

## Breeding and Genetics: Beef Cattle

### M72 Association of a single nucleotide polymorphism of calpain 1 gene with meat tenderness of the yak.

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The association of a single nucleotide polymorphism (SNP) of calpain 1 (CAPN1) gene with shear force of 2.54 cm steaks from *M. longissimus dorsi* from Gannan yaks (*Bos grunniens*, n = 181) was studied. The experimental design was a repeated measures with the main unit in a completely randomized design with a factorial arrangement of treatments (age at harvest x SNP) and the repeated subunit was aging days. Individual animal was used as the experimental unit. Yaks were harvested at 2, 3, and 4 yr of age (n = 51, 59, and 71, respectively), and samples of each yak carcass were aged at 4°C for 0, 1, 3, 7, 14 or 21d. Shear force for each sample was determined at each of 6 postmortem aging times using Warner-Bratzler shear force methodology. Fragments of the yak CAPN1 gene including exon 9 and intron 9 were amplified and subjected to single strand conformation polymorphism analysis. A SNP was found within intron 9 of the CAPN1 gene G5837A, and there were 2 genotypes of GG and GA identified, respectively. The genotypic frequency of GG was 82.87% compared with 17.13% for GA. Statistical analysis was done using SAS PROC MIXED. Interaction of SNP x age at harvest x aging days was demonstrated ( $P < 0.10$ ) for shear force. In 2-yr-old yak, genotype GG had lesser shear force than that of GA at the aging times of 0, 3, and 7 d (0.78, 0.92, and 0.65 kg, respectively;  $P < 0.05$ ); however, in 3-yr- and 4-yr-old yak, genotype GG had lesser shear force than GA at aging time of 14 d (0.71 and 0.58 kg, respectively;  $P < 0.05$ ). Genotype had little effect ( $P > 0.05$ ) on shear force for 3- and 4-yr-old yaks averaged over aging time. In 2-yr-old yak, genotype GG had 0.57 kg lesser shear force than yaks with genotype GA ( $P < 0.05$ ) averaged over aging time. Therefore, results from this research suggest that the CAPN1 SNP affected shear force of *M. longissimus dorsi* but the effect differed depending on age of yak and aging time of the meat.

**Key Words:** yak, calpain, genotype

### M73 The effects of single nucleotide polymorphisms of calpastatin gene on meat tenderness of the yak.

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The association of single nucleotide polymorphisms (SNPs) of calpastatin (CAST) gene with shear force of 2.54 cm steaks from *M. longissimus dorsi* from Gannan yaks (*Bos grunniens*, n = 181) was studied. Yaks were harvested at 2, 3, and 4 yr of age (n = 51, 59, and 71, respectively), and samples of each yak carcass were aged at 4°C for 0, 1, 3, 7, 14 or 21d. Shear force for each sample was determined at each of the 6 postmortem aging-day using Warner-Bratzler shear force methodology. Fragments of the yak CAST gene including exon 3 were amplified and subjected to single strand conformation polymorphism analysis. Two linkage SNPs were found within exon 3 of the CAST gene: G40455A and G40463A, and there were 2 genotypes of GG/AA and GA/GA demonstrated respectively. The genotypic frequency of GG/AA was 72.93% compared with 27.07% for GA/GA. Statistical analysis was done using SAS PROC MIXED. Interaction of genotype x age at harvest x aging time was demonstrated ( $P < 0.05$ ) for shear force. In 2-yr-old yak, GG/AA had lesser shear force than GA/GA at the aging times of 1 and 7

d (1.15 and 0.57 kg, respectively;  $P < 0.05$ ); 4-yr-old yak GG/AA had lesser shear force than GA/GA at aging times of 7 and 14 d (0.64 and 0.49 kg, respectively;  $P < 0.05$ ). Genotype had little effect ( $P > 0.05$ ) on shear force in 2-yr- and 3-yr-old yak averaged over aging time. In 4-yr-old yak, GG/AA had 0.40 kg lesser shear force than GA/GA ( $P < 0.05$ ) averaged over aging time. Therefore, it was concluded that the CAST SNPs affect ( $P < 0.10$ ) shear force of *M. longissimus dorsi* depending on age of yak and aging time of the meat. Further study should focus on the ontogeny of CAST gene mRNA expression.

