feedlot traits based on economic considerations of the production system is important to achieving improved feedlot performance to constant finish.

Key Words: Feed Efficiency, Beef Cattle, Heritability

893 Predicting breeding values for feed intake from individual or pen-fed data. K. M. Olson*, D. J. Garrick, and R. M. Enns, *Colorado State University, Fort Collins*.

The objective of this study was to determine the reduction in accuracy of breeding values when pen-fed rather than individual observations on feed intake (FI) were used. The simulated data set consisted of 1,000 animals with true breeding values (BV) and phenotypes for FI (heritability of 0.34) representing 49 sires and 200 maternal grandsires (MGS). Three approaches were compared to predict breeding values for FI (EBV). The first approach was animal model BLUP (IAM) using 1,000 individual FI records. The second approach used 500, 250 or 100 combined FI observations on pens of i=2, 4 or 10 animals (PAM_i). The residual variance was modified to account for the number of animals contributing to each pen FI observation. The third approach (IPM_i) allocated each animal in the pen the average of the pen FI and incorrectly treated that as a unique FI observation in animal BLUP. Correlations were determined between the BV and EBV for each approach, separately for animals with data, sires and MGS. Correlations were 0.633 for animals, 0.767 for sires and 0.266 for MGS using IAM. These correlations are consistent with expectations based on the heritability and amount of information available. Correlations for animals reduced to 0.532 (PAM_2), 0.470 (PAM_4) and 0.371 (PAM_{10}). Corresponding reductions were 0.774, 0.744, 0.619 for sires and 0.225, 0.107, 0.003 for MGS. When penned animals were treated as if they had individual FI the correlations were 0.531 (IPM_2), 0.465 (IPM_4), 0.365 (IPM_{10}) for the animals, 0.776, 0.742, 0.624 for sires, and 0.218, 0.097, 0.002 for MGS. The reduction in accuracy with penning is consistent with the reduction in available data. The correlations were almost identical whether BLUP was correctly accounting for penning (PAM_i) or allocating pen averages to each individual (IPM_i). The apparent accuracy computed from the coefficient matrix was overstated in IPM_i. Pen data can be effectively used in BLUP analyses when individual FI is not available. Correct account of pen information is recommended for reporting accuracy of EBV.

Key Words: BLUP, Accuracy, Animal Model

894 The use of ultrasound to evaluate growth and carcass quality in Nelore cattle. F. R. C. Araujo[1,2], F. Manicardi[3], J. R. Hofig Ramos[4], C. U. Magnabosco[5,1], T. R. Famula[1], and R. D. Sainz*[1], [1]*University of California, Davis,* [2]*Aval Servios Tecnológicos S/S, Uberaba, MG, Brasil,* [3]*Grupo OMB, Pontes e Lacerda, MT, Brasil,* [4]*Grupo HoRa, Cornélio Procópio, PR, Brasil,* [5]*Embrapa Cerrados, Bolsista CNPq Brasilia, DF, Brasil*.

This study was carried out to support the development of expected progeny differences (EPD) for carcass traits in Nelore cattle raised under tropical grazing systems. Data from 1,721 bulls and heifers raised in central Brazil (Grupo OMB and Grupo HoRa) were collected at approximately 15, 18, 21 and 24 months of age. The animals were weighed (BW) and scanned for longissimus muscle area (ULMA); backfat thickness between the 12th and 13th ribs (UFAT); and fat thickness over the rump (URFAT), at the P8 site. Mean (and SD) scan data were: Age, 19 (SD = 2.6) months; BW, 321 (SD = 58) kg; ULMA, 47.80 (SD = 8.85) cm^2; UFAT, 1.5 (SD = 0.62) mm; URFAT 2.0 (SD = 0.97) mm. Data were analyzed using a mixed model. Fixed effects were age in months (AGEm), month of scanning (MONTH), contemporary group (including management group; CGxMG). The interaction between AGEm and MONTHSCAN was used to test the slopes for homogeneity, and the individual animal within contemporary and management group was included to account for repeated measures on the same animal. A large portion of observed variance in response variables was accounted for by GCxMG and AGEm ($P < 0.001$). Month of scanning (i.e., season) had no effect on BW or ULMA ($P > 0.05$) when the contemporary and management groups were properly accounted for. UFAT was not significantly influenced by MONTH or by AGEm ($P > 0.05$), nor was there any significant AGEm x MONTH interaction. By contrast, URFAT was significantly affected by AGEm ($P < 0.01$), indicating that it is a more sensitive fat deposit. The repeatabilities of measurements were very low for UFAT (0.035) but high for URFAT (0.62) and moderate for ULMA (0.44). Nelore cattle raised on tropical pastures exhibit growth patterns and carcass compositions that are very different from those observed in *Bos taurus* cattle raised on high-concentrate diets, but once the contemporary group and management were accounted for, seasonality had no effect on carcass traits and body weight.

