to 28 ($P \le 0.01$) and 1 to 35 d ($P \le 0.031$). The BW gain, feed:gain, feed intake, mortality and foot ash were unaffected when available P was reduced by 0.10% or phytase supplementation in low DCP diets. The results of the present study demonstrated bone ash, bone meal and TSP a superior source than that of DCP. Lowering of available P by 0.10% and addition of phytase in low available P diets did not affect the growth performance or foot ash of the broilers raised on low ME and CP diets.

Key Words: Feed Phosphates, Enzyme, Broiler

Physiology & Endocrinology - Livestock and Poultry: Metabolic Physiology

965 Plane of nutrition by tick burden interaction in cattle: Effect on metabolic indicators in plasma. D. Tolleson*, G. Carstens, T. Welsh, P. Teel, O. Strey, S. Prince, K. Dean, and L. Slay, *Texas A&M University.*

Previous studies concerning the effect of external parasites on intake, performance, and metabolism in cattle utilized a single moderate quality (14% CP, 60% TDN) diet. The effects of an external parasite burden may be exacerbated in cattle grazing low quality forage. The objective of this study was to examine the interaction between plane of nutrition and a Lone Star (Amblyomma americanum) tick burden as expressed by metabolic indicators in cattle. Twenty eight growing beef steers $(194 \pm 3.0 \text{ kg})$ were randomly assigned to one of four treatments in a 2 \times 2 factorial arrangement: moderate (M; 14.0 \pm 1.0% CP, 60 \pm 1.5% TDN) vs low (L; 7.0 \pm 1.0% CP, 58 \pm 1.5% TDN) plane of nutrition (PON), and control (no tick) vs tick treatment (300 pair of adult A. americanum per treated animal). Steers were individually fed M and L diets ad libitum for 35 d prior to and 21 d following the start of tick infestation (day 0), with peak tick feeding occurring on d 10 to 14. Animal weight and BCS were obtained on d -35, 0, and 21. Blood was sampled on d -7, 0, 7, 8, 9, 10, 11, 12, 13, 17 and 21. Plasma was harvested and analyzed for urea nitrogen (BUN), glucose (GLU), non-esterified fatty acids (NEFA), and beta-hydroxy-butyrate (BHBA). PON affected (P < 0.01) BUN and GLU but not (P > 0.1) BHBA and NEFA. The effect of day was significant (P < 0.01) for BUN, BHBA and NEFA but not (P > 0.1) GLU. Across PON, tick burden did not affect (P > 0.1) any constituent. A model containing BUN, GLU, and NEFA at d 12 and 21 described 54.9, 66.4, and 75.5 % of the variation in d 21 BCS, d 21 weight and d 0 to d 21 average daily gain (P < 0.01). PON but not tick burden affected metabolism of growing beef steers.

 Table 1. Effect of tick treatment and plane of nutrition on metabolic indicators in cattle (mean, SE).

Constituent	Tick		Control		Moderate		Low	
BUN GLU	4.91 95.24	0.20	5.05 96.72	0.22	7.01 101.42	0.15	2.89 90.38	0.08
BHBA	93.24 473.39	1.20	426.49		455.37	1.13	90.38 444.36	
NEFA	0.27 MT	0.01	0.24 MC	0.01	0.25 LT	0.01	0.26 LC	0.01
BUN	6.83	0.21	7.19	0.21	2.97	0.12	2.82	0.12
GLU	102.85	1.25	100.01	1.87	87.52	1.71	93.28	0.68
BHBA	482.45	19.65	428.65	19.93	464.21	22.87	424.24	16.57
NEFA (meq/l)	0.25	0.01	0.25	0.01	0.30	0.02	0.22	0.01

Key Words: Tick, Plane of Nutrition, Metabolic Indicator

966 Using serum components and ultrasound measurements at weaning to predict feedlot gain and carcass merit. J. S. Thurlow*¹, T. L. Perkins², S. T. Reiter¹, A. H. Brown Jr.¹, and C. F. Rosenkrans Jr.¹, ¹University of Arkansas, Fayetteville, ²Missouri State University, Springfield.

