alive as well as birth weights of piglets were recorded immediately after farrowing. At d 110 of gestation, maternal body weight (P=0.603) and backfat thickness (P=0.349) did not differ between the control and treatment groups. The total number of pigs born did not differ (P=0.102) between the two groups of gilts. However, compared with the control group, arginine supplementation increased the number of pigs born alive by 23% (11.23 vs. 9.12, P=0.029) and litter birth weight by 28% (15.80 vs. 12.37 kg, P=0.005). These results demonstrate, for the first time, that dietary L-arginine supplementation improves pregnancy outcome in gilts. Supported by Texas Tech Univ., Texas A&M Univ., Ajinomoto, and USDA/NRI.

Key Words: Gestation performance, Gilts, Arginine

22 QTL mapping in an F_2 Duroc x Pietrain resource population: II. Carcass and meat quality traits. D. B. Edwards*[1], C. W. Ernst[1], N. E. Raney[1], M. E. Doumit[1], M. D. Hoge[1,2], and R. O. Bates[1], [1]*Michigan State University*, *East Lansing*, [2]*Western Illinois University*, *Macomb*.

Pigs from the F_2 generation of a Duroc x Pietrain resource population were evaluated to discover quantitative trait loci (QTL) affecting carcass composition and meat quality traits. Carcass composition phenotypes included primal cut weights, skeletal characteristics, backfat thickness, muscle pH, and carcass temperature. Meat quality data collected on boneless *longissimus* muscle chops included objective and subjective color information, marbling and firmness scores, and drip loss. Additionally, chops were analyzed for moisture, protein, and fat composition as well as cook yield and Warner-Bratzler shear force measurements. Palatability of chops was determined by a trained sensory taste panel. A total of 510 F_2 animals were genotyped for 124 microsatellite markers evenly spaced across the entire genome. Data were analyzed with line cross least squares regression interval mapping methods using sex and litter as fixed effects and carcass weight or harvest age as covariates. Significance thresholds of the F-statistic for additive, dominance, and imprinted QTL were determined on chromosome- and genome-wise levels by permutation tests. A total of 94 QTL for 35 of the 38 traits analyzed were found to be significant at the 5% chromosome-wise level. Of these 94 QTL, 16 were significant at the 1% chromosome-wise, 13 at the 5% genome-wise, and 14 at the 1% genome-wise significance thresholds. Putative QTL were discovered for 45 min pH and pH decline on SSC 3, marbling score and carcass backfat on SSC 6, carcass length and number of ribs on SSC 7, marbling score on SSC 12, and color measurements and tenderness score on SSC 15. These results will facilitate fine mapping efforts to identify genes controlling carcass composition and meat quality traits that can be incorporated into marker-assisted selection programs to accelerate genetic improvement in pig populations.

Key Words: Meat quality, Pigs, Quantitative trait loci

23 Differential gene and protein expression in gilt and sow derived oocytes. M. Paczkowski*, D. Terry, C. Bidwell, and R. Krisher, *Purdue University*, *West Lafayette, IN*.

Gilt derived oocytes matured in vitro demonstrate decreased ability to undergo embryonic development compared to sows, suggesting reduced oocyte competence. Gene transcripts present in oocytes may reflect developmentally important mechanisms. Alternatively, identifying possible regulatory proteins involved in successful oocyte maturation could result in methods to enhance the competence of oocytes from prepubertal pigs and increase developmental potential. We hypothesize that by comparing gene expression and protein complement in oocytes with high and low developmental potential, we can identify differentially expressed genes that may play a role in mechanisms controlling oocyte competence. Sow and gilt cumulus-oocyte-complexes (COC) were collected from 2 to 6mm follicles and matured for approximately 43 h in either defined Purdue Porcine Media (PPMmat), or TCM199 medium (supplemented with 10% porcine follicular fluid, 0.5 mM cysteine, 0.91 mM pyruvate, and 3.05 mM glucose) for microarray and protein analysis, respectively. After maturation, COCs were denuded and assessed for maturation, as indicated by polar body extrusion. Dynabead Direct mRNA isolation reagents were used to isolate poly A+ mRNA (n=200 oocytes) for input into the Affymetrix microarray two-cycle amplification and labeling system. Two dimensional gel electrophoresis was performed on oocyte samples (n=3000) and gels were stained with silver nitrate. Protein spots (n=14) were digested with trypsin and analyzed by mass spec. The results of these preliminary experiments show that pig oocytes express about 8,800 transcripts (36% of the probe sets) that are detectable by the pig Affymetric GeneChip. Differential expression was observed in 292 proteins; 120 proteins identified in gilts were absent in sows, while only 55 proteins were identified in sows that were absent in gilts. Seven proteins were identified with high confidence. Differentially expressed genes and proteins will be further analyzed and their potential roles in developmental competence of oocytes investigated.

