## BREEDING AND GENETICS: APPLICATIONS AND METHODS IN ANIMAL BREEDING— BEEF

### 0929 (M043) Effects of functional polymorphisms on beef carcass merit.

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To develop a resource to identify polymorphisms present in common beef cattle breeds, and relate those polymorphisms to phenotypic differences, low-coverage genomic sequence was obtained on 186 purebred bulls from 15 predominant breeds in the United States and 84 crossbred sons of these bulls. These bulls were influential in the USMARC Germplasm evaluation population (GPE), enabling sequence-derived genotypes to be imputed throughout the population of individuals genotyped with the BovineHD (HD; $n$ = 1027) and BovineSNP50 ($n$ = 8697) platforms. Variants detected from these sequences were classified according to predicted effect on gene function, with 4699 predicted to cause a loss of gene function (LOF); 66,484 non-synonymous (NS) SNP causing an amino acid change in the protein produced by a gene, and 59,092 that may have a role in gene regulation (REG), occurring in annotated non-coding RNA or regions immediately surrounding a gene. Imputed genotypes of 685 purebred genotyped grandsires in the GPE population (18 to 74 bulls per breed) were used to represent each breed to assess diversity and determine breed effects on carcass merit. Relative genetic distances between breeds were consistent regardless of the set of genotypes considered. Brahman was furthest from any other breed, and Hereford the most distant from any other taurine breed. Similar distances were obtained using HD and ND SNP. The mean between-breed distance estimated with REG variants was about 10% higher than HD or NS, and distances using LOF variants were about 30% lower. Heritability estimates from GBLUP considering records of 5990 genotyped carcasses and treating breeds as genetic groups, ranged from 0.49 for ribeye area to 0.59 for marbling score when using only HD genotypes. Similar estimates were obtained in independent analyses using NS and REG, but the LOF estimates were lower, between 0.29 and 0.32. In four-component analyses with different genomic relationship matrices for HD, NS, REG, and LOF, 68% to 76% of additive variance was attributed to HD, and 2% or less to LOF. Contributions of both NS and REG were between 10 and 16% for carcass weight, marbling, and fat thickness. For ribeye area, the REG component was 31% of additive variance, and NS was nil. The GBLUP breed solutions were consistent with breed differences estimated in previous analyses. USDA is an equal opportunity employer and provider.

**Key Words:** beef cattle, genomic prediction, functional polymorphisms

### 0930 (M044) Steers' carcass characteristics with different genetic predominance fed with diets containing substitution levels of grain corn by millet grain.

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This study aimed to evaluate the crossbred steers' carcass and meat characteristics with European or Zebu genotypic predominance. Considering that commercial animals were used, these animals were divided by genotypic predominance by visual evaluation. Feedlot finished with high diets concentrated percentage (80%), containing different levels of grounded millet grain as replacement for grounded corn grain (0, 33, 66, and 100%). Forty-five steers with European predominance and 44 steers with Zebu predominance, with initial average weight of 317.8 and 320.7 kg, respectively, and average age of 21 mo, were allocated in 16 collective pens. In the total, 89 animals were used from the beginning to the end of the feedlot. For the slaughter evaluation, 6 steers were used from each treatment for carcass evaluation. The animals from each genetic predominance were randomly chosen within of each level of corn substitution by millet grain. The experimental design was completely randomized with factorial arrangement 4 (diets) × 2 (genetic groups– predominance) × 6 (animals). The corn grain replacement by millet grain did not influence significantly slaughter weight (480.4 kg) ($P > 0.05$), hot carcass weight (259.5 kg) ($P > 0.05$), carcass yield (54.1%) ($P > 0.05$), or subcutaneous fat thickness (3.95 mm) ($P > 0.05$). Steers of predominantly European genotype showed significant higher values for slaughter weight (507.6 vs. 453.3 kg) ($P < 0.001$), hot carcass weight (269.6 vs. 249.3 kg ($P < 0.001$), and *Longissimus dorsi* area (65.34 vs. 56.83 cm2) ($P < 0.001$); however, they were lower in carcass yield (53.2 vs. 55.0%) ($P < 0.001$). Millet grain can be used in corn grain substitution for finishing steers since it does not change carcass traits of economic interest. Steers with European predominance are heavier at slaughter, presenting heavier and better carcass conformation.