Key Words: Beef Cattle, Carcass, Ultrasound

Breeding and Genetics: Swine

895 Validation of QTL's in a swine population selected for ovulation rate. M. R. Mousel*, G. A. Rohrer, K. A. Leymaster, and R. K. Christenson, *U.S. Meat Animal Research Center, USDA-ARS, Clay Center, NE*.

Variations in allele frequency of a four-breed, white composite population of swine selected for ovulation rate (OR) were evaluated. Animals were selected for 11 generations for increased OR and compared to unselected controls (CO). The selection line had an increase of 3.0 corpora lutea and an increase of 0.3 pigs in total litter size as compared to controls. DNA was collected from 146 CO and 156 OR gilts and boars at generations 10 and 11. A QTL analysis for OR identified loci on chromosomes 3, 8, and 10 in a Meishan-White composite population. Three microsatellite markers were selected for chromosomes 3 (17-42 cM) and 10 (85-96 cM) and six for chromosome 8 (1-13 cM) for utilization with selected and control lines. Allele frequencies of markers contained within QTL peaks were analyzed by logistic regression to ascertain any difference in allele frequency due to selection. All markers on chromosome 3 had significant ($P<0.01$) changes between lines in allele frequency. Odds ratio of the most significant marker ($P<0.0001$), SW2429 contained 7 distinct alleles, the 125 base allele was 530.2 times more likely to be present in homozygous OR animals than CO. Chromosome 8 had 3 of 6 markers with significant ($P<0.02$) changes in allele frequency. The marker SW2651, which contained 3 alleles, was most significant ($P<0.0001$) with an odds ratio of 2.6 for the 100 base allele in homozygous OR animals. Significant ($P<0.01$) changes in allele frequency were found on chromosome 10 with all markers. An odds ratio of 7.3 was calculated for the 107 base allele in homozygous OR animals for the most significant ($P<0.0001$) marker SWR1829 which had 8 alleles. Selection for OR has changed the allele frequency of markers from the three QTL regions studied. The QTL discovered in a Meishan cross population are likely segregating in occidental germplasm. The selection line will be useful to identify causative genes and genetic markers for use in the industry.

Key Words: Swine, Ovulation Rate, Allele Frequency

896 Identification of quantitative trait loci affecting reproduction and early growth in pigs. J. Holl*[1], J. P. Cassady[2], D. Pomp[1], and R. K. Johnson[1], [1]*University of Nebraska, Lincoln,* [2]*North Carolina State University, Raleigh*.

Quantitative trait loci (QTL) in a 3-generation population of a cross of low-indexing pigs of a randomly selected control line with high-indexing pigs of a line selected 10 generations for increased index of ovulation rate and embryonic survival were investigated. Birth weight (BWT, n = 428), weaning weight (WWT, n = 405), age at puberty (AP, n = 295), ovulation rate (OR, n = 423), number of fully formed pigs (FF, n = 370), number of pigs born alive (NBA, n = 370), number of mummified pigs (MUM, n = 370), and number of stillborn pigs (NSB, n = 370) were collected in F_2 females. Grandparent, F_1, and F_2 animals were genotyped for 151 microsatellite markers. Previous analyses with single Mendelian QTL models identified 16 putative QTL ($P < 0.10$). Data were reanalyzed with composite interval mapping (CIM) including models incorporating genomic imprinting. More QTL for reproductive traits than in the earlier scan (31 vs 16, $P < 0.10$) and two QTL for birth weight were identified. Mendelian QTL affected **FF** (C11, 52 cM, $P < 0.05$), **NBA** (C11, 71 cM, $P < 0.05$), **NSB** (C13, 100 cM, $P < 0.05$; C5, 131 cM, $P < 0.10$; C12, 37 cM, $P < 0.10$), **NN** (C11, 47 cM, $P < 0.05$; C8, 20 cM, $P < 0.05$; C7, 62 cM, $P < 0.05$), **AP** (C8, 172 cM, $P < 0.05$; C7, 1 cM, $P < 0.05$; C7, 58 cM, $P < 0.10$; C18, 40 cM,