**Key Words:** yak, calpastatin, tenderness

### M74 Estimation of inbreeding and effective population size of fullblood Wagyu cattle registered with the American Wagyu Association.

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The founders of the American Wagyu herds were imported from Japan during a period when inbreeding was high and the effective population size of the Japanese Wagyu was low. The effective population size represents the number of breeding animals in an ideal population where each male and female has an equal chance of contributing to the next generation. The objectives of this research were to estimate the inbreeding and effective population size of the Wagyu breed using pedigree information from 2504 fullblood animals registered with the American Wagyu Association and from genotypes of 50 fullblood Wagyu animals representing 8 prominent sire lines. The Illumina BovineSNP50 BeadArray was used to genotype the Wagyu samples. Excess homozygosity was used to estimate inbreeding by genotype using PLINK (Purcell et al. 2007) while inbreeding based on pedigree was estimated with FSspeed Pro (<http://www.tensemt.co.uk/fspeed/fspeed.html>). The effective population size was estimated for the period of 1990 to 2007 as described by Nomura et al. (2001) where the annual rate of inbreeding ( $\Delta F_{ST,y}$ ) was used to estimate the annual effective population size ( $N_e$ ). The estimated level of inbreeding for American Wagyu based on pedigrees was 5.8% which reflects that inbreeding is underestimated for foundation animals with shallow pedigrees. The estimated inbreeding based on pedigrees and genotypes in the 8 sire lines are shown in Table 1. The effective population size averaged 8.8 between 1990 and 2007, with a low of 1.5 in 1991 and a high of 16 in 2007. Wagyu in America are the result of a small number of cattle imported from Japan between 1976 and 1999 and additional importations in the near future are not expected. Strategies to increase genetic diversity and limit inbreeding should be considered to maintain this unique breed of cattle.

**Table 1.** The percent inbreeding for each of 8 sires based on their 5 generation pedigree and genotypes from the SNP50 BeadArray

Sires	%Inbreeding: Pedigree	%Inbreeding: Genotype
TF Itomichi 1/2	0	25
Kitaguni Junior	0	18.4
TF Kikuhana	18.7	39.1
Kitateruyasudoi	9.4	27.3
Michifuku	6.2	28.1
Sanjirou	12.9	33.1
Takazakura	12.5	31.2
JVP Fukutsuru 068	9.4	21.9

**Key Words:** Wagyu, inbreeding, population

**M75 Genetic network update for economically important traits in a Wagyu x Limousin reference population.** Z. Jiang<sup>\*1</sup>, J. J. Michal<sup>1</sup>, T. F. Daniels<sup>1</sup>, J. Chen<sup>1</sup>, Z. X. Pan<sup>1</sup>, T. Kunej<sup>1</sup>, M. D. Garcia<sup>2</sup>, C. T. Gaskins<sup>1</sup>, J. R. Busboom<sup>1</sup>, L. J. Alexander<sup>3</sup>, R. W. Wright Jr.<sup>1</sup>, and M. D. MacNeil<sup>3</sup>, <sup>1</sup>Washington State University, Pullman, <sup>2</sup>Louisiana State University, Baton Rouge, <sup>3</sup>USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT.

In the present study, 84 genes representing 6 different biological pathways were investigated for their associations with 5 carcass, 6 eating quality and 8 fatty acid composition traits in a Wagyu  $\times$  Limousin reference population, including 6 F1 bulls, 113 F1 dams, and 246 F2 progeny. A total of 157 mutations, mainly single nucleotide polymorphisms were genotyped using a Sequenom assay, but only 135 tagged mutations were selected by the HAPLOVIEW analysis for the association study. Single marker-trait association runs revealed 153 significant associations ( $P < 0.05$ ), which were then placed into 3 groups of quantitative trait modes (QTM)s with additive, dominant and overdominant effects if a marker had 3 genotypes with at least 9 animals for each group of genotypes. All significant markers and their QTM's associated with each of these 19 traits were involved in a linear regression model analysis, which confirmed single-gene associations for 4 traits, but revealed 2-gene networks for 9 traits and 3-gene networks for 4 traits. Such genetic networks involving both genotypes and QTM's resulted in high correlations between predicted and actual values of performance, thus providing evidence that the classical Mendelian principles of inheritance can be applied in understanding the genetic complexity of complex phenotypes. Our present study also indicated that carcass, eating quality and fatty acid composition traits rarely share genetic networks. Therefore, marker-assisted selection for improvement of one category of these traits would not interfere with improvement of another.

