

Breeding and Genetics: Applications and Methods in Animal Breeding—Beef

T179 Genetic analysis of female weights via random regression and multiple trait models in a multibreed beef cattle population.

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The objective was to obtain REML estimates of covariance functions and variance ratios for weights taken during the productive life of beef cows from a multibreed Angus-Brahman population using random regression models. The dataset contained 40,009 weights from 1,792 cows. Genetic analyses were performed using random regression models (RRM) with Legendre polynomials (LP). Reference heritabilities at birth, weaning, and 1, 2, 3, 4 and 5 years of age were estimated using 2-trait mixed models (MTM). Fixed effects for RRM were contemporary group (year-period of measurement), and cubic LP covariates for age of female, interactions between age of female and expected Brahman fractions of female and her dam, and direct and maternal heterozygosity. Random effects were cubic LP age covariates for direct and maternal additive genetic and direct permanent environment, and residual. Two-trait models for weights up to one year had contemporary group (year-period of measurement), age of female, expected Brahman fractions of female and her dam, and direct and maternal heterozygosity as fixed effects. Random effects were direct and maternal additive genetic, maternal permanent environment and residual. Two-trait models for weights taken after one year of age ignored maternal effects. Legendre polynomials behaved badly at extreme ages. The MTM direct heritability estimates were similar to RRM values, except for birth weight (0.3 ± 0.06 for MTM and 0.02 ± 0.02 for RRM). The RRM direct heritability increased from near zero at birth to 0.59 ± 0.05 at 764 d and then decreased to 0.39 ± 0.09 at 2,500 d of age. Maternal heritability reached its maximum value at 222 d (0.09 ± 0.02) and decreased towards 2,500 d (0.02 ± 0.05). Direct permanent environment variance ratios increased from 0.04 ± 0.02 at birth to 0.57 ± 0.08 at 2,500 d of age. Results suggested that this dataset should be reanalyzed using functions less sensitive at extreme age values such as splines to obtain reasonable estimates of variance ratios over the entire range of ages.

Key Words: cattle, multibreed, random regression

T180 Ranking of Nellore cattle at agricultural shows: Genetic and phenotypic parameters with production traits.

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Although livestock judging does not use techniques of genetic evaluation and the population samples are not comprehensive in terms of the number of animals evaluated, agricultural shows exert an effect on breed improvement since the champion animals are rapidly disseminated in the population through semen or oocytes. Records (28,279) of 17,141 Nellore cattle participating in 26 agricultural shows, born from 1994 to 2009, from 764 sires, were used to estimate genetic and phenotypic parameters between animal rank in cattle judging and growth traits (yearling weight-YW, hip height-HH, body length-BL, heart girth-HG), scrotal circumference (SC) and ultrasound carcass traits (longissimus muscle area-LMA, backfat-BF, rump fat thickness-RF). Two traits

were defined for animal rank in cattle judging: value 1 was attributed to animals ranked 1st to 3rd place within the age category and value 0 to the remaining animals (TOP3); and, value 1 was attributed to animals ranked 1st to 5th place within the age category and value 0 to the remaining animals (TOP5). TOP3 and TOP5 were evaluated from weaning to 36 months of age as repeated traits and YW, HH, BL, HG, SC, LMA, BF and RF were evaluated as single traits at 365 days of age. The (co) variance components were estimated by Bayesian inference under a two-trait threshold-linear animal model. The heritabilities posterior means estimated for TOP3 and TOP5 were 0.182 ± 0.010 and 0.260 ± 0.012 , and the repeatabilities were 0.341 ± 0.007 and 0.400 ± 0.007 . Genetic correlation between TOP3, TOP5 and YW were higher (0.941 ± 0.016 and 0.943 ± 0.014) than the estimates between TOP3, TOP5 and HH, BL, HG (from 0.535 ± 0.098 to 0.757 ± 0.038). Low genetic correlations were estimated between animal rank traits and SC (0.439 ± 0.072 and 0.382 ± 0.067) and carcass traits (from 0.341 ± 0.114 to 0.231 ± 0.145). The highest phenotypic correlations were estimated between TOP3, TOP5 and YW (0.485 ± 0.010 and 0.535 ± 0.009), followed by the phenotypic correlations with HG (0.379 ± 0.019 and 0.390 ± 0.018), suggesting that judges are most influenced by these two traits at the time of awarding prizes.

Key Words: *Bos indicus*, categorical trait, Zebu

T181 Genetic parameters and genetic trends for preweaning growth in an Angus-Brahman cattle population in the Colombian tropics.

