W250 Effect of season on high bulk milk somatic cell count in northern Thailand. S. Rojstian*, V. Punyapornwittaya, W. Tiwanuntakorn, S. Boonyayatra, J. Younggad, C. Apairoj, and W. Suriyasathaporn, *Department of Clinic of Ruminant, Faculty of Veterinary Medicine, Chiangmai University, Chiangmai, Thailand.*

The objective of this study was to evaluate the effect of season on bulk milk somatic cell count (BMSCC) in Northern Thailand. Data of BMSCC from 123 dairy farms within 4 milk-collecting centers in Chiang Mai and Lumphun provinces, Thailand, were collected once a month between October 2000 to August 2001. By the definition from Thai Meteorological Department, seasons in Thailand are comprised of winter (Nov.Feb.), summer (Mar.-May), and rainy season (Jun.-Oct.). High BMSCC was defined when farms had BMSCC higher than 500,000 cells/ml. The percentage of farms with high BMSCC from each milk-collection center and each month was a dependent variable. Seasons and milk-collecting center factors were fixed effects. Data was analyzed using mixed model analysis (Proc Mixed, SAS v.8). Results showed that both season and milk-collecting center were related to the proportion of high BMSCC farms ($P < 0.05$). The percentages of high BMSCC of all centers were ranged between 5.4 and 37.9. The percentage of high BMSCC in rainy season (30.7 %) was significantly higher than summer (20.7 %) and winter (22.4 %). We concluded that a problem of sub-clinical mastitis for dairy farms in northern Thailand is highest during the rainy season.

Key Words: Bulk Milk Somatic Cell Count, Season, Cows

W251 Growth and parasite burdens of St. Croix White and Dorper X St. Croix White lambs grazing native pasture during the wet season in the US Virgin Islands. R. E. Dodson*, A. J. Weis, and R. W. Godfrey, *University of the Virgin Islands, Agricultural Experiment Station, Kingshill, VI.*

St. Croix White (STX; n = 16) and Dorper X STX (DRP; n = 14) ewe and wether lambs were used to evaluate the growth of lambs grazing during the wet season under tropical conditions. Two wk after weaning, at 63 d of age, lambs were placed in guinea grass (Panicum maximum) pastures (0.5 ha) in a rotational grazing system for 147 d. Daily rainfall amounts were recorded during the grazing period. Lambs were moved between pastures every 20 ± 3 d. Forage quantity was determined at the start and end of grazing within each pasture. Each week for the first month and every two weeks thereafter lamb weight, fecal egg count (FEC) and packed cell volume (PCV) were determined for each lamb. The pastures received 978.7 mm of rain with 64.5% of the rain falling by d 45 of the grazing period. Forage quantity was 1264.2 ± 413.9 and 627.5 ± 126.2 Mg/ha at the time of entry into and exit from pastures, respectively. Forage contained 13.3 ± 0.7 % crude protein and 60.8 ± 0.6 % TDN. Average daily gain was higher ($P < 0.05$) for DRP than for STX lambs (76.8 ± 3.8 vs 64.8 ±4.3 g/d, respectively) and wethers had higher ADG ($P < 0.009$) than ewes (79.2 ± 4.1 vs 62.5 ± 4.1 g/d, respectively). Wether lambs were heavier than ewe lambs within breed ($P < 0.001$) during the grazing period but there was no difference ($P > 0.10$) between breeds. There was no breed x gender interaction for ADG or BW. There was no difference ($P > 0.10$) between DRP and STX lambs in FEC or PCV during the grazing period. Packed cell volume was negatively correlated ($P < 0.0001$) with FEC in DRP and STX lambs (r = -0.71 and -0.67, respectively). Weight was positively correlated ($P < 0.009$) with PCV in DRP and STX lambs (r = 0.15 and 0.16, respectively).). In 3 lambs that died FEC was 2350 egg/g and PCV was 10% the week immediately prior to their death. These results indicate that DRP lambs grow faster and have similar parasite burdens when compared to STX lambs grazing native pasture during the wet season under tropical conditions.

Key Words: Sheep, Parasites, Grazing

W252 Phylogenetic relationship and distribution of bacteria in the mucosa of chicken guts: from the crops to ceca. J. Gong[1], W. Si*[1], R. Huang[2], F. Deng[1], Y. Yin[1], H. Yu[1], and Y. Han[3], [1]*Food Research Program, Agriculture and Agri-Food Canada, Guelph, Ontario,* [2]*Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha China,* [3]*3Maple Leaf Foods Agresearch, Guelph, Ontario.*

Bacterial populations in the mucosa of adult chicken guts at different regions, including the crop, gizzard, duodenum, jejunum, ileum, and cecum, were studied by molecular analysis of 16S rRNA genes. Bacteria in the mucosa of tested gut regions were mainly Gram-positive. Ceca had the most diverse bacterial population in the guts. Eleven out of 100 cloned 16S rDNA sequences from the cecum had less than 95% homology to database sequences. There were 56 phylogenetic types of bacteria (from 100 16S rDNA clones) detected in the cecum, as compared to 8 phylogenetic types (from 51 clones) in the crop, 3 phylogenetic types (from 51 clones) in the gizzard, 15 phylogenetic types (from 52 clones) in the duodenum, 11 phylogenetic types (from 50 clones) in the jejunum, and 7 phylogenetic types (from 50 clones) in the ileum. Bilophila capilosu and E. coli comprised the largest groups among the clones from the cecum, representing 12 and 11%, respectively. Lactobacilli were predominant (181 out of 254 clones) in the upper gastrointestinal tract (from crops to ilea) with the highest diversity being found in the crop. L. aviarius was the predominant species of Lactobacilli detected in the gizzard and duodenum. It also comprised the largest group of bacteria in the jejunum and ileum. This report is the first comprehensive study of mucosa-associated microbiota from different gut regions in broiler chickens.