**Key Words:** quantitative traits, genetic networks, beef cattle

**M76 Genetic trends for image analysis traits in Japanese Black cattle.** Y. Nakahashi\*, S. Ido, and K. Kuchida, Obihiro University of A & VM, Obihiro-shi, Hokkaido, Japan.

Intramuscular fat has been a concern in genetic improvement of Japanese Black cattle. Beef Marbling Standard (BMS) has been used as an indicator of the amount of marbling. However, there are factors other than marbling that are known to affect BMS, such as the coarseness or fineness of marbling flecks. In the present study, we investigated genetic trends and the relationships between traits related to BMS. A total of 10,556 of Japanese Black cattle that were shipped to a meat processing plant in Hokkaido, Japan, were used in the study. High quality digital images were collected and analyzed to calculate the marbling percent (MP) and coarseness index of marbling (CIM). The AIREMLF90 program was used for estimation of genetic parameters. Genetic trends were calculated as the average of standardized breeding values (BV) of the dams by birth year for every trait. Regression coefficients ( $\beta$ ) were used to compare the genetic trends. The estimated heritabilities of BMS, MP, and CIM were  $0.63 \pm 0.04$ ,  $0.74 \pm 0.04$ , and  $0.51 \pm 0.04$ , respectively. The genetic correlation coefficients of BMS with MP and CIM were 0.58 and 0.96, respectively. The trend in average BMS BV was flat from 1937 to 1970 ( $\beta = -0.01$ ), increasing from 1970 to 1990 ( $\beta = 0.04$ ), and accelerating after 1990 ( $\beta = 0.18$ ). Similarly, the genetic trends for MP and CIM also increased. These results indicated that the genetic improvement of BMS is occurring, but at the same time genetic merit for the undesirable trait of marbling coarseness is also increasing. To achieve improvement of BMS without increasing coarseness of marbling, it is suggested to utilize image analysis in genetic evaluation, as this technology can indicate detailed characteristics of marbling.

**Key Words:** genetic trend, image analysis, Japanese Black cattle

**M77 Multivariate analyses of weight traits fitting reduced rank and factor analytic models in Nellore cattle.** A. A. Boligon<sup>\*1</sup>, A. B. Bignardi<sup>1</sup>, M. E. Z. Mercadante<sup>2</sup>, and L. G. Albuquerque<sup>1</sup>, <sup>1</sup>FCAV/UNESP, Jaboticabal, São Paulo, Brazil, <sup>2</sup>Instituto de Zootecnia, Sertãozinho, São Paulo, Brazil.

A total of 61,528 records from 12,246 animals from the Nellore Cattle Breeding Program were used to estimate genetic parameters using multivariate analysis (MV). Reduced rank analyses fitting the first  $m = 2, 3, 4$  and 5 genetic principal components (RR) and analyses that fitted a factor analytic structure considering  $m = 2, 3, 4$  and 5 factors (FA), were carried out. The traits evaluated were: birth weight (BW), weaning weight (WW), weight at 365 (W365) and 550 d of age (W550), and weight at 2, 3, 4, 5 and 6 year of age (W2Y, W3Y, W4Y, W5Y and W6Y, respectively). Genetic additive direct effects and residual effects were considered as random. For BW and WW, the genetic maternal and maternal permanent environment effects were included as random effect. Contemporary group (farm, sex, year, and month of birth) was included as a fixed effect. Linear and quadratic effects of animal age at recording (except BW), and dam age at calving (for BW, WW, W365 and W550) were included as covariables. The residual, genetic maternal and permanent environment covariance matrix was assumed to have full rank throughout. Models were compared by Akaike's Information Criterion (AIC) and Schwarz's Bayesian Information Criterion (BIC). The model containing the largest number of parameters - MV (96 parameters) showed the worst fit. For models with the factor number equal to the principal component number, the value of  $\log L$  was very similar. In general, the results indicate that RR models with 3 principal components (RR-PC3) are sufficient to model the genetic covariance structure among the weight traits. The 3 principal components explained more than 90% of the genetic variation. Genetic correlation estimates between weights traits ranged from 0.42 to 0.96. Results from RR-PC3 agreed closely with estimates from MV analyses and literature results. The RR estimation decreased computational requirements relative to MV analyses.