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The objective of this research was to estimate genetic parameters and trends for birth weight (BW) and weaning weight adjusted to 270 d of age (WW270) in a beef cattle population composed of Angus and Brahman straightbred and crossbred animals located in a Colombian premontane humid forest. Data were from 561 calves born from 1999 to 2010. The 2-trait model included the fixed effects of contemporary group (year-season-sex), age of dam, breed direct genetic effects, breed maternal genetic effects, individual heterosis, and maternal heterosis. Random effects were calf direct genetic, dam maternal genetic, permanent environmental maternal, and residual. Variance components and genetic parameters were estimated by restricted maximum likelihood. Program AIREML was used to perform computations. Heritabilities estimates for additive direct genetic effects were 0.08 ± 0.005 for BW and 0.10 ± 0.006 for WW270. Maternal heritability was 0.04 ± 0.002 for BW and 0.08 ± 0.005 for WW270. Low direct and maternal preweaning heritabilities suggest that nutrition should be improved to allow fuller expressions of calf direct growth and cow maternal ability. The correlation between additive direct genetic effects for BW and WW270 (0.18 ± 0.03) indicated that genes affecting BW also affected WW270. The genetic correlations between direct and maternal additive effects were negative for BW (-0.51 ± 0.02) and for WW270 (-0.21 ± 0.03) suggesting that genes increasing weight would lower maternal ability. Calf weighted yearly means showed near zero trends during these years for direct and maternal effects for BW and WW270. This indicated that the intensity of selection applied to this multibreed population

was insufficient to influence direct and maternal genetic yearly EBV means during this 12-yr period. To make genetic progress for direct and maternal growth traits, a selection program that utilizes direct and maternal animal EBV to select replacement sires and dams will need to be implemented in this population.

Key Words: beef cattle, genetic parameters, genetic trends

T182 Population structure and relation among inbreeding coefficient and breeding values in Guzera beef cattle. D. G. F. Guidolin^{1,3}, N. V. Grupioni^{2,3}, N. C. Tramonte^{2,3}, I. Urbinati^{3,5}, T. C. S. Chud^{2,3}, R. B. Lobo⁴, and D. P. Munari^{3,5}, ¹*Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, CAPES, Brasília, DF, Brazil*, ²*Fundação de Amparo a Pesquisa do Estado de São Paulo, FAPESP, São Paulo, SP, Brazil*, ³*Universidade Estadual Paulista Júlio de Mesquita Filho, UNESP, Jaboticabal, SP, Brazil*, ⁴*Associação Nacional de Criadores e Pesquisadores, ANCP, Ribeirão Preto, SP, Brazil*, ⁵*Conselho Nacional de Desenvolvimento Científico e Tecnológico, CNPq, Brasília, DF, Brazil*.

The aim of this study was to estimate population parameters and inbreeding coefficients and its relation with breeding values and with the index indicated for the Guzera breed (MGT). The reason to do that was to provide information for the breeding program held by ANCP. For this we used pedigree data from 26,160 animals, born between 1943 and 2009, bred in 43 herds participant in the Guzera Breeding Program (PAGR). The population parameters estimated were average inbreeding coefficient (F), inbreeding per generation (DF), effective population size (Ne), generation interval, effective number of founders (Nf) and number of ancestors (Na). The traits studied were age at first calving (AFC), scrotal circumference at 365 and 450 days of age (SC365) and (SC450), body weight at 365 and 450 days of age (BW365) and (BW450). Ne presented equal to 78.59, indicated low genetic diversity in the herds studied. The generation intervals observed in the population is considered to be high, 9.1 years. The F observed was 0.93% and DF was 0.64%, this indicates that the inbreeding coefficient is increasing through the period studied. Although it was observed that the inbreeding coefficient does not influence animal performance. Despite the fact that inbreeding depression was not observed in this study, mating related animal is not recommended.

Key Words: parameter, selection, zebu

T183 Genetic parameters and trends for productive, reproductive and carcass traits in Guzera beef cattle. D. G. F. Guidolin^{1,3}, N. V. Grupioni^{2,3}, N. C. Tramonte^{2,3}, P. A. Bernardes^{3,5}, G. B. Nascimento^{1,3}, G. Vargas^{1,3}, R. B. Lobo⁴, and D. P. Munari^{3,5}, ¹*Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, CAPES, Brasília, DF, Brazil*, ²*Fundação de Amparo a Pesquisa do Estado de São Paulo, FAPESP, São Paulo, SP, Brazil*, ³*Universidade Estadual Paulista Júlio de Mesquita Filho, UNESP, Jaboticabal, SP, Brazil*, ⁴*Associação Nacional de Criadores e Pesquisadores, ANCP, Ribeirão Preto, SP, Brazil*, ⁵*Conselho Nacional de Desenvolvimento Científico e Tecnológico, CNPq, Brasília, DF, Brazil*.

