

no associations between vacuum chewing and other performances were found. No postural behaviors and other stereotypies were found to be related with reproductive performance. Additionally, farrowing rate was not associated with any postural behaviors and stereotypies in logistic regression models ($P>0.05$).

Key Words: Vacuum Chewing, Stereotypies

8 The effect of toys on performance and behavior of weanling pigs housed in littermate or mixed groups. C. M. Wood*, B. Osborne, S. Meder, A. Young, A. Damon, J. Joseph, M. Ashby, T. O'Hare, and L. A. Kuehn, *Virginia Tech*.

Two trials were conducted to determine if the addition of a commercially available toy and the mixing of litters had any effect on weanling pig behavior and performance. In each trial, crossbred pigs ($n=96$) were assigned to treatments at weaning from outcome groups based on litter, gender, and weight. Both trials were conducted in two similar environmentally controlled nursery rooms containing 12 double deck pens each. Each pen (84 cm x 117 cm x 60 cm) housed four pigs. Treatments (toy/no toy and littermate/mixed) were randomly assigned to pens within room in a 2x2 factorial arrangement. All pigs received the same diets, which met or exceeded NRC requirements. Trial 1 lasted two weeks, and Trial 2 lasted four weeks. In Trial 1, five observers recorded pig behavior for a defined period of time in 13 sessions. In Trial 2, one of the five observers recorded behavior four times during the study. In Trial 1 (avg. initial wt = 8.5 kg), pigs with toys tended to gain more ($P < .06$) than pigs without toys. Pigs with toys also displayed fewer vices ($P < .05$), but fought more often ($P < .05$) than pigs without toys. Mixing of litters did not affect growth rate, but pigs in mixed pens did fight more ($P < .05$) than littermates housed together. In Trial 2 (avg. initial wt = 7.5 kg), littermates gained faster the first week ($P < .05$), but there was no effect of toy on gain throughout the trial. There were more pig-to-pig interactions among pigs without toys ($P < .05$) but there were no other significant behavioral differences. There were very few behavioral differences between mixed and littermate pigs, although pigs in mixed pens were observed to drink more often ($P < .05$). The results of these trials suggest that toys can be effective in reducing unwanted

behavioral vices in weanling pigs and may help them to gain faster, but more work needs to be done to clarify results.

Key Words: Weanling Pigs, Behavior, Growth Rate

9 Use of dietary seaweed treatment to reduce heat strain in cattle. L.E. McVicker*, D.E. Spiers, J.E. William, K.J. Barnhart, L.N. Thompson, A. Al-Haidary, and D.P. Colling, *University of Missouri-Columbia*.

Heat stress results in an increase in heat load in cattle, which ultimately reduces productivity. A 50-day study was conducted to determine if a seaweed-derived feed additive, Tasco Meal™ can reduce heat strain in cattle. Twenty-four steers (avg. BW 300 kg) were housed in the Brody Climatology Laboratory at the University of Missouri-Columbia. Each animal was randomly assigned to treatment groups that received either a top dressing of Tasco Meal or control feed daily. Initially half of the animals were exposed to a 13-day heat challenge (HC) reaching air temperatures of 36C during the day and 26C at night. A second 10-day HC period increased night low temperature to 33C and left the high at 36C. During the last portion of the study, animals that had been continuously housed at thermoneutral (TN) were exposed to HC for 12 days to evaluate their heat stress response after receiving Tasco for an extended period. Steers were fed twice daily at 0800 and 1600 with water available ad libitum. Feed intake was recorded daily. Thermal status was measured using telemetric, temperature transmitters (CowTemp, Model BV-010) implanted in the peritoneal cavity. Skin temperatures and respiration rate were taken four times daily. Few significant differences ($p \geq 0.05$) were noted between Tasco-treated and control groups. Animals fed Tasco and initially exposed to heat exhibited a visibly lower core temperature ($\sim 0.5C$) than control animals. However, there were no significant group differences ($p \geq 0.05$) in core temperature. In contrast, animals that received Tasco and were exposed to TN conditions initially showed a visible increase in core temperature above the control animals when exposed to HC after 37 days with no differences in group temperature. Treatment with a seaweed-derived feed additive appears to offer some benefit during early heat stress, but additional studies are needed to verify this benefit.

Key Words: Cattle, Heat Stress, Seaweed

Breeding and Genetics

10 An equivalent single trait animal model to obtain standard errors for estimates of genetic correlations between two traits measured on distinct subsets of animals. K. A. Nephawé*¹, S. D. Kachman¹, and L. D. Van Vleck², ¹*University of Nebraska, Lincoln, NE*, ²*USDA, ARS, USMARC, Lincoln, NE*.

Estimates of genetic correlations among traits are required for economic selection indexes for calculation of expected responses to selection. Such correlations are often estimated using bivariate REML methodology with, for example, MTDFREML programs of Boldman et al. (1995). With two-trait analyses, MTDFREML is able to estimate parameters for bivariate models but the package does not calculate the approximate sampling variances for the estimated (co)variances unless the two traits are measured on all animals. When the two traits are measured on two non-overlapping subsets of animals, the appropriate standard errors can be calculated by reparameterizing the bivariate model to an equivalent single trait model. Reparameterization is done by assigning dummy levels to all fixed and random factors associated with the missing trait when the other trait was measured so that the reparameterized data file contains no missing values. Under the equivalent single trait model, the two direct genetic effects are fitted as two correlated genetic effects so that their covariance is the direct genetic covariance between the two traits. A limitation of the software (not of the approach) is that this equivalent model works only for situations with no true maternal genetic effects for the two traits. The two models can be shown to have the same residual covariance structures. The equivalence was further demonstrated with a numerical example. The standard error for genetic correlation was computed using the equivalent single trait model. An equivalent single trait model could be useful for obtaining the standard error of estimate of genetic correlation between two traits for some situ-

ations for which the MTDFREML program currently will not compute the sampling variances.