**Key Words:** growth traits, genetic parameters, principal component analysis

**M78 Genetic parameters for weight traits from birth to 630 days of age in Guzera cattle by random regression models.** I. S. Silva<sup>\*1</sup>, I. U. Packer<sup>2</sup>, L. O. C. Silva<sup>3</sup>, C. M. R. Melo<sup>4</sup>, and R. A. A. Torres Junior<sup>3</sup>, <sup>1</sup>University of Brasília - UnB, Brasília /DF, Brazil, <sup>2</sup>University of São Paulo - USP/ESALQ, Piracicaba/SP, Brazil, <sup>3</sup>Embrapa Gado de Corte, Campo Grande/MS, Brazil, <sup>4</sup>Federal University of Santa Catarina - UFSC, Florianópolis/SC, Brazil.

A total of 60,782 body weight records belonging to Guzera breed from birth to 630 d of age were analyzed to estimate the variance components and the genetic parameters by random regression models and the REML methodology. Ten regression models were analyzed with contemporary group as fixed effect and age of dam as a covariate. Covariance functions of different order were analyzed for direct additive genetic random (kA), animal permanent environmental (kC), maternal permanent environmental (kQ) and residual effects with homogeneous (r1) and heterogeneous variance structures, with 5 (r5) or 10 (r10) residual variance classes. Models were compared by the Likelihood Ratio Test, the Akaike Information Criterion (AIC) and the Schwarz's Bayesian Information Criterion (BIC). The variance estimates in the analyses by the regression models were relatively similar. AIC values showed that the adjustment of the model with order of covariance functions of 6 for kA, kC, kQ (Reg666) and r10, was superior in relation to the other models. BIC values showed that the most parsimonious model

had order of covariance functions of 6 for kA, 5 for kC and 3 for kQ (Reg653), and r10, was optimal among the models with 10 residual variance classes. The heritability estimates for weights at birth (WB), 205 (W205), 365 (W365) and 550 (W550) days of age were 0.13, 0.43, 0.46, 0.48 for the model Reg666-r10, and 0.13, 0.46, 0.54, 0.56, for the model Reg653–10. The phenotypic, genetic, animal and maternal permanent environmental correlations were all positive and were similar for all models. Considering the most parsimonious model, Reg653 and r10, the genetic correlations between WB/W205, WB/W365, WB/W550, W205/W365, W205/W550 and W365/W550 were 0.40, 0.40, 0.42, 0.68, 0.74 and 0.81, respectively. Models with variance homogeneity were inadequate. It was observed that division of the residual variance into 10 distinct classes was the most suitable model for describing variation in the weights studied herein.

**Key Words:** beef cattle, variance components, random regression

**M79 Principal component analysis of traits contributing to genetic evaluation of Brahman bulls in Brazil.** J. C. Souza<sup>\*1</sup>, L. O. C. Silva<sup>2</sup>, A. Gondo<sup>2</sup>, P. B. Ferraz Filho<sup>3</sup>, J. A. Freitas<sup>4</sup>, C. H. M. Malhado<sup>5,7</sup>, R. L. Weaber<sup>6</sup>, and W. L. Lamberson<sup>6,1</sup> *Mato Grosso do Sul Federal University - UFMS, Aquidauana, MS, Brazil, <sup>2</sup>Empresa Brasileira de Pesquisa Agropecuaria - EMBRAPA, Campo Grande, MS, Brazil, <sup>3</sup>Mato Grosso do Sul Federal University - UFMS, Tres Lagoas, MS, Brazil, <sup>4</sup>Parana Federal University - UFPR, Palotina, PR, Brazil, <sup>5</sup>UESB, Jequie, BA, Brazil, <sup>6</sup>Animal Sciences, MU - USA, Columbia, MO, <sup>7</sup>Scholarship of CNPq, Brasilia, DF - Brazil.*