Key Words: 16S rRNA, Bacteria, Chicken Gut

Breeding and Genetics II

W253 A computerized approach to minimize inbreeding of breeding plans. John R. Garbe* and Yang Da, *Department of Animal Science, University of Minnesota, St Paul.*

Inbreeding is an important issue in animal breeding. Since inbreeding is often associated with detrimental effects, minimizing inbreeding is often desired. Theoretical prediction of inbreeding levels for breeding plans is difficult in real animal populations due to the complex pedigree structures formed over many generations. As computing power rapidly improves, predicting inbreeding levels based on exhaustive calculation of inbreeding coefficients resulting from all potential matings becomes feasible. We developed a computer program named MiniInbred to identify a breeding scheme that minimizes inbreeding. This program predicts inbreeding level in the next generation by identifying matings that yield the lowest inbreeding level in the offspring. The inbreeding coefficient resulting from all potential matings of the current breeding animals (generation 1) are calculated, and the potential matings among the current breeding animals that yield the lowest inbreeding level are identified. The program also has the option to predict the lowest inbreeding available in the third generation. In this case, the hypothetical offspring (generation 2) of the current breeding animals are treated as parents, and the inbreeding coefficient resulting from all potential matings between the hypothetical parents are calculated, and the potential matings among the hypothetical parents that minimize inbreeding are identified. This computerized approach is illustrated and evaluated using two large animal pedigrees.

Key Words: Inbreeding, Breeding, Animal

W254 Full pedigree analysis of QTL affecting growth, carcass, and meat quality in pigs. 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], and E. Kalm[2], [1]*Animal AG,* [2]*Institute of Animal Breeding and Husbandry, Kiel, Germany.*

Quantitative trait loci (QTL) detection methods in swine are often based on full- or half-sib families and ignore additional relationships among animals. In this study, a full-pedigree analysis based on a variance component (VC) approach was applied to a three-generational pedigree from a line-cross experiment involving Pietrain and Large White x Landrace hybrid. The pedigree included 17 F0, 118 F1, and 1014 F2 animals originating from repeated matings of four F1 sires to 33 full-sib F1 dams. All animals were genotyped for 27 microsatellite markers on SSC2, SSC6, and SSC7. Phenotypes on 31 growth, carcass, and meat quality traits were available on F2 animals. The analyses were performed using an animal model with random polygenic and QTL effects. The (co)variance

matrix of the polygenic effect was an additive genetic relationship matrix. The (co)variance matrix of the QTL effect contained probabilities that alleles shared by two individuals were identical-by-descent (IBD). The IBD probabilities were calculated for each pair of gametes independently, using a deterministic method that combines a recursive algorithm for general pedigree structure with the method to estimate IBD between sibs, and then combined to obtain IBD probabilities at the individual's level. The VC analysis was performed and LOD scores were obtained at every 1cM. Significant evidence of QTL (LOD>2) affecting daily gains, most fatness traits, meat reflectance and conductivity was found on SSC2. For some traits, more than one significant peak was found, indicating possible presence of two or more linked QTL. There was suggestive evidence (LOD>1.5) of several QTL affecting fatness traits on SSC6. On SSC7, we found a very significant (LOD=14.5) QTL for carcass length. Full pedigree analysis provides stronger evidence of existing QTL and more precise estimates of their positions than traditional methods.

Key Words: Swine, QTL Mapping, General Pedigree

W255 Efficiency of selection on multiple QTL in a crossbred population. N. Piyasatian*, R. Fernando, and J. Dekkers, *Iowa State University, Ames*.

The efficiency of marker-assisted selection on multiple known QTL for a trait with heritability of 0.1 in a line-crossing program was evaluated on the basis of frequencies of favorable QTL alleles and genetic gain over ten generations. Three biallelic unlinked additive QTL were simulated with known QTL positions. Polygenic effects were simulated based on the sum of 100 additive and unlinked loci. Different analyses and criteria for selection were evaluated by considering the effects of factors included in the models and three alternative levels of effects at the QTL (each QTL explaining 10.8, 3.57, and 0.9% of the genetic variance). In each generation 5% males and 25% females were selected out of 500 progeny. Two alternative analyses were considered:

Model A: $\mathbf{Y} = \mathbf{X_n}\,\beta_\mathbf{n} + \mathbf{X_g}\beta_\mathbf{g} + \mathbf{Zu} + \mathbf{e}$, and Model B: $\mathbf{Y} = \mathbf{X_n}\beta_\mathbf{n} + \mathbf{Zu} + \mathbf{e}$

where $\mathbf{Y}$ is the observed phenotypes; $\beta_\mathbf{n}$ and $\beta_\mathbf{g}$ are non-genetic and genetic fixed effects (= number of favorable QTL alleles); $\mathbf{X_n}$ and $\mathbf{X_g}$ are incidence matrices; $\mathbf{u}$ are additive polygenic effects; and $\mathbf{e}$ are the environmental effects. Selection was based on the sum of BLUE of $\beta_\mathbf{g}$ and BLUP of $\mathbf{u}$. A total of 50 replicates were run.

