606 Genomic technologies to increase production of Certified Angus Beef (CAB). J. D. Nkrumah*[1], P. Boddhireddy[1], M. Kelly[1], S. L. Northcutt[2], M. McCully[3], K. Anderson[1], J. Rumph[1], W. Herring[1], J. Osterstock[1], and S. DeNise[1], *[1]Pfizer Animal Genetics, Kalamazoo, MI, [2]Angus Genetics Inc., St Joseph, MO, [3]Certified Angus Beef, Wooster, OH.*

Genomic technologies can be used as part of genetic improvement strategies to allow Angus cattle producers to both improve growth performance and increase the potential for animals to achieve the Certified Angus Beef (CAB) brand quality specifications. We applied data mining and machine learning methods to genotype and phenotype data on a total of ~4,000 animals with AAA marbling and postweaning gain EPDs and ~9,600 animals with feedlot growth and carcass marbling phenotypes to select an optimum subset of markers from the Illumina BovineSNP50 chip. Selected SNPs predict the genetic potential of Angus cattle to qualify for the CAB brand due to superior genomic merit for marbling, and to affect profitability through growth. Marker effects estimated based on cross-validations using 2/3 of each data were used to compute molecular breeding value predictions, which were then tested in the remaining independent 1/3 of each data set. The independent internal validation results showed that the markers explained between 17 to 36% of the genetic variation in both the EPDs and phenotypes for marbling and growth, depending on the trait. Subsequently, the SNP effects were used to generate predictions on a second completely independent set of ~5,400 animals with genotypes. These new molecular breeding value predictions were sent to Angus Genetics Inc. (AGI), where they were combined with their respective phenotypes and evaluated for their genetic correlations with phenotypes using single-trait animal models. The estimated genetic correlations in the AGI analysis ranged from 0.40 to 0.50, depending on the trait. These predictions provide commercial cattlemen the opportunity to use simple and cost-effective genomic tools to inform early selection, management, and marketing decisions related to genetic potential for marbling and growth.

Key Words: Certified Angus Beef, genomic technologies, molecular value predictions

607 Genomic selection for dry matter intake using a combined European and Australian reference population. Y. de Haas*[1], J. E. Pryce[3], M. P. L. Calus[1], E. Wall[2], M. P. Coffey[2], H. D. Daetwyler[3], B. J. Hayes[3], and R. F. Veerkamp[1], *[1]Animal Breeding and Genomics Centre of Wageningen UR Livestock Research, Wageningen, the Netherlands, [2]Sustainable Livestock Systems Group at Scottish Agricultural College, Easter Bush, Midlothian, United Kingdom, [3]Biosciences Research Division of Department of Primary Industries Victoria, Bundoora, VIC 3083, Australia.*

Dairy cow dry matter intake (DMI) data from Australia (AU), the United Kingdom (UK) and the Netherlands (NL) were combined (1801 cows) for this study. The aim was to explore the impact on the accuracy of genomic estimated breeding values of pooling data across key reference populations. A total of 843 Australian growing heifers with records on DMI measured over 60 to 70 d at approximately 200 d of age, 359 Scottish and 599 Dutch lactating heifers with records on DMI during the first 100 d in milk were included in the data set. Genotypes were obtained using the Illumina BovineSNP50 BeadChip for European (UK+NL) cows, and Illumina High Density Bovine SNP chip for AU heifers. The AU and EU genomic data were matched on SNP-name and genotypes were compared for quality control using 40 bulls that were genotyped in both data sets. This resulted in a total of 30,949 SNPs being used in the analyses. Genomic predictions were with both single-trait and multi-trait genomic REML models, using ASReml. The accuracy of genomic prediction was evaluated in 11 single-country validation sets, and the reference set (where animals had both DMI phenotypes and genotypes) were either a reference set within AU or EU, or with a multi-country reference set consisting of all data except the validation set. When DMI was considered to be the same trait for each country, using a multi-country reference set, the accuracy of genomic prediction for DMI increased for EU and UK, but not for AU and NL. Extending to a bivariate (AU-EU) or trivariate (AU-UK-NL) model increased the accuracy of genomic prediction for DMI in all countries. The highest accuracies were estimated for all countries when data was analyzed with a trivariate model, with increases of up to 5.5% compared with a single-trait analysis with a multi-country reference set.