P < 0.10; C8, 101 cM, P < 0.10; C8, 136 cM, P < 0.10; C12, 56 cM, P < 0.10), **MUM** (C12, 98 cM, P < 0.10; C12, 70 cM, P < 0.05; C2, 6 cM, P < 0.10; C6, 64 cM, P < 0.10; C6, 165 cM, P < 0.10), and **BWT** (C12, 17 cM, P < 0.10). Partially imprinted QTL affected **OR** (C9, 1 cM, P < 0.01), **BWT** (C6, 155 cM, P < 0.05), and **MUM** (C6, 81 cM, P < 0.05). Paternally imprinted QTL affected **NN** (C6, 85 cM, P < 0.05; C6, 171 cM, P < 0.10; C15, 64 cM, P < 0.10; C15, 109 cM, P < 0.10), **AP** (C15, 98 cM, P < 0.05), and **MUM** (C6, 191 cM, P < 0.10). Maternally imprinted QTL affected **NSB** (C14, 104 cM, P < 0.10), **NN** (C1, 155 cM, P < 0.10), and **MUM** (C2, 29 cM, P < 0.10). Power to detect QTL with small effects increases with CIM with imprinting compared to single QTL models.

Key Words: Pigs, Imprinting, Quantitative Trait Loci

897 Mapping genes affecting scrotal hernia condition in domestic pigs. F.-X. Du*, N. Mathialagan, C. J. Dyer, M. D. Grosz, L. A. Messer, A. C. Clutter, T. Wang, M. M. Lohuis, and J. C. Byatt, *Animal AG Monsanto Company*.

Scrotal hernia (SH) is a congenital defect that results from protrusion of part of the intestine through the abdominal opening of the inguinal canal and into the scrotum. The SH condition is affected by both genetic and environmental factors; however, the effect of ill-defined environmental factors and plausible involvement of multiple genes with likely incomplete penetrance complicate attempts to identify genetic determinants. To map SH genes, a whole genome scan (using microsatellite markers) was performed using 7 independent SH-affected paternal families from 3 commercial pig lines. An identity-by-descent based nonparametric linkage analysis of this dataset identified 3 chromosomes with suggestive statistical evidence for segregation of SH genes. Twenty-seven additional paternal SH families with 2 SH piglets were genotyped for 33 microsatellite markers on these 3 chromosomes, and the subsequent linkage analysis provided additional suggestive statistical evidence for 2 chromosomes: SSC2 and SSC12. Subsequently, an approximately 50 cM chromosomal region on SSC2 and a number of candidate genes from SSC2 and SSC12 were selected. Sequencing a panel of 24 animals identified multiple polymorphic single nucleotide polymorphisms (SNP) in both candidate genes and anonymous sequences derived from bacterial artificial chromosomes mapping to the targeted SSC2 region. Ultimately, 137 polymorphic SNP assays (107 on SSC2 and 30 on SSC12) were validated. Approximately 2,000 animals (sires, affected or unaffected offspring) of 143 paternal families (with at least 1 affected progeny or at least 80 progeny all absent of SH) from Pietrain sires were genotyped for all 137 SNP markers. Linkage disequilibrium analyses of this dataset provided additional statistical evidence for segregation of genes affecting SH on both SSC2 and SSC12, and helps to refine the map of SH genes and to identify associated candidate genes.

Key Words: Scrotal Hernia, Nonparametric Linkage Analysis, Linkage Disequilibrium Mapping

898 Prospecting for pig SNPs in the human genome: have we struck gold? L. Grapes*[1], S. Rudd[2], R. Fernando[1], K. Megy[3], D. Rocha[3], and M. Rothschild[1], [1]*Iowa State University, Ames,* [2]*Institute for Bioinformatics, GSF-National Research Center for Environment and Health,* [3]*University of Cambridge, Cambridge, UK*.