The objective of this study was to determine if weaning characteristics could be used to predict subsequent feedlot gain and carcass composition. The following items were collected at weaning and used as predictor variables: lactate dehydrogenase (LDH) activities, lactate, cortisol, insulin-like growth factor I (IGF-I), and prolactin concentrations and ultrasound measurements. Forty-six crossbred steers $(203 \pm 1.7 \text{ kg})$ were weaned $(216 \pm 2.6 \text{ d})$ and blood samples collected. Calves were weighed every 21 d and ADG calculated. Longissimus dorsi muscle area (REAU and REAU2), rib fat thickness (FTU and FTU2), intramuscular fat (IMFATU and IMFATU2), and rump fat (RUMP) were determined using ultrasonic measurements at weaning and at d 57 of the feedlot phase. Hot carcass weight (HCW), rib fat thickness (RF), longissimus dorsi muscle area (REA), marbling score (MARB), yield grade (YG), and quality grade (QG) were determined at harvest. Weaning FTU correlated with YG (r = 0.28; P < 0.05), and weaning REAU correlated with HCW and REA (r = 0.55 and 0.60; P < 0.01). Lactate concentrations at weaning tended (P < 0.10) to be negatively correlated with YG (r = -0.27). Serum activity of LDH tended (P < 0.10) to be negatively correlated (r = -0.25) with MARB. Serum IGF-I concentration correlated with REAU2 and FTU2 during the feedlot phase (r = 0.29 and 0.41 respectively; P < 0.05), and HCW, REA, and RF at harvest (r = 0.40, 0.38, and 0.39; P < 0.01). Serum components and ultrasound measurements at weaning did not accurately predict feedlot gain. However, weaning measurements of lactate concentration, serum LDH activity, and ultrasound measurements may be useful in predicting carcass composition.

Key Words: Feedlot, Carcass Composition, Ultrasound

967 Use of infrared thermal imaging to measure changes in body temperature following lipopolysaccharide (LPS) administration in hair sheep ewes. R. W. Godfrey^{*1}, R. C. Ketring¹, and S. T. Willard², ¹University of the Virgin Islands, Agricultural Experiment Station, St. Croix, US Virgin Islands, ²Mississippi State University, Mississippi State.

Previous work in our lab has shown a high correlation of rectal and vaginal temperature (RT and VT, respectively) with maximum eye temperature (MAX) measured using digital infrared thermal imaging in hair sheep ewes. The objective of this study was to evaluate the relationship of VT, RT and MAX in hair sheep ewes after the administration of LPS to induce a febrile state. Rectal temperatures

and infrared images of the right and left eyes of each ewe were taken at -12, -1, 0, 1, 2, 3, 4, 6, 12, 24, 36 and 48 hr. Temperature data loggers, programmed to record at 5-min intervals, were inserted into the vagina of each ewe at -12 hr and removed after the 48 hr sample collection. At 0 hr ewes were administered saline (CONT; n = 7; 0.5 mL i.v.) or LPS (n = 7; 0.2 ug/kg BW i.v.). Infrared images of the right and left eye were analyzed to obtain an average MAX for each ewe at each time point. Analysis consisted of measuring the change in RT, VT and MAX over time and determining the correlation among RT, VT and MAX. Ewes given LPS had higher (P < 0.008) RT and VT than CONT ewes from 1 hr after treatment through 12 hr. Ewes given LPS had higher (P < 0.01) MAX than CONT ewes from 1 hr after treatment through 6 hr. Within ewes given LPS, MAX was lower than VT (P < 0.02) during the entire sampling period and lower than RT (P < 0.03) from 3 hr through 48 hr after treatment. Within CONT ewes, MAX was lower than RT and VT (P < 0.01) during the sampling period. There was no difference (P > 0.10) between RT and VT within either the CONT or LPS ewes. Overall, VT and RT were highly correlated (r = 0.96, P < 0.0001) and MAX was highly correlated with RT (r = 0.96, P < 0.0001)0.82, P < 0.001) and VT (r = 0.93, P < 0.0001). In agreement with our previous work, these results suggest that thermography of eye, using maximum eye temperature, may have application as a non-invasive method to measure elevated body temperatures in the ewe.

Key Words: Thermography, Eye, Sheep

968 Effects of plane of nutrition and selenium on colostrum quality and mammary development in ewes. T. J. Swanson^{*1}, C. J. Hammer¹, J. B. Taylor², D. A. Redmer¹, K. A. Vonnahme¹, J. S. Luther¹, T. L. Neville¹, J. J. Reed¹, J. S. Caton¹, and L. P. Reynolds¹, ¹North Dakota State University, Fargo, ²USDA-ARS, U.S. Sheep Experiment Station, Dubois, ID.

