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*

Cientifico e Tecnologico (CNPq), Brasilia, DF, Brazil, [3]Universidade de Sao Paulo, Faculdade de Zootecnia e Engenharia de Alimentos, Pirassununga, SP, Brazil.

The objective of this study was to identify genomic regions associated with beef fatty acid profile (FA) in Nellore males finished in feedlot using the single-step method. A total of 1,616 genotypes and 963 phenotypes were used. Animals were genotyped using the high-density BovineHDBeadChip panel, which contains 777,962 SNP markers distributed throughout the genome. Quality control (QC) criteria were: i) SNPs with minor allele frequency ≤5%, call rate ≤90% (CR); ii) Only samples with CR ≥90% were considered. A total of 470,007 SNPs and 1,556 samples remained in the data set. The FA profile was measured in *Longissimus thoracis* muscle using a gas chromatography, with a 100 m capillary column. The following FA were analyzed: total saturated FA (SFA), total monounsaturated FA (MUFA), total polyunsaturated FA (PUFA), omega-3 (n-3) and omega-6 (n-6). Contemporary groups (CG) were defined as farm, year of birth, and yearling management group. Variance components estimation model included random additive direct genetic effects, fixed effects of CG, and animal's slaughter age as a covariable (linear and quadratic effect). For SFA, MUFA, PUFA, n-3 and n-6, a total of 31, 19, 40, 6 and 6 genomic regions that explain 1% or more of the additive genetic variance were found, respectively. Preliminary studies showed that many of these regions were not previously detected in other cattle breeds. Genes like *PRKAR1A* (protein kinase), *ELOVL5* (fatty acid elongase 5), *FASN* (fatty acid synthase) and *SCD* (esterol-CoA desaturase) were also identified. This study found several genomic regions associated with meat fat acidy profile in Nellore cattle that can be used for further studies to contribute for the production of healthier meat. This work was supported by Sao Paulo Research Foundation (FAPESP) grant #2009/16118-5 and grant #2011/21241-0.

Key Words: fatty acid composition, molecular marker, SNP

W73 An SNP association study evaluating Brahman and Brahman-influenced steers for growth and carcass traits. Amanda Royer[1], Chris Shivers[3], David Riley[4], Mauricio Elzo[5], and Matthew Garcia*[1,2], *[1]Louisiana State University School of Animal Sciences, Baton Rouge, LA, [2]LSU AgCenter, Baton Rouge, LA, [3]American Brahman Breeders Association, Houston, TX, [4]Department of Animal Science, Texas A&M University, College Station TX, [5]Department of Animal Science, University of Florida, Gainesville, FL.*

Brahman cattle are important in tropical regions due to the breed's ability to tolerate excessive heat and parasite presence. However Brahman cattle exhibit lower yielding, lower quality carcasses as compared with *Bos taurus* breeds. The objective of the current study was to evaluate potential SNP associations on 4 candidate genes for growth and carcass traits in a population of Brahman and Brahman-influenced steers. A total of 42 Brahman and Brahman-influenced steers born between 2009 and 2014, at Louisiana State University Central Research Station in Baton Rouge, Louisiana, were utilized. Steers were evaluated through the American Brahman Breeders Association (ABBA) carcass evaluation project in Gonzales, Texas, for growth, feedlot performance, and carcass quality and composition traits. Growth traits measured at the Central Research Station beef unit before shipment to the feedlot include birth weight, weaning weight, and hip height. Traits measured in Gonzales, Texas, included feedyard entrance weight, harvest weight, and average daily gain. Carcass traits measured include hot carcass weight, ribeye area, marbling score, yield grade, quality grade, dressing percent, and Warner-Bratzler shear force score. A mixed model design with growth, carcass traits and individual SNP genotype fit as dependent variables and breed type, year, dam fit as independent variables was utilized to evaluate potential SNP associations. Sire was fit as a random variable in the model. Four known candidate genes were chosen for SNP analysis based on previous association with growth and carcass traits. Candidate genes include calpastatin (CAST), calpain (CAPN), thyroglobulin (TG), and adiponectin (ADIPOQ). A total of 20 SNP were chosen for each CAST and CAPN, and a total of 30 SNP were chosen for each TG and ADIPOQ. All SNP were selected equidistantly spaced across each candidate gene. Although multiple SNP in the current study were significantly ($P < 0.05$) associated with growth and carcass traits, they must first be validated in much larger and diverse populations before implementation into selection strategies.