With increasing interest in performing genome-wide association studies in livestock, rapid identification of genetic markers is becoming a necessity. Single nucleotide polymorphism (SNP) discovery in pigs could be increased using in silico methods. In addition, if closely related species have similar SNP frequencies in their coding regions, SNP discovery in pigs could be increased by screening pig coding regions that are homologous to SNP-dense human coding regions. To test this hypothesis, we identified pig SNPs in silico. All porcine expressed sequence tags (ESTs) were downloaded from EMBL (www1.embl-heidelberg.de) and clustered. Clusters containing 8 or more ESTs were analyzed using the SNiPper algorithm, which assigns a score to a deviation within an EST relative to the consensus sequence. Of the clusters containing 8 or more ESTs, 452 contained at least one putative, high-scoring SNP, totaling 1,394 SNP loci. From these SNPs, 231 were located to the coding regions of 80 porcine genes or hypothetical proteins. Using pig coding SNPs (cSNPs) from 25 of these genes and validated human cSNPs from dbSNP (www.ncbi.nlm.nih.gov/SNP) in homologous genes, the correlation between the gene-specific frequency of human and pig cSNPs was high (0.77; P < 0.00001) given stringent parameters used to identify pig SNPs in silico. This human-pig correlation represents a lower bound of the true correlation due to false-positive and false-negative results known to occur with in silico SNP detection methods. Using validated mouse and human cSNPs from dbSNP in 50 homologous genes, the correlation between the gene-specific frequency of human and mouse cSNPs was only moderate (0.48; P < 0.0005). These results follow the expectation that closely related species have similar mutation frequencies within their coding regions, which could be attributed to their high level of sequence identity. From 15 porcine in silico SNPs, 9 (60%) have been experimentally validated, indicating that EST-based in silico methods will increase the rate of SNP discovery in pigs. Also, the high human-pig correlation indicates that comparative methods can be used to capitalize on the large supply of human SNP information for rapidly identifying cSNPs in pigs.

Key Words: SNP, Pigs, Bioinformatics

899 An evaluation of performance and carcass characteristics between pigs sired by boars from two different time periods. C. R. Schwab*, T. J. Baas, D. W. Newcom, and K. J. Stalder, *Iowa State University, Ames*.

This study was conducted to evaluate differences in performance and carcass traits between pigs sired by boars currently available and pigs sired by boars from the mid 1980's. Two lines were developed by splitting and randomly allocating littermate and $\frac{1}{2}$ sib pairs of females for mating to current (CTP) or old (OTP) time period boars. Matings by CTP boars were made using fresh semen and matings by OTP boars were made using frozen semen. Subsequent boar, barrow, and gilt progeny from two replications were weighed on test at a mean pen weight of 39.8 kg. Off test ultrasonic measurements of 10th rib loin muscle area (LMA), backfat (BF10), and intramuscular fat percentage (IMF) were collected on a total of 789 pigs at a mean pen live weight of 109 kg. Records on pigs sired by CTP boars (n=556) were from 23 sires while pigs sired by OTP boars (n=231) were from 15 sire groups. All available barrows and randomly selected gilts (n=277) were then sent to a commercial abattoir and measurements of tenth-rib backfat (CBF10), last rib backfat (CLRBF), last lumbar backfat (CLLBF), and loin muscle area (CLMA) were collected. Time period differences were assessed by the use of a mixed model that included fixed effects of sire time period, replication, sex, contemporary group, and the interaction of sex by time period. Sire and dam nested within time period were included as random effects. There was no difference in average daily gain or adjusted days to 113.5 kg between the two time periods; however, pigs sired by CTP boars had significantly greater lean gain per day on test. Pigs sired by CTP boars had larger (P<0.05) LMA measurements and less BF10, while pigs sired by OTP boars had significantly more IMF. Carcass evaluation revealed more CLMA, and significantly less CBF10, CLRBF, and CLLBF for pigs sired by CTP boars when compared to pigs sired by OTP boars.

Key Words: Swine, Performance, Carcass

900 Characterization of a line of pigs selected for increased litter size for two RFLPs identified in *follistatin*. C. D. Blowe*, E. J. Eisen, O. W. Robison, and J. P. Cassady, *North Carolina State University, Raleigh*.

The objective of this study was to characterize changes in allelic frequencies for two RFLPs associated with the *follistatin* gene in a line of pigs selected for increased litter size (LS). The LS line was selected for increased number of fully formed pigs, and litters were standardized at birth so replacement gilts were reared in litters of ten or fewer pigs. A contemporary control line (C) was maintained. In generation nine, estimated mean breeding values for litter size differed between lines by 0.63 pigs (P < 0.01). *Follistatin*, a cysteine-rich glycoprotein encoded by a single gene, was investigated. Based on expression patterns and implications from studies involving *follistatin* function, it can be concluded that *follistatin* may play an important role in determining litter size. Intronic regions were amplified using PCR, and two different RFLPs, characterized by *Msp*I *(FS1)* and *Fnu*4HI *(FS2)*, were identified. Frequencies of the B allele of *FS1* increased in LS, and allele frequencies differed between LS and C by 0.25 and 0.18 in generations 10 and 11, respectively. The change in allele frequency for *FS1* differed from 0 in generations 10 (P < 0.01) and 11 (P < 0.057). Standard errors were adjusted to determine if random drift could be excluded as the cause of

