compounds significant for interactions, 11 compound signatures may prove to be relevant as predictors for animals that will or won't lose excessive weight and backfat thickness during the course of lactation. Further investigations into the specific identities and validation of all significant compounds will provide potential nutraceuticals to offset intensive depletion of energy stores in young dams during lactation. *USDA is an equal opportunity provider and employer.*

Key Words: gilts, lactation, metabolome

ASAS EARLY CAREER WINNER

Small RNA expression and function during oocyte maturation and embryo development in the pig. B. J. Hale, C.-X. Yang, E. C. Wright, and J. W. Ross* *Department of Animal Science, Iowa State University, Ames.*

Following germinal vesicle breakdown (GVBD), the genome of an immature oocyte becomes transcriptionally inactive and changes in mRNA and protein abundance rely on interactions with the surrounding cumulus oophorus and cellular processes occurring within the oocyte and early embryo prior to the maternal to zygote transition. Thus, molecular events regulating oocyte recruitment and maturation may have a significant impact on the developmental ability of subsequent embryos. MicroRNA (miRNA), in addition to several RNA binding proteins, have a demonstrated ability to regulate both mRNA and protein repertoires through their ability to confer post transcriptional gene regulation (PTGR). To better understand the biological roles of miRNA in the pig oocyte during meiotic progression and during early embryonic development, we characterized expression patterns of miRNA and other small RNA molecules using deep sequencing. Following mapping of our sequencing reads to the pig genome, we identified the expression of several hundred miRNA in cumulus cells, oocytes and in the 4- to 8-cell stage and blastocyst stage embryos following in vitro fertilization. In addition to miRNA, we were able to identify the expression patterns of other small, non-coding RNA, such as piwi-interacting RNA (piRNA), and siRNA. Based on total small RNA expression in the oocyte and the ability of those small RNA to map to intronic and exonic regions of mRNA, we were able to predict mRNA that may be subject to small RNA mediated PTGR in the oocyte. We have also pursued the characterization of miRNA, including MIR21 and its target, programmed cell death 4 (PDCD4), during in vitro maturation and the implications of MIR21 inhibition for developmental competency. We have demonstrated a temporal relationship between MIR21 and PDCD4 protein abundance exists and can be altered during in vitro maturation by prematurely elevating MIR21 abundance or through the use of MIR21 antagonists. We have also further characterized expression of dead end homolog 1, an RNA binding protein with the potential to interact with specific mRNA and spare those molecules from miRNA mediated PTGR, during follicle development, in vitro maturation and during early embryo development. *These projects were supported by USDA National Institute of Food and Agriculture grant no. 2008-35205-05309 and 2008-35205-18712.*