Breeding and Genetics: Genomic Selection and Whole-Genome Association II

329 Use of the Illumina Bovine3K BEAD chip in dairy genomic evaluation. G. R. Wiggans[1], T. A. Cooper*[1], K. M. Olson[2], and P. M. VanRaden[1], *[1]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, [2]National Association of Animal Breeders, Columbia, MO.*

Genomic evaluations using genotypes from the Illumina Bovine3K BEAD chip became available in September 2010 and made official in December 2010. The approximately 4,000 samples a month submitted for this low cost chip are 79% hair, 10% blood, 10% nasal and 1% semen and tissue, and 93% are from females. To integrate the 3K genotypes into the evaluations, they are imputed from the 2,614 single nucleotide polymorphisms (SNP) used from the 3K chip to the 42,503 used in evaluation. Reliability is discounted to recognize errors associated with imputation. The average 3K genomic evaluation reliability is 5 points lower than for 50K evaluations. The accuracy of imputation is dependent on an animal's relationship to the genotyped population. The average imputed call rate for 3K genotypes is 95.2% and ranges from 71.0% to 97.0%. Animals that have a low imputed call rate are those who have unknown pedigree or no genotyped relatives. Animals tested using the 50K chip have at least one genotyped parent 94.5% of the time, whereas only 84.2% of 3K genotyped animals do. For approximately 8% of 3K genotypes, the sire is determined to be incorrect. If the true sire of an animal is genotyped, it can be identified with > 99% certainty. Other errors such as dam conflicts, unidentified identical twins / split embryos and breed conflicts prevent genotypes from being used. The chemistry used for the 3K chip is different from that of the 50K chip and causes greater variability in the accuracy of the genotypes. Because of this, a 3K specific check was added which excludes approximately 1% of samples. They are rejected because they have a high proportion of conflicts between SNP of the sire/dam and progeny. The performance of SNP also differed between chips, resulting in 272 SNP that were usable on the 50K chip being not usable on 3K. The 3K chip has been successful in extending genotyping to a larger portion of the cow population. The evaluation system has been modified to accommodate the characteristics of the chip. Improvements in accuracy of imputation and other improvements will further improve the accuracy of 3K based genomic evaluations.

Key words: 3K, genomic evaluation, parentage

330 Properties of different density genotypes used in dairy cattle evaluation. P. M. VanRaden[1], M. E. Tooker*[1], K. M. Olson[2], T. A. Cooper[1], G. R. Wiggans[1], and C. P. Van Tassell[3], *[1]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, [2]National Association of Animal Breeders, Columbia, MO, [3]Bovine Functional Genomics Laboratory, ARS, USDA, Beltsville, MD.*

Dairy cattle breeders have used a 50K chip since April 2008 and a less expensive, lower density (3K) chip since September 2010 in genomic selection. Evaluations from 3K are less reliable because genotype calls are less accurate and missing markers are imputed. After excluding genotypes with <90% call rate and other edits, marker properties were compared for 8,305 animals with 3K, 54,643 with 50K version 1, 2,602 with 50K version 2, and 353 with a higher density (777K) chip. Animals were of 3 breeds, and all 4 chips were from Illumina. Numbers of markers selected were 2,614 from the 3K chip, 42,503 from 50K version 1, 41,019 from 50K version 2, and 632,665 from the 777K. Markers selected each had <20% missing genotypes and <2% parent-progeny conflicts, with proportionally stricter limits for markers with minor allele frequencies <0.5. The selected 3K markers averaged 0.7% missing genotypes vs. 0.4% for the 50K markers. Parent-progeny conflicts averaged 0.07% for the selected 3K markers vs. 0.01% for the 50K markers. Properties of the 777K chip are similar to the 50K chips, but only 38,201 markers that match the 50K chip currently are used. Genomic evaluations were examined for 319 animals that had 3K genotypes in December and then 50K in February. Means were nearly identical (within 1 pound for fat and protein). The 3K evaluations had SD about 96% as large as 50K, in agreement with the 95% expected from the lower published reliability (64 vs. 71% for net merit). The correlations ranged from 0.92 to 0.96 across traits as compared with 0.46 to 0.66 for parent average with 50K. Version 2 of findhap.f90 will improve the 3K correlations to 0.94 to 0.97, improve average reliability by 2%, and improve the percentage of correctly imputed genotypes to 96.3% from 93.8% with version 1. Breeders can increase reliability affordably using lower density to impute higher density genotypes.