Key Words: *Bos indicus*, carcass trait, growth

W74 Major loci associated with growth traits on BTA14 in Hanwoo (Korean cattle). Seung Hwan Lee*[1,3], Ki Yong Chung[1], Cedric Gondro[2], Chang Gwan Dang[1], Hyeong Cheul Kim[1], Sidong Kim[1], and Hee Ceol Kang[1], *[1]National Institute of Animal Science, Pyeongchang, Gangwon, Korea, [2]University of New England, Armidale, NSW, Australia, [3]Chungnam National University, Daejeon, Chungnam, Korea.*

Genome-wide single marker regression using Bovine 50K BeadChip was performed on growth traits from 1,012 Hanwoo steers in Hanwoo (Korean Cattle). SNPs were excluded from the analysis if they failed in over 5% of the genotypes, had median GC scores below 0.6, had GC scores under 0.6 in less than 90% of the samples, deviated in heterozygosity more than 3 standard deviations from the other SNPs and were out of Hardy-Weinberg equilibrium for a cutoff *P*-value of $1E^{-5}$. Unmapped and SNPs on sex chromosomes were also excluded. A total of 32,696 SNPs were used in this analysis. To test an association between SNP and QTL, single marker regression analysis was implemented in this study. SNP was assumed to be in LD with QTL in close proximity and the effect evaluated was additive effect (QTL allele substitution effect). The Bonferroni-corrected genome wide significant association ($P < 1.5 \times 10^{-6}$) was applied to detect significant SNPs for the GWAS. The GWAS identified one major QTL for body weight at 6, 12, 18 and 23 mo ranging 23Mb to 25Mb on BTA14. The most significant SNP was Hapmap32241-BTC-054753 (24Mb, $P = 1.8 \times 10^{-6}$) for BW6, Hapmap27934-BTC-065223 (25Mb, $P = 1.2 \times 10^{-10}$) for BW12, BW18 and BW23 in Hanwoo. The most significant SNPs accounted for 8 to 10% of additive genetic variance, which is quite large proportion against total additive genetic variance. The Hapmap27934-BTC-065223 has 12.97 kg of allele substitution effect in body weight at 12 mo (BW12). The results revealed that growth traits was affected by major QTL with large effect and many other SNP with small effects with the normal distribution.

Key Words: genome-wide association study, major loci, BTA14

W75 Identification of shared copy number variation among Spanish beef cattle. T. B. R. da Silva*[1], A. González-Rodríguez[3], E. Mouresan[3], J. J. Cañas-Álvarez[5], L. Varona[3], D. P. Munari[1], M. J. Carabaño[2], C. Avilés[4], P. Martínez-Camblor[6], and C. Díaz[2], *[1]Univ Estadual Paulista, Jaboticabal, SP, Brazil, [2]Instituto Nacional de Investigacion y Tecnologia Agraria y Alimentaria, Madrid, MD, Spain, [3]Univ de Zaragoza, Zaragoza, AR, Spain, [4]Univ de Cordoba, Córdoba, AN, Spain, [5]Univ Autonoma de Barcelona, Barcelona, CT, Spain, [6]Univ De Valladolid, Valladolid, CL, Spain.*