changes in allele frequency, and differences were retested (P < 0.29) and (P < 0.31), respectively. Results for *FS2* were similar to those of *FS1*. The additive effect of the B allele of *FS1* on estimated breeding value for pigs born live in LS (n = 207) was +0.09. Marker-assisted selection has the potential to be highly advantageous in selection for lowly heritable and sex-limited traits, such as litter size. Changes in allele frequency to the exclusion of random drift were not detected; however, sufficient evidence exists to support further investigation of *follistatin* as a candidate gene for litter size in pigs.

Key Words: Pigs, Reproduction, Selection

901 Detection of quantitative trait loci for growth, carcass, and meat quality traits in a Pietrain x (Large White × Landrace) line cross. N. Vukasinovic*[1], F.-X. Du[1], L. A. Messer[1], J. C. Byatt[1], M. M. Lohuis[1], A. C. Clutter[1], J. Bennewitz[2], N. Reinsch[2], G. Otto[2], K. Sanders[2], N. Borchers[2], C. Looft[2], and E. Kalm[2], [1]*Animal AG Monsanto Company,* [2]*Institute of Animal Breeding and Husbandry, Christian-Albrechts University of Kiel, Germany.*

An analysis of quantitative trait loci (QTL) affecting growth, carcass and meat quality traits in swine was conducted on an F2 population created by crossing Pietrain boars with Large White × Landrace hybrid sows at Christian-Albrechts University of Kiel, Germany. Four F1 sires were repeatedly mated to 33 full-sib F1 sows to produce 1014 F2 offspring. All F0, F1, and F2 animals were genotyped for 27 microsatellite markers on chromosomes 2, 6, and 7. Data on eight growth traits (weights and daily gains at various ages), 16 carcass traits (hot carcass and ham weights and percentages, carcass length, loin eye area, and various fatness measurements), and seven meat quality traits (pH, meat color, and conductivity) were analyzed using line cross (LC) and half-sib family (HS) regression methods. LC analysis revealed very strong evidence (P < 0.001) of QTL for daily gain, hot carcass weight, and fatness traits (backfat thickness, abdominal fat, loin fat area, meat:fat ratio, and lean percentage) located near the proximal end of chromosome 2. Chromosome 2 also carried a significant QTL (P<0.001) at 34cM for meat reflectance. The significant QTL in the proximal region of chromosome 2 were imprinted. There was a very significant QTL (P<0.001) affecting carcass length around 90cM on chromosome 7. HS analysis of four large paternal families (each with 250 offspring) was performed to detect QTL segregating within the lines. HS analysis confirmed the QTL found by LC analysis. Additional significant QTL (P<0.01) were found on chromosome 2 for ham weight and ham percentage at 2cM, and for loin pH at 113cM. There was suggestive evidence (P<0.05) of several QTL affecting daily gain and fatness traits on chromosomes 6 and 7. These results indicate that some QTL segregate within, rather than between the lines.

Key Words: QTL Mapping, Line Cross, Half-Sib Analysis

902 An evaluation of meat and eating quality traits between pigs sired by boars from two different time periods. C. R. Schwab*, T. J. Baas, D. W. Newcom, and K. J. Stalder, *Iowa State University, Ames.*