Key Words: Reparameterization, Sampling Variances, Genetic Parameters

13 Models for a composite trait such as litter weight weaned for Polypay ewes. L. D. Van Vleck*¹, K. J. Hanford¹, and G. D. Snower², ^{1,2}*USDA, ARS, USMARC, Lincoln, NE*, ²*Clay Center, NE*.

Litter weight weaned (LWW, kg) is the product of a rate trait (number of lambs weaned) and the average weight per lamb weaned and, in this case, is a composite maternal trait of the ewe. Litter weight weaned can be defined on a per ewe exposed basis, on a per ewe lambing basis, or on the basis of a ewe weaning at least one lamb. Depending on which definition is used, the biological and economic meanings of the trait will be different. Variance components for these definitions were estimated from analyses of 9,075 records of 3,487 Polypay ewes from the USSES, Dubois, Idaho. The basic model included fixed effects of age of ewe, year of birth, type of birth and rearing, and random genetic and permanent environmental effects associated with the ewe. For a specific per ewe definition, various covariates which affect LWW also will affect the biological interpretation of estimates of variance components. For example, on a per ewe exposed basis with no other fixed effects, estimates of heritability, repeatability, and phenotypic variance were: 0.04, 0.08, and 531. With 3 covariates to account for fraction of litter weaned being wether or ram or ewe lambs, the estimates were: 0.04, 0.07, 181. With the covariate of number of lambs born, the estimates were: 0.06, 0.11, and 432. With the covariate of number of lambs weaned, the estimates were: 0.11, 0.12, and 45. This pattern was similar per ewe lambing or weaning at least one lamb. When analyzed with either number of lambs

born or weaned with fixed effects of age of ewe and year of birth, estimates for LWV were similar to estimates from single trait analyses. The exception was that when analyzed with number weaned and with the 3 covariates for gender of litter, estimates were 0.04, 0.08, and 412 per ewe exposed, 0.04, 0.08, and 405 per ewe lambing, and 0.07, 0.09, and 205 per ewe weaning at least one lamb. An obvious conclusion is that for genetic evaluations which include a composite trait such as LWV, models must be developed carefully for what the specific goals are.

Key Words: Genetic Parameters, Sheep, Variance Components

14 Evaluation of serially measured body weight data in young Angus bulls and heifers. A. Hassen*, D. E. Wilson, and G. H. Rouse, *Iowa State University, Ames, IA.*

Data in the current analysis came from 927 purebred Angus bulls and heifers born during the spring of 1998 to 2001. Each year animals were weighed 4 to 10 times starting at birth to 461 d of age. The broad objective of this study was to identify statistical procedures to be used in modeling serially measured phenotypic data and their possible application in evaluating component ultrasound traits. The specific objectives were to describe body weight changes of bulls and heifers, to evaluate current industry age of calf adjustment factors, and to estimate heritability of growth curve parameters. Both linear and nonlinear(logistic) regression models were used to describe body weight changes. Model R^2 , RMSE, and percent absolute bias (PABS) for the best linear model based on bull data were 0.91, 47.9 kg, and 11%, respectively. The corresponding values for heifers were 0.90, 38.59 kg and 11.6%, respectively. Logistic models also showed similar R^2 , RMSE, and PABS. For both model types, individual animal regressions showed a better fit as evidenced by lower mean RMSE (9 to 10 kg), PABS (1.8 to 2%), and higher R^2 (0.99) values than those used on data pooled within sex. Bulls showed a higher mean predicted mature weight (763 kg) than heifers (542 kg). Predicted daily weight gain and age at inflection point for bulls were 1.75 kg/d and 296 d, respectively, as compared to 1.24 kg/d and 261 d for heifers. When compared to data adjusted to 205 d using all within animal serial data (ADWT), current industry age of calf adjustment factors introduced an average bias amounting to 2% to 11% of ADWT. Heritability of growth parameters ranged from 0.17 to 0.20, suggesting limited directional changes if selection is based entirely on these parameters. Statistical models that allow for individual animal information may provide an alternative for studying compositional changes. However, with limited number of observations per animal and restricted range of ages at scan, nonlinear growth functions may not provide any better description of changes in body composition than simple linear regression models.

Key Words: Cattle, Growth, Regression

15 Relationship between intramuscular fat percentage predicted from real-time ultrasound and meat quality traits in pigs. D.W. Newcom*¹, T.J. Baas¹, and R.N. Goodwin², ¹*Iowa State University, Ames, IA*, ²*National Pork Board, Des Moines, IA.*

Data from two national progeny testing programs were used to compare the relationships of intramuscular fat percentage of the loin predicted using real-time ultrasound (PIMF) and chemical intramuscular fat percentage (CIMF) with meat quality traits in pigs. A total of 821 purebred (Yorkshire, Duroc, Chester White, Poland China, and Berkshire) barrows and gilts were ultrasonically scanned 5 d prior to harvest with an Aloka 500 SSD ultrasound machine. A minimum of four longitudinal and one cross-sectional ultrasound image were collected. Intramuscular fat percentage was predicted using a model which included image parameters from the longitudinal images and backfat from the cross-sectional image. Chemical intramuscular fat percentage was determined by lab analysis of a slice from the loin at the 10th rib. Meat quality traits measured were: Minolta reflectance, Hunter L, and pH (24 and 48 h); water holding capacity and subjective visual scores for color, marbling, and firmness (48 h); Instron tenderness, cooking loss, and trained sensory panel evaluations (5 d). Traits were grouped for analysis and each group included chemical and predicted IMF. The heritabilities for CIMF and PIMF were 0.45 and 0.52, respectively, and the genetic correlation between them was 0.76. Estimates were consistent across trait groups. Genetic correlation estimates for PIMF and CIMF with pH measured 48 hours post-mortem were 0.40 and 0.27, respectively. The genetic correlations between PIMF and tenderness, juiciness, and flavor

evaluated by a sensory panel were 0.29, 0.67, and 0.66, respectively. The genetic correlations between CIMF and tenderness, juiciness, and flavor were 0.35, 0.53, and 0.54, respectively. Genetic correlation estimates for PIMF and CIMF with water-holding capacity were -0.40 and -0.25, respectively. The genetic correlations of PIMF and CIMF with remaining meat quality traits were similar. Selection for intramuscular fat percentage estimated from chemical analysis or by real-time ultrasound should yield similar correlated responses in meat quality traits in pigs.