Key Words: genomic selection, dry matter intake, international collaboration

608 Whole transcriptome sequencing of seven bovine tissues reveals gene expression profiles, splicing variants, and novel coding regions to improve genome annotation. J. Thomson*[1], U. Basu[1], Y. Meng[1], X. Liao[1], S. Moore[2], and P. Stothard[1], *[1]University of Alberta, Edmonton, AB, Canada, [2]University of Queensland, Brisbane, Qld, Australia.*

A comprehensive annotation of the transcriptome is essential for understanding the genome biology of cattle. The objectives of this work include characterizing the transcriptome of 7 bovine tissues with the aim of identifying additional splice variants, novel coding regions, and tissue-specific gene expression. Liver, adipose, hypothalamus, muscle, kidney, duodenum, and lung tissues were profiled using RNA-Seq Reads were mapped to the bovine reference sequence using TopHat and gene expression values normalized as FPKM (fragments per kilobase of exon per million fragments mapped) were generated using Cufflinks. A total of 24,617 genes were identified and quantified in at least 1 of the 7 tissues. Several thousand transcript variants were also identified. Functional annotation of the expressed genes will provide insight into tissue functions and may stimulate future lines of research. This work adds to the current knowledge base by identifying expressed transcripts and quantifying their expression in several important tissues. Novel transcribed regions that are not currently available in the database may be identified. Additional information about gene function can be used to improve our understanding of ruminant biology.

Key Words: gene expression, genomics, physiology

609 An ensemble-based approach to imputation of high-density genotypes for genomic selection with application to purebred Angus cattle. C. Sun*[1], X.-L. Wu[1,2], K. A. Weigel[1], G. J. M. Rosa[2,3], S. Bauck[4], B. W. Woodward[4], R. D. Schnabel[5], J. F. Taylor[5], and D. Gianola[2,3], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]Department of Animal Sciences, University of Wisconsin, Madison, [3]Department of Biostatistics and Medical Informatics, University of Wisconsin, Madison, [4]Merial Limited, Duluth, GA, [5]Division of Animal Sciences, University of Missouri, Columbia.*

Imputation of high-density genotypes from low-density panels is of increasing interest in genomic selection because it can reduce genotyping costs markedly. Imputation software packages vary in imputation accuracy, and imputed genotypes may be inconsistent among procedures. Hence, an AdaBoost-like approach is proposed to combine imputations from several different software packages. Six such packages were used: Beagle (v3.3), IMPUTE (v2.0), fastPHASE (v1.4), AlphaImpute, findhap (v2), and Fimpute (v2), each serving as a basic classifier in an ensemble-based system. This method computed weights sequentially for all classifiers, and then combined results from the component methods via weighted majority voting, to produce a final vote for unknown genotypes. The data included 3,078 purebred Angus cattle, each genotyped with the Illumina BovineSNP50 BeadChip. SNP genotypes on 3 chromosomes (BTA1, BTA16, and BTA28) were used to compare imputation accuracy among various methods, and the application involved imputation of 50k genotypes covering 29 chromosomes based on a set of 7k SNPs contained on the Illumina BovineLD chip. Beagle and Fimpute had the greatest accuracy, which varied between 0.87 and 0.99, among the 6 imputation softwares. The ensemble method outperformed the independent packages; however, the sequence of independent packages in voting affected imputation accuracy. The ensemble systems yielding the best imputation accuracies were those that had Beagle as the first classifier, followed by one or 2 methods that utilized pedigree information. A salient feature of the ensemble method is that it provides a way of solving imputation inconsistencies among different imputation methods, hence leading to a more reliable system for imputing genotypes relative to any of the individual procedures.