The objectives of this study were to estimate genetic parameters and genetic trends for traits evaluated by the Guzera Breeding Program (PAGR), in order to provide support for the genetic improvement of the breed. Records on 18,491 animals from 43 farms were used. Traits studied were rib eye area (REA), fat thickness between the 12th and 13th rib (FT), rump fat thickness (RF), age at first calving (AFC), scrotal circumference at 365 (SC365) and 450 (SC450) days of age, gestation

length (GL), mature weight of the cow (MWC), body weight at birth (BWB), 120 (BW120), 210 (BW210), 365 (BW365), 450 (BW450 days old) and cumulative productivity in females (CP). Genetic parameters and breeding values were estimated by restricted maximum likelihood, by one and two-trait analysis whose general model included additive genetic random effect and fixed effect of contemporary groups (CG), for CP, AFC, SC365 and SC450. For GL, BWB, BW120, BW210, BW365 and BW450, a maternal additive random genetic effect and the fixed effect (linear and quadratic) of the cow's age at calving were added to the base model. For carcass traits, the fixed effect (linear) of weight at ultrasound was included. Genetic trends were obtained by linear regression of average annual breeding values (obtained by one-trait analysis) on year of birth (1987 to 2009). The t statistic was used and the null hypothesis considered the regression coefficient as zero. Most traits showed sufficient additive genetic variation, except CP, FT and RF, which expressed low genetic correlations with other traits. The trend graphs indicate that genetic change is occurring in the average breeding value of animals over time, with the exception of CP, GL and the maternal genetic effect for BWB. The inclusion of RF in a selection index proposed by ANCP is recommended.

Key Words: zebu, heritability, breeding

T184 Genetic trend on growth traits in Hanwoo. Y.-S. Choi¹, S.-W. Kim¹, K.-S. Kim¹, S.-K. Lee¹, D.-J. Yu¹, A.-A. Yun¹, M.-J. Ku¹, D.-H. Park¹, J.-W. Lee², and W.-H. Kim¹, ¹*Livestock Research Institute Jeollanamdo Agricultural Research & Extension Service (JARES), Gangjin-gun, Jeollanamdo, Republic of Korea*, ²*Chonnam National University, Gwangju, Republic of Korea*.

The objectives of this study were to figure out factors affecting growth performance of Korean native cattle called Hanwoo and to analyze phenotypic correlations among carcass traits. Birth and weaning weights and carcass traits were considered for prediction of potential ability on growth. Linear model was used to analyze sex of calves, dam parity and age, birth year, birth season, slaughter season were used as fixed factors in this study. Birth and weaning weights by sex of calves were 27.32 ± 2.26kg and 83.84 ± 14.23kg in bull and 26.24 ± 3.08kg and 82.44 ± 14.34kg in heifer, respectively. Birth weight in bull was significantly heavier than those in heifer ($P < 0.05$). Carcass weight by the sex of calves was 399.07 ± 56.25 kg in steer and 302.16 ± 56.25 kg in cow. Eye muscle area was 87.37 ± 11.36 cm² in steer and 73.37 ± 13.02 cm² in cow. Birth weight by parity of dam was significantly different ($P < 0.05$). Birth and weaning weights at 4th parity was 28.86 ± 2.86 kg and 88.00 ± 14.29kg, respectively. Birth and weaning weights by birth season were not different. But carcass weight born in summer season was 386.85 ± 67.28 kg which was heavier than those of them born in spring season ($P < 0.05$). Backfat thickness by slaughter season was significantly different ($P < 0.05$). Carcass weight and eye muscle area slaughtered at winter were 379.38 ± 68.53 kg and 84.27 ± 14.20cm². Phenotypic correlation coefficient between carcass weight and eye muscle area was 0.84 in cow and 0.66 in steer. Other correlation coefficients of carcass traits were positive. Phenotypic correlation coefficient by birth season winter was negative between eye muscle area and backfat thickness and the other traits of correlation coefficient were positive 0.84 in cow and 0.66 in steer. Other correlation coefficients of carcass traits were positive. Especially phenotypic correlation coefficients between carcass weight and eye muscle area were 0.86 in spring, 0.81 in summer, 0.79 in fall, and 0.73 in winter, respectively. These results indicated that age of dam should be an important factor for better growth performance and eye muscle area could be used as a selection indicator to increase carcass weight.

Key Words: Korean native cattle, genetics, growth trait

T185 Genetic and phenotypic (co)variance component estimation of reproductive traits in a multibreed beef cattle population.