This study was conducted to evaluate differences in meat and eating quality traits between pigs sired by boars currently available and pigs sired by boars from the mid 1980's. Two lines were developed by splitting and randomly allocating littermate and $\frac{1}{2}$ sib pairs of females for matings by current (CTP) or old (OTP) time period boars. Matings by CTP boars were made using fresh semen and matings to OTP boars were made using frozen semen. Subsequent boar, barrow, and gilt progeny from two replications were weighed off test at a mean pen weight of 109 kg. All available barrows and randomly selected gilts were sent to a commercial abattoir and used for meat and eating quality evaluation. Records on pigs sired by CTP boars (n=178) were from 23 sires while pigs sired by OTP boars (n=98) were from15 sire groups. Chemical intramuscular fat percentage was determined by lab analysis of a sample from the loin at the 10th rib. Additional meat and eating quality traits measured were: Minolta reflectance and Hunter L color (24 and 48 h); pH (24 h and 7 d); water holding capacity and subjective visual scores for color, marbling, and firmness (48 h); Instron tenderness, cooking loss, and trained sensory panel evaluations (7 d). Time period differences were assessed by the use of a mixed model that included fixed effects of sire time period, replication, sex, contemporary group, and the interaction of sex by time period. Sire and dam nested within time period were included as random effects. Pigs sired by OTP boars had a greater (P<0.05) intramuscular fat percentage and higher subjective marbling and color scores than pigs sired by CTP boars. There were no differences between time periods for the evaluations of Minolta reflectance, Hunter L (24 and 48 h), water holding capacity, Instron tenderness, pH (24 h and 7 d), or subjective firmness scores. Trained sensory evaluations revealed higher (P<0.05) flavor scores and lower off-flavor scores for OTP sired pigs; however, no differences in tenderness score, juiciness score, chewiness score, or cooking loss were found between the two lines.

Key Words: Swine, Meat Quality, Eating Quality

903 Growth and carcass composition in pig lines divergently selected for testosterone production and their crossbred progeny. J. M. Bender* and J. P. Cassady, *North Carolina State University, Raleigh.*

The objective of this study was to characterize growth and carcass composition in two Duroc lines of pigs divergently selected 10 generations for testosterone production and then maintained by random within line selection. In generation 21 endogenous testosterone production in the high (HTL) and low (LTL) testosterone lines averaged 49.0 ng/ml and 27.8 ng/ml (P < 0.01), respectively. Eight LTL and 10 HTL boars were used to create 29 LTL and 33 HTL litters. These same boars were mated to a common line of white composite (WC) females to generate 11 WC by LTL litters (WLT) and 23 WC by HTL litters (WHT). Barrows and gilts were then selected LTL (n=55), HTL (n=61), WLT (n=102), and WHT (n=101) for testing. Pigs were weighed and scanned using real-time ultrasound 48 h prior to one of two slaughter dates. Data were analyzed with a mixed model including fixed effects of genetic group, slaughter date, sex, and random effect of sire nested within line. All possible interactions among fixed effects were tested. Traits analyzed included days to 114 kg (D114), average daily gain (ADG), back fat adjusted to114 kg (BF114), loin eye area adjusted to 114 kg (LEA), predicted percent lean (%LEAN) and marbling 24 h post-mortum. Lines did not differ for LEA. The HTL had fewer D114 (P < 0.011), greater ADG (P < 0.004), greater BF114 (P < 0.001), and lower %lean (P < 0.001) than LTL. For crossbred progeny WHT had greater ADG (P < 0.010) and greater BF114 (P < 0.025) than WLT and tended to have fewer D114 (P < 0.068) and lower %lean (P < 0.08) than WLT. Least square means for marbling score for HTL, LTL, WHT, and WLT were 3.63, 3.61, 3.03, and 3.03, respectively. Pure line progeny were more highly marbled than crossbred progeny (P < 0.01). Pigs selected for increased testosterone production grew faster and produced fatter carcasses than pigs selected for decreased testosterone. Because of their high marbling scores these lines may be useful in developing premium products.

Key Words: Growth, Carcass Composition, Pigs

904 Detection of quantitative trait loci segregation within pure breeds in a Berkshire x Yorkshire F_2 population. H. Zhao*[1], J.-J. Kim[1], M. Perez-Enciso[2], and J. C. M. Dekkers[1], [1]*Iowa State University, Ames,* [2]*Universitat Autonoma de Barcelona, Spain.*

Segregation of quantitative trait loci (QTL) within commercial breeds is of great interest because most marker-assisted selection is implemented within breeds. The objective here was to implement a variance component analysis method to detect and characterize QTL in an F_2 cross between two Berkshire grand sires and nine Yorkshire grand dams with data on 525 F_2 progeny. A model that combines fixed between-breed and random within-breed QTL effects and random polygenic effects was used to analyze back fat traits on chromosomes 7 and 12. These chromosomes were partitioned into segments based on previous results from QTL mapping using least squares regression: 0-35, 35-65, 65-95, 95-125 and 125-138 cM for chromosome 7, and 0-45, 45-80 and 80-96 cM for chromosome 12. For each segment, identity by descent probabilities were obtained by a Monte Carlo Markov Chain algorithm. Each segment was first tested separately for presence of a QTL effect, by comparing the full model with a model with only the polygenic effect, and for segregation of the QTL within the parental breeds, by dropping the variance of the segment. All significant segments were then fitted in a full model and tested vs. a reduced model where the effects of one segment were dropped. For chromosome 7, segments 35-65 cM and 95-125 cM had significant (p<0.05) effects on average backfat, tenth rib backfat and lumbar backfat. The variance of segment 35-65 cM was significant for average backfat and lumbar backfat. Both fixed and random effects were significant for segment 65-95 cM for last rib backfat. For chromosome