The objective of this study was to evaluate the contribution of each trait contributing to genetic evaluation of Brahman sires. The data were from the 2006 summary of Brahman bulls published by EMBRAPA/CNPGC. Estimates of EPD were obtained using a multiple trait animal model including: weight to maternal phase – 120 d (PM); weight total maternal phase (TMMP); weaning weight (WW); total maternal weaning weight (TMW); yearling weight (YW); pre-weaning gain (GNW) (g/day); total maternal pre-weaning gain (TMPG); post-weaning gain (YGP); age (days) at first calving (IPP); interval between the 1st and 2nd calving (I2P); interval and other calving (IOP); scrotal circumference measurements (SC); and genetic qualification index (IQG = 10% \* PM + 15% \* WW + 20% \* TMW + 30% \* YW + 10% \* IPP + 10% \* I2P + 5% \* SC)) of 542 bulls. The characteristics were evaluated by using the PRINCOMP procedure of SAS. The eigenvalues and proportions of the first 5 principal components were 6.72, 0.52; 1.78, 0.14; 1.49, 0.11; 1.18, 0.09; 0.61, 0.05, respectively; the first eigenvalue totaled 0.52; first 2 0.65; the first 3 0.77, the first 4 0.86, and a total of 5 0.91. The estimated contribution of the first principal component for each trait was WW (0.3757); IQG (0.3749); YGP (0.3724), YW (0.3573); TMW (0.3569); TMPG (0.3526); TMMP (0.3161); YGP (0.2316), SC (0.1515), IOP (0.1347), IPP (0.0527), PM (-0.0060); and I2P (-0.0528). The traits that most contributed were weaning weight, genetic qualification index and post-weaning gain. The traits which contributed least were weight to maternal phase and interval between 1st and 2nd calving. The largest genetic correlations were between weaning weight and post-weaning gain (0.96); yearling weight (0.97); and IQG (0.9556).

**Key Words:** gain, principal components, Zebu

**M80 Allelic frequencies of polymorphisms associated with feed efficiency in Aberdeen Angus cattle in Uruguay.** A. I. Trujillo, P. Grignola, I. Pandulli, P. Nicolini, A. Casal, A. Espasandin, F. Peñagaricano, and M. Carrquiry\*, *Universidad de la Republica, Montevideo, Montevideo, Uruguay.*

We are interested in selecting cattle with improved feed efficiency by searching for residual feed intake (RFI) candidate genes. In confinement systems, neuropeptide Y (NPY), leptin (LEP) and insulin growth factor-1 (IGF-1) have shown association with feed efficiency. Since frequencies of single nucleotide polymorphisms (SNP) of NPY, LEP and IGF-1 are unknown in beef cattle population in Uruguay, our objective was to study the distribution of these SNP in the Aberdeen Angus breed. This is a first step in evaluating the associations of these SNP with RFI and investigating their use as molecular markers for assisted selection in pasture-based system. A totally of 130 genetically unrelated calves from 5 Aberdeen Angus herds (the major contributors to the national genetic pool) were sampled. DNA was extracted from fresh blood using the “salting out” procedure. High resolution melting (HRM) of PCR small amplicons in presence of SYBR Green dye was used to genotype. An A/G SNP located in intron 2 of the NPY gene, a C/T SNP located in exon 2 of the LEP gene and a C/T SNP located in the promoter region of IGF-1 gene, were the markers genotyped. The allelic frequencies of SNP were 0.76 and 0.24 (A and G) for NPY, 0.46 and 0.54 (C and T) for LEP, and 0.61 and 0.39 (C and T) for IGF-1. The SNP frequencies distributions were similar across different herds ( $P \geq 0.05$ , Chi-squared test). This data shows that the frequency of “favorable” alleles is lower than the “unfavorable” alleles in Aberdeen Angus cattle in Uruguay. These results support our proposal that it is possible to improve feed efficiency by using marker-assisted selection in the context of a national program.