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Accurate (co)variance estimates are necessary to optimize selection response in reproductive traits of economic importance for commercial beef cow/calf operations. The objective of this research was to determine the heritability of and relationship among 5 reproductive traits in a multi-breed beef cattle population. Records on 1369 cows from 505 sires and 1360 dams were collected between the years 2002 and 2011. Binary traits of first-service conception rate (FSCR) and pregnancy rate (PR), a categorical trait (number of service per conception, NS) were analyzed by a threshold model, while interval traits of gestation length (GL) and days to calving (DC) were analyzed using a linear model. Models included fixed effects of contemporary group (herd, year, breeding season and breeding method), age of cow, age of dam and linear regressions on breed proportions of Angus, Limousin, Charolais, Simmental, Gelbvieh and Piedmontese. Additive genetic and permanent environment due to repeated records on cows were included as random effects with service sire fitted in the threshold model as random univariate and bivariate animal models were fitted using ASReml (Gilmour et al, 2008). Estimates of heritabilities (repeatabilities) for FSCR, PR, NS, GL and DC were 0.121 (0.149), 0.143 (0.143), 0.016 (0.045), 0.211 (0.211) and 0.068 (0.096), respectively, which were relatively high compared to previous research. Genetic correlations between FSCR and PR, DC and GL were positive and high ($r_G = 0.985$ and 0.744). Furthermore, in addition to the negative correlation between the FSCR and GL ($r_G = -0.562$), the other traits appeared to be genetically independent. Phenotypically, reproductive traits were correlated with low to moderate correlation coefficients from -0.249 to 0.537 . These parameters indicate genetic progress in reproductive traits of a multibreed beef cattle population would be possible.

Key Words: beef cattle, reproduction, genetic correlation

T186 Genetic analysis of a temperament trait in a Nellore cattle population in Brazil.

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Temperament in cattle is generally assessed as the reaction of an animal to a stressful event, such as human handling. Flight speed (FS) is a temperament trait measured the time the animal takes to exit a squeeze chute over a given distance. A lower FS is indicative of a calmer animal, which is then easier to handle and manage. In addition, FS has been found to influence the productive performance of herds, due to its correlation with other traits such as carcass quality, daily gains, pregnancy rate and feed efficiency. However, almost nothing is known regarding the genetic landscape controlling FS variation in cattle. Thus, the objectives of this study were to identify genomic regions and biologically relevant pathways associated with FS in a Nellore cattle population in Brazil. The analysis included 599 Nellore males belonging to 34 paternal half-sib families born between 2007 and 2009 at the experimental farms Embrapa Cattle-Southeast and Embrapa Beef Cattle, and three additional farms in the State of Mato Grosso do Sul, Brazil. The genomic information consisted of 563,672 single nucleotide polymorphisms (SNPs). Asso-

ciations between SNPs and FS were assessed using a series of linear mixed models, one for each SNP, including a random polygenic effect and a permanent environmental effect. These analyses were performed using the pedigreemm package in R. Gene set enrichment analysis also was conducted in order to find potential Gene Ontology (GO) terms related to this trait. Estimated SNP effects indicated some genomic regions that might be associated with FS, such as in chromosomes 5, 13 and 15. Additionally, we found a total of 28 GO terms significantly enriched with genes associated with FS. Interestingly, several of these functional categories are related to stress, such as cellular adhesion (GO: 0007155) and process of cellular response to toxins, physical stresses and inflammatory cytokines which occur by signaling via the stress-activated protein kinase (IPR017441). Results of this study shed some light regarding the genetic architecture underlying this trait in beef cattle. Financial support: FAPESP, EMBRAPA.

Key Words: beef cattle, gene ontology, GWAS

T187 The effects of winter hair coat shedding of Angus dams on adjusted weaning weight of calves.

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Heat stress is a major concern for some beef cattle producers. Methods to select cattle that are resistant to the negative effects of heat stress are economically important for these producers. Decreases in feed intake, conception rates and milk production lead to reduced gains for cows and calves. A visual scoring method of how winter hair coat is shed may help identify cattle more resistant to heat stress. The objectives of the study were to collect hair coat shedding scores (HCS) on registered Angus dams throughout the Southeast, Missouri and Texas and to explore the relationship between HCS of the dam and adjusted weaning weight (WW) of her calf. Hair coat shedding scores were collected from 18 farms in 2011-2012 in North Carolina, South Carolina, Virginia, Tennessee, Kentucky, Missouri, Alabama, and Texas. Hair coat shedding scores were on a 1-5 scale with 5 being a cow with a full winter hair coat and a 1 being a slick summer coat. Two technicians independently scored each cow. Using the average of the two scores, cows were assigned to one of three categories for analysis. If a cow had an average HCS of less than 3, she was assigned to HCS1. If a cow had an average HCS between 3 or 4, she was assigned to HCS3. If a cow had an average HCS of 4 or greater, she was assigned to HCS5. Data were separated into two groups by calving season and analyzed separately. Regions were considered as Southeast, Missouri, and Texas. Data were analyzed in SAS using PROC GLM. There were no differences in HCS for cattle in Texas. However, for the lactating cows in Missouri and Southeast, calves from dams that were a HCS1 weighed, on average, 4.84 ± 1.62 kg ($P < 0.01$) heavier than calves from dams that were a HCS5. Calves from dams that were a HCS3 weighed, on average, 3.71 ± 1.72 kg ($P < 0.05$) heavier compared to calves from dams that were a HCS5. Calf WW did not differ between HCS1 and HCS3 dams. Regional differences observed in this project maybe due to forage differences such as the presence or absence of endophyte infected fescue. In conclusion, HCS can be a visual method to help producers determine if their cattle are suffering from heat stress.