Key Words: Pigs, Meat Quality, Genetic Parameters

16 Effect of selection for testosterone production on testicular morphology and daily sperm production in pigs. S. Walker*, O.W. Robison, C.S. Whisnant, and J.P. Cassady, *North Carolina State University, Raleigh.*

The objective of this study was to determine effects of divergent selection for testosterone on morphological testicular characteristics and daily sperm production. Duroc boars from lines divergently selected for testosterone production in response to GnRH challenge for 10 generations followed by random selection were used. In generation 21 endogenous testosterone in the high testosterone line (H, n=54) and low testosterone line (L, n=44) averaged 490 ng/dl and 278 ng/dl ($P<0.01$), respectively. Body weight, testicular weight, and epididymal weight were recorded for boars from H (n=82) and L (n=44) castrated at an average age of 211 d and 97 kg. For animals castrated in generation 20 (H, n=46 and L, n=13) tissue samples were also taken, and volume densities for leydig cells and seminiferous tubules were determined along with daily sperm production per gram of testis. After adjustment for body weight, average paired testicular weights for H and L were 417 kg and 457 kg ($P<0.01$), respectively. Adjusted epididymal weights also differed between lines ($P<0.02$), with H having larger epididymal weights. Line H (n=46) had greater volume densities of leydig cells than L (n=13) ($P<0.02$). Volume density of seminiferous tubules tended to differ between the lines ($P<0.07$). Daily sperm production per gram of testes once adjusted for age did not significantly differ between lines. Selection for testosterone production in response to a GnRH challenge was an effective method of changing testosterone levels, testicular size, epididymal weight, and volume density of leydig cells and seminiferous tubules. However, no significant difference in daily sperm production per gram of testes was seen with respect to selection for testosterone. At this time selection for testosterone in order to increase sperm production is not recommended.

Key Words: Selection, Reproduction, Pigs

17 Response to selection in purebred and crossbred swine populations selected for growth traits on a maternal index. M. B. Munthala*, T. S. Stewart, A. P. Schinckel, and M. M. Schutz, *Purdue University, West Lafayette, IN USA.*

The objective was to evaluate the correlated response to selection for a maternal index on days to 105 kg (d105) and backfat at 105 kg (BF) in crossbred and purebred pigs. Three replicates of purebred Yorkshire and Landrace, boars and gilts were selected on maternal index (including number born alive, pigs survival to weaning, litter 21-dayweight, d105 and BF). Adjusted d105 and BF were calculated by National Swine Improvement Federation guidelines. Contemporary purebred and crossbred offspring were produced over a period of 7 years. Data were analyzed with purebreds and crosses together (n = 5540) and with subsets of each breed composition category LL (n = 1437), YY (n = 1411), LY (n = 1452), YL (n = 1240). Model included replicate, farrowing group nested in replicate, sex and covariates of birth weight, and weaning weight. Fixed effects of sire and dam breed were included for full data. All effects were found to be significant ($P<0.05$). Average d105 was 185.32d ($\pm 24.2d$) and average BF was 19.3mm ($\pm 5.5mm$). Heritability estimates and genetic correlations were obtained with REML and breeding values were BLUP using PEST. Heritability for d105 ranged from 0.34 to 0.68 (full data 0.48, LL 0.34, YY 0.38, LY 0.55, and YL 0.68). Heritability of BF ranged from 0.38 to 0.56 (full data 0.42, LL 0.38, YY 0.52, LY 0.52, and YL 0.56). Small non-significant genetic correlations (ranging from -0.095 to 0.0163) were found between d105 and BF. Over a period of 7 years, genetic trend for both d105 (d/yr) and BF (mm/yr) decreased, with regression coefficients -1.00 and -0.3 respectively. The breed-wise genetic trend per year for d105 (d/yr) and BF (mm/yr) respectively was LL -0.75, -0.31; LY -0.37, -0.025; YL -0.025, 0.074; YY -0.43, -0.32. The breed-wise phenotypic trend per year for d105 (d/yr) and BF (mm/yr)

respectively was LL 4.28, -0.89; LY 4.18, -0.4; YL 5.94, -0.68; YY 4.76, -0.8. Selection for maternal trait index has resulted in a genetic decrease in d105 and BF.

Key Words: Days to 105 kg, Backfat, Response

18 Effects of sire line, sire, and sex on plasma urea nitrogen (PUN), body weight, and backfat thickness in offspring of Duroc and Landrace boars and heritabilities. J. Klindt*, R. M. Thallman, J. T. Yen, and T. Wise, *USDA-ARS, U.S. Meat Animal Research Center.*

In pork production, efficiency of dietary protein (nitrogen) utilization is low, <50%, resulting in urinary excretion of large quantities of nitrogen as urea. Dietary protein accounts for 20 to 25% of the cost of diets and efficiency of its use affects economic efficiency. Utilization of protein and formation of urea are under enzymatic regulation, suggesting genetic regulation. The present study examines the effect of sire line, sire, and sex on growth characteristics and PUN concentrations in the offspring of 11 Duroc sires and 11 Landrace sires bred to Yorkshire-Landrace dams. Plasma samples were obtained at 107, 128, and 149 d of age from 511 boars, gilts, and barrows group-penned and fed a standard finishing diet. Body weight (kg) and backfat (BF, mm, mean of measurements at 1st rib, last rib and last lumbar vertebra) were recorded at time of blood sample collection. Sire line, sire, sex, age, age*sex, and age*line*sire influenced ($P < 0.01$) BW, BF, and PUN. Single observation traits; i.e., ADG (kg/d), BW at 21wk (BW21wk, kg), avg. daily change in BF (ADCBF, mm/d), BF at 21wk (BW21wk, mm), and mean of three PUN measures (mPUN, mg/dL) were generated. All traits were influenced ($P < 0.01$) by sire and sex, and line influenced ($P < 0.01$) all traits except ADCBF ($P > 0.65$). Phenotypic correlations of mPUN with growth traits are: ADG, 0.05; BW21wk, 0.21; ADCBF, 0.23; and BF21wk, 0.42. Genetic correlations of mPUN with growth traits are: ADG, 0.12; BW21wk, 0.44; ADCBF, 0.22; and BF21wk, 0.62. Heritabilities (h^2) are: ADG, 0.64; BW21wk, 0.47; ADCBF, 0.40; BF21wk, 0.57; and mPUN, 0.35. Determination of PUN, as herein, may be with sufficient precision to allow its use in a selection protocol. Selection of pigs with superior growth performance and low PUN may result in greater efficiency of dietary nitrogen utilization and reduced negative environmental impact.