**Key Words:** SNP NPY LEP IGF-1, feed efficiency, Aberdeen Angus breed

**M81 Techniques for sifting inconsistent data points from repeatedly weighed beef cattle.** S. E. Speidel\*, C. M. McAllister, D. H. Crews Jr., and R. M. Enns, *Colorado State University, Fort Collins.*

Prior to their inclusion in genetic evaluations, phenotypic records are typically sifted following Beef Improvement Federation guidelines to exclude erroneous data points. Random regression techniques allow the use of data points regardless of age at measurement. Given the range of ages typically seen in field data sets, it can be challenging to identify problematic observations. The objective of this study was to compare data sifting procedures that can be implemented on a large scale for the purpose of identifying individual data points inconsistent within an individual animal's growth curve. The data set consisted of 1372 animals with an average of 10.98 weight observations per animal ranging from 0 to 519 d of age. Three methods were used to identify inconsistent data within a given animal. First individual animals with  $R^2$  values less than 0.90 for the linear regression of weight on age were examined. Second, residuals from this regression were compared with residuals on all animals, to identify observations with residuals greater than 4, 5, and 6 standard deviations (SD) from 0. Finally, each weight was compared with the overall variability of weight within age window across years, to identify those greater than 4, 5, and 6 SD from the mean. This last method was the least robust of all 3 failing to identify any erroneous data points. The  $R^2$  method was not sensitive enough in this data set given that only 5 animals possessed an  $R^2$  less than 0.90, although one individual animal was identified with a data point not consistent with his remaining values. The most sensitive method compared each individual residual value to the overall residual variability. Here, a total of 10, 2

and 0 animals were identified with residuals greater than 4, 5, and 6 SD from the mean, respectively. For this data set, the inclusion of birth and weaning weights along with the test weights gave better predictions of average daily gain by more precisely estimating the intercept for each regression line. Since the  $R^2$  values were so high the residual method easily found those observations inconsistent with the remaining records on the individuals.

**Key Words:** beef cattle, data sifting, longitudinal data

**M82 Use of principal component approach to predict direct genomic breeding values for meat traits in Italian Simmental Bulls.** M. A. Pintus<sup>1</sup>, G. Gaspa<sup>1</sup>, N. P. P. Macciotta\*<sup>1</sup>, P. Carnier<sup>2</sup>, E. L. Nicolazzi<sup>3</sup>, C. Dimauro<sup>1</sup>, D. Vicario<sup>4</sup>, P. Ajmone-Marsan<sup>3</sup>, A. Nardone<sup>5</sup>, and A. Valentini<sup>5</sup>. <sup>1</sup>Università di Sassari, Sassari, Italia, <sup>2</sup>Università di Padova, Padova, Italia, <sup>3</sup>Università di Piacenza, Piacenza Italia, <sup>4</sup>ANAPRI, Udine, Italia, <sup>5</sup>Università della Tuscia, Viterbo, Italia.

In the current study, principal component (PC) analysis was used to reduce the number of predictors in the estimation of direct genomic breeding values (DGV) for meat traits in a sample of 457 Italian Simmental bulls. SNP marker genotypes were determined with the 54K Illumina beadchip. After edits, 40,179 SNPs were retained. PC extraction was carried out separately for each chromosome and 2,466 new variables able to explain 70% of total variance were obtained. Bulls were divided into reference and validation population. Three scenarios of the ratio reference/validation were tested: 70:30, 80:20, 90:10. Effect of PC scores on polygenic EBVs was estimated in the reference population with a BLUP model. Traits analyzed were daily live weight gain, size score, muscularity score, feet and legs score, beef index (economic index), calving ease direct effect, and cow muscularity. Accuracy was calculated as correlation between DGV and polygenic EBV in the validation bulls. Muscularity, feet and legs, and the beef index show the highest accuracies (Table 1), calving ease the lowest. In general, accuracies are slightly higher (Table 1) when reference animals are selected at random and the best scenario is 90:10.

**Table 1.** Accuracy of GEBV for 7 meat traits

Trait	Scenarios					
	Sorted by birth year			Random		
	70:30	80:20	90:10	70:30	80:20	90:10
Daily live weight gain	0.38	0.35	0.53	0.47	0.37	0.63
Size score	0.44	0.47	0.54	0.49	0.47	0.47
Muscularity score	0.71	0.67	0.80	0.71	0.70	0.79
Feet and leg score	0.72	0.74	0.85	0.76	0.77	0.83
Beef index	0.63	0.57	0.74	0.63	0.60	0.77
Calving ease direct effect	0.23	0.23	0.24	0.34	0.26	0.29
Cow muscularity	0.80	0.85	0.83	0.82	0.84	0.82

**Key Words:** principal component analysis, genomic selection, meat trait

**M83 Genetic analysis of visual score data with different distributions and genetic parameters using linear and nonlinear models.** F. Barichello\*<sup>1</sup>, M. M. Alencar<sup>2</sup>, and R. A. A. Torres Júnior<sup>3</sup>, <sup>1</sup>Unesp, Jaboticabal, SP, Brazil, <sup>2</sup>Embrapa Southeast Livestock, São Carlos, SP, Brazil, <sup>3</sup>Embrapa Beef Cattle, Campo Grande, MS, Brazil.

