

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. Espasandin*¹, Diego Gimeno^{2,1}, Jorge Urioste¹, and Fernando Pereyra¹, ¹Udelar, School of Agronomy, Bernardo Rosengurt Experimental Station, Cerro Largo, Uruguay, ²Uruguayan Wool Secretariat, Montevideo, Uruguay.

A diallelic experiment between 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 ($g_A^i - g_H^i$) and maternal ($g_A^m - g_H^m$) breed differences, as well as individual (h_{AH}^i) and maternal (h_{AH}^m) 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 ($g_A^i - g_H^i$), as well the heterosis were not significant for BW ($P > 0.05$). For WW, the difference between maternal effects ($g_A^m - g_H^m$) was positive, with 4.87 ± 1.01 kg ($P < 0.0001$), and individual heterosis was 5.12 ± 1.24 kg ($P < 0.0001$). The h_{AH}^i for %W was 0.22 ± 0.03 . The h_{AH}^m was significant for WW (11.58 ± 1.48 kg, $P < 0.0001$). Crossbred dams were higher than pure breed by 0.04 points in BCS (3.79 vs. 3.75), being different HH and HA vs. AA and HA ($P < 0.05$). At birth, calves HH, AH and HA were heavier than AA. For %W, crossbred dams averaged 24.7 points higher than pure breeds (85.0% vs. 60.3%). Crossbred breed dams weaned calves significantly heavier (means 159.1 ± 4.1 kg) to purebred cows. Hereford breed dams weaned calves with significantly less weight (means 143.3 ± 2.7 kg). The estimations of breed genetic effects show reductions in birth weight related to a Angus breed (g^i), as well an increment in weaning weight due to a maternal Angus effect (g^m). Superiority in crossbred dams were evidenced in individual and maternal heterosis.

Key Words: breed effect, crossbreeding, heterosis

T78 Estimates of genetic parameters for reproductive traits in Brahman cattle breed. Ligia Cavani*¹, Diogo Anastácio Garcia², Luis Orlando Duitama Carreño², Rafael Keith Ono², Henrique Torres Ventura³, and Ricardo Fonseca¹, ¹São Paulo State University (Unesp), Dracena, São Paulo, Brazil, ²São Paulo State University (Unesp), Jaboticabal, São Paulo, Brazil, ³Brazilian Association of Zebu Breeders (ABCZ), Uberaba, Minas Gerais, Brazil.

This study was designed to estimate genetic parameters for the following traits of Brahman cattle in Brazil: age at first calving (AFC), calving interval (CI), rebreeding (REB), and stayability (STAY). The data were provided by Brazilian Association of Zebu Breeders (ABCZ), and included Brahman cattle that were born between 1994 and 2012. For REB, the value 1 was assigned to heifers that rebreed and calved after first calving, and the value 0 was assigned to heifers that failed to rebreed after first calving. Likewise, for STAY, the value 1 was assigned to heifers that calved at least 3 times when they were 6-yr-old; otherwise, the value 0 was assigned. We utilized bivariate analysis using linear-threshold animal model to estimate co-variances components by using the software GIBBSF90 and THRGIBBS1F90 from BGF90. The

model included fixed effects, random effects that represented additive genetic direct effects of each animal, permanent environmental effects, included as random, and residuals. For AFC and STAY, the fixed effects were composed only by contemporary group. Besides that, for REB and CI, the fixed effects were composed by contemporary group, calf birth year and calf birth season. Also, the covariate dam age at calving was included for CI. The permanent environmental effects only were included in the model for CI. The contemporary groups were composed from farm, type of gestation (AI or natural service) and birth year of dam; and in addition, only for STAY, birth season of dam (rainy or dry). The mean h^2 were 0.10, 0.02, 0.22, and 0.10 for AFC, CI, REB, and STAY; respectively. The genetic correlations were -0.13 between AFC and CI, -0.35 between AFC and REB, -0.57 between AFC and STAY, and 0.32 between REB and STAY, which reveal that cows that remain productive for longer periods in the herd, also start breeding younger and present greater chances to 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 Cavani*¹, Rafael Medeiros de Oliveira Silva², Michel Marques Farah³, Rafael Keith Ono², Luis Orlando Duitama Carreño², Henrique Torres Ventura⁴, and Ricardo Fonseca¹, ¹São Paulo State University (Unesp), Dracena, São Paulo, Brazil, ²São Paulo State University (Unesp), Jaboticabal, 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, fa, fg, fe/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, fa, fg, fe/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, fa,

fg, fe/fa and fg/fe; respectively. The number of ancestors to explain 50% of the genetic variability in Pt was 46, in Ppt was 41 and in Pst was 24. The results showed a reduction in genetic variability, because $fe > fa > fg$. Values close to 1 observed for fe/fa and fg/fe showed no genetic bottleneck and a small process of genetic drift. Thus, genetic variability has been reduced in Brahman cattle population, especially on those from Pst.