Key Words: heat stress, beef

T188 Characterization and genetic selection for beef tenderness in polled Nellore cattle.

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Brazil is the world's largest beef exporter, but receives low prices due to quality issues. The predominant Zebu breeds (80% Nellore) are well adapted to the tropics but generally lack tenderness. This project aims to establish the foundations for selection of Nellore animals of high genetic merit for tenderness. A base population was established by Guaporé Pecuária, using data from progeny tests of 25 sires representative of the Nellore breed and *inter se* matings of the animals with greatest potential for producing beef with high and low shear force (WBSF). A total of 82 bull calves from the third generation resulting from those matings were used in this study. Calves were born at the Guaporé Pecuária ranch in Mato Grosso, then transported to Embrapa for growing on pasture with supplementation and finally finished in a feedlot (40% corn silage + 60% concentrate, 14% CP). Calves were harvested at a minimum backfat of 4 mm in five lots after 54, 96, 104, 137 and 166 days on feed. Steaks were taken from the Longissimus muscle at the 12th rib, aged for 7 days and frozen pending measurement of shear force. Data were subjected to analysis of covariance, with Group as the main effect and age and weight at the beginning of finishing as covariates, using the GLM procedure (Minitab v. 16, State College, PA). Average initial weight of the animals was 215.3 ± 39.5 kg. There were no differences ($P > 0.10$) between Tender and Tough groups in ADG (1.443 ± 0.272 kg/d), final weight (529 ± 37.6 kg), dressing % (56.0 ± 1.38%), marbling score (Slight-) or pH (6.08 ± 0.30). There was a trend ($P = 0.072$) for greater fat thickness in the Tender group (7.3 mm) compared to the Tough group (6.5 mm). Animals in the Tender group produced beef with lower WBSF in comparison to animals in the Tough group (4.10 and 4.92 kg, respectively; $P = 0.05$). These data confirm that there is genetic variability in beef tenderness within the Nellore breed, and indicate that this trait will respond to genetic selection. Future studies will attempt to identify molecular markers to assist in genetic improvement programs for Zebu cattle.

Key Words: beef, tenderness, breeding

T189 Genetic association between heifers rebreeding and reproductive traits in Nellore heifers. R. B. Costa^{1,2}, A. P. N. Terakado^{*1,3}, and L. G. Albuquerque^{1,3}, ¹Universidade Estadual Paulista (UNESP) - FCAV, Jaboticabal, SP, Brazil, ²Fundacao de Amparo a Pesquisa do Estado de Sao Paulo (FAPESP), Sao Paulo, SP, Brazil, ³Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brasília, DF, Brazil.

The aim of this study was to estimate genetic correlations between heifer rebreeding and other reproductive traits in Nellore heifers, and verify the possibility to include these traits as selection criteria in beef cattle breeding programs. Data from 231,473 Nellore females belonging to Agropecuaria Jacarezinho LTDA were used. Primiparous heifer rebreeding (PHR) was defined by assigning value 1 (failure) or value 2 (success) for heifers that did not calve or calved, respectively, given that they had previously calved. Early pregnancy occurrence (P16) was defined based on the conception and calving of the heifer, given that heifers entered the breeding season around 16 months of age. For heifers that calved before 31 months of age it was assigned the value 2 (success) and those who failed, the value 1 (failure). Age at first calving (AFC) and Days to first calving (DFC) were also analyzed. Genetic parameters were estimated by Bayesian inference in two-trait analyses, assuming a linear animal model for AFC and DFC and a threshold model for PHR and P16. For all traits, the additive direct effect was considered as random and the effect of contemporary group, as fixed. For PHR, the linear effect of the number of days between the first calving date and the second conception

date was used as covariable. For P16, the linear effect of the covariable age of the heifer at the beginning of the breeding season was used. Heritability estimates were 0.18 ± 0.02; 0.05 ± 0.01, 0.20 ± 0.03, and 0.56 ± 0.03 for PHR, DFC, AFC, and P16, respectively. Genetic correlation estimates between PHR and DFC (-0.59 ± 0.04), AFC (-0.68 ± 0.05), and P16 (0.72 ± 0.03) suggest that selection to improve any of these traits will result in an increase in re-conception rate.