The aim of this study was to evaluate the effect of the way (Y) of assigning discrete visual scores (VS, 6 levels) for the values of a continuous underlying scale (USC) on the estimated breeding values (BV) for 2 heritability values ( $h^2$ : 0.25 and 0.49) and 2 magnitudes of contemporary

group variance (CG: 0.25 and 1.00). Three different models (M) (linear, threshold, and linear with transformed data) were used for the analysis. Herds with 40 sires and 1,200 dams, mated at random, were simulated for 20 years. Direct and maternal BV, maternal permanent environmental, CG, and age of dam effects were generated and combined with an independent error term to form the phenotype in the USC. The USC were assigned, as a function of CG, according to normal relative ( $Y_1$ ) and normal fixed ( $Y_2$ ) distributions. The BVs were estimated using the GIBBS2F90 and THRGIBBS1F90 programs with previously estimated variance components. The procedure was repeated 10 times for each combination. Correlations (R) between estimated and true BV were obtained for each animal class (sires, dams and offspring). Significant effects of Y on R for all animal classes were found. The  $Y_1$  distribution presented better estimates than  $Y_2$  distribution for all animal classes (sires: 0.92 vs 0.91; dams: 0.61 vs 0.60; offspring: 0.69 vs 0.68). For dams and offspring, significant effect of  $h^2$  on R was found, where high level of  $h^2$  provided greater correlation between true and estimated BV (dams: 0.67 vs 0.55; offspring: 0.74 vs 0.63). For sires, significant effects of  $h^2 \times CG$  interaction on R were found (at  $h^2 = 0.49$  no differences were found between levels of CG, but at  $h^2 = 0.25$  greater R values were found with a low level of CG). M had no effect on R. The results indicate slightly better performance of the  $Y_1$  way of assigning VS to US values, and all M yielded consistent results for VS evaluation.

**Key Words:** breeding value, threshold model, transformed data

**M84 Multibreed genetic evaluation of calving ease and birth weight using a threshold-linear model in Gelbvieh cattle.** S. Tsuruta\*, A. H. Nelson, J. K. Bertrand, and I. Misztal, University of Georgia, Athens.

Multibreed genetic evaluation (MBE) was implemented for calving ease (CE) and birth weight (BW) using a threshold-linear model applied to data from the American Gelbvieh Association. Data included 138,072 CE records (3 categories) and 941,811 BW records from 1972 to 2008. The pedigree file contained 1,204,867 animals. Heterosis priors of CE were not available from the literature, so they were constructed by making them proportional (0.02) to the BW priors. Priors of unknown parent group within breeds (breed effects) for CE were also constructed in proportion to those for BW. Priors of external BW and CE EPD for Angus sires in the Gelbvieh data set were provided by the American Angus Association. The computer program used a preconditioned conjugate gradient and iteration on data method. The MBE converged when priors for heterosis and breed effects were used without considering prior external EPD information; however, analyses did not converge when the external EPD priors were included. Correlations between EPD with and without heterosis and breed effect priors were 0.95 and 0.99 for CE and BW, respectively. Correlations of the Angus sire EPD computed in the Gelbvieh MBE with the external EPD of the same Angus sires were 0.23 and 0.33 for CE and BW, respectively, indicating that the external EPD for Angus sires were not good priors in the Gelbvieh data. When low accuracies were assumed for the external Angus EPD for CE and BW, the program converged. This indicates that CE provided from an Angus sire mated to a Gelbvieh female may not be representative of the Angus sire's performance based on external EPD, which were the result of mating Angus sires to Angus dams. This result may suggest that the external EPD priors for BW only should be used in the MBE because informative external EPD priors may not be available for CE.

**Key Words:** multibreed evaluation, calving ease, threshold-linear model

**M85 Comparison of a feed efficiency measure for steer progeny produced from divergently mated sires and dams phenotyped for residual feed intake.** N. O. Minton\*, R. L. Weaber, R. L. Kallenbach, and M. S. Kerley, *University of Missouri, Columbia*.