Key Words: Plasma Urea Concentrations, Growth, Genetic Influences

19 Mapping of porcine genes related to human diabetes. C.J. Otieno*, S. Vleck, C. Jelks, K.S. Kim, N.T. Nguyen, and M.F. Rothschild, *Iowa State University, Ames.*

The link between diabetes and obesity is well known, and the pig may present a good model system for studying these complex traits. Resistin (RSTN), an adipocyte hormone, counteracts the effects of insulin while 11 beta hydroxysteroid dehydrogenase isoform 1 (HSD11B1) catalyzes glucocorticoid conversion, and both have been implicated in insulin resistance, impaired glucose tolerance, diabetes and obesity. Protein kinase B Akt2 (AKT2) mediates insulin signaling in muscle and fat cells. We identified polymerase chain reaction-restriction fragment length polymorphisms (PCR-RFLPs) in the porcine RSTN, HSD11B1 and AKT2 genes. A 14 base-pair insertion/deletion SmlI PCR-RFLP in intron 2 of the RSTN gene was detected and used to genotype a reference family generated by intercrossing Berkshire and Yorkshire pig breeds. According to linkage analysis, the RSTN gene was mapped to pig chromosome 2 between the markers SW1686 and SW766. Similarly, we identified a StuI PCR-RFLP in intron 3 of HSD11B1, and linkage analysis mapped this gene to pig chromosome 9 between the markers SW2116 and SW1651. Using the French pig/rodent somatic cell hybrid panel containing 27 cell lines, we physically mapped the AKT2 gene to pig chromosome 6 in the region q21. This study has added three new markers to the pig genome map, and further investigations on these genes in pigs may provide useful information on genetic factors underlying diabetes and obesity.

Key Words: Pig, Gene, Diabetes

20 Characterization of a line of pigs selected for increased litter size for genes known to affect reproduction. C. D. Blowe*, E. J. Eisen, O. W. Robison, and J. P. Cassady, *North Carolina State University, Raleigh.*

The purpose of this study was to characterize changes in allelic frequencies in a line of pigs selected for increased litter size. Genes to be examined were chosen based on results of previous studies, which indicated that a particular polymorphism was associated with an increase in litter size. Pigs were selected from the largest litters where litter size was based on number of fully formed pigs. Litters were standardized at birth so that no replacement gilts were reared in a litter greater than 10 pigs. A contemporary control line was maintained also. In generation nine, the estimated mean breeding value for litter size was 0.63 pigs larger in the select line than in the control line. DNA was extracted from white blood cells. Alleles were detected using previously published primers and enzymes. Estrogen receptor (ESR) and retinol binding protein 4 (RBP4) loci were amplified using PCR. Product from PCR reactions was then digested with restriction enzymes that have been shown in previous studies to produce restriction fragment length polymorphisms. Digestion using *Pvu* II and *Msp* I were used for ESR and RBP4, respectively. No segregation of ESR alleles was detected in either population. Frequencies of the A allele for RBP4 were 0.266 and 0.207 in the select and control lines, respectively. The frequencies were not significantly different between the two lines. Molecular genetics has the potential to be highly advantageous in selection for lowly heritable and sex-limited traits, such as litter size. It may be concluded that changes in litter size observed in this population were not associated with either the ESR or RBP4 locus.

Key Words: Pigs, Reproduction, Litter Size

21 Modeling variance and covariance of total sperm cells over the active lifetime of AI boars. S.-H. Oh*¹, M. T. See¹, T. E. Long², and J. M. Galvin², ¹North Carolina State University, Raleigh NC, ²NPD USA, Roanoke Rapids NC.

The objective of this study was to model the variances and covariances of total sperm cells ($\times 10^9$) over the active lifetime of AI boars. Data from boars ($n = 833$) selected for AI were provided by NPD USA. Total number of records and animals were 19,629 and 1,045, respectively. Parameters were estimated for total sperm cells by age of boar classification under a random regression model using the Simplex method and DxMRR procedures. The analysis model included breed, collector and year-season as fixed effects. Random effects included additive genetic effect, permanent environmental effect of boar, and measurement error. All measurement errors were assumed to be equal. Observations were removed when the number of data at a given age of boar classification was less than 10. Preliminary evaluations showed the best fit with fifth order polynomials indicating that the best model would have fifth order fixed regression and fifth order random regressions for animal and permanent environment effects. In this study, all combinations within the fifth order were fit to evaluate the best polynomial covariance function. Goodness of fit for models was tested using Akaike's Information Criterion and Schwarz Criterion. The maximum log likelihood value was observed for fifth, seventh, and fourth order polynomials for fixed, additive genetic and permanent environmental effects, respectively. However, the best fit as determined by Akaike's Information Criterion (AIC = 5.799) and Schwarz Criterion (SC = 5.801) was by fitting fifth, sixth, and sixth order polynomials for fixed, additive genetic and permanent environmental effects, respectively. Heritability estimates for total sperm cells ranged from .27 to .61 across age of boar classifications. In addition, heritability for total sperm cells tended to increase with age of boar classification. The cyclic nature of heritability for total sperm cells that was observed over the active lifetime of boars may be due in part to number of observations across seasons limiting our ability to correct for seasonal effects on sperm production.

