Breeding and Genetics: Genomic methods and application—Beef

W66 GWAS between single nucleotide polymorphisms with beef fatty acid profile in Nellore cattle using the single-step procedure. Marcos V. A. Lemos*[1], Hermenegildo L. J. Chiaia[1], Mariana P. Berton[1], Fabiele L. B. Feitosa[1], Carolyn Aboujaoude[1], Adrielle M. Ferrinho[2], Lenise F. Mueller[2], Joyce J. M. Furlan[2], Angelica S. C. Pereira[2], Lucia G. Albuquerque[1], and Fernando Baldi[1], *[1]State University of São Paulo, Jaboticabal, São Paulo, Brazil, [2]University of São Paulo, Pirassununga, São Paulo, Brazil.*

The aim of this study was determine genomic regions associated with the profile of beef fatty acid (FA) of Nellore cattle finished in feedlot using the single-step method. A total of 1,616 genotypes and 963 phenotypes were used. The FA profile was analyzed in *Longissimus thoracis* samples using a gas chromatography, with a 100-m capillary column. The following fatty acids were analyzed: lauric (C12:0), palmitic (C16:0), stearic (C18:0), oleic (C18:1 *cis*-9), linoleic (C18:2 *cis*-6), CLA (C18:2 *cis*-9 *trans*-11), CLA (C18:2 trans10 cis12), linolenic (C18:3 n3), myristic (C14:0), myristoleic (C14:1), docosahexaenoic (C22:6 n3), elaidic (C18:1 n9t), vaccenic (C18:1 t11), arachidonic (C20:4 n-6) eicosatrienoic (C20:3 n6 cis-8,11,14) and alfa-linolenic (C18:3 n6). The animals were genotyped with the BovineSNP BeadChip (High-Density Bovine BeadChip). After quality control of genotypes, a total of 470,000 SNPs and 1,556 samples remained. The model used for the (co)variance and genetic parameter estimation included the random genetic additive direct effect, the fixed effect of the contemporary groups, and the animal's slaughter age as a covariable. To determine the areas of QTL, segments that were ≥ 1% of the additive genetic variance were chosen. For identification and positioning of these segments, the database available in the "National Center for Biotechnology Information" and Ensembl Genome Browser were used. A total of 115 genomic regions (1-Mb SNP windows) associated with the FA profile were identified many of these regions were previously detected in other cattle breeds, like the gene *ELOVL5* (fatty acid elongase 5) associated with the C20:4 n-6 FA, the *ESRRG* (estrogen receptor-related gamma gene) was associated with the C12:0 FA and the *PCYT1A*, TCTEX1D and *GALNTL6* were associated with C18:2 cis-9 cis-12 n-6, C14:0 and C16:0 FA. The genes present in these regions may help to explain the genetic basis of FA profile in Bos indicus cattle, contributing to better selection of these traits associated with improvement of human health.

Key Words: *Bos indicus*, fatty acid composition, genetic markers

W67 Genotype imputation and haplotype-phase inference using trio based reference panel in Hanwoo (Korean cattle). Dajeong Lim*, Jung-Woo Choi, Hyung-Chul Kim, Han-Ha Chai, and Yong-Min Cho, *National Institute of Animal Science, Suwon, South Korea.*

In recent years, large numbers of cattle have been genotyped with SNP arrays from 3K to 800K. These platforms can be available to increase the efficiency and accuracy of breeding programs by implementing genomic selection. As for cattle, there are currently several imputation/phasing methods used in genomic selection, genome-wide association (GWA) studies, or genetic diversity analysis. Currently, many imputation and phasing methods are introduced to reduce the number of missing genotypes and to infer the haplotypes from these genotype data. Despite these efforts, imputation or phasing errors are still present. Next-generation sequencing (NGS) price has been consistently dropped, various population genomic theories and breeding program can be now applied to the sequencing data obtained from population of each breed of interest. For example, long-range haplotype sequencing technology can phase 99% of single-nucleotide variants (SNVs) in sequencing data without imputation process; current technologies typically phase ~95–97% in human. Therefore, we describe the phasing study using Hanwoo trio sample. First, we selected the representative trio sample from pedigree analysis in Hanwoo population. Genotyping was performed based on the Illumina 800K. Imputations for genotype data in this study were done using BEAGLE and FIMPUTE, genotype imputation tools that use a reference panel of haplotypes to estimate phase and impute missing genotypes in trio data. Second, We sequenced the trio data using Illumina Long-read haplotyping technology known as Moleculo. The short sequence reads producing from each molecule are assembled into synthetic long-reads. These fragments assign haplotype to homologous chromosomes in the phasing application. Finally, we compared accuracy of imputation/phasing based on the SNP array and sequencing data of an optimal reference panel of maternal/paternal haplotypes. These results help in improving selection and breeding value estimation and in avoiding imputation errors from SNP information.