Key Words: ancestor, inbreeding

T80 Use of a robust Bayesian regression model in genome-wide association study of growth traits in Brangus heifers. Sunday O. Peters*¹, Kadir Kizilkaya², Dorian J. Garrick³, Rohan L. Fernando³, Ikhide G. Imumorin⁴, and Milton G. Thomas⁵, ¹Berry College, Mount Berry, GA, ²Adnan Menderes University, Aydin, Turkey, ³Iowa State University, Ames, IA, ⁴Cornell University, Ithaca, NY, ⁵Colorado 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 π , 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 \times 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 π , 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. Carolyn A. Santos¹, Angélica S. C. Pereira², Fabieli L. B. Feitosa¹, Marcos V. A. Lemos¹, Hermenegildo L. J. Chiaia¹, Mariana P. Berton¹, Adrielle M. Ferrinho², Lenise F. Mueller³, Joyce M. Furlan², Monica R. Mazalli³, and Fernando S. Baldi*¹, ¹Universidade Estadual Paulista, Faculdade de Ciências Agrárias e Veterinárias, Departamento de Zootecnia, Jaboticabal, São Paulo, Brazil, ²Universidade de São Paulo, Faculdade de Medicina Veterinária e Zootecnia, Departamento de Nutrição e Produção Animal, Pirassununga, São Paulo, Brazil, ³Universidade de São Paulo, Faculdade de Zootecnia e Engenharia de Alimentos, Pirassununga, São Paulo, Brazil.

The present study aimed to estimate (co)variance components and genetic parameters for beef fatty acid (FA) composition in 937 Nellore bulls, finished in feedlot (period of 90 d) and slaughtered with an average age of 24 mo, weighing 500–550 kg. The FA profile was analyzed in *Longissimus thoracis* samples using a gas chromatography, with a 100-m capillary column. The contemporary groups (CG) were organized based on farm and year of birth, and management group at yearling. The following 14 FAs were quantified: C16:0, C18:0, C18:1 *cis*-9, C18:2 *cis*-6, C18:2 *cis*-9,*trans*-11 and C18:2 *trans*-10,*cis*-12, C18:3n-3, C14:0, C14:1, C18:1n-9 *trans*, 18:1 *trans*-11, C20:3n-6 *cis*-8,11,14, C20:3n-3 *cis*-11,14,17, and C20:4. The (co)variance components were estimated using an animal model which included random additive genetic effects, fixed effects (CG), and the slaughter age as a covariable (linear and quadratic effect). The restricted maximum likelihood method was used (REMLF90 computer program) and 2 multi-trait analysis were performed, one including 14 individual FA and the other the total SFA, MUFA, PUFA, n-3, n-6 and n-9. The individual FAs with the highest heritability estimates were C18:2 *trans*-10,*cis*-12 (0.38) and C18:3n-3 (0.41). The C18:0, C16:0, C18:1 *cis*-9, 18:1 t11, C18:2 *cis*-9,*trans*-11 and C20:4 FAs resulted in low heritability estimates, indicating that these FAs should respond slowly to selection. With the exception of the C18:2 *trans*-10,*cis*-12 FA, the genetic associations between individual PUFAs were high and positive. The genetic correlation estimates between the total of SFA with PUFA and n-6 were high and negative (–0.84 and –0.88), and with n-3 were moderate (–0.62). It is expected that the response to direct selection for polyunsaturated, n-3 and n-6 fatty acids would be fast. In general, the correlations between the most important fatty acids are favorable and therefore indirect selection may be used to improve the fatty acid profile. This study revealed the existence of genetic variation and hence the possibility of genetic improvement of meat fatty acid composition in zebu cattle.