For the large QTL, QTL frequencies approached fixation (>0.9) in generations 6 and 10 for Models A and B. For the smaller QTL, it required more generations to approach fixation, in particular for Model B. In generation 2 (F2), genetic gain from Model A was 70% greater than gain from Model B for the large QTL, 20% greater for the medium QTL, and 10% poorer for the small QTL. The latter likely results from the large standard errors of QTL effect estimates for the small QTL. For the large and medium size QTL, extra gains of Models A over B declined over generations. Results show that QTL detected in breed crosses can be used to increase genetic gain in populations that are developed from those crosses. Additional analyses will evaluate the impact of having markers at various distances from the QTL.

Key Words: QTL, Marker-Assisted Selection, BLUP

W256 Comparison of normalization and models for the analysis of gene expression data. S. L. Rodriguez-Zas*[1], M. R. Band[2], R. E. Everts[1], B. R. Southey[1], Z. L. Liu[1], and H. A. Lewin[1,2], [1]*University of Illinois at Urbana-Champaign*, [2]*W. M. Keck Center for Comparative and Functional Genomics, University of Illinois at Urbana-Champaign*.

The influence of different normalization and parametric models on the analysis of gene expression from three cattle tissues (rumen, large intestine and small intestine) was evaluated. Fluorescence intensities were recorded in cDNA microarrays that included over 6000 double-spotted cattle genes. A total of six microarrays were used in a reference design with reverse labeling. Prior to normalization, individual spots were filtered if the fluorescence intensity was weak or extreme relative to the sample mean for each gene. The fluorescence intensity normalization methods used were log2 transformation, loess transformation, and linlog at 30% intensity transformation and the combination of loess and linlog transformations. Normalized data were then analyzed using three response variable-model combinations, tissue intensity divided by reference intensity (RATIO), reference intensity treated as a response variable together with the tissue intensities (ABSOLUTE) and reference intensity included in the model as a covariate dependent variable (COVARIATE). A linear mixed effects model including the effects of dye and tissue was fitted and model adequacy was determined by the mean square error criterion. Across all normalization methods, the ABSOLUTE model provided the worst fit and the RATIO and COVARIATE models provided similar fit. However the ABSOLUTE model provided the most significant genes and the COVARIATE model the fewest significant genes. The average difference across normalization methods in the number of genes differentially ($P < 1x10^{-8}$) expressed among tissues was 201 between the ABSOLUTE and COVARIATE models. The log2 transformation provided the worst fit and the combined transformation provided the best fit across all models. The combination transformation provided the most significant results and the linlog provided the fewest. The average difference across models in the number of genes of differentially ($P < 1x10^{-8}$) expressed was 76 between the combined and linlog normalization methods. The variation in results indicates that every cDNA microarray experiment must be studied using different normalizations and models.

Key Words: Gene Expression, Normalization, Mixed Effects Model

W257 Graphical visualization of two large complex populations using Pedigraph 2.0. J. R. Garbe* and Y. Da, *Department of Animal Science, University of Minnesota, St. Paul*.

This poster presents pedigree drawings for two large and complex pedigrees to evaluate the capabilities of Pedigraph 2.0 developed by the authors. Pedigree 1 is a sub population of the entire US registered Jersey population with 1.3 million daughters from 579 sires in 8 generations. The pedigree drawing used the summarization option that displays the sires and their parents, as well as the counts of daughters of each sire according to the performance of pregnancy rate. The program took 43 minutes to draw the full pedigree on a 2 GHz PC computer. To print out the entire drawing with readable entries would require a piece of paper 17 feet wide and 4 feet tall. Pedigree 2 is the European royal genealogy data (unofficial data available from the internet) with 48,605 individuals spread out over 106 generations, with entries as early as 827 BC and as recent as 1997. The program took 43 minutes to draw the full pedigree on a 2 GHz PC computer. Color lines connecting parents and offspring were used to enhance the visibility of parent-offspring relationship. Using zoom in would allow a clear view of any part of the pedigree. However, to print out the main body of the entire drawing with readable entries would require a piece of paper 80 feet wide and 200 feet tall. Using Pedigraphs option of extracting partial pedigrees, we produced the pedigree drawing of Victoria Hanover, Queen of Britain. This partial pedigree contains 5,124 individuals, 3,975 ancestors and 1,148 descendants, and is viewable without the need of an excessively large print. The results show that pedigree graphing for large complex populations is possible. The main limitation is the size of the pedigree printout, which could be too large to be practical.

Key Words: Pedigree, Genealogy, Visualization

W258 Spanish buck β-B inhibin/activin (INHBB) microsatellite polymorphisms. R. Realivasquez*[1], S. A. Ericsson[1], S. F. Spiller[1], W. T. Campbell[1], K. L. Sternes[1], P. H. Purdy[2], H. D. Blackburn[2], and J. M. Dzakuma[3], [1]*Sul Ross State University, Alpine, TX*, [2]*USDA-ARS-National Animal Germplasm Program, Fort Collins, CO*, [3]*Prairie View A&M University, TX*.