**Key Words:** carcass weight, subcutaneous fat, zebu.

### 0931 (M045) Genome-wide association analysis for beef traits in Marchigiana cattle breed.

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Genome-wide association studies (GWAs) are procedures that enable to correlate huge amounts of genetic and phenotypic data to find genomic regions that affect traits of economic importance. Several studies have been conducted for dairy cattle while few reports are available for beef cattle. In this study a GWA was performed on Marchigiana breed cattle, one of the most important beef breeds farmed in Italy. Phenotypes were body weight (BW), average daily gain (ADG), carcass weight (CW), dressing percentage (DP), pH at slaughtering (*P*H), shank circumference (SC) and head weight (HW) measured on 408 Marchigiana young bulls slaughtered between 16 and 24 mo of age. Animals were genotyped with the Illumina 54K bead-chip. Edits were on the call rate ( > 0.99), number of missing ( > 2, 5%), MAF ( > 0.01). Data were analyzed with a mixed linear model that included the fixed effects of herd, date of slaughtering, fixed covariables of age at slaughtering, SNP genotype (coded as 0, 1, 2), and the random effect of the sire to account for population stratification. A permutation test with 10,000 replications for each marker was performed to account for multiple testing. Significant markers (Permutation corrected $P < 0.05$) were 12 for BW, 124 for ADG, 36 for CW, 28 for DP, 9 for pH, 19 for SC, and 41 for HW, respectively. Annotated genes in genomic regions corresponding to significant SNP were derived from the UCSC Genome Browser Gateway (http://genome.ucsc.edu/) using intervals of 500 Kbp (0, 25 Mbp upstream and downstream of the significant region). Among identified genes, some were related to bone metabolism, as the OSTN (Osteocrin), SPARC (secreted protein acid cystein rich), muscle physiology as MEF2C (myocyte enhancer factor 2) and CA3 (carbonic anhydrase III, muscle specific) feeding behavior as HCRTR2 (hypocretin (orexin) receptor 2) and fatty acid biosynthesis as ACACB (acetyl-CoA carboxylase β) and ACAD8 (Acyl-CoA dehydrogenase family, member 8), respectively. Of interest were also some genes that could be related to meat quality as FPGS (folylpolyglutammate synthase) on BTA11, TTPA (tocopherol (α) transfer protein) on BTA 14 and GGPS1 (geranylgeranyl diphosphate synthase 1) on BTA28. These genes are involved in the metabolism of antioxidants such as vitamins A, E and folate that are effective molecules in preventing oxidative stress.

**Key Words:** GWA, beef traits, Marchigiana cattle

### 0932 (M046) Estimation of genetic parameters for reproductive traits in a multibreed population of beef cattle.

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Reproductive traits are very important economically relevant traits in beef cattle production, and estimation of genetic parameters for these traits is necessary to optimize selection response and improve profitability of beef production. The objective of this research was to determine genetic parameters for the reproductive traits of heifer pregnancy (HPG), stayability (ST), rebreeding rate (RR) and calving ease (CE) in a multi-breed cattle population. We analyzed a dataset of 10,245 HPG and ST records, 8740 RR records and 11,779 CE records from a large commercial operation in Nebraska that included pedigree information, contemporary groups and sire breed. Hierarchical threshold mixed models based on a probit link specification were used for the bivariate analysis of HPG and ST records and for the univariate analysis of RR and CE with maternal records. The posterior means and 95% posterior probability intervals of additive variance were estimated to be 0.227 ± 0.103 [0.104, 0.418] for HPG and 0.123 ± 0.043 [0.049, 0.215] for ST, and 0.211 ± 0.101 [0.074, 0.449] for RR and 0.216 ± 0.147 [0.04, 0.549] for CE, respectively. Also, the posterior mean and 95% posterior probability interval (*P*PI) of direct maternal variance were estimated to be 0.702 ± 0.229 [0.355, 1.230] for CE. Posterior mean inferences on direct heritability were found to be 0.056 ± 0.019 [0.025, 0.099] for HPG and 0.065 ± 0.021 [0.028, 0.111] for ST, 0.138 ± 0.053 [0.056, 0.254] for RR and 0.08 ± 0.05 for CE, respectively. Posterior mean inferences on maternal heritability were found to be 0.263 ± 0.07 [0.145, 0.417] for CE. The posterior mean of genetic correlation between HPG and ST was low and negative (-0.174 ± 0.289) and insignificant with [-0.665, 0.353] of 95% PPI. The posterior mean and 95% PPI of direct maternal genetic correlation was -0.235 ± 0.132 [-0.509, 0.024] for CE. The low heritability values observed in this study are similar to literature values and the low and negative correlation between HPG and ST indicate that genetic improvement geared towards improving HPG may have antagonistic effect on ST, but this effect is not statistically significant.