Key Words: Porcine Oocyte, Microarray, Protein Analysis

24 Effects of L-carnitine and gestation length on growth factor messenger RNA (mRNA) expression in maternal tissues. K. R. Brown*[1], R. D. Goodband[1], M. D. Tokach[1], S. S. Dritz[1], J. L. Nelssen[1], J. E. Minton[1], D. M. Grieger[1], J. C. Woodworth[2], and B. J. Johnson[1], [1]*Kansas State University*, *Manhattan*, [2]*Lonza, Inc*, *Allendale, NJ*.

Fifty-nine gestating gilts (BW=137.7 kg) were used to determine the effects of dietary L-carnitine on the IGF system expression in maternal reproductive tissues. Treatments were designed as a 2 × 3 factorial arrangement with diet (L-Carnitine or control) and gestation day (40, 55, or 70) as main effects. Gilts were fed a gestation diet once daily (1.75 kg) with a 50-g top dress containing either 0 (n=30) or 88 mg (50 ppm) of L-carnitine (n=29) from breeding through d 40, 55, or 70 of gestation when maternal reproductive tissues were collected. Real-time quantitative PCR was used to measure growth factor messenger RNA (mRNA) levels in uterine, myometrial, and endometrial tissues. There were no interactions between diet and gestation day. Supplementing gilts with L-carnitine increased endometrial IGFBP-3 (P=0.05) and IGFBP-5 (P=0.01) mRNA abundance, and numerically increased IGF-I (P=0.16; 4.52 vs. 3.34). Endometrial IGF-I, IGF-II, IGFBP-3, and IGFBP-5 mRNA levels were not different among gestation lengths. Carnitine did not influence myometrial or placental IGF-I, IGF-II, IGFBP-3, and IGFBP-5 mRNA abundance. As gestation increased from d 40 to 55, IGF-I, IGFBP-3, and IGFBP-5 mRNA abundance decreased (P<0.04) in the myometrium with no differences as gestation increased from d 55

to 70. Placental IGF-I tended to increase (P=0.08) as gestation length increased. This data suggests supplementing gilts with L-carnitine affected expression on IGF-I, IGFBP-3 and IGFBP-5 mRNA in the endometrium of the porcine uterus, therefore altering the IGF system in the uterine environment. In addition, changes occurred in growth factor expression in the myometrium of the porcine uterus and placental tissue as gestation length increased. These data may aid in the explanation of the improvements in fetal birth weight and litter size from sows fed L-carnitine observed in previous studies.

Key Words: Carnitine, Gilt, Messenger RNA

25 Pretreatment of swine jejunal epithelial cells (IPEC-J2) with *Bacillus licheniformis* (BL) prevents *Salmonella enterica* serovar Typhimurium (ST)-induced basolateral interleukin 8 (IL-8) secretion. K. A. Skjolaas*, T. E. Burkey, and J. E. Minton, *Kansas State University*, *Manhattan*.

Although no single class of alternatives has emerged to replace the enhanced growth performance afforded by in-feed antibiotics in weaned pigs, a number of products appear to recapture a portion of the advantage. Direct-fed microbials are among those products, including those containing *Bacillus* spp. However, the mechanism of action by which *Bacillus* functions in the gut has yet to be fully understood. Direct-fed microbials may affect inflammatory signaling in the gut epithelium in response to invasive enteric pathogens. Thus, the objective of the current study was to evaluate IL-8 secretion induced by ST in IPEC-J2 cells pre-exposed to BL. IPEC-J2 cells were grown to confluency and treated apically overnight with 10^6, 10^7, or 10^8 BL (BL6ST, BL7ST, BL8ST, respectively) followed by a 1 hr apical ST (10^8) challenge. Cells were then washed and media containing 50 Mg/mL gentamicin was added to kill remaining extracellular bacteria. Three control treatments included cells exposed to 10^8 BL alone, 10^8 ST alone, or cells not exposed to any bacteria (CTL). Supernatants were collected 5 hr after ST challenge and IL-8 secretion was quantified by ELISA. The secretion of IL-8 was significantly increased as compared to CTL in both the basolateral and apical directions by ST ($P < 0.0001$) with significantly greater basolateral polarization ($P < 0.05$). The BL treatment and all BL and ST co-treated cells (except BL8ST) increased IL-8 secretion above CTL, but only apically ($P < 0.05$ for BL, BL6ST and BL7ST), and not in the basolateral direction. The data demonstrate that porcine jejunal epithelial cells increase IL-8 secretion in both the apical and basolateral directions in response to ST, but in the presence of BL, ST stimulated secretion of IL-8 is inhibited in the basolateral direction.