To examine the effects of plane of nutrition and selenium supplementation on colostrum quality and mammary development in pregnant ewe lambs, 82 Rambouillet ewe lambs were allotted randomly to one of six treatments in a 3×2 factorial design. Groups included dietary levels of Se [adequate Se (ASe, 7.4 µg/kg BW) vs. high Se (HSe, 85 µg/kg BW)], and plane of nutrition [60% (RES), 100% (CON), and 140% (HIGH) of NRC requirements for ewe lambs]. Basal diets were fed once daily in complete pelleted form and HSe ewes received a Se pellet to meet the required Se level. Upon parturition lambs were immediately separated from their dams. Three hours post lambing colostrum was stripped from the udder. Colostrum yield was measured and samples obtained for milk component and IgG analysis. Ewes were slaughtered within 24 h of parturition and mammary tissues collected for RNA, DNA, and protein analysis. Plane of nutrition decreased (P<0.05) mammary gland weight in RES (670.1 g) compared to CON (838.9 g) and HIGH (815.3 g). In contrast, Se had no effect on ewe mammary weight. Colostrum weight and volume were lower (P<0.01) in RES (343.8 g and 325.9 mL respectively) and HIGH (364.0 g and 364.0 mL respectively) compared to CON (585.7 g and 575.1 mL respectively). Total IgG was lower (P<0.02) in RES (32 g/L) and tended (P<0.06) to be lower in HIGH (34 g/L) compared with CON (43 g/L). Plane of nutrition decreased (P<0.02) butter fat, lactose, and nonfat solids in colostrum of RES and HIGH compared to CON. Milk urea nitrogen increased (P < 0.02) with increasing plane of nutrition. There was no effect of Se on any colostrum components measured. Total DNA and RNA in mammary tissue was lower (P < 0.03) in RES (1.52 g and 2.21 g respectively) compared to CON (2.18 g and 3.42 g

respectively). Total RNA in RES was also lower (P<0.01) compared to HIGH. Results indicate plane of nutrition plays a fundamental role in both colostrum formation and mammary gland development in pregnant ewe lambs.

Key Words: Colostrum, Selenium

969 Evaluating nutritional status of Dorper and Rambouillet ewes in a range sheep production system. T. R. Whitney*, D. F. Waldron, T. D. Willingham, and B. O. Payne, *Texas A&M Agricultural Experiment Station, San Angelo.*

Nutritional status of Dorper and Rambouillet ewes, originating from multiple flocks and grazing a common pasture was investigated. Forty-six Dorper and 33 Rambouillet ewes that lambed within the first 45 days of the lambing season (January 12 to February 26) were used. Data were analyzed with a model that included breed and age of ewe as fixed effects, BW at the start of the breeding season as a linear covariate, and flock of origin of the ewe as a random effect. Blood samples were collected from ewes at the start of the breeding season (August 9 and 16), mid-gestation (October 28 and November 9), and late gestation (December 13 and 20). Dorper ewes had greater insulin-like growth factor-1 (IGF-1; P<0.05) concentrations except on August 16, and had greater non-esterified fatty acid concentrations than Rambouillet ewes on August 9 and 16 and November 9. Since IGF-1 has been shown to be directly related to performance and reproduction efficiency, these results suggest that Dorper ewes could possibly have greater production efficiency than Rambouillet ewes on rangelands. In contrast, higher NEFA concentrations suggest that Dorper ewes were at times, catabolizing more fat than Rambouillet ewes. Dorper ewes had greater body condition (BC; P < 0.05) than Rambouillet ewes at the beginning of the study. Thus, either Dorpers were more capable of using stored energy reserves (e.g. fat) during periods of poor nutrition, or they have higher NEFA concentrations than Rambouillets due to genetics. Results are not conclusive since serum metabolite and hormone concentrations must be analyzed over longer periods of time and interpreted along with other measures. Data from the second year of this study need to be analyzed to make better inferences.

Key Words: Insulin-like Growth Factor-1, Sheep, Physiology

970 Variation in metabolic parameters in dairy cattle kept in a constant environment. K. L. Ingvartsen*, T. Larsen, P. Berg, and N. C. Friggens, University of Aarhus, Faculty of Agricultural Sciences, Tjele, Denmark.