Key words: genomic evaluation, imputation, marker density

331 Use of the partial least-squares regression to impute missing markers when some animals are genotyped with low-density SNP platforms. C. Dimauro*[1], S. Sorbolini[1], E. Pintus[1], J. T. van Kaam[2], and N. P. P. Macciotta[1], *[1]Università di Sassari, Sassari, Italy, [2]Associazione Nazionale Allevatori Frisona Italiana, Cremona, Italy.*

In genomic selection direct genomic values (DGV) are predicted by using genotype information provided by high-density SNP platforms. At present, genotyping process is very expensive and problems arise when genomic data extracted from different SNP platforms has to be joined. Recently, several algorithms aimed at imputing marker information not directly collected in some animals, have been suggested. In this work the partial least squares regression (PLSR) imputation method, previously developed by using only simulated data, was tested on a real experiment. Data were from 1,042 Italian Holstein sires genotyped with the Illumina BovineSNP50 BeadChip. Animals were divided in 2 groups. 900 old bulls constituted the training population with all SNP markers considered known. The remaining 142 young bulls were the prediction population where only 3,072 markers, corresponding to the Illumina Bovine 3K BeadChip, were considered known. Efficiency of PLSR imputation method was tested through the mean imputation error rate and the mean imputation accuracy. The first refers to the mean proportion of incorrectly imputed genotypes, the second to the mean correlation coefficient between actual and PLSR imputed genotypes. Moreover, DGV accuracies for milk, fat percentage and protein percentage were evaluated both for original and PLSR predicted data. The ratio between DGV accuracies obtained by using PLSR imputed data and original data was used as synthetic index of goodness of prediction. Results for mean imputation accuracy and mean imputation error rate were 0.70 and 0.18, respectively, whereas the DGV ratios were 0.975 for milk, 0.993 for fat percentage and 0.957 for protein percentage. These results are better than those obtained in a simulated scenario with a more favorable number of animals. Therefore, the PLSR imputation method works better with real than simulated data, thus promising a higher efficiency in SNP marker prediction if the number of genotyped animals increases.

Key words: imputation, genomic selection

332 Reduced dimensionality in GS models through Lassoed supervised principal components. C. Maltecca* and K. A. Gray, *North Carolina State University, Raleigh.*

The availability of high-density SNP panels and sequencing information poses a challenge in genomic data analysis due to highly over-parameterized models. Identification of linear combinations that exhibit large variation through principal components analysis is often employed to reduce model dimensionality. In this work we investigated the use of supervised principal components, an extension of principal components analysis aiming at obtaining a combination of features with both high variance and significant correlation with the outcome. De-regressed breeding values for milk, fat, and protein yield, were obtained for approximately 8,000 US-HOL bulls genotyped with the Illumina 50K chip. For each of the 36,768 SNPs available for the analysis a standardized univariate regression coefficient was calculated. For each value, of a threshold θ ($0 < \theta1 < \theta2... < \theta k$), a reduced data matrix was formed, consisting only of features that exceeded the absolute value θ. For features exceeding θ the first 3 principal components were calculated. Optimal values of θ for each trait were obtained through cross-validation. Soft thresholding employing the correlation of each feature with the supervised PC predictor was used in obtaining a reduced number of features. Subsequent genomic breeding value predictions were obtained through the use of Bayesian LASSO. Values of θ of 3.5, 3.1 and 3.6 were found for milk, fat and protein yield respectively. These values resulted in reduced panels of 1,213, 1,189, and 958 SNPs, respectively. Correlations between GEBVs and BV in a prediction set obtained splitting the data chronologically were of 0.691 (0.712 whole panel), 0.713 (0.743 whole panel), and 0.708 (0.731whole panel), while slopes for the regression of GEBV on BV in the prediction set were of 0.780 (0.765 whole panel), 0.801 (1.125 whole panel), and 0.804 (1.198 whole panel), respectively for milk, fat and protein. For all traits, reduced models recovered more than 90% of the overall information at a fraction of the computing cost.