Key Words: Heritability, Semen, Pigs

22 Performance of mice divergently selected for sensitivity to fescue toxicosis when challenged with endophyte-infected fescue and heat stress. S. Bhusari*¹, E. Antoniou¹, D.E. Spiers¹, W.D. Hohenboken², P.A. Eichen¹, and W.R. Lamberson¹, ¹University of Missouri-Columbia, ²Virginia Polytechnic Institute and State University, Blacksburg.

Mice, previously selected for sensitivity to endophyte-infected fescue seed diets based on rapid (R) or slow (S) gain, were used to study the effects of fescue toxicosis during heat stress. Ninety-five mice from the lines were randomly allocated to either heat stress (HS, 34 ± 1°C) or thermoneutral (TN, 24 ± 1°C) conditions and diets containing 50% endophyte positive (E+; 6 ppm ergovaline) or negative (E-) fescue seeds. Mice were exposed to conditions of HS and endophyte diets from 47 to 60 days of age. Body weights were measured on the first day of the experiment (d1), day 7 (d7) and day 14 (d14). At study end, mice were euthanized and the livers weighed (Lwt) and frozen for future study of gene expression. Dependent variables, Lwt, body weight gain from d1 to d7, d7 to d14 and d1 to d14, and body weight at d7 and d14, were fitted to a model including the effects of selection line, air temperature, diet, and all possible interactions using the GLM procedure of SAS. The R line gained more weight from d1 to d14 than the S line (1.8 ± 0.16 g vs. 0.95 ± 0.14 g, respectively, P<0.01). Body weight gain from d1 to d14 on E+ diet was less than on E- diet (0.91 ± 0.15 g vs. 1.85 ± 0.16 g, respectively, P<0.01). There was a Line x Treatment x Diet interaction for Lwt adjusted for differences in body weight (P=0.02). Liver weights were heavier in both R and S mice fed E+ at HS than at TN. In mice fed the E- diet, air temperature did not affect the liver weight within either the R or S line. Interaction among factors for liver weight indicates differences in susceptibility of lines to fescue toxicosis.

Key Words: Fescue Toxicosis, Heat Stress, Endophyte

23 Relationships among Charolais sire expected progeny differences and progeny performance in commercial herds. S. C. Clark*¹, D. W. Moser¹, and R. E. Williams², ¹Kansas State University, Manhattan, KS, ²American International Charolais Association, Kansas City, MO.

Data on Charolais-sired calves were analyzed to evaluate progeny performance relative to sire EPD in a large data set of commercial crossbred cattle in 31 herds across the United States. The traits analyzed were birth weight (n=3,558) and weaning weight (n=3,615) of crossbred progeny from 224 nationally evaluated sires. Birth weight (BW) and weaning weight (WW) were used to assess response to selection in crossbred progeny. Random regression coefficients estimated for progeny BW on sire EPD were 1.03 ± 0.09 kg/kg of BW EPD, and for progeny WW, 0.66 ± 0.11 kg/kg of WW EPD. Published sire BW EPD and WW EPD were averaged and weighted on published accuracy. The average weighted sire BW EPD was 0.39 kg and WW EPD was 7.30 kg with an average accuracy of 0.79 and 0.75, respectively. Correlations for sire effect solutions in commercial herds with published sire BW EPD and WW EPD were 0.59 and 0.39, respectively. Sire EPD for birth and weaning weights were positively related to actual progeny performance. Therefore, selection based upon sire EPD should result in change of crossbred progeny performance. This further validates use of EPD as a selection tool for BW and WW in commercial herds. However, WW response was lower than expected, possibly a result of management practices in commercial herds compared to purebred herds.

Key Words: Expected Progeny Differences, Progeny Performance, Sire Effect

24 Relationships between live animal ultrasound predicted intramuscular fat and shear force in fed cattle. L. D. Keenan*, D. W. Moser, D. R. Eborn, and T. T. Marston, Kansas State University, Manhattan, KS.

Simmental sired (n=136) and Hereford (n=148) feedlot steers were ultrasonically evaluated for intramuscular fat deposition at the 12-13th rib site using CPEC and Critical Vision, Inc. ultrasound systems. Warner-Bratzler Shear Force (WBSF) measurements were taken on postmortem steaks from the 13th rib region of the hindquarter to determine whether shear force values were associated with amount of intramuscular fat projected by the ultrasound systems. Differences between ultrasound and actual marbling measurements were corrected for bias and identified as

CPECDEV and CVIDEV, respectively. Simple Pearson correlation coefficients of CPECDEV and CVIDEV with WBSF were .18 and .15, respectively. This indicates that animals overestimated for marbling had a tendency to have higher WBSF values. A linear model was used to describe effects of marbling, WBSF, breed, and breed x WBSF interaction on CPECDEV and CVIDEV. WBSF and breed x WBSF were not statistically significant effects (P>.05) on CPECDEV or CVIDEV. This research indicates that animals with higher ultrasound marbling predictions as compared to the actual carcass marbling score are not associated with higher WBSF values. Thus, CPEC and CVI predictions of intramuscular fat are not biased by differences in WBSF.

Key Words: Intramuscular Fat, Ultrasound, Warner-Bratzler Shear Force

25 Functional genomics as a tool for integrated polygene discovery for complex traits. D. Pomp*, University of Nebraska-Lincoln.