12, segment 0-45 cM was significant for average backfat and last rib backfat without significant variance. In conclusion, multiple and segregating QTL were detected for backfat traits on chromosome 7 and QTL was detected on one segment on chromosome 12. The variance component approach is a useful method to detect QTL in crosses between outbred breeds and to identify those that segregate within breeds.

Key Words: QTL, Segregation, Variance Component Analysis

905 PACE: An integrated pig genome database. J. W. M. Merks*[1], T. J. A. van Kampen[2], R. van Wijk[1], B. Harlizius[1], A. Rattink[3], G. Albers[3], and M. A. M. Groenen[2], [1]*IPG, Institute for Pig Genetics BV, Beuningen, The Netherlands,* [2]*Department of Animal Sciences - Animal Breeding and Genetics Group, Wageningen University and Research Centre, Wageningen, The Netherlands,* [3]*Nutreco Breeding Research Centre, Boxmeer, The Netherlands.*

Knowledge of farm animal genomes has increased enormously over the last decade. A large part if this information is publicly available for a variety of species and through specific databases such as for pigs; PiGBASE for mapping data, Pig EST Database, TIGR SsGI for genes and data on their expression patterns and the INRA Comparative and Cytogenetic mapping home pages. Potentially these databases provide comprehensive public repositories for genome research. However, these data are difficult to combine from the different sources or with private data, but also with genome data of model organisms. This strongly hinders comparative mapping and positional fine-mapping. A new pig genome database - PACE was set up in the Netherlands to enable integration of data from the different sources. For this, the widespread database system of AceDB has been adapted and links with existing farm animal databases but also databases like LocusLink, Genbank, MGI, GeneCards are included to facilitate an efficient comparative mapping with human and mouse. In addition published information on porcine QTL has been included. This database with more than 5000 genetic markers and loci and about 500 QTL's will be available publicly from July 2004.

Key Words: Pigs, Genome Map, Database

906 Estimation of genetic parameters for farrowing mortality, litter size and test performance of first parity Large White sows. J. Arango*[1], I. Misztal[1], S. Tsuruta[1], M. Culbertson[2], and W. Herring[2], [1]*University of Georgia, Athens,* [2]*Smithfield Premium Genetics, Roanoke Rapids, NC.*

Selection to increase prolificacy and performance traits may be affecting piglet survivability at different production stages. To investigate this complex of traits, genetic correlations were estimated among total born (TB), number born alive (BA) and number of pigs born dead (PD) from 47,454 first-parity Large White sow records. Data were from 22 pure-line farms. Additional performance data (n=30,832) were available for ultrasound backfat (BF) at end of the test, and days to reach 113.3 kg (AD). Univariate, all pair-wise bivariate, and four sets of trivariate (TB-PD-AD, TB-PD-BF, BA-PD-AD and BA-PD- BF) analyses were carried out using AI-REML. Models included the fixed effects of contemporary group (farm-farrowing year- farrowing month for litter traits and batch-sex-farm-barn for test traits). Analysis of BF included measurement weight as linear and quadratic covariates. Random effects of animal additive genetic and residual error were also included. Estimates of heritability averaged over analyses were 0.09, 0.08, 0.06, 0.37 and 0.31 for TB, BA, PD, AD and BF, respectively, and were similar across individual analyses. Estimates of genetic correlations averaged over analyses were 0.94, 0.39, 0.03, -0.02 for TB-BA, TB-PD, TB-AD and TB-BF; 0.02, 0.08 and 0.06 for BA-PD, BA-AD and BA-BF; -0.13 and -0.21 for PD-AD and PD-BF, and -0.23 for BF-AD, respectively. The genetic relationship of PD with TB was moderate and positive while negative with AD and BF. Response to selection for increasing litter size may increase piglet mortality at birth. Intense selection for faster growth and increased leanness may increase piglet mortality from first parity sows in this population.

