Breeding and Genetics: Application and methodology in animal breeding—Beef

T77 Genetic parameters for breeding phase in Hereford x Aberdeen Angus crosses in grazing system of Uruguay. Ana C. Espasandin¹, Diego Gimeno², Jorge Urioste¹, and Fernando Pereyral.¹, ¹Udelar, School of Agronomy, Bernardo Rosengurt Experimental Station, Cerro Largo, Uruguay; ²Uruayan Wool Sectarariat, Montevideo, Uruguay.

A diallelic experiment hereford (HH) and aberdeen angus (AA) beef breeds, developed between 1994 and 2002 at the Bernardo Rosengurt Experimental Station, College of Agriculture-University of the Republic, Uruguay (32°35′ S, 54°15′ W, and 94 of altitude). The data set totalized a set of 57 sires and 1365 dams. The individual (g_A - g_H), and maternal (g_mA - g_mH) breed differences, as well as individual (h²_HH) and maternal (h²_mH) heterosis were estimated using additive linear models for cow body condition score at calving (BCS), calf birth weight (BW) and weaning weight (WW), and generalized linear models for weaning percentage (%W). Effects of genetic group, year and month/year) at birth, dam age, and calf sex were included as fixed effects, and individual or sire as random effects. The effect of the difference between individual breed genetic (g_A - g_H), as well the heterosis were not significant for BW (P > 0.05). For WW, the difference between maternal effects (g_mA - g_mH) was positive, with 4.87 ± 1.01 kg (P < 0.0001), and individual heterosis was 5.12 ± 1.24 kg (P < 0.0001). The h²_HH for %W was 0.22 ± 0.03. The h²_mH was significant for WW (11.58 ± 1.48 kg, P < 0.0001). Crossbred dams were higher than pure breed by 0.04 points in AFC and REB; however, heifers that calved too young may present problems, such as calving difficulty, that may increase CI. The selection of Brahman cattle for reproductive traits, such as AFC, CI, REB, and STAY, will render low magnitude and long-term responses.

Key Words: heritability, rebreeding, stayability

T79 Assessment of genetic variability of Brazilian Brahman cattle raised either on pasture or stabled by pedigree analysis. Ligia Cavani¹, Rafael Medeiros de Oliveira Silva², Michel Marques Farah³, Rafael Keith Ono², Luis Orlando Duitama Carreño², Henrique Torres Ventura³, and Ricardo Fonseca¹,¹ São Paulo State University (Unesp), Jaboticabal, São Paulo, Brazil; ²São Paulo State University (Unesp), Dracena, São Paulo, Brazil; ³Brazilian Agricultural Research Corporation (Embrapa), Juiz de Fora, Minas Gerais, Brazil; ⁴Brazilian Association of Zebu Breeders (ABCZ), Uberaba, Minas Gerais, Brazil.

The aim of this study was to assess the genetic variability of Brahman cattle in Brazil by analyzing information obtained by genealogical records. The pedigree data were obtained from the Brazilian Association of Zebu Breeders and was formed by 207,747 Brahman animals from different regions of Brazil. In this data set, cattle were born between 1994 and 2012 and they were analyzed in 3 ways: considering all the pedigree information (Pt), and dividing the pedigree data according to animals raised either on pasture (Ppt) or stabled (Pst). The software R was used for data consistency and to generate the file with the following information: animal, sire, dam, birth date, and sex. The software Pedig was used to determine the inbreeding, generation intervals and the results of the parameters based on the probability of gene origin: number of founders (Nf), effective number of founders (fe), effective number of ancestors (fa) and founder genome equivalents (fg). Average inbreeding coefficients (F) were 0.31%, 0.30% and 0.22% for Pt, Ppt and Pst, respectively. However, mean F values for inbred animals were 5.94%, 5.13% and 6.52% for Pt, Ppt and Pst, respectively. In addition, average generation intervals were 4.73, 4.65 and 4.81 years for Pt, Ppt and Pst, respectively. For Pt, the results based on probability of gene origin were 13,764, 101.4, 97.07, 75.02, 1.04, 0.74 for Nf, fe, fg, fa and fg/fe; respectively. For Ppt, the results based on probability of gene origin were 6,906, 94.4, 91.57, 72.93, 1.03, 0.80 for Nf, fe, fg, fa and fg/fe; respectively. For Pst, the results based on probability of gene origin were 2,407, 68.8, 66.36, 58.42, 1.04, 0.88 for Nf, fe, fg, fa and fg/fe; respectively. For Pst, the results based on probability of gene origin were 2,407, 68.8, 66.36, 58.42, 1.04, 0.88 for Nf, fe, fg, fa and fg/fe; respectively.
T80 Use of a robust Bayesian regression model in genome-wide association study of growth traits in Brangus heifers. Sunday O. Peters*, 1 Kadir Kizilkaya, 2 Dorian J. Garrick, 3 Rohan L. Fernández, 3 Ikhide G. Imumorin, 4 and Milton G. Thomas, 5 Berry College, Mount Berry, GA, 2 Adnan Menderes University, Aydin, Turkey, 3 Iowa State University, Ames, IA, 4 Cornell University, Ithaca, NY, 5 Colorado State University, Fort Collins, CO.