**Key Words:** reproductive traits, genetic parameters, threshold model

### 0933 (M047) Copy number variation in the genome of Nellore cattle.

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The aim of this work was to study the distribution of CNVRs (regions of copy number variation) in the genome of Nellore cattle. A total of 3022 animals (females and males) finished in feedlot conditions were used. For genotyping, a panel with more than 777,000 SNP markers (High-density Bovine BeadChip) was used. Samples with Call rate lower than 90% were excluded. The PennCNV algorithm (Wang et al., 2007) was used for CNVs detection. To maintain the quality of the samples, samples with LRR (Log R ratio) standard deviation above 0.30, BAF (frequency of allele B) higher than 0.05 and waviness factor higher than 0.01, were excluded from the analyses (Liu et al., 2013), reducing the number of animals to 1561. The regions of CNVs (CNVRs) were generated by overlapping 73,073 CNVs identified by the CNVRuler program (Kim et al., 2012). Initially, different CNVs length were considered with a minimum size of 10kb, 50kb and all sizes, which resulted in 4459, 1365, and 6399 CNVRs, respectively. When all CNV sizes were considered, the average CNVRs length was 36.4 kb, ranging from 0.65 to 1310 kb. There was a higher incidence of CNVRs at BTA1 (483), BTA6 (381), and BTA2 (380). The chromosomes that showed lower incidence of CNV regions were BTA25 (85), BTA27 (104), and BTA28 (117). Considering the CNVs of all sizes, 35.7, 41.0, and 23.3% of the CNVRs were copy gain, copy loss and both (gain and loss in the same region), respectively. The 6399 CNV regions estimated in the present study coverage approximately 8.80% of the bovine genome (UMD_3.1, 2649,685,063 bp). This study confirms the existence of large structural variations in the genome of Nellore cattle and it would support the genetic improvement of this breed and elucidate the genetic mechanisms involved in the expression of productive traits.

**Key Words:** CNV, CNVR, Nellore

### 0934 (M048) Seasonality and fresh semen quality from Pantaneira and Nellore bulls raised in Brazilian Pantanal.

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Taurine cattle (*Bos taurus*) when subjected to tropical conditions have reduced fertility compared to zebu cattle (*Bos indicus*). The Pantaneira breed (*Bos taurus*) was recently recognized as a Brazilian native breed adapted into climatic conditions of Brazilian Pantanal. However, the seminal parameters of this breed are unknown. Thus, the aim of this work were knowing the seminal parameters Pantaneira breed and evaluate what breed (Pantaneira or Nellore breed) raised on pasture in the southern Brazilian Pantanal region is more adapted to regional climatic conditions. Seven Pantaneiro bulls and three Nellore bulls were used. Semen was collected by electroejaculation. Immediately after collection were evaluated: sperm motility (MOT), vigor (VIG), primary defects (PRIMDEF), secondary defects (SECDEF) and total defects (TOTDEF) semen concentration (CONC), sperm viability (SVIAB) and integrity of acrosomal membrane (ICM). The experiment was conducted in a 2 × 2 factorial arrangement (two breed and two seasons) and data were analyzed by ANOVA and Tukey test, with $\alpha = 5\%$. Seminal parameters in Pantaneira bull are within recommended standards for bovine. SVIAB was lower in winter in both breeds (95.76 ± 1.77% vs. 87.07 ± 4.78%, $P = 0.03$). Nellore bulls showed a higher amount of sperm with SECDEF in summer (2.16 ± 1.09% vs. 0.57 ± 0.31%; $P = 0.02$), and higher percentage of PRIMDEF (61.91 ± 5.92 vs. 26 ± 3.83%, $P = 0.01$) and TOTDEF (62.58 ± 5.63% vs. 27.33 ± 3.91%, $P = 0.03$) in winter. Were not found effects of breed, season, or interaction ($P > 0.05$) in other parameters evaluated. Although Pantaneira breed to be considered a taurine breed (*Bos taurus*), it passed a natural selection process by about 300 yr, adapting to high temperatures in central Brazil and probably has become more resistant to testicular degeneration process. In contrast, Nellore bulls appear to be more sensitive to heat stress by cold. Therefore, it is concluded that Pantaneira breed is most suitable breed to edaphoclimatic conditions in the Brazilian southern Pantanal.