Most phenotypes with agricultural and biomedical relevance are multifactorial traits controlled by complex contributions of genetic and environmental influences. Genetic predisposition results from combinations of relatively small effects of genetic variations within a large number of polygenes, known as quantitative trait loci (QTL). Molecular biology has yielded advancements in understanding many complex traits at the metabolic and physiological levels; however, despite the mapping of many QTL for important traits (e.g. growth, body composition, reproduction) across several mammalian species including mouse, rat, pig, sheep, cattle and human, little has been learned regarding the identity and nature of the underlying genes due to the inherent inaccuracy of QTL localization and the inability to differentiate between co-localization and co-occurrence. This wide gap between our knowledge of physiological mechanisms underlying complex traits and the nature of genetic predisposition to complex traits significantly impairs polygene discovery efforts. Integration of experimental approaches to jointly evaluate predisposition and physiology should increase success of polygene discovery and characterization by combining the power of recombination with functional analysis. For example, key transcriptional, proteomic, metabolomic and endocrine pathways can be phenotyped in large populations for which marker genotypes are available. By measuring such sub-phenotypes within the framework of a structured gene mapping population, we can bridge the gap between physiology and predisposition to facilitate accurate selection of candidate genes representing QTL, thus enabling complex trait polygene identification and characterization. Such efforts would advance our understanding of the overall genetic architecture of complex traits by testing the central hypothesis that genes controlling predisposition to a complex trait are primarily involved in trans-regulation of the physiological pathways that directly regulate the trait.

Key Words: Genomics, Microarray, Gene Discovery

26 Proteomic analysis of skeletal muscle calcium homeostasis. M. Zece*, S. Jones, R. Cerny, J. Schultz, N. Palmer, and B. Kornilav, University of Nebraska, Lincoln.

Calcium homeostasis is a critical process in muscle because this cation represents the trigger for several physiological functions including metabolism, contraction and protein turnover. There is also evidence that calcium level is linked to apoptosis and programmed cell death. Abnormal regulation of calcium level is widely held as the principle cause of pathological conditions such as malignant hyperthermia and central core disease in humans. Malignant hyperthermia is also manifest as stress syndrome in meat animals. This condition often results in premature death or poor quality meat (PSE). Significant progress has been made in the past decade regarding our understanding of calcium regulation and in the identification of potential causes for its abnormalities. The discovery of a single mutation in ryanodine receptor (RyR1) protein stirred hopes that definitive testing would eliminate or reduce the incidence of PSE in pigs. However, this has not yet been realized. A more complicated picture has emerged from recent research. For example, numerous (>20) mutations have been identified in RyR1 that correlate with malignant hyperthermia in humans. It has also been shown that calcium homeostasis results from the coordinated interaction of several SR-associated proteins including: RyR1, dihydropyridine receptor, calsequestrin, tradin, junctin and calmodulin. These proteins form a functional complex that is responsible for calcium

release following their interaction. Thus there may be multiple mutations in porcine muscle that collectively contribute to elevated calcium level and its adverse consequences for meat animals.

Our group has taken a proteomic approach to investigate this complex protein system. Two-dimensional electrophoresis in combination with mass spectrometry methods are being used to separate, identify and characterize constituent SR proteins. This group of membrane proteins represents significant challenges to widely used proteomic methods. Thus we have developed techniques to enable their assessment. We are particularly interested in investigating whether additional polymorphisms exist in the porcine form of RyR1 protein. The results of this work including separations of SR-associated proteins and their identification will be presented.

Key Words: Calcium Homeostasis, Proteomics, PSE

27 Design and analysis of cDNA microarrays in animal science. R. J. Tempelman*, Michigan State University, East Lansing.

Gene expression experiments based on cDNA microarrays have established a new paradigm for animal science research. Until very recently, however, not enough consideration had been given to experimental design issues such as randomization and biological versus technical replication. Furthermore, the nature of cDNA microarray data seems to require the use of various data adjustments or 'normalization' procedures and the consideration of multiple sources of variation. Design and data quality considerations pertinent to cDNA microarray experiments are discussed. Analyses of cDNA microarray data currently appears to require two types of data normalization: 1) a dye-intensity based normalization and 2) a second normalization based upon a mixed effects model analysis. Both analyses are readily computed using SAS statistical software. Nevertheless, plenty of design and data analysis issues remain unresolved and require further investigation, including the use of control genes, inference involving low level transcripts, non-normal data, and multiple testing.

Key Words: Design of Experiments, Functional Genomics, Mixed Effects Models

28 Application of expression profiling technology to animal agriculture. J. C. Byatt*, N. Mathialagan, and C. J. Dyer, Monsanto Company, St. Louis, MO.

The advent of technologies that allow relative expression of thousands of transcripts to be examined simultaneously has made possible a multitude of potential discovery projects that promise to enhance our knowledge of gene function and gene interactions. As expression profiling technology has become more widely available it has been enthusiastically implemented by animal scientists, but several challenges remain with respect to designing meaningful experiments, analyzing and sharing data and generating results with obvious utility. These issues are particularly acute when applied to industrial research, because ultimately a cost/benefit analysis must be carried out for research projects and there should be a clear application of technology investments to a final product. In the case of expression profiling, there are two obvious applications of this technology to product development for animal agricultural companies. The first is to use this technology to identify targets for therapeutic drugs and productivity enhancers. This parallels the pharmaceutical industry's use of expression profiling to identify "druggable" targets. The second application is to use gene expression data to identify potential candidate genes in which genetic variation contributes to QTL. In theory, identification of genes, levels of expression of which are associated with commercially important phenotypes, helps identify positional candidate genes for QTL. In practice, the case for using expression profiling to identify positional candidates will depend on many factors, including 1) number and type of tissues that could express genes controlling the trait, 2) whether these tissues are amenable to serial sampling, 3) the ability to manipulate the phenotype or select and sample animals with a large degree of phenotypic variation and 4) resources for discovering polymorphisms in a potentially very large number of gene candidates. These issues will be explored and illustrated with some examples from a number of expression profiling studies.

Key Words: Expression Profiling, Candidate Gene

31 Estimate of heritability and genetic change for survival of Hereford cows. G. E. Martinez*¹, R. M. Koch¹, L. V. Cundiff², K. E. Gregory², S. D. Kachman¹, and L. D. Van Vleck^{2,3}, ¹University of Nebraska, Lincoln, NE, ^{2,3}USDA, ARS, USMARC, ²Clay Center, NE, ³Lincoln, NE.