Key words: genomic selection, supervised principal components, shrinkage estimators

333 FImpute - An efficient imputation algorithm for dairy cattle populations. M. Sargolzaei*[1,2], J. P. Chesnais[1], and F. S. Schenkel[2], *[1]L'Alliance Boviteq, Saint-Hyacinthe, QC, Canada, [2]University of Guelph, Guelph, ON, Canada.*

Imputation consists of approximating the high density (HD) genotype of an individual using information from its lower density (LD) genotype and from the HD genotypes of other individuals, which can be relatives of the imputed individual (family-based imputation) or members of the population at large (population-based imputation). An efficient imputation algorithm and program (FImpute) was developed using family followed by population imputation and optimized for memory and CPU time. The algorithm was first tested on a group of 6,246 Holstein animals genotyped for the 50K panel, which was representative of younger animals recently genotyped in the North America. Only the SNP used in the 3K panel were retained, and 50K genotypes were approximated using information from these SNP and the 50K genotypes of older animals in the North American Holstein population. Overall, the percentages of SNP imputed correctly, incorrectly and missing were 96.8, 1.44 and 1.76%, respectively. As expected the correct call rate was the highest when both parents where genotyped with 50K, but it remained above 90% for 96.2% of animals. A validation study was carried out to assess the effect of using imputed genotypes on GPA accuracy. The realized reliabilities for the GPA of validation bulls (n = 498) were only slightly lower when using imputed genotypes compared with actual 50K genotypes, by a range of 0 to 0.04 depending on the trait. FImpute was also used in the Jersey and Brown Swiss breeds, yielding imputation accuracies high enough to make adequate genomic predictions. When using the 3K panel, most of the imputation accuracy comes from family rather than population imputation. Population imputation would contribute more with a larger LD panel, e.g., when imputing from 50k to 777K. Using both types of imputation, as in FImpute, will nevertheless be required to obtain maximum imputation accuracy. FImpute is now used for imputation from 3k to 50k for official genomic evaluations in Canada.

Key words: imputation, software, validation

334 Estimation of linkage disequilibrium in four US pig breeds. Y. M. Badke*[1], R. O. Bates[1], C. W. Ernst[1], C. Schwab[2], and J. P. Steibel[1], *[1]Department of Animal Science, Michigan State University, East Lansing, [2]National Swine Registry, West Lafayette, IN.*

The success of marker assisted selection depends on the amount of linkage disequilibrium (LD) across the genome. To implement marker assisted selection in the swine industry information about extent and degree of LD is essential, and LD can be used to estimate effective population size. The objective of this study was to estimate LD in 4 US breeds of pigs (Duroc, Hampshire, Landrace, and Yorkshire). To estimate LD, 351 animals from 117 sire/dam/offspring trios were genotyped using the Illumina Porcine SNP60 BeadChip. DNA was isolated from samples (blood or semen) obtained from purebred animals recorded with the National Swine Registry. The number of trios per breed was 30, 26, 29, and 32 for the Duroc, Hampshire, Landrace and Yorkshire breeds, respectively. After excluding SNP for low genotyping rate, failure to meet Hardy Weinberg equilibrium, and minor allele frequency below 5%, an average of 36,421 SNP with an average intermarker distance of 66Kb were used for the analysis. The genotypes were phased and pairwise r^2 was computed. Average r^2 across all chromosomes was 0.36 (sd = 0.028) in Landrace, 0.38 (sd = 0.039) in Yorkshire, 0.43 (sd = 0.036) in Hampshire and 0.45 (sd = 0.041) in Duroc. For markers 1Mb apart, r^2 ranged from 0.13 (sd = 0.037) in Landrace to 0.18 (sd = 0.057) in Duroc and Hampshire. The LD between neighboring markers was $r^2 > 0.3$ for 43% of marker pairs in Landrace, 47% in Yorkshire, 51% in Hampshire and 53% in Duroc. The current average estimated effective population size based on estimated r^2 was 105 for Hampshire, 111 for Landrace, and 125 for both Yorkshire and Duroc. These estimates of LD are lower than previously reported values based on a smaller marker panel, and lower than recently reported estimates for Finnish Landrace and Yorkshire pigs based on the SNP60 BeadChip. Estimates of effective population size in Finnish Landrace and Yorkshire pigs using genotypes and pedigree information were smaller than our estimates. Results of this study are relevant to the US purebred seedstock industry and critical for the design of programs of whole genome marker assisted evaluation and selection.