Key Words: age at first calving, beef cattle, early pregnancy

T190 Evaluation of sire breed type on growth and carcass characteristics utilizing multigenerational Angus sired calves versus Charolais-sired calves. J. Bailey*, M. J. Canal, T. R. Howard, G. T. Gentry, and M. D. Garcia, Louisiana State University, Baton Rouge.

The objective of this study was to evaluate the effect of sire breed type on growth, performance, and carcass characteristics. This study compared the effects of sire breed type between calves sired by either multigenerational Angus sires or Charolais sires. A total of 132 calves were evaluated for growth performance traits were collected at the Central Research Stations in Baton Rouge, LA, and included birth weight, weaning weight, hip height, and average daily gain. Carcass quality and composition traits were also collected and included hot carcass weight (HCW), rib eye area (REA), back fat (BF), and marbling score (MARB). Analyses were conducted by breed using a means separation analysis with simple t-test procedures in SAS. Mean birth weights were significantly higher ($P < 0.05$) for Charolais-sired steers and heifers as compared to Angus-sired heifers. Charolais-sired steers had a significantly higher ($P < 0.05$) birth weight than Angus steers. Mean weaning weights however were significantly higher ($P < 0.05$) for Angus-sired steers and heifers as compared to Charolais-sired heifers. No significant differences were reported between the two groups for hip height, average daily gain, or hot carcass weight. Charolais-sired calves had a significantly larger ($P < 0.05$) rib eye area when compared to the Angus-sired calves. A significant difference ($P < 0.05$) was reported for back fat with the Angus-sired calves having a larger recorded measurement than the Charolais-sired calves. A significant difference ($P < 0.05$) was reported for marbling with the Angus-sired calves having a greater measurement than the Charolais-sired calves. The results of a larger rib eye area and lesser amount of marbling and back fat in the Charolais-sired calves as compared to the multigenerational Angus sired calves is in agreement with previous reports describing the differences in growth and carcass traits associated with each of these breeds.

Key Words: growth trait, carcass quality, carcass composition

T191 Genetic association between carcass, growth and visual scores traits in Hereford × Nellore cattle. A. P. N. Terakado*, R. B. Costa, D. R. Ayres, R. Carvalheiro, and L. G. Albuquerque, Universidade Estadual Paulista (UNESP) - Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Sao Paulo, Brazil.

The use of genetic evaluation is an important tool to increase farming profitability, allowing the identification and selection of superior genetically animals. The aim of this study was to estimate genetic associations among post-weaning daily gain (PWG), loin eye area (LEA) and backfat thickness (BT) measured by ultrasound, and visual scores of body structure (S), finishing precocity (F) and muscling (M) in Hereford × Nellore animals, to verify the possibility to include these traits as selection criteria in beef cattle breeding programs. Data from 231,354 animals from Conexão Delta G breeding program were used. The animals were scanned for LEA between the 12th and 13th ribs and for BT over the

longissimus muscle at a point 3/4 the length ventrally of LEA. Scores ranging from 1 to 5 were attributed to the traits S, F and M, with 5 corresponding to the highest expression of the trait and 1 corresponding to the lowest expression. For all traits, the individual and maternal breed compositions were considered as a fixed effects and the yearling age (linear and quadratic effects) as a covariate. For LEA and BT, it was considered the yearling weight (linear and quadratic effects) as a covariate. The genetic parameters were estimated by Bayesian inference in multi-trait analysis, under a linear animal model. Heritability estimates for PWG, LEA, BT, S, F and M were 0.13 ± 0.008 ; 0.20 ± 0.047 ; 0.09 ± 0.029 ; 0.16 ± 0.011 ; 0.16 ± 0.012 and 0.25 ± 0.012 , respectively. Genetic correlations between PWG and visual scores ranged from 0.31 to 0.46, thus selecting to increase PWG will lead to genetic changes in the same direction in S, F and M. Otherwise, correlations between PWG and carcass traits were -0.22 (LEA) and -0.33 (BT), suggesting that selection for higher PWG will decrease LEA and BT. The genetic correlation estimates between S, F, M and carcass traits were practically null, -0.01 (S \times LEA); 0.07 (S \times BT); 0.08 (F \times LEA); 0.05 (M \times LEA) and 0.13 (M \times BT), thus visual scores are not good indicators of those traits. However, a moderate genetic correlation was found between F \times BT (0.44), this indicates that selection for F will increase BT.