The aim of this study was to describe normal changes in selected physiological variables dependent on breed, lactation number and time in lactation in a constant environment and describe phenotypic and genetic variation in physiological variables. The experimental design has been published earlier (Nielsen et al., 2003, LPS 79, 119-133) as has the blood sampling and univariate analysis (Ingvartsen & Friggens, 2005, DAE 29, 294-304). In short, a total of 317 cows (Danish Red (RD), Danish Holstein (DH) and Jersey (DJ)) and 634 lactations (parity 1, 2, \geq 3) were included. Blood samples collected weekly from -28 d to 298 d relative to calving, a total of 10809 samples, were analyzed for selected hormones, metabolites, and minerals (only non-esterified fatty acids (NEFA), β -hydroxybutyrate (BHBA) and glucose included here). Mixed models using random regression techniques (LeGendre

polynomials) were set up to analyze the systematic effects comprising combinations of breed, line, feeding, parity and time in lactation using the MIXED procedure in SAS. Variance components were estimated across breeds using a package for multivariate mixed models (DMU-program, Madsen & Jensen, 2000). A significant interaction between breed and parity was observed for NEFA, these were higher concentration (P<0.05) in DH compared to DJ for parity 2 and 3. RD had generally lower NEFA compared to DH. While DH and DR showed marked differences in BHBA profiles due to parity DJ did not, causing an interaction (P<0.05). Also for glucose an interaction between breed and lactation was found. In general glucose was lowest in DJ, particularly for primiparous cows, and the concentration did not increase as quick after nadir as in DH and DR. For both NEFA, BHBA and glucose the between cow variation was highest in early lactation. The intra-class (intra-cow) correlation during the first 4 weeks declined from 0.71 to 0.46 for NEFA, 0.44 to 0.36 for BHBA and 0.44 to 0.27 for glucose. The large between cow variation and relatively high intra-class correlation indicates that these parameters may be of use to describe animal status.

Key Words: Metabolites, Variation, Dairy Cattle

971 Uncovering adaptive hepatic gene networks due to prepartum plane of dietary energy and physiological state in periparturient Holstein cows. M. Bionaz*, J. K. Drackley, S. L. Rodriguez-Zas, H. M. Dann, N. A. Janovick Guretzky, R. E. Everts, R. Oliveira, H. A. Lewin, and J. J. Loor, *University of Illinois*, *Urbana.*

Gene network assembly from bovine tissue microarray studies could advance our understanding of function and molecular events underlying complex traits (e.g., fatty liver, ketosis). Joint ANOVA using MIXED was conducted on liver microarray data (174 arrays) from 2 of our published studies (Physiol. Genomics 23:217-226, 27:29-41) using a platform with 7,872 bovine cDNA inserts. Liver microarray data were generated from Holstein cows fed control (100% of NRC), ad libitum (ca. 150% of NRC; AA), or restricted (ca. 80% of NRC; RR) energy diets and biopsied at -65, -30, -14, 1, 14, 28, and 49 d relative to parturition. The statistical model included cow as random effect and time, diet, and time \times diet as fixed effects. A total of 1,555 genes showed a time \times diet interaction (P < 0.0001). Ingenuity Pathways Analysis software recognized and mapped 798 genes. A cut-off of \geq 1.5-fold change in expression on d -14, 1, 14, 28, and 49 relative to -30 was used. Analysis showed that on d -14, 1, and 14, cell-to-cell signaling (20-28 genes) molecular transport (10-13 genes), and tissue development (16-24 genes) were among the most affected molecular functions in cows fed AA. In cows fed RR gene transcription (12-76 genes), protein synthesis (8-30 genes), and immune response (17-23 genes) were among the most enriched molecular/physiological functions. Fewer genes changed by \geq 1.5-fold relative to d -30 in control liver. Several canonical pathways enriched in the data set also were observed, e.g. Integrin and Actin cytoskeleton signaling (AA primarily), protein ubiquitination and complement cascade (RR primarily), and ERK/MAPK and IGF-1 signaling (control primarily). Results confirmed that RR and AA prepartum affected liver genomic adaptations differently. However, one of the most striking observations from this analysis was the marked effect of prepartum dietary energy on expression of genes associated with functions (e.g. transport, gene transcription) supporting tissue remodeling.