When alternative models are used for genome-wide association studies (GWAS), not a single one of them has been recognized as universally best across all traits. One explanation is that different traits may have different genomic architecture characterized by different distributions for marker effects. Further, it is known that results from BayesA and BayesB models can be heavily influenced by the value of hyperparameters assumed known, namely pi, the scale factor and degrees of freedom. Our objective was to use a robust Bayesian regression model for GWAS that treated these hyperparameters as unknown and apply this model to 3 growth traits in Brangus (3/8 Brahman × 5/8 Angus) heifers. Genotypes for each heifer were obtained from BovineSNP50 Infinium beadchips. Phenotypes included data on birth weight (BW), weaning weight (WW) and yearling weight (YW) from 830 individuals from 67 sires. Simultaneous association of all SNP for each of BW, WW and YW were tested in a robust model that treated SNP effects as random. Fixed effects included cohort groups as class effects (defined for animals with the same calving season, location, and trait contemporary group) and dam age (in years) as classes. Several genomic locations were associated with variation in these growth traits in heifers. The top 10 regions by SNP effects were found on chromosomes 1, 2, 5, 6, 14 and 26 for BW, chromosomes 1, 2, 3, 5, 6, 16 and 28 for WW and chromosomes 5, 6, 7, 11, 12, 14, 16, 18, 20 and 29 for YW. Results confirm many previously reported regions associated with variation in these growth traits in both taurine and indicine cattle breeds but also included new associations. Results demonstrated the utility of regression models with unknown hyperparameters of pi, scale and degrees of freedom in GWAS of growth traits in Brangus heifers.

Key Words: robust Bayesian regression, genome-wide association, growth

T81 Genetic parameter estimates for fatty acid profile of Longissimus thoracis beef from Nellore cattle finished in feedlot. Carolyne A. Santos, 1 Angelica S. C. Pereira, 2 Fabieli L. B. Feitosa, 1 Marcos V. A. Lemos, 1 Hermenegildo L. J. Chardulo, 1 Fabieli L. B. Feitosa, 1 Marcos V. A. Lemos, 1 Hermenegildo L. J. Chardulo, 1 Adnan Menderes University, Aydin, Turkey, 1 Universidad Estadual Paulista, Botucatu, SP, Brasil, 2 Universidade Federal de Viçosa, Viçosa, MG, Brasil, 3 Universidade Federal de Viçosa, Viçosa, MG, Brasil, 4 Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brasil, 5 Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brasil.

The aim of this study was to estimate genetic parameters and determine ratio efficiency of selection for weaning weight (W205), weight at 450 d (W450) and weight gain from weaning to 450 d (PWG450) in Brahman cattle. Traits were studied through multivariate analyses. Variance components were estimated by restricted maximum likelihood performed by the software MTDFREML. The Statistical model included the fixed effects of contemporary group (composed by farm, crop and birth season, sex, and weaning and yearling management groups) and the linear covariate age, the random effect of animal and residual. For weaning weight, the management group at yearling was excluded from the analysis because the fixed effect of dam at calving age (3 to 9 years and more than 9 years) and the effect of permanent environmental were included. Purpose of ratio efficiency was verifying the efficiency of genetic gain as a function of indirect selection. Observed means of W205, W450 and PWG450 were 197 ± 34, 320 ± 74, 118 ± 59. Estimated heritability of W205, W450, and PWG450 were 0.18, 0.16 and 0.12. W205 and W450 had very high genetic correlation (0.89). GPW450 had high genetic correlation with W450 (0.79), but relatively lower correlation with W205 (0.43). For all traits, the direct selection was more efficient. Information obtained suggests slow genetic gain for W205, W450 and PWG450. GPW450 was appropriate to use as an indirect selection criterion for W205 and W450.

Key Words: Bos indicus, genetic variation, meat
selection criteria because it showed less influence of weaning weight, and high correlation with W450.

**Key Words:** beef cattle, genetic correlation, weaning weight

**T83** Effect of prediction method and cross-validation approach on accuracy of DGV for feed efficiency traits. Rafael M. O. Silva1, Daniela A. L. Lourenco2, Breno O. Fragomeni2, Luciana Takada1, Rafael Espigolan1, Maria E. Z. Mercadante1, Fernando Baldi1, Guilherme C. Venturini1, Joslaine N. S. G. Cyrillo3, Ignacy Miszta1, Roberto Carvalheiro1, and Luciana G. Albuquerque1. 

**T84** Genetic correlation estimates between the profile of individual beef fatty acids of meat and carcass traits and meat in Nellore cattle finished in feedlot. Fabieli Loise Braga Feitosa1, Fabiele Loise Braga Feitosa1, Guilherme Costa Venturini1, Carolyn Aboujaoude1, Marcos Vinicius Antunes de Lemos1, Mariana Piatto Berton1, Rafael Lara Tonussi1, Rafael Espigolan1, Joyce de Jesus Mangini Furlan2, Angelica Simone Cravo Pereira2, and Fernando Baldi1. 