Key Words: phasing, imputation, Hanwoo

W68 Genome-wide association study analysis for meat traits of beef cattle. Hoyoung Chung*, *National Institute of Animal Science, Suwon, KY, Korea.*

To identify genomic loci with an effect on meat quality traits in Hanwoo cattle, 3,000 animals with carcass phenotypes were genotyped with a customized 56K Affymetrix SNP chip. Genome-wide association studies (GWAS) were performed for marbling (MAR), maturity (MAT), backfat thickness (BFT), loin eye area (LEA), carcass weight (CAW), meat quality grade (MQG), and meat yield grade (MYG). Multiple statistically significant SNP were identified for MAT (674 SNP), MAR (595), CAW (754), LEA (506), BFT (440), MYG (496), and MQG (2,850) with chromosomes 14 and 23 having extreme significant associations for CAW and MYG, respectively. A 66-bp insertion in *ADIPOQ* from 81966364 to 81966419 was genotyped by agarose gel electrophoresis in 3,000 animals to verify the associations of GWAS loci located in the *ADIPOQ* region. The *ADIPOQ* insertion was significantly associated with MAR ($P = 0.034$), BFT ($P = 0.004$), LEA ($P = 0.014$), CAW ($P = 0.002$), and MYG ($P = 0.003$). This study's significant SNP may be used in marker-assisted selection programs to improve meat quality traits in beef cattle.

Key Words: GWAS, SNP, meat trait

W69 Admixture analysis in Brazilian synthetic cattle. Marcos E. Buzanskas*[1], Ricardo V. Ventura[2], Tatiane C. S. Chud[1], Daniel J. A. Santos[1], Priscila A. Bernardes[1], Thiago B. R. Silva[1], Mauricio A. Mudadu[3], Luciana C. A. Regitano[3], Marcos V. G. Barbosa da Silva[4], Changxi Li[5], Flavio S. Schenkel[2], Maurício M. Alencar[3], and Danísio P. Munari[1], *[1]UNESP – Univ Estadual Paulista, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, SP, Brazil, [2]University of Guelph, Guelph, ON, Canada, [3]Embrapa Southeast Livestock, São Carlos, SP, Brazil, [4]Embrapa Dairy Cattle, Juiz de Fora, MG, Brazil, [5]University of Alberta, Edmonton, AB, Canada.*

The development of synthetic breeds in Brazil from crosses between *Bos taurus indicus* (Bti) and *Bos taurus taurus* (Btt) is very useful when it

is desired to combine the fitness and carcass yield. The Canchim breed (CA), which has expected proportions of 62.5% Charolais and 37.5% zebu (Nellore breed), have been the focus of several studies because this breed has high carcass quality and adaptability to extensive production system. The aim of this study was to estimate the genetic composition in the Canchim breed using single nucleotide polymorphism (SNP) data. Canchim animals (285 individuals) were genotyped with the Illumina BovineHD BeadChip (777962 SNPs). To estimate the genetic contribution of Btt and Bti, 814 animals from the Nellore breed (NE) and 405 animals from the Charolais breed (CH) were genotyped with the Illumina BovineHD BeadChip and BovineSNP50 BeadChip (54609 SNPs), respectively. The PLINK v.1.9 software was used to combine the data, perform genotype quality control, and estimate the linkage disequilibrium (r^2). The ADMIXTURE software was used to estimate the genetic contributions. Genotype quality control resulted in 283, 811, and 405 animals from the CA, NE, and CH breeds and 29716 SNPs. The genetic contributions of Btt and Bti in the Canchim breed were, in average, 72.5% and 27.5%, respectively. Minimum and maximum proportions of Btt and Bti ranged from 66.0% to 89.0% and 11.0% to 34.0%, respectively, in Canchim cattle. The differences between the expected proportions and the estimated proportions of Btt and Bti were due to the patterns r^2, which are greater in shorter distances (0–0.04 Mb) for CH (0.20), followed by CA (0.16), and NE (0.15). When the r^2 between adjacent SNPs are high, recombination rates should be low, which may be indicative of greater contribution of CH animals in the composition of CA breed. The maximum proportion of 16.0% of Btt was observed for NE, indicating remote crossbreeding, which could have contributed to higher Btt proportion in CA animals.

Key Words: beef cattle, genomics, genetic structure

W70 Genome-wide association analysis and gene ontology enrichment of meat tenderness in Polled Nellore cattle in Brazil. Leticia M. Castro[1,4], Claudio U. Magnabosco[2,3], Fernando B. Lopes[2,4], Roberto D. Sainz*[2,5], and Guilherme J. M. Rosa[6], *[1]Federal University of Goias, Goania, GO, Brazil, [2]Embrapa-Brazilian Agricultural Research Corporation, Brasilia, DF, Brazil, [3]CNPq-National Council for Scientific and Technological Development, Brasilia, DF, Brazil, [4]Capes-Coordination for the Improvement of Higher Education Personnel, Brasilia, DF, Brazil, [5]University of California, Davis, CA, [6]University of Wisconsin, Madison, WI.*