Key words: swine, linkage disequilibrium, effective population size

335 A major QTL for response to porcine reproductive and respiratory syndrome virus in pigs. N. Boddicker*[1], D. J. Garrick[1], J. M. Reecy[1], R. Rowland[2], M. F. Rothschild[1], J. P. Steibel[3], J. K. Lunney[4], and J. C. M. Dekkers[1], *[1]Iowa State University, Ames, [2]Kansas State University, Manhattan, [3]Michigan State University,*

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Porcine reproductive and respiratory syndrome (PRRS) is an important disease in swine production. The objective of this study was to discover the genetic basis of host response to PRRS virus using data from the PRRS Host Genetics Consortium PRRS-CAP project by conducting a genome-wide association analysis. Three groups of 200 commercial crossbred pigs were infected between 18 and 28 d of age with virus isolate NVSL 97–7985. Blood samples and body weights were collected up to 42 d post infection (dpi). Pigs were genotyped with the Illumina Porcine 60k Beadchip. Whole genome analyses focused on viral load (VL = area under the curve for log-transformed RT-PCR based serum virus from 0 to 21 dpi) and weight gain (WG = gain from 0 to 42 dpi). Heritabilities estimated using pedigree information were 28 and 26% for VL and WG, with maternal effects estimates of 14 and 11%. Phenotypic and genetic correlations between VL and WG were −0.25 and −0.34. Associations with SNPs were identified using BayesB of Gensel software. Using Porcine sequence build 10, a 33 SNP region associated with both VL and WG was found on chromosome 4. The favorable correlation between the genomic estimated breeding values for VL and WG for the 33 SNP region was −1.0. The region explained 15.7% of genetic variance for VL and 11.2% for WG. The unfavorable allele for the most significant SNP had a frequency of 0.84 and estimated allele substitution effects were significant ($P < 0.01$) for each of the 3 groups when fitting the SNP as a fixed covariate in ASREML, with estimates of −3.9, −4.7, and-4.8 units for VL (phenotypic SD = 6.9), and 3.0, 1.5, and 1.9 kg (phenotypic SD = 3 kg) for WG. This region explains a substantial proportion of the genetic variance in response to experimental challenge with a specific strain of the virus. The SNPs in this region are in high LD, which makes further fine mapping difficult. This region may provide opportunities to select pigs for PRRS resistance, but validation is required. This work was supported by the PRRS CAP, USDA NIFA Award 2008-55620-19132, the NRSP-8 Swine Genome and Bioinformatics coordination projects, and by the breeding companies that provided pigs.

Key words: swine, PRRS, GWAS

336 Use of sample pooling in a genome-wide association study identifies chromosomal regions affecting incidence of bovine respiratory disease. L. A. Kuehn*, J. W. Keele, E. Casas, S. A. Jones, D. A. King, T. G. McDaneld, T. P. L. Smith, and T. L. Wheeler, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