Key Words: AdaBoost, imputation, ensemble-based system

610 Gene expression analysis of longissimus and semitendinosus muscle from Angus and Charolais finishing steers. J. W. Buchanan*[1], A. K. Sexten[2], J. W. Dillwith[1], C. R. Krehbiel[1], and R. G. Mateescu[1], *[1]Oklahoma State University, Stillwater, [2]Kansas State University, Manhattan.*

Fatty acid profile is an important component in determining the healthfulness of beef products. However, the fatty acid profile of beef is variable among breeds and within different cuts in the same breed. Genetic regulation of fatty acid profile is known to vary among breeds and within different muscles. The objective of this study was to analyze gene expression in both longissimus and semitendinosus muscles in 6 Angus and 6 Charolais heifers finished on concentrate for 140 d. Expression of *ADIPOQ* (*adiponectin*), *FASN* (*fatty acid synthase*), *DGAT2* (*diglyceride acyl transferase 2*), *PPARG* (*peroxisome proliferator activated receptor gamma*), and *GPAM* (*glycerol-3 phosphate acyltransferase muscle type*) were analyzed for differences between both muscle and breed. Total RNA was extracted from intramuscular samples and gene expression was quantified using SYBR Green real-time PCR. Delta CT (threshold cycle) values for each gene were analyzed for differences between breed and muscle using the GLM procedure in SAS (Cary, NC) and means were separated with the PDIFF option. In Angus cattle, *ADIPOQ* and *FASN* were upregulated 6.7- and 4.1-fold respectively in semitendinosus compared with longissimus muscle ($P < 0.05$). In Charolais, *PPARG* was upregulated 43-fold in semitendinosus compared with longissimus ($P < 0.05$). In longissimus, *ADIPOQ*, *FASN*, *PPARG*, and *DGAT* were upregulated 7.6-, 6.0-, 5.0-, and 6.1-fold in Charolais compared with Angus ($P < 0.05$). In semitendinosus, *PPARG* was upregulated 35.8-fold in Charolais compared with Angus ($P < 0.05$). Significant differential expression differences across both muscle and breed indicates these genes are likely affecting fatty acid metabolism in the tissues analyzed.

Key Words: beef, fatty acid, gene expression

611 Single nucleotide polymorphisms in the NPY, leptin, and IGF-1 genes in Angus cattle: I Effects on feed efficiency. A. I. Trujillo,* A. Casal, and P. Chilibroste, *Universidad de la Republica, Facultad de Agronomia, Montevideo, Montevideo, Uruguay.*

Single nucleotide polymorphisms (SNP) that showed associations with residual feed intake (RFI) may be useful for marker-assisted selection. There is limited research about specific gene mutations and RFI. Neuropeptide Y (NPY), leptin (LEP), and insulin-like growth factor-1 (IGF-1) are candidate genes due to their role in the regulation of feed intake, growth and energy balance. Thus, our aim was to study the associations of SNP previously identified in NPY (A/G, intron 2), LEP (C/T, exon 2) and IGF-1 (C/T, promoter region) genes to dry matter intake (DMI), metabolizable energy intake (MEI), average daily gain (ADG) and RFI. Female Angus calves carrying 3 putative favorable alleles simultaneously (V = validation group; n = 19; 187 ± 33 kg BW, 260.6 ± 34 d old at the beginning of test (BT)) and calves carrying 3 putative unfavorable alleles (C = control group, n = 19, 185 ± 33 kg BW, 263.9 ± 17 d old at BT) were fed a TMR diet (60:40 concentrate: alfalfa hay, as fed) twice a day during 56 d. DMI was estimated by the difference between feed offered and refused; BW was recorded every 2 wk. RFI_K was residual from a regression of DMI on ADG and mid-test $BW^{0.75}$. RFI_{SCA} was residual from regressing DMI on DMI predicted from Australian feeding standards. RFI_{NRC} was residual from regressing DMI on DMI expected from net energy system (NRC_{1984}) and RFI_{ME} was the same as RFI_{NRC} but expressed in ME values. Mean DMI, MEI, ADG and RFI_K were 7.16 ± 1.08 kg DM, 18.53 ± 2.78 Mcal ME, 1.24 ± 0.19 kg BW, and 0.00 ± 0.41, respectively. Mean values for RFI_{SCA}, RFI_{NRC}, and RFI_{ME} were 0.00 ± 0.49, 0.00 ± 0.50, 0.00 ± 1.27, respectively. Calves of V group had lower DMI and MEI ($P = 0.046$, $P = 0.032$, respectively) and similar ADG ($P = 0.195$) than calves of C group when initial BW (covariate) and age (random effect) were included in a linear mixed model. Calves of V group were more efficient ($RFI_{NRC} = -0.181$, $RFI_{SCA} = -0.171$, $P < 0.05$; $RFI_{ME} = -0.3279$, $RFI_K = -0.111$, $P < 0.1$) than calves of C group. Spearman rank correlation between RFI methods was highly significant ($P < 0.001$). These results indicate that there is an association between the SNP of NPY, LEP and IGF-1 and RFI.