DNA markers could be useful in selecting for potential spermatozoal fertility. The purpose of this study was to determine if β-B inhibin/activin microsatellite polymorphisms were present in Spanish buck DNA. An α (INHA) subunit and a β-B (INHBB) subunit can dimerize to form inhibin. The β-B subunit can hetero-dimerize with a β-A (INHBA) or with another β-B subunit to create activin. Inhibins impede and activins stimulate spermatogenesis through FSH regulation. Two primer sets designed for human INHBB microsatellite polymorphisms, polymerase chain reaction and electrophoresis were utilized to examine purified DNA from 23 Spanish bucks. The first primer set (forward AAACAGCAAGACCCTGACTC, reverse TTAGCGTGCCATCCTCAT) showed distinctive bands located at 284 base pairs (bp) (1 hd), 282 bp (2 hd), 280 bp (14 hd), 278 bp (1 hd), or no detectable bands (5 hd). The second

primer set (forward AACTCCATCCCGGTGC, reverse ATGTGTGC-CTGTGGGTTTAG) also showed distinctive bands that were located at 248 bp (6 hd) and 246 bp (7 hd) or no detectable bands (10 hd). Significant deviation from the Hardy-Weinberg equilibrium were observed for both primer sets due to excess homozygosity. These potential polymorphic bands may imply genetic diversity, and could be used for selection strategies. Additional studies will be needed to identify specific QTL.

Key Words: Inhibin, Activin, INHBB

W259 Mapping QTL in complex pedigrees. G. Freyer*[1] and N. Vukasinovic[2], [1]*Research Institute for the Biology of Farm Animals, Dummersdorf, Germany,* [2]*Animal AG, Monsanto Company.*

Traditional methods for detection and mapping of quantitative trait loci (QTL) in dairy populations are based on daughter design (DD) or granddaughter design (GDD). Although these designs are well established and usually successful in detecting QTL, they consider sire families independently from each other, thereby ignoring relationships among other animals in the population and consequently, reducing the power of QTL detection. In this study, we compare a traditional DD with a full pedigree design (FPD) and assess the precision and power of both methods for detecting and locating QTL in a simulated complex pedigree. The pedigree included seven large sire families with overlapping generations and inbreeding. QTL search was considered within a 54cM long chromosomal segment, covered with 11 moderately polymorphic and randomly distributed markers. Marker genotypes were available for all animals. Pedigree information was available for daughters, sires, and two generations of their male ancestors, but not for dams. Phenotypic records were available for daughters and some of the dams. One QTL was placed close to the end of the segment. QTL analyses were performed under the variance component model containing a random QTL and a random polygenic effect. The covariance matrix of the polygenic effect was a standard additive relationship matrix. The (co)variance matrix of the random QTL effect contained probabilities that QTL alleles shared by two individuals are identical-by-descent (IBD). In the DD analysis, IBD probabilities were calculated using sires and daughters marker genotypes. In the FPD analysis, IBD probabilities were obtained using a deterministic approach. Estimation of QTL position and variance components was conducted using REML algorithm. Although both methods were able to find the exact position of the QTL, the FPD method showed better precision of QTL position estimates (narrower, better defined peak) and significantly higher power (3-4 x higher test statistics) than the DD method.

Key Words: QTL Mapping, Daughter Design, Pedigree

W260 INHA microsatellite polymorphisms in Angora bucks. S. F. Spiller*[1], S. A. Ericsson[1], R. Realivasquez[1], W. T. Campbell[1], K. L. Sternes[1], P. H. Purdy[2], H. D. Blackburn[2], and J. M. Dzakuma[3], [1]*Sul Ross State University, Alpine TX,* [2]*USDA-ARS-National Animal Germplasm Program, Ft. Collins CO,* [3]*Prairie View A&M University, TX.*

Genetic mediation and variability of sperm production has been hypothesized, however previous heritability estimates have always been low, therefore making selection for semen characteristics difficult. The objective of this study was to determine if α-inhibin (INHA) microsatellite polymorphisms, a dimeric subunit playing a pivotal inhibitory role in the regulation of spermatogenesis, were present in the DNA of Angora bucks. Inhibins are dimeric molecules composed of an α and one of two β subunits (βA or βB) that exert a negative feedback system on the pituitary release of FSH. Using a primer set originally developed to amplify ovine INHA microsatellite polymorphisms, purified DNA from 24 mature Angora bucks was amplified and examined using polymerase chain reaction and electrophoresis. The INHA primer set (forward primer AGCGTGTGAAGCTGGAGAT and reverse primer ACGTGATCAC-TACCACAGTACGGA) produced multiple homozygous and heterozygous banding patterns with varying numbers of base pairs (bp). Homozygous bands were detected at 195 bp (1 hd) and 200 bp (3 hd). The following heterozygous banding patterns (bp) were identified: 185, 215 (2 hd); 195, 200 (1 hd); 195, 225 (1 hd); 195, 240 (1 hd); 200, 225 (4 hd); 200, 230 (1 hd); 205, 220 (1 hd); and 205, 225 (1 hd). No banding was observed in 8 goats. This data demonstrated significant deviations of genotype counts from Hardy-Weinberg equilibrium. The presence of these INHA polymorphisms suggests a range of genetic variation that could be utilized in selection strategies, with further work required to identify specific associations between potential markers and semen characteristics.