Key Words: beef cattle, crossbred, genetic correlation

T192 Evaluation of growth and performance characteristics of crossbred calves sired by Charolais, Simmental, or Braunvieh sires. M. S. Mizell*, T. Page, K. Harborth, M. Canal, A. Canal, and M. D. Garcia, *Louisiana State University, Baton Rouge.*

The objective of the current study was to evaluate the growth and performance characteristics for a crossbred calf crop sired by three different paternal breeds of sires. The sire breeds consisted of Braunvieh, Charolais, and Simmental cattle that all originated from herds in the southeastern United States. The three sire types were mated to a population of crossbred cattle that are classified by the breed types comprising the MARC germplasm cycle 8 dams. A total of 44 Simmental calves, 34 Charolais calves, and 32 Braunvieh calves were calved at the LSU AgCenter Central Research Station and all had birth weights, weaning weights, and hip height measurements collected. Birth weight measurements were recorded within 48 hours of birth. Weaning weight and hip height measurements were recorded at weaning on approximately day 210 days of age. The average birth weight, weaning weight, and hip height for the Simmental heifers were 37.57 kg, 282.79 kg, and 113.77 cm. The average birth weight, weaning weight, and hip height for the Simmental steers were 40.01 kg, 307.24 kg, and 115.87 cm. The average birth weight, weaning weight, and hip height for the Charolais heifers were 34.98 kg, 266.67 kg, and 111.48 cm. The average birth weight, weaning weight, and hip height for the Charolais steers were 39.01 kg, 300.93 kg, and 115.14 cm. The average birth weight, weaning weight, and hip height for the Braunvieh heifers were 36.88 kg, 255.08 kg, and 111.53 cm. The average birth weight, weaning weight, and hip height for the Braunvieh steers were 35.28 kg, 270.91 kg, and 112.67 cm. Utilizing the mixed model procedure and the LSMEANS function of SAS it was observed that Simmental sired calves had a significantly higher birth weight ($P < 0.05$) than both the Braunvieh- and Charolais-sired calves. Simmental-sired calves also had a significantly ($P < 0.05$) higher hip height measurement than Braunvieh-sired calves but were not taller than Charolais-sired calves. No significant differences were reported between sire breeds for weaning weight.

Key Words: growth, birth weight, weaning weight

T193 An evaluation of 55 years of performance trends from the Dean Lee Research Station performance bull test. T. R. Howard, S. DeRouen, K. Harborth, K. Bondioli, and M. D. Garcia*, *Louisiana State University, Baton Rouge.*

The objective of this study was to evaluate genetic trends for bulls that have comprised the LSU AgCenter Dean Lee performance bull test that has been conducted for the past 55 years. The LSU AgCenter Performance bull test at the Dean Lee Research Station has collected data on yearling bulls on 112d of test for the last 55 years. To date 7,488 yearling bulls from 34 breeds have been evaluated for such traits, including birth weight (BW), initial weight, 112-day weight, average daily gain (ADG), adjusted yearling weight, and scrotal circumference (SC). The top 4 represented bull breeds with greater than 500 animals being tested were included in a Angus, Charolais, Hereford, and Simmental. In 1958, initial weights averaged 249.38 kg and 112-day weights averaged 362.19 kg. Initial weights and 112-d weights in 2011 averaged 332.52 kg and 510.49 kg, respectively. Analyses revealed that all growth traits for all animals regardless of breed demonstrated a linear increase across the years with BW and SC being the lone exceptions. Initial weight increased 1.61 kg/year, 112-d weight increased 2.63 kg/yr, ADG increased .0091 kg/day/year and adjusted yearling weight increased 3.67 kg/year while BW and SC decreased -0.44 kg/year and -0.23 cm/year respectively. The mixed model procedure of SAS and interval regression analyses were utilized to evaluate the positive slope increase observed for all traits over the past 55 years for the four highest represented breeds. Analysis of each individual breed's performance across all years indicated that the Simmental breed had the greatest increase ($P < 0.05$) in initial weight with 3.92 kg/year over Angus (1.92 kg/year), Charolais (0.12 kg/year), and Hereford (1.21 kg/year) ($P < 0.05$). Results for 112-day weight indicated that the Simmental breed made a greatest increase ($P < 0.05$) of 3.79 kg/year when compared to Angus (3.23 kg/year), Charolais (1.99 kg/year), and Hereford (2.24 kg/year). Charolais displayed the largest increase ($P < 0.05$) in ADG across all years with 0.02 kg/day/year while Angus, Hereford, and Simmental increased 0.01, 0.009, and 0.001 respectively.

Key Words: bull test, performance testing, genetic trend

T194 Multivariate heavy-tailed distribution modeling of residuals in estimation of genetic parameters of carcass traits in beef cattle. S. O. Peters^{1,2}, K. Kizilkaya^{3,4}, D. J. Garrick³, R. L. Fernando³, E. J. Pollak⁵, M. De Donato^{1,6}, T. Hussain^{1,7}, and I. G. Imumorin^{*1}, ¹Cornell University, Ithaca, NY, ²Berry College, Mt Berry, GA, ³Iowa State University, Ames, ⁴Anadn Menderes University, Aydin, Turkey, ⁵US Meat Animal Research Center, Clay Center, NE, ⁶Universidad de Oriente, Cumana, Sucre, Venezuela, ⁷University of Veterinary and Animal Sciences, Lahore, Pakistan.