Genetic parameters for survival measured in years between first calving and disposal were estimated using records for 2,053 Hereford cows born from 1964 to 1979 from a selection experiment with three lines selected for weaning weight (WWL), yearling weight (YWL), and an index of yearling weight and muscle score (IXL), and a control line (CTL). The model included year of birth as the only fixed factor and sire as the only random factor. The numerator relationship matrix accounted for all known relationships among sires. The survival analysis was carried out with a Weibull model with a penalized quasi-likelihood function. A record was considered censored if a cow was still alive at the end of the experiment or was sold or culled for reasons not related to the experiment. Genetic trends were estimated by regressing weighted means of estimated breeding values (EBV) of sires for years of birth of their daughters on birth year of the daughters. Environmental trends were estimated by regressing means of solutions for year of birth of the daughters on birth year. The estimate of the Weibull parameter was 1.30 ± 0.14 , which indicates that the hazard for being culled increased with age. The overall median survival time was 5.2 years. The estimate of heritability \pm SE for survival was: 0.06 ± 0.02 on the log scale and 0.15 when transformed to the original scale (years). Estimates of annual genetic change for survival were nearly zero for all lines. Selection of sires whose daughters are more likely to remain longer in the herd would be possible in a breeding program but could be relatively slow due to the low estimate of heritability. Comparison of changes in survival time for the selection and control lines showed that selection for weights at weaning and yearling ages had little effect on survival time in this experiment.

Key Words: Beef Cattle, Longevity, Selection

32 Birth and weaning traits of topcross progeny of Hereford, Angus, Brangus, Beefmaster, Bonsmara, and Romosinuano sires. Larry V. Cundiff, USDA, ARS, U.S. Meat Animal Research Center.

The objective of this experiment was to characterize breeds representing diverse sources of germplasm for preweaning traits that are important in beef production. Data were obtained on 1,270 calves born in the spring of 2001 and 2002 and 1,231 calves weaned resulting from artificial insemination matings of Hereford (H, 22 sires), Angus (A, 22), Brangus (Bg, 21), Beefmaster (Bf, 22), Bonsmara (Bo, 19), and Romosinuano (Ro, 20) bulls to Hereford, Angus, and composite MARC III (1/4 each Angus, Hereford, Red Poll, and Pinzgauer) cows. Data on gestation length (GL), unassisted calving percentage (CE), survival to weaning (SW), birth weight (BW), and 205-d weaning weight (WW) were analyzed by least squares procedures using a model that included random effects for sire in sire breed and fixed effects for sire breed, dam breed, sex of calf, age of dam (4.5,...10 yr), birth year, sire breed x dam breed, and any other two factor interactions that were significant ($P < .05$) for each trait. Effects of sire breed were significant ($P < .01$) for GL, BW, and WW, but not for CE or SW. The means for H, A, Bg, Bf, Bo, and Ro sired progeny were 283.7, 281.6, 284.9, 286.6, 286.7, and 288.9, respectively for GL with a mean least significant difference ($LSD < .05$) of 1.6 d. Corresponding sire breed means were 94.4, 97.2, 96.9, 95.6, 97.7, and 99.2% for CE ($LSD < .05 = 3.4\%$); 41.3, 39.5, 41.1, 43.3, 41.0, and 38.4 kg for BW ($LSD < .05 = 1.3$ kg); 96.9, 98.1, 96.8, 96.4, 94.7, and 98.6% for SW ($LSD < .05 = 3.3\%$); and 242.4, 245.6, 248.9, 254.0, 242.0, and 230.1 kg for WW ($LSD < .05 = 4.9$ kg). H and A, which have evolved in temperate climates, had significantly shorter GL than Bf, Bo, and Ro, which are considered more tropically adapted. Ro and A had significantly lighter BW than Bo, Bg and H which were in turn lighter than Bf. WW were significantly heavier for Bf than all other breeds. Bg had significantly heavier WW than H and Bo. WW of Ro were significantly lighter than all other breeds.

Key Words: Beef Cattle, Breeds, Germplasm

33 Evaluation of predicted milk yield and weaning weight in Polled Hereford, Angus, Brangus, Gelbvieh, Limousin, Salers, and Simmental Breeds of beef cattle. J. P. Cassidy*, C. H. Brown, and O. W. Robison, *North Carolina State University, Raleigh.*

The objective of this experiment was to measure breed differences in predicted milk yield (PMY, a trait of the cow) and weaning weight (WW, a trait of the calf). Data included 935 records from a breed evaluation project at the North Carolina Department of Agriculture Tidewater Research Station, Plymouth, NC. Breeds included were Polled Hereford (PH), Angus (AN), Brangus (BN), Gelbvieh (GV), Limousin (LM), Salers (SA), and Simmental (SM). Milk yields were predicted from three measurements of milk production. The model included fixed effects of calving year (CY), age of dam at calving (ADC), sex of calf, and age of granddam at time of dam's birth (AGD). Calf birth weight and breed type were treated as fixed regression covariates. Direct genetic breed effects were estimated as deviations from the mean performance of PH. Fixed effects of CY and ADC ($P < 0.01$) and AGD ($P < 0.07$) were important. Calf birth weight affected PMY ($P < 0.01$). All possible combinations of single degree of freedom contrasts between breed types were done. Direct genetic effects of PH reduced PMY when compared to AN, BN, GV, SA, and SM ($P < 0.05$). Simmentals had a greater PMY than AN, BN, and SA ($P < 0.05$), and GV had greater PMY than LM ($P < 0.05$). Simmental's greater PMY was expected because SM was developed as dual-purpose breed and thus, selected for milk yield as well as meat production. For WW fixed effects of CY, ADC, sex of calf, and AGD were significant. Birth weight was also important ($P < 0.05$). Direct genetic effects of AN, BN, GV, SA, and SM increased WW as compared to PH ($P < 0.05$). Direct genetic effect of SM increased WW as compared to SA and LM ($P < 0.05$), and direct genetic effect GV increased WW as compared to LM ($P < 0.05$). Breed differences do exist for PMY and WW. Maximizing net return on assets should be the goal of all beef producers. Increasing calf-weaning weight while lowering cow maintenance costs and increasing rebreeding rates would be expected to improve net return on assets for cow-calf producers.