Key Words: Angora, Inhibin, Activin

W261 Effects of the *Compact* mutant myostatin allele $Mstn^{Cmpt\text{-}dl1Abc}$ introgressed into a high growth mouse line on skeletal muscle cellularity. C. Rehfeldt*[1], G. Ott[2], D.E. Gerrard[3], L. Varga[4], W. Schlote[5], J.L. Williams[6], and L. Bünger[7], [1]*Research Institute for the Biology of Farm Animals, Dummersdorf, Germany,* [2]*University of Applied Sciences, Lemgo, Germany,* [3]*Purdue University, West Lafayette, IN,* [4]*Agricultural Biotechnology Center, Godollo, Hungary,* [5]*Humboldt University , Berlin, Germany,* [6]*Roslin Institute (Edinburgh) , Roslin Midlothian, UK,* [7]*ICAPB University of Edinburgh, UK.*

The murine *myostatin* mutation $Mstn^{Cmpt\text{-}dl1Abc}$ (*Compact; C*) was introduced into an inbred mouse line with extreme growth (DUHi) by marker-assisted introgression. To study the allelic effects on muscle fiber hyperplasia and hypertrophy, myonuclear proliferation, protein accretion, and muscle fiber metabolism, samples from *Rectus femoris* and *Longissimus dorsi* muscles of animals wild-type (+/+), heterozygous (*C*/+), and homozygous (*C/C*) for the $Mstn^{Cmpt\text{-}dl1Abc}$ allele were examined by histological and biochemical analyses. *C/C*mice exhibited lower body (-12%) but higher muscle weights (+38%) than +/+ mice. Total muscle fiber number was increased (+24%), whereas fibre size was not affected. Protein and DNA concentrations and DNA/protein ratios as well as creatine kinase activity remained unchanged implying increases in the total contents of DNA and muscle protein. Fiber type distribution was markedly shifted to the white glycolytic (+17%units) at the expense of red oxidative fibers. Capillary density was substantially lower in *C/C*than in +/+ mice as seen by lower number of capillaries per fiber (-35%) and larger fiber area per capillary (+77%). However, the *C* allele was partially recessive in heterozyogous mice for both fiber type frequencies and capillary density. The results show that hypermuscularity caused by mutations in the *myostatin* gene results from muscle fiber hyperplasia rather than hypertrophy, and from balanced increases in myonuclear proliferation and protein accretion. However, capillary supply is adversely affected and muscle metabolism shifted towards glycolysis, which could have negative consequences for physical fitness.

Key Words: DUHi, Muscle Fiber, Capillary

W262 Detection and characterization of microsatellite loci based on PCR. H. Y. Chung*, J. M. Ha, S. J. Oh, and S. W. Lee, *National Livestock Research Institute, Omokchon.*

Tri repeat microsatellite loci have been isolated based on PCR detection procedures in Korean cattle. The pooled genomic DNA samples, which were digested with Sau3A restriction enzyme, were separated onto agarose gels. DNA fragments were recovered for 3 sections (200 to 500 bp, 500 to 1000, 1000 to 1,500). A total of 6 genomic libraries were constructed by a PCR-enrichment procedure with biotined oligo probes, which were used microsatellite selection process. A total of 3,800 clones were analyzed for (ATG)n, (TAA)n, (GGC)n, (CAT)n, (GCA)n, and (CTG)n repeat sequences. Most clones (89%) were contained repeat regions and more than 70% clones contained single nucleotide polymorphisms. Effective clones, which contained repeat sequences that used in this study, were 45%. On the Blast search, 65% of clones were hit, 20% of clones were identified as known microsatellite loci, and 15% of clones were identified as unknown genes.

Key Words: Microsatellite, PCR, Cattle

W263 Using plasma IGF-I concentration for genetic improvement of feed efficiency in beef cattle. R. M. Herd[1], D. J. Johnston[2], K. Moore[2], H-U. Graser[2], and P. F. Arthur*[3], [1]*NSW Agriculture - Armidale, Australia,* [2]*Animal Genetics and Breeding Unit, Armidale, Australia,* [3]*NSW Agriculture - Camden, Australia.*

Providing feed for animals is the single most expensive cost of beef production. Individual animal feed intake is difficult and expensive to measure, and this drawback highlights the need for alternative cost effective measures for genetic improvement of feed efficiency. Recent research in Australia has shown that plasma IGF-I concentration is moderately heritable (0.32 to 0.43) in beef cattle, and is genetically correlated (0.39 to

0.63) with residual feed intake (RFI), a measure of feed efficiency that accounts for differences in size and growth rate. Plasma IGF-I concentration is also genetically correlated with subcutaneous fat depth (0.35 to 0.62) and with intramuscular fat (0.26 to 0.47). The application of IGF-I for genetic improvement of livestock is now a patented technology licensed to Primegro Limited, an Australian company. For 2004, the Australian genetic improvement system (BREEDPLAN) utilised these genetic parameters to incorporate IGF-I information in the generation of estimated breeding values (EBVs) for RFI. The accuracy of EBVs for RFI generated using an animal's actual feed intake information alone is approximately 63%. While the IGF-I measure is relatively inexpensive and convenient, the EBVs for RFI generated from IGF-I information alone have low accuracies (approximately 40%). To improve accuracy, strategies that combine measurement of IGF-I in all breeding animals, and actual feed intake measurement in strategically selected individuals in the herd in a two-stage selection process will be required.