Key Words: *Bos indicus*, genetic variation, meat

T82 Genetic evaluation of growth traits in Brahman cattle. A. M. Matorano², M. E. Z. Mercadante³, J. N. S. G. Cyrillo³, L. A. L. Chardulo¹, and J. A. V. Silva*¹, ¹Universidade Estadual Paulista, Botucatu, SP, Brasil, ²Universidade Estadual Paulista, Jaboticabal, SP, Brasil, ³Instituto de Zootecnia, Sertãozinho, SP, 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 contemporary group and 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 GPW450. GPW450 was appropriate to use as

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. Silva*¹, Daniela A. L. Lourenco², Breno O. Fragomeni², Luciana Takada¹, Rafael Espigolan¹, Maria E. Z. Mercadante³, Fernando Baldi¹, Guilherme C. Venturini¹, Joslaine N. S. G. Cyrillo³, Ignacy Misztal², Roberto Carneiro¹, and Lucia G. Albuquerque¹, ¹Univ Est Paulista Julio de Mesquita Filho, FCAV-UNESP, Jaboticabal, SP, Brazil, ²The University of Georgia, Athens, GA, ³APTA Center for Beef Cattle, Animal Science Institute, Sertãozinho, SP, Brazil.

Accuracies of direct genomic values (DGV) for feed efficiency traits obtained with different methods and cross-validation approaches were compared. After quality control 437,197 SNP genotypes were available for 761 Nellore cattle provided by the Institute of Animal Science, SP, Brazil. Methods of analysis were traditional BLUP, ssGBLUP, GBLUP, and BayesC π . The traits were residual feed intake (RFI), feed conversion ratio (FCR), average daily gain (ADG) and dry matter intake (DMI). Model included fixed effects of contemporary groups (sex, year of birth, and pen), month of birth, and the covariable age of dam (linear and quadratic effects); and, as random, the additive animal effects. Three cross-validation approaches were considered: WPRO – validation was done on animals that did not have progeny; UNREL – the data set was split into 3 less related subsets; RAN – the data set was randomly divided into 4 subsets and the validation was done in each subset at a time. The accuracy of DGV was calculated as the Pearson correlation between corrected phenotype and the DGV divided by square root of heritability. Accuracies ranged from 0.01 (with UNREL) to 0.78 (with RAN) for studied traits. The inclusion of genomic information increased more than 10% of the average accuracy of predictions over traditional BLUP; on average, GBLUP showed more accurate predictions of DGV than BayesC π (0.33 and 0.29, respectively). For the RAN cross-validation approach, accuracies were 50% higher with ssGBLUP than GBLUP, especially for traits with high heritabilities (ADG- $h^2 = 0.55$, and DMI - $h^2 = 0.58$). The most accurate predictions were obtained using RAN, ranging from 0.28 to 0.78. On the other hand, the UNREL cross-validation approach provided the less accurate predictions, ranging from 0.001 to 0.29. With WPRO accuracies of DGVs were from 0.12 to 0.69. These results show that accurate genomic prediction can be obtained for all analyzed traits, especially for those with high heritability. Accuracies of DGV are higher when animals in validation are more related to those in training. São Paulo Research Foundation (FAPESP) grant 2013/01228-5 associated to 2009/16118-5.

Key Words: beef cattle, genomic selection

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 Feitosa, Carolyn Aboujaoude, Marcos Vinícius Antunes de Lemos, Mariana Piatto Berton, Guilherme Costa Venturini, Rafael Lara Tonussi, Rafael Espigolan, Bianca Ferreira Olivieri, Lucia Galvão de Albuquerque, and Fernando Baldi*, *Universidade Estadual Paulista, FCAV-UNESP, Jaboticabal, São Paulo, Brasil.*

The aim of this study was to evaluate the genetic-quantitative relationships between the beef fatty acid profile with carcass and meat traits and meat in Nellore cattle. Data from 1616 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 \times 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*

T85 Genetic parameter estimates for carcass and meat quality traits in Nellore cattle finished in feedlot. Bianca Ferreira Olivieri¹, Fabiele Loise Braga Feitosa¹, Hermenegildo Lucas Justino Chiaia¹, Guilherme Costa Venturini¹, Carolyn Aboujaoude¹, Marcos Vinícius Antunes de Lemos¹, Mariana Piatto Berton¹, Rafael Lara Tonussi¹, Rafael Espigolan¹, Joyce de Jesus Mangini Furlan², Angélica Simone Cravo Pereira*², Lucia Galvão de Albuquerque¹, and Fernando Baldi¹, ¹Universidade Estadual Paulista, FCAV-UNESP, Jaboticabal, São Paulo, Brazil, ²Universidade de São Paulo, FMVZ-USP, Pirassununga, São Paulo, Brazil.

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 1616 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 with 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