Copy number variations (CNV) are defined as structural variation with 1 kb or larger, and are present in the genome in several forms. Gene

expression and gene dosage can be affected by CNV, therefore it can be associated with diseases and livestock economic traits. Local Spanish breed such as Asturiana de los Valles (AV); Avileña Negro-Ibérica (ANI); Morucha (Mor); Pirenaica (Pi) and Retinta (Ret) breeds play an important role in the beef market in Spain. The aim of this paper was to identify CNVs being shared among the 5 breeds and verify the functional annotation of the genes within these CNVs. The 366 animals were genotyped with the Illumina BovineHD BeadChip, which 75 are from AV; 74 from ANI; 75 from Mor; 74 from Pi and 68 from Retinta. Each breed had 25 families composed by father-mother-offspring, exception those breeds that had not 75 individuals, which had 25 incomplete families (mother-offspring). The families within breed were selected to have greater genetic variability. The Penncnv software was applied to detect and filter the CNVs, which considers the BAF (B Alelle Frequency) and LRR (Log R Ratio) signals. We used the trio calling option to identify the CNVs, which consider the pedigree information after the individual CNV calling. We found CNVs being shared among breeds, varying from 87 between Pi and Ret to 514 between AV and Mor. These results suggest evidence that the formation of these breeds may be connected to common ancestry. We found the same CNV in different copy number between breeds, which means, one CNV that is a deletion in certain breed, is an insertion in another one and some of these CNVs encompassed genes. Those genes were WC1.8, PRAME, HSFY2, OAS1X, CD163L1, BOLA-DQA2, OR4P4, OR5J2, TRAC, and they are related to immune system, MHC (Major Histocompatibility Complex) and Olfactory System. Our findings speculate that some CNVs seem to be species specific and the difference of gene copy number among breeds can influence the response to environmental and pathogens challenges.

Key Words: genomic, single nucleotide polymorphism, structural variant

W76 Whole-genome resequencing analysis for identifying genome-wide SNPs and signatures of selection. Dajeong Lim*, Jung-Woo Choi, Bong-Hwan Choi, Won-Hyong Chung, and Seung-Soo Lee, *National Institute of Animal Science, Suwon, South Korea.*

Over the last 30 years, Hanwoo has been selectively bred to improve economically important traits. Hanwoo is currently the representative Korean native beef cattle breed, and it is believed that it shared an ancestor with a Chinese breed, Yanbian cattle, until the last century. However, these 2 breeds have experienced different selection pressures during recent decades. Here, we whole-genome sequenced 10 animals each of Hanwoo and Yanbian cattle (20 total) using the Illumina HiSeq 2000 sequencer. A total of approximately 3.12 and 3.07 billion sequence reads were mapped to the bovine reference sequence assembly (UMD 3.1) at an average of approximately 10.71- and 10.53-fold coverage for Hanwoo and Yanbian cattle, respectively. A total of 17,936,399 single nucleotide polymorphisms (SNPs) were yielded, of which 22.3% were found to be novel. By annotating the SNPs, we further retrieved numerous nonsynonymous SNPs that may be associated with traits of interest in cattle. Furthermore, we performed whole-genome screening to detect signatures of selection throughout the genome. We located several promising selective sweeps that are potentially responsible for economically important traits in cattle; the *PPP1R12A* gene is an example of a gene that potentially affects intramuscular fat content. These discoveries provide valuable genomic information regarding potential genomic markers that could predict traits of interest for breeding programs of these cattle breeds.

Key Words: whole-genome sequencing, Hanwoo, Yanbian

W77 Genome-wide association on growth traits in Nellore Cattle. Rafael M. O. Silva*[1], Daniela A. L. Lourenco[2], Breno O. Fragomeni[2], Luciana Takada[1], Rafael Espigolan[1], Maria E. Z. Mercadante[3], Fernando Baldi[1], Guilherme C. Venturini[1], Joslaine N. S. G. Cyrillo[3], and Lucia G. Albuquerque[1], *[1]Univ Est Paulista Julio de Mesquita Filho–FCAV-UNESP, Jabiticabal, SP, Brazil, [2]The University of Georgia, Athens, GA, [3]APTA Center for Beef Cattle, Animal Science Institute, Sertaozinho, SP, Brazil.*