Key Words: Cattle, Feed Efficiency, IGF-I

W264 Growth hormone gene polymorphisms differentially predict ADG and carcass traits in performance tested Angus and Brangus bulls. M. G. Thomas[1], R. M. Enns[2], G.A. Silver*[1], M. D. Garcia[1], K. L. Shirley[1], V. R. Beauchemin[1], and D. M. Hallford[1], [1]*New Mexico State University, Las Cruces*, [2]*Colorado State University, Ft. Collins*.

Growth hormone is necessary for growth and fat metabolism. Relationships of GH gene polymorphisms to ADG and yearling ultrasound carcass measures were evaluated in performance tested Angus and Brangus bulls (n = 361 from 36 sires). Bi-allelic polymorphisms were an intron 4 Msp-I RFLP (+/+, +/-, -/-) and an exon V L-leucine to V-valine single nucleotide polymorphism (SNP). Bulls were spring-born and fall-weaned and then gain tested for 112-d as they approached 1 yr of age with a ration formulated to yield 1.58 kg gain/d. Birth weight, adjusted 205- and 365-d weights, and longissimus muscle area per 100 kg of BW were similar among breed groups. Means for these traits were 37.2 $\pm$ 1.2, 268.8 $\pm$ 11.9, and 463.8 $\pm$ 10.2 kg and 6.2 $\pm$ 0.2 cm2/100 kg of BW, respectively. Angus bulls had greater ($P < 0.05$) ADG and ribfat thickness than Brangus bulls (1.59 > 1.53 $\pm$ 0.05 kg/d and 0.66 > 0.48 $\pm$ 0.05 cm). Angus bulls had high frequencies (> 0.68) of the homozygous +/+ and LL genotypes, whereas genotypic frequencies were evenly distributed in Brangus bulls. Mixed model analyses revealed that the Msp-I and LV genotypes within breed were significant ($P < 0.05$) sources of variation in prediction of ADG and ribfat. The interaction between Msp-I and LV genotypes was a significant ($P < 0.05$) predictor of intramuscular fat and ribfat. In Brangus bulls, the heterozygous Msp-I genotype had the highest rate ($P < 0.05$) of ADG and the heterozygous LV genotype had the highest ($P < 0.05$) level of intramuscular fat relative to the homozygous genotypes. Concomitantly, homozygous -/- and VV genotypes had greater ($P < 0.05$) amounts of ribfat and ADG relative to the other genotypes in Angus bulls, but these genotypes were observed at very low frequencies (i.e., 0.06 and 0.03). Results suggest that GH gene polymorphisms are informative predictors of ADG and carcass measures in growing Angus and Brangus bulls. However, it appears genotypes of the two polymorphisms differentially predict these traits within the breed groups of Angus and Brangus.

Key Words: Bull, GH, SNP

W265 An improved approximation of the gametic covariance matrix for marker assisted genetic evaluation by BLUP. F. Pita*[1], R. Fernando[2], and L. Totir[2], [1]*Newsham Genetics, LC*, [2]*Iowa State University, Ames*.

Marker Assisted Best Linear Unbiased Prediction (MABLUP) with large livestock pedigrees depends critically on efficient algorithms to invert the gametic covariance matrix for the marked QTL. These algorithms are based on tracing the QTL alleles of an individual to its grandmother or grandfather. When marker information is complete, there are simple rules to compute the probabilities (PDQs) of these events. When marker information is incomplete, even if the PDQs are computed exactly, the efficient algorithms would be approximate. Further, computing the exact PDQs becomes difficult when marker information is incomplete. In this study , we examined the effect of estimating the PDQs by MCMC on response to MABLUP. The MCMC method applied is based on the concept of segregation indicators. A pedigree with 96 individuals and four generations was simulated. Two or four bi-allelic markers were simulated flanking a QTL which accounts for 2.85% of the genetic variation. The candidate individuals for selection did not have phenotypic information. In a previous study, use of an analytical approximation of PDQs was shown to result in a loss of about 50% of the response to MABLUP. The results of this study show that by estimating the PDQs by MCMC the loss in response was of 19.2% and 2.4% when information from 2 or 4 markers was used, respectively. Because the PDQs in this study were estimated accurately by MCMC using all available marker information, the approximation in the inverse is almost due to use of the efficient algorithm. The small loss in response that we observed here indicates that the approximation introduced through the recursive equation is small.

Key Words: Gametic Matrix, MABLUP, MCMC

W266 Identification of quantitative trait loci for carcass and growth traits in swine using principal components analysis. T. M. Stearns*, S. L. Rodriguez-Zas, J. E. Beever, M. Ellis, F. McKeith, B. R. Southey, J. Hartschuh, and R. J. Feltes, *University of Illinois at Urbana-Champaign, Department of Animal Sciences*.