Key Words: Microarray, Liver, Genomics

972 Liver fatty acid binding protein (FABP) and acyl-CoA synthase (ACSL) isoform gene expression due to plane of dietary energy prepartum in dairy cows. M. Bionaz*, J. K. Drackley, H. M. Dann, and J. J. Loor, *University of Illinois, Urbana*.

Specific isoforms of FABP and ACSL may work in concert to partition fatty acids towards discrete metabolic pathways in liver, particularly after parturition when NEFA influx increases dramatically. The main objective of this study was to examine mRNA expression by qPCR of FABP (1, 3, 4, 5, 6) and ACSL (1, 2, 3, 4, 5, 6) family members in liver from Holstein cows fed control (100% of NRC) or ad libitum (ca. 150% of NRC; AA) energy diets and biopsied at -14, 1, and 14 d relative to parturition. Expression of 14 genes with key functions in fatty acid oxidation (LPIN1, ACOX1, CPT1A, PPARA, PPARGC1A, CYP4A11), lipid synthesis and desaturation (DGAT1, SCD, HMGCR), fatty acid transport (CD36), lipid droplet synthesis (S3-12, LSDP5, ADFP), and RP9 (reference gene) also were analyzed. ANOVA using MIXED was used for statistical analysis. All ACSL isoforms and the 1, 4, and 6 FABP isoforms were affected by day relative to parturition $(P \le 0.10)$. Relative to d -14, ACSL1 increased on d 1 whereas ACSL isoforms 2 through 6 decreased. Similarly, FABP4 and FAPB6 increased on d 1 whereas FABP1 decreased relative to d -14. A significant interaction effect was observed for ACSL3, ACSL4, FABP4, and FABP5. Expression of FABP isoforms was 4 to 11-fold greater with AA vs. control on d 1. Cows fed control had greater overall expression of ACSL3 and FABP3. Among other genes examined, expression of HMGCR and SCD in cows fed control vs. AA experienced a marked decrease by d 1 and then increased by d 14 resulting in an interaction effect. The opposite response was observed for CD36 expression. Expression of PPARA on d 14 was higher in cows fed control vs. AA. ADFP and PPARGC1A expression increased over time, reaching peak values on d 1. Results indicate that prepartum plane of dietary energy affects expression of FABP and ACSL family members to different extents primarily on d -14 and 1. The fate of exogenous fatty acids (e.g., fatty acid oxidation vs. esterification) in the liver could be dictated at least in part by the expression pattern of specific ACSL and FABP isoforms.

Key Words: Liver, Gene Expression, Dairy Cows

973 The use of nicotinic acid as antilipolytic agent to induce sustained low plasma NEFA concentrations in feed restricted Holstein cows. J. A. A. Pires* and R. R. Grummer, *University of Wisconsin, Madison.*

The objectives were to determine the effects of nicotinic acid (NA) on blood metabolites (experiment 1) and whether successive doses of NA can induce sustained reductions of plasma nonesterified fatty acid (NEFA; experiment 2) in feed restricted non-lactating Holstein cows. Experiment 1 was a 4 × 4 Latin Square with 1 wk periods. Each period consisted of 2.5 d of feed restriction to increase plasma NEFA and 4.5 d of ad libitum feeding. Treatments were abomasal administration of 0, 6, 30 or 60 mg/kg BW of NA, given as a single bolus 48 h after initiation of feed restriction. Plasma NEFA concentration decreased (treatment and treatment × time: P < 0.001) from 546 uEq/L to 208 uEq/L at 1 h after the infusion of 6 mg NA/kg BW, and to less than 100 uEq/L at 3 h after the abomasal infusion of the two highest doses of NA. A rebound occurred after the initial decrease of plasma NEFA concentration during which NEFA increased transiently above 1,200 uEq/L. The rebound lasted up to 9 h for 30 mg NA/kg BW dose, and up to 6 h for 6 mg NA/kg BW dose. Experiment 2 was a randomized complete block design with 3 treatments and 6 cows. Starting at 48 h of feed restriction, cows received nine hourly abomasal infusions of 0, 6 or 10 mg/kg BW of NA. Plasma NEFA concentrations was 553 uEq/L immediately before the initiation of treatments, and decreased to less than 100 uEq/L during infusions of 6 or 10 mg NA/h per kg BW (treatment × time: P < 0.001). Data suggest that the maximal antilipolytic response was achieved with the lowest dose of NA. NEFA concentrations rebounded to over 2,100 uEq/L 4 h after termination of NA infusions. The profile of insulin and glucose concentration suggests a state of insulin resistance during NEFA rebound in both experiments. This model for altering plasma NEFA concentrations by abomasal infusions of NA can be used to study the metabolic ramifications of elevated vs. reduced NEFA concentrations. The data demonstrate potential benefits and pitfalls of using NA to regulate plasma NEFA and prevent lipid related metabolic disorders.