Key Words: beef cattle, residual feed intake, single nucleotide polymorphism

612 Single nucleotide polymorphisms in the NPY, Leptin, and IGF-1 genes in Angus cattle: II Effects on serum IGF-1 and leptin concentrations. A. I. Trujillo,* A. Casal, and P. Chilibroste, *Universidad de la Republica, Facultad de Agronomia.*

Single nucleotides polymorphisms (SNP) in the leptin (LEP) and insulin-like growth factor (IGF-1) genes or its promoters, have been associated with differences in serum LEP and IGF-1 concentrations and others relevant traits including residual feed intake (RFI). The aim of the study was to evaluate the relationship of the SNP, previously

identified in NPY (A/G, intron 2), LEP (C/T, exon 2) and IGF-1 (C/T, promoter region) genes, with serum LEP and IGF-1 concentrations. Female Angus calves, genotyped at mentioned SNP, were classified as carrying 3 putative favorable alleles simultaneously (n = 19; 187 ± 33 kg BW; 260.6 ± 34 d old; V = validation group), or 3 putative unfavorable alleles (n = 19; 185 ± 33 kg BW; 263.9 ± 17 d old; C = control group). Calves were fed a TMR diet (60:40 concentrate: alfalfa hay, as fed) during 56 d. Dry matter intake (DMI) was estimated as the difference between feed offered and refused; BW was recorded every 2 weeks. RFI_{ME} was residual from regressing energy metabolizable intake (EMI) on EMI expected from net energy system (NRC1984). Blood samples were collected by jugular venipuncture at sampling date at the beginning (SD1) and at the end of test (SD2). Data was analyzed as a repeated measure using a mixed model and means were considered to differ when $P < 0.05$. Mean serum concentration of IGF-1 and LEP were 281.8 ± 110.8 and 2.92 ± 0.97 ng/mL, respectively. IGF-1 concentration did not differ between groups, was affected by initial BW (iBW; $P < 0.0001$) and was greater in SD2 than in SD1 (348.8 vs. 214.9 ± 12.2 ng/mL, respectively). LEP concentration did not differ between groups and tended to be affected by iBW ($P < 0.1$). In addition, IGF-1 concentration was moderate and positively correlated with DMI (r = 0.40, $P < 0.05$) while LEP concentration was moderate and negatively correlated with RFI_{ME} (r = −0.40, $P < 0.05$). Although the SNPs considered were not associated with any of the studied hormones our data show a correlation between LEP concentration and RFI_{ME}. Further studies are needed but these results suggest that LEP serum concentration could be use as an indicator of efficiency in beef cows.

Key Words: single nucleotide polymorphism, IGF-1, leptin

613 A distributed parallel computing approach for tuning Bayesian regression models for genomic selection with application to Angus cattle. X.-L. Wu*[1,2], H. Okut[2], C. Sun[1], G. J. M. Rosa[2], S. Bauck[3], B. W. Woodward[3], R. D. Schnabel[4], J. F. Taylor[4], and D. Gianola[1,2], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]Department of Animal Sciences, University of Wisconsin, Madison, [3]Merial Limited, Duluth, GA, [4]Division of Animal Sciences, University of Missouri, Columbia.*