Key Words: Swine, Farrowing Mortality, Litter Size

907 Comparison of deposition rates for loin muscle area, backfat, and intramuscular fat percentage among breeds in the 2003 National Barrow Show Sire Progeny Test. B. D. Martin*, T. J. Baas, C. Schwab, D. W. Newcom, J. F. Lampe, and K. J. Stalder, *Iowa State University, Ames.*

Weights and serial ultrasonic measurements of 10^{th} rib loin muscle area (LMA), 10^{th} rib backfat (BF), and intramuscular fat percentage (IMF) were used to assess deposition rates and growth patterns of purebred pigs entered in the National Barrow Show Sire Progeny Test. Yorkshire (30), Duroc (71), Chester White (49), and Berkshire (154) barrows and gilts were weighed and scanned for LMA, BF, and IMF every two weeks beginning at a live weight of approximately 68 kg. Off test ultrasonic measurements were taken at approximately 109 kg. Five scans were taken on each animal. At each scan period, BF, LMA, and IMF were analyzed with a mixed model that included fixed effects of breed, sex, contemporary group, and the interaction of breed by sex. Sire and dam within breed were included as random effects. Weight at each scan period was included as a linear covariate. Deposition rates were calculated for LMA, BF, and IMF using intra-pig linear and quadratic regressions for the independent variable live weight. Intra-pig linear and quadratic regression coefficients and y-intercepts were analyzed as dependent variables in a mixed model that included fixed effects of breed, sex, contemporary group, and the interaction of breed by sex. Across all scans, Yorkshires and Durocs were significantly leaner than Berkshires, and gilts were leaner than barrows. At scans 3, 4, and 5, Durocs were significantly leaner and had more ($P<0.05$) LMA than Chester Whites. Durocs had more ($P < 0.05$) LMA than Yorkshires and Berkshires at all five scan periods. Chester White pigs had the largest linear regression coefficient for LMA and the smallest y-intercept. Mean deposition rates for IMF were not significantly different between breeds. Gilts had more ($P < 0.05$) LMA than barrows at periods 3, 4, and 5. Barrows had more ($P < 0.05$) IMF than gilts at scan intervals 2, 3, 4, and 5. Quadratic regression coefficients for BF were significantly different between barrows (-0.00002) and gilts (-0.00001).

Key Words: Swine, Ultrasound, Regression

Nonruminant Nutrition: Feed Ingredients & Management

908 Effect of whey and lactose source on nursery pig performance. A. M. Gaines*, B. W. Ratliff, P. Srichana, and G. L. Allee, *University of Missouri, Columbia.*

A 25 d growth assay experiment was conducted to determine the effects of whey and lactose source on nursery pig performance. At weaning, a total of 276 pigs (TR-4 × C22; 5.8 ± 0.03 kg) reared in a commercial research facility were fed one of two diets containing spray-dried whey and crystalline lactose or granular whey and Dairy Lac 80®. Pigs were housed 23 pigs per pen and fed in three dietary phases. Each diet contained the same inclusion of whey and other specialty ingredients. Diets were formulated to be lactose equivalent with additional lactose being added from crystalline lactose in the spray dried whey diets or Dairy Lac 80® in the granular whey diets. For the phase 1 period (0-7 d), phase 2 period (7-14 d), and phase 3 period (14-25 d) the level of inclusion of whey in the diets was 20.0%, 10.0%, and 0.0%, respectively. A whey source was not included in phase 3; however, both the spray-dried and granular whey treatments did contain 7% lactose derived from crystalline lactose or Dairy Lac 80®, respectively. During the Phase 1 period there was no effect of whey and lactose source on ADG ($P = 0.91$), ADFI ($P = 0.29$), or G/F ($P = 0.54$). Similarly, there was no effect of whey and lactose source on ADG ($P = 0.57$), ADFI ($P = 0.37$), or G/F ($P = 0.63$) during the Phase 2 period. However, during the Phase 3 period pigs fed Dairy Lac 80® had improved ADG ($P = 0.07$) as compared to pigs fed crystalline lactose. Improvements in ADG were due to improvements in ADFI ($P = 0.08$). There were no differences in G/F ($P = 0.76$) among the lactose sources. For the overall period (d 0-25) pigs fed granular whey and Dairy Lac 80® had improved ADG ($P = 0.05$) and ADFI ($P = 0.04$) as compared to pigs fed spray-dried whey and crystalline lactose. There were no differences in G/F ($P = 0.44$). Based on the results, whey and lactose source did not influence growth performance during the early nursery period. However, growth perfor-