Key Words: Nicotinic Acid, NEFA, Bovine

974 Reduction of plasma NEFA concentration by nicotinic acid enhances the response to insulin in feed restricted Holstein cows. J. A. A. Pires*, J. B. Pescara, and R. R. Grummer, *University of Wisconsin, Madison.*

The objective was to study the effects of lowering plasma nonesterified fatty acid (NEFA) concentration, using supraphysiologic doses of nicotinic acid (NA) as an antilipolytic agent, on the responses to intravenous glucose tolerance test (IVGTT) in feed restricted Holstein cows. Six non-lactating, non-gestating, ruminally cannulated Holstein cows were blocked by body condition score, and randomly assigned to a sequence of two treatments in a cross-over design. Cows were offered legume/grass hay ad libitum, supplemented with minerals and vitamins and allowed free access to water and trace mineralized salt block. Mobilization of body reserves was stimulated by withdrawing forage for 48 h before initiation of treatments. Treatments consisted of eleven hourly abomasal infusions of water (control) or NA (6 mg/h per kg BW). Intravenous glucose tolerance test (0.25g glucose/kg BW) was performed 8 h after initiation of treatments and was followed by 3 h of blood sampling. Infusions of NA decreased (P < 0.001) plasma NEFA concentration from 545 µEq/L to around 100 µEq/L within 2 h after initiation of treatments and significant differences were maintained throughout infusions. The reduction of plasma NEFA concentration led to significantly greater glucose clearance rate (1.9 vs. 1.2 %/min, P = 0.002) and to decreased glucose half life (37 vs. 58 min; P < 0.001), time to reach basal concentration (81 vs. 114 min; P < 0.001) and glucose response area under the curve during 180 min of sampling (AUC180; 6942 vs. 10085 (µIU/mL)*180 min; P < 0.001). Enhanced glucose clearance was achieved despite lower (P = 0.05) insulin concentration (70.0 vs. 97.9 ± 13.4 µIU/mL) and a tendency (P = 0.11) for smaller AUC180 (7646 vs. 12104 ± 2587 (µIU/mL)*180 min) when plasma NEFA was reduced by NA, reflecting increased response to endogenous insulin. Based on literature, we do not expect NA to have altered glucose metabolism directly. Therefore, this experiment demonstrates a cause-effect relationship between elevated NEFA and insulin resistance in Holstein cows.

Key Words: NEFA, Insulin Resistance, Nicotinic Acid

975 Effect of short-term feeding of a plant botanical during late-gestation on temperature and physiological responses of piglets challenged with LPS. J. L. Salak-Johnson*¹, J. M. Suchomel¹, S. R. Niekamp¹, S. Block², and R. Balsbaugh³, ¹University of Illinois at Urbana-Champaign, Urbana, ²ADM Animal Nutrition Research, Decatur, IN, ³ADM Alliance Nutrition, Inc., Quincy, IL.