Predicting genetic merit of candidates for breeding purposes using an optimal subset of whole-genome markers is a model selection problem. A BayesCπ model, for example, postulates that a portion, π, of all SNP markers have no effect on the quantitative trait. Inferring π, however, adds extra complexity to the Bayesian regression model, which is dependent on the extent of data and the underlying trait genetic architecture, and requires more computing time. It is also questionable whether the π parameter optimized in training data necessarily leads to best prediction when generalized to testing data particularly for traits governed by the infinitesimal model. Here, we propose a distributed parallel computing (DPC) approach to choose optimal π values in Bayesian regression models, based on their cross-validation performance in testing data sets. Several Bayesian regression models were computed in parallel in computer clusters, each assuming a distinct value of π. These 2 approaches to choosing π were applied to prediction of marbling score in 3,078 registered Angus bulls. It was found that the π values obtained directly from BayesCπ fitted to the training data were smaller than those obtained from the DPC approach as supported by testing data. This reflected that BayesCπ fit more SNP markers in the model than the DPC approach. In general, the π obtained from BayesCπ was > 95% with a 50K SNP panel, and it was moderate (40–70%) with a 3k SNP panel. In contrast, the DPC approach consistently yielded the best predictions using from 600 to 900 SNP markers. Hence, a model that describes variation in a training set well does not necessarily lead to the best predictions when generalized beyond the training set. With a low-density SNP panel, however, interpretation of SNP markers having putatively nonzero effects should be done with caution, because many could be distant from functional genes or quantitative trait loci.

Key Words: distributed parallel computing, genomic selection, single nucleotide polymorphism

614 Quantitative traits and genomics of heterosis in Wagyu × Angus F_1 progeny. L. F. Zhang[1,2], J. J. Michal[1], J. V. O'Fallon[1], Z. X. Pan[1,3], C. T. Gaskins[1], J. J. Reeves[1], J. R. Busboom[1], M. V. Dodson[1], R. W. Wright Jr.[1], and Z. Jiang*[1], *[1]Department of Animal Sciences, Washington State University, Pullman, [2]College of Animal Sciences, Zhejiang University, Hangzhou, Zhejiang, China, [3]College of Animal Sciences and Technology, Nanjing Agricultural University, Nanjing, Jiangsu, China.*

The objective of the present study was to understand the genetic complexity of economically important traits in beef cattle. A total of 91 genes were investigated for their associations with 6 carcass and 24 fatty acid composition traits in a Wagyu × Angus population, including 43 Wagyu bulls and their potential 791 F1 progeny. Parentage assignment was performed using the Cervus package, while the association analysis was conducted using the PROC MIXED procedure of SAS. All significant markers along with their quantitative trait modes (QTMs) for each phenotype were then integrated into a linear regression analysis to identify genetic networks. Of the 182 SNPs evaluated, 102 SNPs that were in Hardy-Weinberg equilibrium with minor allele frequencies (MAF) > 0.15 were selected for parentage assignment. Linkage disequilibrium analysis further identified 75 of these 102 SNPs derived from 54 genes as tagged SNPs for association analysis. After Bonferroni correction, single-marker analysis revealed a total of 113 significant associations between 44 genes and 29 phenotypes (adjusted $P < 0.05$). Multiple-marker analysis confirmed single-gene associations for 10 traits, but revealed 2-gene networks for 9 traits and 3-gene networks for 8 traits, respectively. These associations/networks were orchestrated by only 19 genes, including ATP-binding cassette A1, apolipoprotein B, ankyrin repeat and SOCS box-containing 3, calpains 1 and 12, calpastatin, corticotropin releasing hormone, dermatan sulfate epimerase-like, EGF containing fibulin-like extracellular matrix protein 1, fatty acid desaturase 2, guanine nucleotide binding protein gamma 3, lipase, hormone-sensitive, phospholipid transfer protein, regulator of calcineurin 1, solute carrier family 27 A1 and A2, tumor necrosis factor, transcription factor B2, mitochondrial and urotensin 2 receptor. In addition, we observed an interesting phenomenon that crossbreeding of different breeds might change gene actions to dominant and overdominant modes, thus explaining the origin of heterosis in their F1 progeny. The present study further confirmed that these pathway-based genes are useful targets for improving meat quality traits and healthful beef products in cattle.

Key Words: quantitative traits, genetic networks, beef cattle