Evaluation of carcass quality and estimation of genetic parameters for carcass traits are of considerable importance in the genetic improvement for beef cattle. Assumption of normality of residuals in linear mixed models for carcass evaluation may make inferences vulnerable to the presence of outliers. Heavy-tail densities are viable alternatives to normal distributions. We compared estimates of genetic parameters by fitting Multivariate Normal (MN), Multivariate Student's-*t* (MS*t*) or Multivariate Slash (MS) and treating degrees of freedom (ν) as unknown for residuals in data of hot carcass weight (HCW), longissimus muscle area (REA) and 12th to 13th rib fat (FAT) traits in beef cattle. A total of 2,476 HCW, REA and FAT records were obtained from a large commercial operation in Nebraska between 2007 and 2008. The data set included pedigree information, contemporary groups, feed lot and breed types. Models included fixed effects of contemporary group of year and pasture and also feed lot type and sire breed. Deviance information criteria for

model comparisons favored MS_t over MS and MN models respectively. The posterior means (PM) (and 95% posterior probability intervals, PPI) of ν for the MS_t and MS models were 5.90 ± 0.86 (4.37, 7.70) and 2.02 ± 0.17 (1.70, 2.38) respectively. Smaller values of posterior densities of ν for MS_t and MS models confirm that the assumption of normally distributed residuals is not adequate for the analysis of HCW, REA and FAT datasets. Posterior inference on additive heritabilities for HCW, REA and FAT using MN, MS_t , and MS models indicated that they are similarly and moderately heritable and were comparable to those reported in literature. PM of genetic correlations for the HCW, REA and FAT were variable but positive except for the correlation between REA and FAT, which shows an antagonistic relationship. The 95% PPI estimates from MN and MS_t models for HCW did not overlap indicating significant difference between PM estimates from MN or MS_t models.

Key Words: cattle, genetic parameter, residual

T195 Heritability and correlations of immune response parameters in cattle treated for bovine respiratory disease. R. R. Cockerum^{*1}, S. E. Speidel¹, J. L. Salak-Johnson², C. C. L. Chase³, R. K. Peel¹, R. L. Weaber⁴, H. Van Campen¹, G. H. Loneragan⁵, J. J. Wagner¹, P. Boddhireddy⁶, M. G. Thomas¹, K. Prayaga⁶, and R. M. Enns¹, ¹Colorado State University, Fort Collins, ²University of Illinois, Urbana, ³South Dakota State University, Brookings, ⁴Kansas State University, Manhattan, ⁵Texas Tech University, Lubbock, ⁶Zoetis, Kalamazoo, MI.

We hypothesized that cattle vary in their innate immune response, which may serve as indicators of developing bovine respiratory disease

(BRD). The objectives of this study were to determine the heritability and associative relationships among immune response parameters. Two contemporary groups of crossbred steer calves ($n = 2869$) were received approximately 83 d post-weaning (221.7 ± 24.34 kg) at a commercial feedlot in Southeastern Colorado. Upon receiving, jugular blood was collected via silicone-coated vacutainer tubes for immune response analyses. Immune response measures were collected at 227 d and 238 d for contemporary groups one and two, respectively. Heritability estimates for immunoglobulin G (IgG), immunoglobulin G1 (IgG1), immunoglobulin G2, (IgG2), IgG1 to IgG2 ratio (IgG1:IgG2), cortisol, and interleukin 8 (IL8) were estimated from a sire model using ASREML. Estimated heritability was low to moderate for the following immune response parameters: IgG (0.13), IgG1 (0.02), IgG2 (0.27), IgG1:IgG2 (0.13), cortisol (0.15), and IL8 (0.30). Furthermore, incidence of BRD as measured from observed clinical signs was heritable (0.21). Correlations among phenotypes and genotypes for traits of interest were calculated. There were low to high positive phenotypic correlations ($0.12-0.87 \pm 0.02$; $P < 0.001$) between IgG, IgG1, IgG2, and IgG1:IgG2. Low negative phenotypic correlations ($P < 0.001$) were estimated between cortisol and IgG (-0.15 ± 0.02), IgG1 (-0.08 ± 0.02), and IgG1:IgG2 (-0.07 ± 0.02). Interleukin 8 had a low positive phenotypic correlation (0.04 ± 0.02 ; $P = 0.033$) with IgG. Moderate to high positive genetic correlations were observed between IgG1 and IgG2 (0.34) and cortisol (0.57), and a moderate negative genetic correlation was observed with IL8 (-0.36). Results from this study suggest that immune response parameters are heritable suggesting that immune response may be improved through genetic selection.

Key Words: bovine respiratory disease, cattle, immunity