Crossbred sows were fed a control (n = 10) or treated (n = 15; control +plant botanical) diet for 14 d prior to farrowing to determine the impact of feeding a gestation diet supplemented with a plant botanical on piglet temperature and physiological responses to lipopolysaccharide (LPS). At birth, piglets were weighed and rectal temperatures were recorded. Eight piglets/litter were randomly chosen to receive a saline (n = 90) or LPS (n = 90); 25 μ g/kg of BW) challenge at 24-h or 72-h of age with 2 pigs assigned per challenge category. Rectal temperature was recorded frequently and blood samples were collected 2 h post-challenge. Data were analyzed with the MIXED procedure of SAS. Diet×LPS×age interaction was observed for piglet rectal temperature. Piglets from sows fed treated diet had greater (P < 0.05) temperature response to LPS than did pigs from control sows at 24 h. Piglets farrowed by treated sows had greater (P < 0.05) temperature at 72 h than did 24 h piglets regardless of challenge. Piglets farrowed by control sows and challenged at 72 h with LPS had greater (P < 0.05) temperature than did piglets from sows fed treated diet. Diet or LPS had an affect on interleukin (IL)-10 and -12, but not IL-6. Piglets farrowed by treated sows had greater (P < 0.05) IL-10 than did control diet×LPS piglets. Plasma IL-12 was less (P < 0.05) in piglets from sows fed treated diet than control and IL-10 was greater (P < 0.001) in LPS pigs than in saline pigs. Cortisol was greater in LPS piglets than saline regardless of diet or age (P < 0.001). But, 24 h pigs had greater (P < 0.05) cortisol in response to LPS than did 72 h pigs. Piglets from sows on control diet had greater (P = 0.14) cortisol response to LPS than did piglets from sows fed treated diet. These data indicate that feeding sows a gestation diet supplemented with plant botanical has modulatory affects on the physiological responses of piglets, but no affect on piglet thermoregulatory processes.

Key Words: Piglet, Immune, Plant Botanical

976 Effects of multiple concurrent stressors on rectal temperature, blood acid-base status, and loin muscle glycolytic potential in market weight pigs. M. J. Ritter^{*1}, M. Ellis², D. B. Anderson³, S. E. Curtis², K. K. Keffaber¹, J. Killefer², F. K. McKeith², C. M. Murphy², and B. A. Peterson², ¹Elanco Animal Health, Greenfield, IN, ²University of Illinois, Urbana, ³Colorado State University, Fort Collins.

Sixty four market weight $(130.0\pm0.65 \text{ kg})$ barrows (n=16) and gilts (n=48) were used in a split-plot design with a 2×2×2 factorial arrangement of treatments: 1) handling intensity (gentle vs. aggressive); 2) transport floor space $(0.39 \text{ vs. } 0.49 \text{ m}^2/\text{pig})$; and 3) distance moved during handling (25 vs. 125 m) to determine the effects of multiple concurrent stressors on the stress responses of pigs. Pigs were moved ~50 m through a course with 0 (gentle) or 8 (aggressive) shocks from an electric goad. Next, pigs were loaded onto a trailer and transported for ~1 h at floor spaces of 0.39 or 0.49 m²/pig. After transport, pigs were unloaded and moved 25 or 125 m through a course using livestock paddles. Rectal temperature was measured and blood samples were collected 2 h before handling procedures and immediately after

distance moved treatments. Longissimus glycolytic potential was also measured after the distance moved treatments on a subset of 32 pigs. Data were analyzed using PROC MIXED and PROC REG of SAS. Handling intensity \times distance moved interactions existed (P<0.05) for several blood acid-base measurements. In general, there was no effect of distance moved on these traits when pigs were previously handled gently. However, when pigs were previously handled aggressively, pigs moved 125 compared to 25 m had higher (P<0.05) blood lactate and lower (P<0.05) blood pH, bicarbonate, and base-excess. Pigs transported at 0.39 compared to 0.49 m²/pig had larger (P<0.01) increases in creatine kinase values, however, transport floor space did not affect any other measurements. Data were also analyzed by the number of stressors (aggressive handling, restricted transport floor space, and moved 125 m during handling) experienced by each pig (0, 1, 2, or 3). As stressor number increased, there was a linear increase (P≤0.01) in rectal temperature, blood lactate, and longissimus lactate and a linear decrease (P<0.01) in blood pH, bicarbonate, and baseexcess. These data suggest that the stressors evaluated had additive effects on rectal temperature, longissimus lactate values, and blood acid-base balance.

Key Words: Pig, Handling, Pre-slaughter Stress

977 Neonatal Fc receptor mRNA expression in fetal pigs and in gastrointestinal tissues from pigs fed diets of varying form with or without irradiated and non-irradiated spay-dried animal plasma. C. N. Groesbeck*¹, T. E. Burkey², J. E. Minton¹, S. S. Dritz¹, R. D.

Goodband¹, M. D Tokach¹, J. M. DeRouchey¹, and J. L. Nelssen¹, ¹Kansas State University, Manhattan, ²University of Nebraska, Lincoln.