**Key Words:** sperm morphology, heat stress, fertility

### 0935 (M049) Sliding window methods to detection of regions under selection in Nellore cattle.

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The directional selection in bovines lead to genetic differences between breeds or herds because the frequency of alleles range in function of trait selected. A frequency of alleles favorable to selected traits increasing and together also increases the frequency of alleles in adjacent loci. Therefore, mutations under selection are characterized as regions where the allelic frequencies are different from expected under chance or absence of selection. The objective in this study was identify regions under selection in Nellore cattle through of calculate of the difference in allelic frequencies between herds under divergent selection. To this end, we used three experimental herds belongs to Estação experimental de Zootecnia de Sertãozinho-SP, Brazil, two herd selected for higher yearling weight (NeS and NeT) and one herd control (NeC) selected since 1968 to weight near the average. We used 67 animals from NeC, 153 from NeS and 421 from NeT genotyped by the Illumina High Density Bovine SNP BeadChip (777K). After quality control were left 456,816 SNPs. We calculated the frequency of allele B for each SNP in each herd and the allelic difference in this frequency between each pair of herds. Then we adopted the method of comparison between populations described by Hayes et al. (2008) termed sliding window average. This one corresponded with the average of the absolute values of differences to each set of 10 adjacent SNPs, where values that exceeding 0.43 are considered significantly higher than expected in no selection. Although the amount of SNPs used in this study is much higher than that used to determine the empirical significance thresholds, the distribution of differences values here calculated show concordance with its patterns. As expected, a difference above 0.43 was not observed in the sliding window average from NeS-NeT if both herds were selected under same criterion, and intensity would not make sense; the difference between them exceeds the threshold established to predict selection effect on the frequencies. In the NeC-NeS and NeC-NeT sliding window averages there were significant values, 74 and 93, respectively, in chromosomes 3, 4, 6, 7, 12, 16, 18, 20, and 24. The correlation between differences from NeC-NeS and NeT-NeS was high ($r = 0.62$) and the region with max difference between herds contained the PPARGC1A gene, (Bta6). Further, we will analyze the role of genes around the regions considered under selection and also match these results with putative signature selections detected with other methods.

**Key Words:** divergent selection, SNPs

### 0936 (M050) Association between copy number variation regions in the Nellore cattle genome and meat tenderness.

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The present study aimed to analyze the association between the copy number variation regions (CNVR) with meat tenderness of 737 Nellore bulls. The animals were finished in feedlot and slaughtered at approximately 2 yr of age. Samples from the *Longissimus dorsi* muscle with 2.5 cm (thickness) were collected to obtain the meat tenderness using a Warner-Bratzler shear force device. A panel with 777,962 SNPs markers (High-Density Bovine BeadChip) was used to genotype the animals. Samples with call rate below 90% were excluded. The parameters used to estimate the CNVs were: Log R Ratio (LRR) and B Allele Frequency (BAF). For quality control, samples with standard deviation values for LRR < 0.30, BAF < 0.05 and waving factor < 0.01 were eliminated. The CNVR were appointed as the CNVs overlaps in the samples, that were located by the CNVRuler software. The shear force data were adjusted for the effects of farm and year of birth, and management groups at birth, weaning and yearling. The model included the state of CNV as a fixed effect and the age of animal at slaughter as a covariate. The average shear force obtained was 5.51 kgf. A total of 4504 CNVRs with an average size of 36.59 kb were detected. There were 10 CNVRs with MAF greater than 0.05, and among them only two significant ($P < 0.05$) associated with meat tenderness (CNVR_1491, CNVR_1130). The CNVR_1491, located on chromosome 7, is in an intergenic region, possibly serving as an indirect marker. This CNVR is between two regions, the first is not characterized, and the second is a pseudogene of transcription factors for heat shock proteins; therefore, the significant *P*-value for this region is an indication that these genes may be influencing this trait. All these LOC regions are "like" regions, areas that have partial or total similarity to genes in other genome regions. The

CNVR_1130, located on chromosome 5, is in theory a intergenic region. There were four regions within this CNVR, two are not characterized and the other two are "like" sequences of the gene associated with butyrophilin protein subfamily 1 member A1, which participates in the formation of fat droplets in milk cattle. Theoretically, this gene may influence the subcutaneous fat thickness and therefore affect meat tenderness. The meat tenderness should be improved in Zebu cattle, and the CNVRs are a tool that can be used to genetic improve this trait.

**Key Words:** chromosomal region, CNVR, shear force

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### 0937 (M051) An evaluation of 6 years of carcass and feedlot performance in Brahman and Brahman-influenced steers tested by the American Brahman Breeders Association (ABBA) National Carcass Evaluation Program.