We hypothesize that genome-wide association (GWA) based on high-density SNP arrays can be used to identify chromosomal regions affecting disease incidence using a case/control type approach. However, the large sample size required to map a lowly heritable trait like susceptibility to bovine respiratory disease complex (BRDC) makes the cost of such an effort prohibitive. We applied pooling of lung samples from slaughter animals with severe lung lesions (a proxy for incidence of respiratory disease) as the case group, and lungs from animals with no visible lesions as the control group (n = 1,000 for each group), to evaluate sample pooling as an approach to reduce the cost of GWA experiments on complex traits. Comparison of allele frequency estimates for each SNP was used to identify chromosomal regions influencing BRDC. We prepared 10 pools of equal volume lung tissue cores from 100 animals in each of the 2 groups (20 total pools), and DNA from each pool was genotyped in duplicate. Bead level data was used to estimate allele frequency for each pool and combined within group for comparison between case and control. Distances between pools and their replicates across 775,996 SNP were calculated and used to form a neighbor-joining phylogeny, such that individual SNP have minuscule effect on the resulting phylogeny. Allele frequency differences between case and control groups were conditionally compared using phylogenetic comparative methods, resulting in SNP with genome-wide significant associations ($P < 0.05$) in 7 chromosomal regions on BTA 9, 10, 13, 18, 20, 21, and 26. Two additional regions on BTA 7 and 17 harbor SNP under marginally less stringent correction (false discovery rate, FDR, 1%), while 1 or 2 regions on all bovine chromosomes are significant with a relaxed FDR of 5%. We conclude that the presence of lung lesions at slaughter is influenced by multiple loci, consistent with expectations from the multifactorial nature of BRDC, and that tissue pooling represents an economical means to dissect the genetic influences on this trait.

Key words: bovine respiratory disease, DNA pooling, genome wide association

337 Genetic analysis of dry matter intake in Holstein cows. D. Spurlock*, A. Wolc, D. Elkins, E. Scalese, J. Dekkers, and R. Fernando, *Iowa State University, Ames.*

Improving feed efficiency of lactating cows is gaining increased interest in the dairy industry. One strategy to improve feed efficiency is to select cows that consume less feed per unit of milk produced. However, selection for improved efficiency may contribute to undesirable correlated changes in fitness traits due to reduced feed intake at the onset of lactation. The objective of this research was to describe the genetic regulation of dry matter intake (DMI) in Holstein cows over the first 150 d in milk (DIM) using both quantitative and genomic approaches. Daily feed intake was recorded for 228 primiparous and 172 multiparous Holstein cows using the Calan Broadbent feeding system, and dry matter content of feed was determined weekly. Random regression models were used to estimate genetic parameters for DMI. Maximum heritability of daily DMI was 0.27 at 25 DIM, and declined to a minimum of 0.18 at 120 DIM. The genetic correlation between DMI on different days was close to unity when less than 60 d apart, and declined to 0.83 between DMI at 10 and 150 DIM. For genomic analyses, DMI was averaged over each of 5 monthly intervals. Genotypes were determined for all cows using the Illumina Bovine 50K SNP platform. Genomic regions associated with variation in DMI were identified using method BayesC implemented in the software package GenSel. Jointly, all genetic markers accounted for 26 to 50 percent of phenotypic variance in average DMI for months one, 2, 3 and 5, but only 4 percent in mo 4. Individual markers had relatively small effects. For each month of lactation, the 10 genomic regions explaining the greatest variance in average DMI were identified. Only 3 of these regions were shared between average DMI for the first and fifth month of lactation. Together, these analyses confirm that DMI is a moderately heritable trait, and that its genetic regulation changes with stage of lactation. The genetic correlation of daily DMI is high throughout the first half of lactation, but use of genetic markers may help to minimize undesirable change in DMI during early lactation as a correlated response to selection for improved efficiency.