The neonatal Fc receptor (FcRn) participates in intracellular trafficking of IgG and the maintenance of circulating IgG. Also, the relationship between the FcRn and IgG may augment host defense immunosurveillance. The current studies evaluated FcRn mRNA from intestinal tissues in fetal pigs and weaned pigs fed meal or pelleted diets with or without irradiated or non-irradiated spray-dried animal plasma. In Exp. 1, fetal pigs were obtained at d 55 and d 70 of gestation (n = 5fetuses/gestational age) and total RNA was isolated from intestinal tissues for quantitative real-time PCR (qPCR) to determine mRNA for FcRn. FcRn transcripts were observed in all samples, and greater levels of FcRn mRNA were observed in d 55 fetuses compared to d 70 fetuses (P < 0.02). In Exp. 2, we and pigs were used in an 11-d growth assay to determine the effects of feeding meal and pelleted diets with irradiated or non-irradiated spray-dried animal plasma (AP 920) on FcRn expression in intestinal tissues. Pigs were blocked by weight and randomly allotted in a 2×2 factorial to one of four dietary treatments. Main effects were diet form (meal or pellet) and either irradiated or non-irradiated spray-dried animal plasma. Jejunal, ileal, and cecal tissues were collected from 24 pigs at the conclusion of the growth assay. Total RNA was isolated to quantify relative mRNA expression of FcRn. FcRn transcripts were again observed in all samples. FcRn mRNA was more abundant in pigs fed diets containing non-irradiated plasma compared with pigs fed the irradiated plasma (P < 0.02, 1.01 vs 0.57). FcRn mRNA was also more abundant in the pigs fed meal diets than pelleted diets (P < 0.05, 0.98 vs 0.59). The results suggest FcRn varies with gestational age in pigs and with factors affecting dietary bacterial load.

Key Words: FcRn Receptor, Irradiation, Pig

Poultry-Breeding and Hatchery Symposium: Semen Evaulation and Fertility Determination in Poultry

978 Using sperm penetration values to evaluate broiler breeder performance and reproductive efficiency. R. K. Bramwell*, *University of Arkansas, Fayetteville.*

The sperm penetration assay is a technique developed to quantitatively assess sperm-egg binding and penetration of the perivitelline layer (PL) enveloping the ovum of the avian egg. The process of sperm-egg binding and penetration represents one of the final steps in fertilization sperm must accomplish in order access the female pronucleus for syngamy. Sperm penetration (SP) values have proven to be beneficial for both research and industry applications as these values are based on a sliding scale as opposed to a binary scale for fertility values. As a research tool, male and or female contribution to infertility can be evaluated with much greater accuracy than using fertility values alone. As an industry tool, SP values are used to evaluate broiler breeder flocks experiencing poor hatchability. From identified broiler breeder flocks, each egg from a 50-egg sample is subjected to the SP assay. Holes in the PL overlying the germinal disc caused by sperm-egg binding and the subsequent acrosome reaction are counted and the values recorded in one of five groups (0-10, 11-30, 31-60, 61-100, over 100 holes). Data is expressed as a percentage of the egg samples that produced values in one of the five groups previously reported. For each age group of broiler breeder flocks, an ideal standard has been determined and each flock can be compared to that standard to determine their reproductive efficiency. From this data, the cause

of poor performance can be determined and recommendations made improve breeder flock performance.

Key Words: Sperm Penetration, Sperm-Egg Binding, Fertility

979 Advances in sperm cell biology stemming from the analysis of sperm mobility. D. Froman*, *Oregon State University*, *Corvallis.*

Sperm mobility is a quantitative trait discovered in the mid-1990s. The term *sperm mobility* denotes the net movement of a sperm cell population against resistance at body temperature. The trait was discovered after development of a test based upon sperm penetration of 6% (wt/vol) Accudenz from an overlaid sperm suspension. This test was proven to be simple, objective, and suitable for semen analysis in the field as well as the laboratory. When applied to populations of males, extreme variation was observed among males. Sperm mobility phenotype was independent of age. The relationship between in vitro sperm mobility and male fecundity warranted a systematic analysis. Sperm mobility was proven to be a primary determinant of fertility based upon competitive and non-competitive fertilization. In fact, fertility was a *function* of sperm mobility phenotype. Heritability (h^2)