Key Words: Direct-fed Microbials, Gastrointestinal Immunology, Interleukin 8

26 Diurnal and dietary impacts on purine derivative excretion from spot samples of urine in finishing heifers. G. I. Crawford*, K. J. Vander Pol, J. C. MacDonald, G. E. Erickson, and T. J. Klopfenstein, *University of Nebraska*, *Lincoln*.

Individually-fed crossbred heifers (n=116; 407 ± 32 kg) were arranged into a randomized complete block design to determine impacts of diet on growth performance and carcass characteristics and the impact of diet and time of sampling on purine derivative (PD; allantoin + uric acid) excretion in spot samples of urine. Treatments were arranged into a 2 x 3 factorial design, with two urine spot sample collection times (0700 and 1700 h; AM and PM) and three diets: 85% steam-flaked corn (SFC); 85% SFC + 1.5% urea (UREA); or 25% SFC, 30% wet corn gluten feed, and 30% corn bran (BYPROD). No collection time x diet interaction was present for any variable ($P > 0.20$). Dry matter intake was greatest with the BYPROD diet and lowest with the SFC diet ($P < 0.05$), averaging 7.9, 8.8, and 10.4 kg/d for SFC, UREA, and BYPROD diets, respectively. Heifers consuming BYPROD and UREA diets gained 1.7 and 1.6 kg/d, respectively ($P > 0.20$), which were both greater ($P < 0.05$) than heifers consuming the SFC diet (1.1 kg/d). Feed efficiencies were 0.138, 0.180, and 0.162 for SFC, UREA, and BYPROD diets, respectively, with UREA being the greatest and SFC the lowest ($P < 0.05$). Heifers fed the BYPROD diet had a greater ($P < 0.05$) PD:creatinine ratio (PD:C) than heifers fed either the SFC or UREA diet, suggesting the BYPROD diet produced greater microbial CP (MCP) flows than either the SFC or UREA diet. Heifers fed the UREA diet had a greater ($P < 0.05$) PD:C than those fed SFC alone, with PD:C measuring 0.94, 1.18, and 1.25 μM PD/ μM creatinine for the SFC, UREA, and BYPROD diets, respectively. Urine spot sampling time had a significant ($P < 0.05$) impact on PD:C, with samples measuring 1.03 and 1.22 μM PD/ μM creatinine for AM and PM samples, respectively. Feeding diets varying in energy and protein produced significant impacts on performance as well as MCP production in heifers. It appears that collecting urine spot samples in PM results in greater estimates of MCP when compared with AM sampling.

Key Words: Heifers, Purine derivatives, Spot samples

27 Diets containing low vitamin A and roasted soybeans affect adipose cellularity and muscle fatty acid profile of beef cattle. M. Gorocica-Buenfil*, C. Reynolds, F. Fluharty, and S. Loerch, *The Ohio State University*, *Wooster*.

A feedlot trial was conducted to determine the effect of low vitamin A diets (LA) and roasted soybean inclusion (SB) on adipose tissue cellularity and muscle fatty acid composition. Angus–based steers (n=168; BW=295 kg) were allotted to 24 pens (7 steers each). Four dietary treatments were investigated: LA (1100 IU/kg DM)–No SB (LA–NS); LA–SB; High vitamin A (HA, 2700 IU/kg DM)–NS; and, HA–SB. Diets included high moisture corn (65–80%), 5% corn silage, 10–20% supplement, and 20% roasted soybean in SB treatments. Steers were harvested on d 168, and longissimus muscle (LM), intramuscular (IM) and subcutaneous (SQ) fat samples were collected from two animals per pen. To measure adipose cellularity, the SQ and IM fat samples were stained with hematoxylin–eosin solution, and cell number and diameter were determined by computer image analysis. Rib samples were taken for muscle fatty acid composition (MFA). Fatty acids were extracted and analyzed by gas chromatography. Adipocyte size and number were affected by diet for the IM ($P<0.05$) but not for the SQ depot ($P>0.05$). A SB × vitamin A (VA) interaction occurred ($P<0.05$) for IM fat cellularity. Steers fed the LA–NS, LA–SB, and HA–SB diets had more and smaller adipocytes than those fed the HA–NS diet (156.6, 154.0, 156.4, and 119.0 adipocyte/mm^2; 85.8, 87.7, 86.3, and 97.8 Mm, respectively; $P<0.05$). Vitamin A did not affect MFA ($P>0.05$). Including SB in-