Key words: dry matter intake, heritability, genomics

338 Genetic markers in bovine chromosome 14 are significant for residual feed intake in steers. A. K. Lindholm-Perry*, L. A. Kuehn, T. P. L. Smith, W. M. Snelling, and H. C. Freetly, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Genetic selection for animals that require less feed while still achieving acceptable levels of production could result in substantial cost savings for cattle producers. The purpose of this study was to identify DNA markers with predictive merit for differences among cattle for traits associated with feed efficiency. Crossbred steers (n = 1,195) were fed a high-corn diet for 140 d and average daily feed intake (ADFI), ADG, and residual feed intake (RFI) phenotypes were obtained. RFI was defined from the regression of ADFI on ADG and mid-metabolic BW. These animals were genotyped with the Illumina Bovine SNP50 BeadChip and an association analysis of these single nucleotide polymorphisms (SNP) was performed. A 1.6 Mb region at BTA14: 22.3 to 23.9 was identified as having significant association (nominal $P = 0.04$ to 0.0006) with RFI. To develop markers with the maximum ability to discriminate favorable alleles, 70 additional SNP, not present on the BeadChip, were genotyped within this chromosomal region. These new SNP were genotyped on the same animals and tested for association with ADFI, ADG, and RFI. The statistical model included fixed effects of year and location; covariates of age, heterosis, and breed percentage; and a random polygenic effect. Ten markers were nominally significant within this region for RFI, the most significant of these were clustered between 23.3 to 23.5 Mb. After conservative correction for multiple testing, one marker at 23.30 Mb remained significant. Many of these markers were also significant for ADG, although none were significant after correction. Alleles with positive effects on ADG correspond to negative effects on RFI, suggesting a marker effect of increased growth without increased feed intake. These markers may be useful as prediction tools for animals that utilize feed more efficiently; however, potential impact of these markers on additional production traits will need to be assessed.

Key words: beef cattle, feed efficiency, genomics

339 QTL-by-feeding period interaction for residual feed intake in crossbred steers: a genome selection approach. O. N. Durunna*[1], D. J. Nkrumah[2], S. S. Moore[1], and Z. Wang[1], *[1]University of Alberta, Edmonton, Alberta, Canada, [2]Pfizer Animal Genetics, Kalamazoo, MI.*

Most feeding trials are conducted within a single feeding period but growing cattle are fed across different feeding periods. It is important to understand whether different feeding periods contribute to differential performance of the QTLs that are associated with residual feed intake (RFI) in growing steers. Our objective was to determine whether similar QTLs associated with RFI in steers are detected during the fall and winter-feeding periods. Feeding trials were conducted over 7 years using crossbred steers fed a finisher diet during the fall (P1) or winter (P2). The number of steers evaluated in P1 and P2 were 319 and 532, respectively. Feed intake was measured with the GrowSafe system, and RFI calculated by linear regression. Genotyping was done using the Illumina BovineSNP50 Beadchip. Genome selection was implemented using a Bayesian approach in Proc QTL using 1407 evenly spaced markers from 40653 SNP. 5000 permutations were used to determine thresholds at 1% and 5% for each group. Group of steers fed in each feeding period was analyzed separately. No QTL was detected on chromosomes 13, 24, 25 and 27 in P1 while QTLs were absent on chromosomes 14 and 22 in P2. More QTLs were observed in the second feeding period than the first feeding period but there was no difference in the number of QTLs that were significant ($P > 0.05$) between the 2 groups at 1% or 5% thresholds. Majority of the QTLs had opposite effects from one feeding period to another. The results indicate that feeding period may contribute to the differential performance of QTLs associated with RFI, therefore it is suggested that effective application of makers in MAS or genome selection should consider their effects in all feeding periods.

Key words: QTL-by-environment interaction, residual feed intake, beef steers

340 Identification of genomic markers for feed efficiency in purebred Simmental, Angus and crossbred steers. N. V. L. Serão*[1], A. D. Markey[1], M. Pérez-Enciso[2], D. B. Faulkner[1], J. E. Beever[1], and S. L. Rodríguez-Zas[1], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]Universitat Autònoma de Barcelona, Barcelona, Catalonia, Spain.*