The purpose of this study was to identify genomic regions which could explain the genetic variation in growth traits in a Nellore cattle population. The data set contained 8702, 8004, 3828, and 3942 records for birth weight (BW), weaning weight (WW), one year weight (YA) and yearling weight (YW), respectively. The animals were genotyped using panels of high-density SNP (Illumina High-Density Bovine BeadChip, 700k). After genomic data quality control, 437,197 SNPs for 631, 635, 342, and 299 animals for BW, WW, YA, and YW, respectively, were also available. SNP solutions were estimated by genome-wide association study using a single-step BLUP approach (ssGWAS). Before the ssGWAS the data was analyzed by a single-step genomic BLUP. Variances were calculated for windows of 200 SNP. Fixed effects in the model included month of birth, age of dam (linear and quadratic effect), contemporary group (sex, year of birth, and pen), plus animal and maternal additive random effects. Moreover, maternal permanent environmental effects were considered as random for all traits but BW. The results showed the top 10 SNP windows for each trait explained a total of 7%, 2.5%, 1.5%, and 3.5% of variance of BW, WW, YA, and YW, respectively. For all of analyzed traits the SNP windows with greatest influences were at chromosome number 14 (BTA14). In all regions of top SNP windows many genes that have been associated with growth in beef cattle were found. Various authors have recommended caution to interpret the results. Even though many SNP windows explained part of variance of all studied traits, it does not necessarily mean those regions cause the phenotypic variation. These results suggest that there are many regions on chromosome 14 associated with growth traits in Nellore cattle. São Paulo Research Foundation (FAPESP) grant 2013/01228-5 associated to grant #2009/16118-5

Key Words: beef cattle, GWAS

W78 Genome-wide association study for flight speed in Nellore cattle. Tiago S. Valente*, Fernando Baldi, Aline C. Sant'Anna, Lucia G. Albuquerque, and Mateus J. R. Paranhos Da Costa, *São Paulo State University, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São Paulo, Brazil.*

The aim of this study was to identify single nucleotide polymorphisms (SNPs) that are significantly associated with temperament, measured by flight speed (FS), in Nellore cattle using the single step procedure (ssGWAS). Temperament was assessed by the speed (m/s) at which each animal exited the crush after yearling weighing. Data were from 16,119 animals with phenotypes and a pedigree file with 162,644 animals. A total of 1,405 animals were genotyped with BovineHD BeadChip. Quality control was performed to exclude SNP markers with unknown genomic position, located on sex chromosomes, monomorphic, MAF < 1%, call rate < 90%, and animal call rate (with less than 90% of SNPs called). After edits, 455,374 SNPs and 1,384 genotyped animals remained. The association analyze was performed by ssGBLUP, a modification of BLUP with numerator relationship matrix $\mathbf{A}^{-1}$ matrix replaced by $\mathbf{H}^{-1}$, that uses the GEBV to estimate the SNPs effects. Variance components and genetic parameters were estimated by Bayesian inference via Gibbs sampling using the softwares GIBBS2F90, PREGSF90 and POSTGSF90, assuming a linear animal model for FS which included

direct additive genetic and residual effects as random effects and contemporary groups as fixed effect. The effects were calculated to segments of 10 sequential SNPs and results interpreted as the percentage (%) of total genetic variance explained by each SNP window. Segments that explained 1% or more of the total genetic variation were considered as canditade region associated with FS. Ten regions were associated with FS: one on BTA1 (1:73354330–73406566, 2.07%), 2 on BTA5 (5:22596661–22604723, 3.04% and 5:119291684–119306475, 1.44%, respectively), one on BTA9 (9:98759214–98767952, 3.33%), BTA11 (11:67385287–67404876, 1.39%), BTA15 (15:16598639–16662233, 1.45%), BTA17 (17:639678–671693, 4.62%), BTA18 (18:34146668–34168795, 1.22%) BTA22 (22:32886184–32904212, 1.08%) and BTA26 (26:47061401–47095621, 1.86%). This result confirms the polygenic architecture related to expression of cattle temperament, resulting from the influence of numerous genes interacting with each other and with environmental factors. Future approaches are required to identify the gene expression associated with the SNP windows found in this study.

Key Words: GWAS, temperament