A three generation resource population including 832 F2 pigs was developed by a parental cross between three Berkshire grand sires and 18 Duroc grand dams. The population was genotyped for ten markers spanning 161.5 cM on chromosome 6 (SSC6), and nine markers spanning 125.5 cM on chromosome 13 (SSC13) based on a sex-averaged CRI-MAP map estimates. Animals were weighed from birth to harvest approximately every 21 d, and carcass and meat quality traits were recorded at harvest (approximately 113 kg). There were significant correlations between the 41 traits recorded and a principal component analysis was used to summarize this high dimensional data into few principal components or orthogonal linear combinations of the traits. A linear mixed effects model was used to detect QTL influencing the principal components and thus the traits of interest. The model included the fixed effects sex, birth year and month, QTL additive, dominance and imprinting coefficients, weight at slaughter and the random effect family. Genetic effects were calculated every 1 cM using a least-squares interval mapping method. The analysis identified QTL influencing groups of traits including tenth rib, last rib, and last lumbar backfat on SSC6 (group SUBFAT6); birth, 21 d, 42 d, and 63 d weight on SSC6 (group WEIGHT6) and fat %, moisture % and marbling on SSC13 (group INTFAT13). The first principal component explained 80.85%, 73.48%, and 77.85% of the variation in SUBFAT6, WEIGHT6 and INTFAT13, respectively. A QTL influencing the first principal component was detected at approximately 70 cM (P < 0.0036), 111 cM (P < 0.0078) and 87 cM (P < 0.0009) in SUBFAT6, WEIGHT6 and INTFAT13, respectively. The location and genetic effect estimates were consistent with univariate analysis. These results indicate that QTL mapping of many correlated traits can be enhanced by principal component analysis.

Key Words: Backfat, Weight, Marbling

W267 Chromosomal assignment of 24 candidate genes for swine efficient growth. M. Grosz*[1], J. Byatt[1], C. Dyer[1], K. Hinds[1], K. Eyer[2], and C. Beattie[2], [1]*Monsanto Company, West Chesterfield, MO*, [2]*University of Nevada-Reno, Department of Animal Biotechnology*.

Candidate genes believed likely to be involved with growth and feed intake were used to screen a BAC library in an effort aimed at identifying chromosomal regions, and ultimately genes and mutations, responsible for phenotypic variation in efficient growth and related traits. Identified BACs were subcloned, sequenced, and primers designed for locus specific re-sequencing and SNP discovery. A subset of SNPs (filtered for sequence context, spacing, disequilibrium, and platform compatibility) were used to genotype several large, two-generation pedigrees. Linkage analysis (CRI-MAP v2.4) identified 27 linkage groups that were "anchored" to porcine chromosomes through linkage to previously assigned loci (http://iowa.thearkdb.org/) or assignment of loci to a porcine radiation hybrid map. The location of the putative human homolog of each gene was identified in silico and used to confirm assignments. This annotation process provided confirmatory evidence for the chromosomal assignment of 24 previously unassigned candidate genes for efficient growth. Subsequent research will now focus on aligning these genes with

QTL detected in various resource populations and comparative sequence analysis to identify functional polymorphisms.

Key Words: Swine, Growth, QTL

W268 Mapping and genetic variation within porcine 70 kiloDalton heat shock protein 2 (HSPA2).

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70 kiloDalton heat shock protein 2 (HSPA2) is expressed in the testis during the meiotic phase of spermatogenesis in humans and mice. Mutations in HSPA2 have been shown to cause sterility in male mice, while not affecting female reproductive capacity. Based on these comparative observations, HSPA2 is a candidate gene for influencing porcine male reproductive phenotypes. To initiate research assessing this possible relationship, the human HSPA2 sequence was used to identify a putative porcine HSPA2 sequence from public EST databases. This EST was used to isolate a Bacterial Artificial Chromosome (BAC) clone containing the porcine homolog of HSPA2. BAC DNA was subcloned, and the porcine HSPA2 locus was defined by sequence assembly and analysis. Extant genetic variation was identified by amplification and re-sequencing of HSPA2 (and flanking regions) with a series of overlapping primer pairs. In total, 11 Single Nucleotide Polymorphisms (SNPs) and 1 single base insertion/deletion were identified in the region spanning from 1062 bases upstream of the start codon to 672 bases downstream of the stop codon. None of the identified SNPs alter the amino acid sequence of the peptide. Two SNPs were converted into PCR-RFLP assays and used to genetically map the HSPA2 locus to chromosome 7, 87 cM, consistent with the syntenic relationship between Hsa14 and Ssc7. Future research can now be directed toward detecting associations between genetic variation and swine reproductive performance and other phenotypes.