**T85** Genetic parameter estimates for carcass and meat quality traits in Nellore cattle finished in feedlot. Bianca Ferreira Olivieri1, Fabiele Loise Braga Feitosa1, Hermengildo Lucas Justino Chiaia1, Guilherme Costa Venturini1, Carolyn Aboujaoude1, Marcos Vinicius Antunes de Lemos1, Mariana Piatto Berton1, Rafael Lara Tonussi1, Rafael Espigolan1, Joyce de Jesus Mangini Furlan2, Angelica Simone Cravo Pereira2, and Fernando Baldi1.

**Key Words:** lipid composition, meat quality, Bos indicus

The aim of this study was to estimate genetic parameters for beef fatty acids profile, carcass and meat traits in Nellore cattle. A total of 1,616 Nellore bulls finished in feedlot (90 d), aged around 2 years old were used. Samples were taken from the Longissimus thoracis muscle in the region of the 12th to 13th ribs of the left half-carcasses 48 h after slaughter. The backfat thickness (BF) was measured using a caliper. The percentage of lipids (LIP) was determined by the Bligh and Dyer method. The fatty acid profile was quantified using SP-2560 capillary column (100 m × 0.25 mm diameter with 0.02 mm thickness, Supelco, Bellefonte, PA). After quality control for genotypes, a total of 470,007 SNPs from 1,556 samples remained. The (co)variances and genetic parameters were estimated using the restricted maximum likelihood method, considering an animal model (ssGBLUP). The heritability estimates for fatty acids were from low to high, ranging from 0.06 to 0.65 for saturated fatty acids, from 0.07 to 0.14 for the monounsaturated fatty acids and 0.05 to 0.62 for polyunsaturated fatty acids. Carcass and meat traits showed low to moderate heritability estimates, ranging from 0.06 (SF) to 0.17 (EGS). Estimates of genetic correlation between BF with C14:0, C18:0, C18:1n-9 cis, C18:2n-6 cis, C18:3n-3, CLA cis-9,trans-11 and CLA cis-10,trans-12 were low to moderate, being 0.38, -0.15, -0.44, 0.18, -0.22, 0.19 and -0.10, respectively. The estimates of genetic correlations between SF with previous fatty acids were low to moderate (0.16, 0.04, 0.04, 0.02, -0.40, 0.35 and 0.60). Estimated genetic correlations between the LIP with C14:0, C18:0, C18:1n-9 cis, C18:2n-6 cis, C18:3n-3, CLA cis-9,trans-11 and CLA cis-10,trans-12 were low to high, being 0.75, 0.70, -0.02, -0.93, -0.62, -0.04 and -0.60, respectively. It is expected that selection for increasing the concentration of mono and polyunsaturated fatty acids by direct selection for carcass and meat traits is less likely to occur.

**Key Words:** lipid composition, meat quality, Bos indicus

The aim of this study was to estimate genetic parameters for beef fatty acids profile, carcass and meat traits in Nellore cattle. A total of 1,616 Nellore bulls finished in feedlot (90 d), and slaughtered with an average of 24 mo of age were used. Samples from the Longissimus thoracis muscle were collected 48 h after slaughter. The proportion of saturated (SFA), monounsaturated (MUFA) and polyunsaturated fatty acids (PUFA), n-3 and n-6 were calculated. The total lipid concentration (LIP) was quantified using the Bligh and Dyer (1959) method. Fatty acids were quantified by gas chromatography (GC-2010 Plus- Shimadzu AOC 20i autosampler) using SP-2560 capillary column. The backfat thickness (BF) was measured using a caliper. Shear force (SF) was measured by the method of Wheeler et al. (1995). The (co)variances and genetic parameters were estimated using the restricted maximum likelihood method, considering an animal model (ssGBLUP), applying the remlf90 software. The animals were genotyped with the BovineSNP BeadChip (High-Density Bovine BeadChip) that contained 777,962 SNP markers. After quality control for genotypes, a total of 470,007 SNPs from 1,556 samples remained. The heritability estimates were low for SFA (0.09), MUFA 0.005, and moderate for PUFA (0.20), n3 (0.08) and n6 (0.20). For SFA, the genetic correlation estimates with SF (0.04) with BF (0.30), and LIP (0.27) were low. The genetic correlation estimates...
between MUFA with carcass and meat traits were low to high, being −0.05 with SF, −0.64 with BF, and 0.88 with LIP. The genetic correlation estimates between PUFA were low with SF (0.22), moderate with BF (−0.41) and LIP (−0.64). For n3, the genetic correlation estimates were low with BF (−0.17) moderate with SF (−0.37) and with LIP (−0.40). The genetic correlation estimates between omega 6 with BF and SF were low (0.05 and 0.10, respectively), and high with LIP (−0.86). It is expected that the selection for carcass and meat traits would change the beef fatty acid composition.

**Key Words:** Bos indicus, heritability, genetic correlation