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The American Brahman Association has made concerted efforts to improve the carcass quality and composition of Brahman and Brahman-influenced cattle. Thus, the objective of the current study was to evaluate genetic trends for Brahman steer calves that have comprised 6 yr (2004–2010) of the American Brahman Breeders Association (ABBA) National Carcass Evaluation Program. A total of 418 steers were evaluated for growth traits, carcass quality, and composition traits. Steers were fed in Gonzalez, TX, until a desirable harvest weight was achieved. Steers were then transported to a commercial harvest facility where carcass quality and composition traits were collected. Growth and performance traits collected in the feedlot that were evaluated in the current study consisted of entrance weight into the feedlot (INWT), harvest weight (HRVWT) and average daily gain (ADG). Carcass quality and composition traits that were evaluated included hot carcass weight (HCW), ribeye area (REA), marbling score (MARSC), yield grade (YG), dressing percent, and Warner-Bratzler shear force (WBS) analysis for meat tenderness evaluation. The PROC REG procedure of SAS was utilized to determine the average increase or decrease of performance for each trait over the six year evaluation period. Entrance weights into the feedlot in 2004 averaged 239.47 kg and HRVWT averaged 494.35 kg. Entrance weights and HRVWT in 2010 had increased to 292.11 kg and 579.26 kg, respectively. Subsequently, all growth traits evaluated in the current study exhibited a linear increase over the six year evaluation period with INWT increasing 5.5 kg/year, HRVWT increasing 11.1 kg/year and average daily gain increasing 0.17 kg/year. When evaluating carcass quality and composition traits, it was revealed that all traits with the exception of MARSC exhibited a linear increase. Marbling score was the only trait observed not to increase over the six year testing period, decreasing at a rate of 3.7 marbling score units per year, respectively. The carcass traits that exhibited a linear increase over the six year evaluation period included HCW (7.2 kg/year), REA (0.55 cm/year), YG (0.04 units/year), WBS (0.41 kg/year) and dressing percentage (0.10/year).

**Key Words:** *Bos indicus*, genetic trends, carcass traits

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### 0938 (M052) Relationship of physical characteristics and reproductive status in crossbred Angus replacement heifers.

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The objective for this study was to measure physical characteristics of developing replacement heifers and to determine if these traits were related to reproductive status at breeding. Contemporary Angus based replacement heifers ($n$ = 89) were managed on pastures containing endophyte infected tall fescue at the University of Arkansas Beef Cattle Research Center near Fayetteville, AK. Measurements that were recorded for each heifer at weaning, yearling, and prebreeding included body weight, pelvic area, hip height, hip width, reproductive tract score, rump fat, back fat, rib eye area, and coat shedding score. A group of heifers ($n$ = 26) were determined to be unsatisfactory for exposure to breeding (NE). Pregnancy status was determined for the remaining heifers ($n$ = 63) following AI and pasture exposure to fertile bulls in a 60-d breeding period. No physical differences were found among the heifers that were exposed and did conceive (EC) ($n$ = 32) compared to heifers exposed that did not conceive (EDC) ($n$ = 31). Mean pelvic height was greater for EC heifers (38.68 ± 4.00) when compared to the NE (35.51 ± 4.00) and EDC (38.00 ± 4.00) heifers ($P$ = 0.056). The NE group had a significantly greater mean coat shedding score than either EDC ($P < 0.01$) or EC heifers ($P < 0.01$), with EC heifers having the lowest mean coat shedding score (3.05, 2.62, vs. 2.52 ± 0.91, respectively). The physical characteristics including body weight, hip height, and rump fat that were measured for the NE group displayed an inverse trend to that of coat shedding score. The NE group exhibited lower ($P < 0.05$) values across all physical measurements compared to EC and EDC heifers. Coat shedding score was further analyzed by dividing the heifers data into two groups, with group one (g1) having coat scores 3 or less and group two (g2) having coat scores 4 or 5. Group one heifers were 10.38 ± 7.23, 21.48 ± 7.78, and 30.18 ± 7.96 kg greater in mean BW when compared to group 2 heifers at weaning, yearling, and prebreeding, respectfully ($P$ = 0.14, $P$ = 0.08, $P < 0.01$, respectfully). In conclusion, these data indicate that coat shedding score was inversely correlated to physical and ultrasound measurements taken at weaning, yearling and prebreeding. Producers selecting replacement heifers may be able to utilize coat shedding score as another characteristics to assess desirable replacement heifers.

**Key Words:** replacement heifer, beef cattle, coat shedding