Brazil has the largest commercial cattle herd worldwide, but its meat quality is highly variable. The national herd is largely composed of *Bos indicus* breeds, which in general have less tender meat than *Bos taurus* cattle, decreasing the product value. This study was carried out to identify genomic regions and biological relevant pathways associated with meat tenderness in Polled Nellore cattle. Data consisted of Warner-Bratzler shear force (WBSF) values of *Longissimus* muscle after 7 d of aging, from 326 Polled Nellore animals born in 3 breeding seasons (2002, 2005 and 2009) at the OB ranch, located in the State of Mato Grosso, Brazil. The animals were genotyped using either the Bovine HD Chip (777k) or the GGP-Indicus Chip (77k). The imputation from the GGP to the HD Chip was performed using FImput software. SNPs were excluded when GenCall <0.7, Call rate <0.90, EHW $P <$ 0.01 (using Bonferroni adjustment), and MAF <0.05. Due to large dispersion of sires (progenies' parents), the population stratification was controlled by the 3 first genomic principal components. Genome-wide association analysis (GWAS) was performed using the Efficient Mixed-Model Association (EMMA) method. The GWAS was complemented with a gene set enrichment analysis of Gene Ontology (GO) terms using the FatiGO procedure. The most significant markers ($P < 0.0001$) were located on chromosomes 2, 3, 7, 10, 11, 17, 20, 21, 24 and 25, indicating several QTLs associated with meat tenderness throughout the genome. Additionally, 48 GO terms were deemed enriched. Several of these functional categories can be related to WBSF in Polled Nellore cattle, such as activities of ion channels, membrane cell transportation, growth factors, and protein serine/threonine phosphatase complex, which participate in processes that inactivate apoptosis components. These results help to elucidate the metabolic pathways related to this trait, which is of extreme economic and social importance to Brazil as Nellore is the dominant beef cattle breed in the country. Financial support: EMBRAPA, CNPq, CAPES.

Key Words: shear force, GWAS, pathway

W71 Genomic-polygenic and genomic predictions of direct and maternal effects for growth traits in a multibreed Angus-Brahman cattle population. Mauricio Elzo*[1], Milton Thomas[2], Dwain Johnson[1], Carlos Martinez[1], Cliff Lamb[1], Owen Rae[1], Jerry Wasdin[1], and Joseph Driver[1], *[1]University of Florida, Gainesville, FL, [2]Colorado State University, Fort Collins, CO.*

The objectives of this research were to compare variance components, genetic parameters, and EBV rankings for birth weight (BW) direct and maternal, weaning weight (WW) direct and maternal, and postweaning gain from 205 d to 365 d (WG) direct using 3 genomic-polygenic and one polygenic model. In addition, trends in EBV were evaluated for each trait and model as Brahman fraction increased from 0% to 100%. The Angus-Brahman multibreed data set included 5,264 animals born between 1987 and 2013. Genomic-polygenic models 1 (GP1; pedigree relationships for all animals; genomic relationships for genotyped animals), 2 (GP2; pedigree relationships for non-genotyped animals only; genomic relationships for genotyped animals), and 3 (GP3; no pedigree relationships; genomic relationships for genotyped animals) used actual and imputed genotypes from 46,768 SNP markers. Variance components and genetic parameters were estimated using REML procedures. Estimates of variance components and genetic parameters from GP1 were the most similar to those from the polygenic model, followed by those from GP2, and the least similar (particularly for maternal traits) were those from GP3. Similarly, the highest rank correlations were those between animal EBV from the polygenic model and GP1 (0.98 to 0.99), followed by those from GP1 and GP2 (0.82 to 0.94) and lastly by those from the polygenic model and GP2 (0.81 to 0.94). Model GP3 performed poorly for maternal traits due to ignoring calf-dam relationships (−0.12 to 0.23). These results indicated that the polygenic model and genomic-polygenic model 1 should be preferred. High genotyping costs could still make the polygenic model preferable for commercial beef cattle operations. Brahman animals tended to have higher EBV for BW direct and WW direct, and lower EBV for WG direct, BW maternal, and WW maternal. However, low regression coefficients for EBV on Brahman fraction ensured that high, medium, and low EBV animals from all breed compositions existed for all growth traits in this multibreed population.

Key Words: cattle, genomic, growth

W72 Genomic regions associated with beef fatty acid profile in Nellore cattle. R. Espigolan*[1], M. V. A. Lemos[1], H. L. J. Chiaia[1], M. P. Berton[1], F. L. B. Feitosa[1], D. G. M. Gordo[1], R. L. Tonussi[1], A. F. B. Magalhães[1], A. M. Ferrinho[3], L. F. Mueller[3], M. R. Mazalli[3], J. J. M. Furlan[3], A. S. C. Pereira[3], L. G. Albuquerque[1,2], F. Baldi[1], *[1]Universidade Estadual Paulista, Faculdade de Ciencias Agrarias e Veterinarias, Jaboticabal, SP, Brazil, [2]Conselho Nacional de Desenvolvimento*

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