Key Words: Beef Cattle, Genetics, Weaning Weight

34 Germplasm evaluation in beef cattle: Cycle IV: Post weaning growth and feed efficiency. G. D. Snowden*¹, L. V. Cundiff¹, R. M. Koch², and K. E. Gregory¹, ¹USDA, ARS, USMARC, Clay Center, NE, ²University of Nebraska, Lincoln, NE.

Breed effects on post weaning growth and feed efficiency traits were compared on 785 F1 crossbred steers out of Angus or Hereford dams and sired by Angus, Charolais, Galloway, Hereford, Longhorn, Nellore, Piedmontese, Salers, or Shorthorn bulls. Steers averaged about 155 d of age at weaning across years (1986 to 1990). Post weaning traits were observed on steers fed within sire breed group in two to three replicated pens per year for approximately 272 d. Steers were slaughtered serially in three or four slaughter groups spanning 56 to 63 d. Quadratic regressions of pen mean weight on days fed and of cumulative metabolizable energy consumption (ME) on days fed were used to estimate gain, ME consumption and efficiency (Mcal ME/kg gain) over time (0 to 226 d on feed) and weight (250 to 500 kg) intervals, and from d 0 to a small degree of marbling and to a 21.6% fat trim end point. Data were analyzed by least squares, mixed model procedures and linear regression to derive contrasts at age-constant, weight-constant, marbling end point, and fat end point. On a time and age constant basis, Charolais and Shorthorn sired crosses were faster growing than other breed types. Growth rates of Longhorn, Galloway, and Nellore-sired crosses were slower compared to other breed types. Rank of sire breeds changed significantly when marbling and percent fat trim end points were considered. Growth rate of Shorthorn-sired crosses to the marbling end point was the slowest. Growth rate of Piedmontese-sired crosses was the fastest to the fat trim end point. Feed efficiency in age and weight constant intervals was highest in Charolais crosses; and lowest in Piedmontese, Nellore, and Longhorn sired crosses. At a marbling or fat trim end point, rank of feed efficiency for Charolais crosses decreased significantly while the rank of Hereford-Angus crosses significantly improved. Breed rankings varied depending on end points.

Key Words: Breed, Biological Type, Marbling

35 Validation of a genetic algorithm for identification of livestock for germplasm preservation. L. L. Melton*¹, P. J. Lamberson², R. A. Breneman³, C. C. Chase, Jr⁴, and W. R. Lamberson¹, ¹University of Missouri-Columbia, ²Columbia University, New York, ³Omaha's Henry Doorly Zoo®, ⁴USDA, ARS, Sub Tropical Agricultural Research Station (STARS), Brooksville, FL.

As livestock production intensifies, a loss of genetic diversity has been observed because of increased use of a few breeds to the exclusion of many others. To preserve diversity the USDA has initiated a program of germplasm preservation through freezing semen. An algorithm to identify least-related animals using pedigree relationships has been developed. Preliminary testing of the algorithm showed that mean relationships between selected animals increased as the proportion of animals preselected increased. In order to test the efficacy of the algorithm in maintaining genetic diversity, data from a pedigreed population of Romosinuano cattle genotyped for 28 microsatellite markers was evaluated. The proportion of total alleles in the population that were maintained in the samples identified for preservation was calculated and comparisons made among methods of identification. An index calculated by summing the inverse of frequencies of all alleles for each individual was determined and animals were ranked on the index. When initiated with a single random seed and 25% of the population was identified by the algorithm for selection, 85% of the alleles in the population were captured in the selected sample. When 40% of the population was selected, the proportion of alleles captured increased to 89%. However, when identifying 25% and the single seed used to initiate the algorithm was the highest indexing animal, 88% of the alleles in the population were captured. When identifying 40% and the single seed used to initiate the algorithm was the highest indexing animal, 93% of the alleles in the population were captured. Additional testing is needed to establish how the algorithm performs with multiple seeds. The algorithm has been used to evaluate the Hereford Swine Association Registry to identify boars for germplasm preservation.

Key Words: Genetic Diversity, Germplasm Preservation, Swine

36 Accuracy of detecting quantitative trait loci by selective DNA pooling. J. Wang*¹, J. Fulton², and J. Dekkers¹, ¹Iowa State University, Ames, ²Hy-Line International, Dallas Center, IA.

Selective DNA pooling is considered an efficient method to detect quantitative trait loci (QTL) but is subject to errors inherent to the creation and evaluation of pools. The objective of this study was to compare QTL detection results using DNA pooling data vs. results using individual genotyping in an F2 family of layer chickens. A total of 192 F2 females from 11 full-sib families were generated by crossing two commercial pure lines. High and low pools were generated for each of 12 egg production traits by pooling DNA from the top and bottom 20% of progeny ranked by BLUP EBV. High and low pool allele frequencies were estimated for a total of 184 microsatellite markers across the entire genome. A Chi-square test for frequency differences was used to identify markers associated with the QTL. Two chromosomes with significant QTL for some traits were chosen for further analysis using individual genotyping of the entire family by least squares regression interval mapping. On these two chromosomes, 22 markers were used for DNA pooling. These, plus 23 additional markers were used for individual genotyping. Individual genotyping resulted in very similar results as DNA pooling despite the larger number of markers genotyped and analysis of the whole family instead of pools of the tails. Graphs of comparison-wise p values (P) across the chromosome were similar for both methods. The correlation between the Chi-square and the F test values based on $\log_{10}(1/P)$ was 0.7 across traits. At $P < 0.01$, a total of 8 QTL were detected for the 12 traits using individual genotyping. Five of these QTL were also significant at $P < 0.01$ using DNA pooling data. Of the 6 QTL detected at $P < 0.01$ with DNA pooling, one was not found using individual genotyping. In conclusion, selective DNA pooling data is extremely useful in capturing most of the information for QTL detection with a reduction in genotyping costs of approximately 100 fold compared with individual genotype data.

Key Words: QTL Mapping, Selective DNA Pooling