The identification of genomic markers associated with feed efficiency in cattle is expected to help in understanding the role of genes, pathways and regulatory elements and accelerate the genetic improvement for this trait of utmost economic importance. The purpose of this study was to identify genomic markers associated with variation in feed efficiency. Genotypes of 703 steers were obtained using the Illumina Bovine SNP50 BeadChip. In total, 2,494 markers found on bovine chromosomes 6 were considered. The indicator of feed efficiency residual feed intake (RFI) was computed based on dry matter intake adjusted for average daily gain and mid-test metabolic weight. A model including the fixed effects of individual SNPs, breed (5 levels; Angus (AN), 3/4 AN, 1/2 AN 1/2 Simmental (SM), 3/4 SM and SM), diet (5 levels), breed-diet interaction, days on feed (covariate) and the random effects of harvest group within contemporary group (27 levels) and additive polygenic effect (pedigree including 3,786 animals) was used to identify SNPs associated with RFI. Maximum likelihood parameter estimation and fixed effects testing were implemented using Qxpak v 5.03. After multiple test adjustment, SNPs were deemed statistical significant at $P < 0.001$. From the 47 SNPs associated with RFI at $P < 0.01$, 7 were associated at $P < 0.001$. Among the 7 SNPs, 2 are harbored on gene regions. SNP rs41870471 is located on the intronic region of Ankrd17, a gene known to affect growth, metabolism, muscle, and aging in mice. SNP rs43451062 is located on the intronic region of Prss12, a member of the trypsin family of serine proteases associated with neurological processes. Breed by Diet interaction had a significant ($P < 0.05$) association with RFI for 6 of the top 7 SNPs. The exception was the model including rs41663978, which exhibited a significant effect of Diet on RFI. SNP rs43451062 had the highest allele substitution effect (1.90 ± 0.01), whereas rs29017713 showed the lowest (0.16 ± 0.01). The incorporation of these markers in genomic selection strategies is expected to accelerate the genetic improvement of feed efficiency.

Key words: residual feed intake, SNP, Association analysis

341 Prediction of genomic estimated breeding values for temperament at weaning in *Bos indicus* crossbreds using Bayesian Inference. L. L. Hulsman*[1], S. O. Peters[2], J. O. Sanders[1], A. D. Herring[1], C. A. Gill[1], and D. G. Riley[1], *[1]Department of Animal Science, Texas A&M University, College Station, [2]Department of Animal and Range Sciences, New Mexico State University, Las Cruces.*

Temperament in cattle influences animals handling and carcass traits. Genetic selection can modify this trait. The objective of this study was to predict GEBV for weaning temperament in crossbred cattle using Bayesian analysis of partitioned data sets for training and validation. Calves (n = 698) were from 13 full-sib embryo transfer Nellore-Angus F_2 families and 4 half-sib families sired by the same bulls in central Texas. Temperament was subjectively assessed by 4 evaluators, where

1 indicated docile and 9 indicated extremely nervous or wild. The average score was used as phenotype. All calves were genotyped using the BovineSNP50 assay (Illumina Inc., San Diego, CA). Markers with call rates <0.9, minor allele frequency <0.05, and Hardy-Weinberg Equilibrium proportions rejected at $P < 0.05$ were removed. Analyses were conducted with 34,980 markers using BayesC procedures. Effects of SNP were random in a mixture model with an inclusion fraction (1 - Π) of 0.001. Fixed effects included birth-year-season, breed of dam, family, and sex. Training was done (1) once using all animals in training, (2) 4 times using the progeny of all but one sire, (3) once using only embryo transfer F_2 progeny, and (4) once by random assignment. Each analysis had GEBV predicted; breeding values were also predicted using an animal model. The average of each animal's GEBV when included in training was compared with the predicted GEBV when included in validation. Each calf was included 5 or 6 times in training and 1 or 2 times in the validation. Correlation (r) between averaged GEBV and predicted GEBV was 0.56. For the best 10% of males, GEBV from Bayesian analyses were re-ranked as compared with traditional prediction (r ranged from −0.64 to −0.32; $P < 0.05$). Generally, GEBV for the best calves ranked similarly (r ranged from 0.24 to 0.84), regardless of their inclusion in training or validation. Re-ranks among analyses could be due to data set size, marker structure, or both.

Key words: Bayesian inference, genomic estimated breeding value, temperament