Key Words: Swine, HSPA2, SNP

Food Safety

W269 Correlation of genomic changes with morphological dimorphism of *Campylobacter jejuni.*

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Campylobacter jejuni is one of the leading causes of human bacterial gastroenteritis. Previous research has shown that variation in pathogenicity of *C. jejuni* may be associated with its polymorphism. The spiral form of *C. jejuni* has been shown to be more highly pathogenic than the coccoid cells of the same strain. The objective of this research was to investigate the possibility of genomic changes associated with the polymorphism in *C. jejuni* using pulsed-field gel electrophoresis (PFGE) and DNA sequencing analysis. *Campylobacter jejuni* isolated from pre-chill, post-chill, and retail chicken carcasses and human stool samples of enteritis patients were cultured on Campylobacter enrichment agar for 18 hours (spiral form) and 72 hours (coccoid form) under microaerobic conditions at 42 °C. All isolates were confirmed as *C. jejuni* positive by using polymerase chain reaction (PCR). The isolates then were embedded in agarose plugs and the DNA was analyzed by PFGE (CHEF-DR III system) after digestion using either *Sma* I and *Sac* II restriction endonucleases. After an ethidium bromide staining, the DNA patterns were analyzed using the molecular analyst fingerprinting software (BIO-RAD). The molecular fingerprint of each isolate in the spiral form was compared to the fingerprint of the same isolate in the coccoid form. No genomic variation in the overall restriction patterns associated with polymorphism was observed in the strains tested. Both forms of *C. jejuni* PFGE profiles showed 100% genetic similarity following *Sma* I or *Sac* II digestion. At same time, PCR products of *fla*A gene from the isolated *C. jejuni*were purified by using Wizard PCR Preps DNA Purification System (Promega Corporation. Madison, WI). The purified DNA samples were tested for DNA sequencing analysis and the DNA sequences of each isolate in both forms were computer analyzed by using SeqMan (DNAstar inc., Madison, WI). For two forms of same isolate, the nucleic acid sequences of *fla*A gene showed 90-100% similarity. It is concluded that the morphological dimorphism of *C. jejuni* is not associated with genetic modification.

Key Words: C. Jejuni, PFGE, DNA Sequence

W270 Risk assessment for antibiotic resistance in foodborne pathogens isolated from poultry products.

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Our initial goal of this study was to determine the prevalence of antibiotic resistant foodborne pathogens in poultry product samples at the retail level. 160 samples of chilled raw poultry meat (thighs, drumsticks, and breasts) and fully cooked turkey hot dogs were sampled from selected stores. One strain from each pathogen-positive sample was selected for susceptibility testing with the E-test method (AB Biodisk North America, Inc.). The E-test was performed for ciprofloxacin, tetracycline, and erythromycin according to the manufacture's instructions. Inocula were prepared by incubating the campylobacter strains for 24 h at 42°C under microaerobic conditions in brucella broth or incubating for 24 h at 37°C in BHI broth for Listeria monocytogenes, Salmonella and E.coli strains. After application of the E-test strips, campylobacter plates were incubated in microaerobic conditions at 42°C for 24 h or 37 C for all other strains. The minimal inhibition concentration (MIC) was read directly from the test strip at the point where the elliptical zone of inhibition intersected the MIC scale on the strip. Our preliminary results indicated that the overall prevalence of tetracycline, ciprofloxacin, and erythromycin resistance in Campylobacter strains was 65.52%, 7.69%, and 7.41% respectively. The overall prevalence of tetracycline, ciprofloxacin, and erythromycin resistance in Listeria monocytogenes strains was 100%, 0%, and 50% respectively. The overall prevalence of tetracycline, ciprofloxacin, and erythromycin resistance in Salmonella strains was 100%, 0%, and 100% respectively. And finally, the overall prevalence of tetracycline, ciprofloxacin, and erythromycin resistance in E. coli strains was 56.25%, 0%, and 100% respectively. These initial results confirm the notion of multiresistant strains in Campylobacter, Listeria monocytogenes, Salmonella and E. coli.

Key Words: Antibiotic Resistance, Foodborne Pathogens, Poultry Products

W271 Risk Assessment of stress factors and Listeria monocytogenes Biofilm formation.

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Differential adherence capabilities and reaction to sanitizers for biofilm removal among tetracycline resistant, quaternary ammonium compound (quat), and sodium hypochlorite (bleach) stressed, acid and alkali adapted, and non- stressed Listeria monocytogenes (LM) were tested by the microtiter bio- screening assay. Cell turbidity and biofilm formation were assessed using a microtiter plate reader at the wavelength of 630 nm. The quantitative analysis of biofilm production was performed by adding 200 ul of 95% ethanol to destain the wells. One hundred microliters from each well was transferred to a new microtiter plate and optical densities (OD) of the crystal violet present in the destaining solution was evaluated. Viable counts were also assessed to determine the efficacy of several sanitizers for the removal of LM biofilm. Results showed significant differences in both biofilm formation and cell turbidity at 630 nm between stressed and non-stressed LM isolates ($p<0.001$). At 630nm, bleach stressed and tetracycline resistant LM formed stronger biofilm compared to the unstressed LM with OD of -2.75 x 10-3, -5.70X10-3 and 3.31x10-3, respectively. There were significant difference in cell turbidity at a 630 nm, between the stressed cells compared to the positive control ($p<0.05$), but there were no difference among the cells subjected to the various stressors. Results of the viable cell counts of the stressed LM in biofilm were significantly higher ($p<0.05$); than the positive controls (average means of 1.8 x 107 +/- 1.6 and 4.5 x 104 +/- 1.16, respectively) when treated with sanitizers. In conclusion, stressed LM cells in biofilm appear to exhibit higher tolerance to sanitizer treatment when compared to unstressed LM cells and this tolerance may influence the efficacy of the sanitizer for biofilm removal.

Key Words: Biofilm, L. Monocytogenes, Stressed Cells