Objectives of this research were to determine feed efficiency of progeny produced from mating RFI phenotyped sires and dams and the effect of test duration (0 to 70 d, 0 to 120 d, and 70 to 120 d) on RFI values of calves. We hypothesized that parent RFI would influence progeny feed efficiency. We further hypothesized that an increase in test duration for RFI is necessary to accommodate for pre-test effects that could alter RFI values of calves. Simmental crossbred heifers ( $n = 12$  RFI- and  $n = 12$  RFI+) were mated with RFI- ( $n = 2$ ) and RFI+ ( $n = 2$ ) bulls. Sire was used as an independent variable to measure the effect of sire on progeny performance. Three dam groups were formed by assigning one SD greater than (INEFF) and one SD less than (EFF) average (AVG) RFI. Steer progeny were placed on feed post weaning where intake and BW were measured over 120 d. Intake and weight data were used to calculate ADG, intake, FCR and RFI. Progeny performance differed among sire groups. Progeny from RFI- sires were more efficient than progeny from RFI+ sires on test durations 0 to 70 d ( $-0.50$  v  $-0.06$ ;  $P < 0.12$ ) and 0 to 120 d ( $-0.51$  v  $-0.05$ ;  $P < 0.15$ ). Unexpectedly, one RFI+ sire's progeny performed similar to progeny of 2 RFI- sires. Progeny from INEFF dams had greater RFI's ( $0.5$  v  $-0.63$ ;  $P < 0.03$ ) from 0 to 70 d and from 0 to 120 d ( $0.55$  v  $-0.72$ ;  $P < 0.03$ ) than progeny of EFF dams. Progeny RFI values were not significantly different from 70 to 120 d between sire and dam groups. Correlations for RFI were high between test durations of 0 to 70 d and 0 to 120 d (0.87) and 0 to 120 d and 70 to 120 d (0.88). Correlations were low for RFI between 0 to 70 d and 70 to 120 d (0.54). We concluded selecting against the lower third of INEFF dams within a population will improve progeny feed efficiency. Furthermore, extending the test duration is required for progeny that are not acclimated to the test facility or ration before intake collection.

**Key Words:** residual feed intake, feed efficiency, beef

**M86 The relationship of bovine respiratory disease and carcass ultrasound measures.** B. W. Brigham<sup>\*1</sup>, C. M. McAllister<sup>1</sup>, R. K. Peel<sup>1</sup>, H. Van Campen<sup>2</sup>, R. L. Weaber<sup>3</sup>, G. H. Loneragan<sup>4</sup>, J. L. Salak-Johnson<sup>5</sup>, C. C. L. Chase<sup>6</sup>, E. J. Pollak<sup>7</sup>, and R. M. Enns<sup>1</sup>, <sup>1</sup>*Department of Animal Science, Colorado State University, Fort Collins*, <sup>2</sup>*Department of Microbiology, Immunology and Pathology, Colorado State University, Fort Collins*, <sup>3</sup>*Department of Animal Science, University of Missouri, Columbia*, <sup>4</sup>*Department of Agricultural Sciences, West Texas A&M University, Canyon*, <sup>5</sup>*Department of Animal Sciences, University of Illinois, Urbana*, <sup>6</sup>*Department of Biology and Microbiology, South Dakota State University, Brookings*, <sup>7</sup>*Department of Animal Science, Cornell University, Ithaca, NY*, <sup>8</sup>*Department of Agricultural Sciences, West Texas A&M University*.

Bovine respiratory disease (BRD) has been identified as an economically relevant trait which lacks selection tools to reduce post-weaning incidence. The lack of sufficient field morbidity data has been a major obstruction to development of tools for genetic improvement. The objective of this study was to investigate the genetic associations among real time carcass ultrasound (US) measures and probability of treatment for BRD. Phenotypes of 2,870 crossbred steers were collected over 2 years (1,551 yr 1; 1,319 yr 2). The US measurements were collected at 3 times during the feeding period; receiving (0d), processing 2 (80d) and pro-

cessing 3 (150d). US measurements included ribeye area (UREA, cm<sup>2</sup>), backfat thickness (UFAT, cm) and percent intramuscular fat (UIMF, %). Morbidity data were collected over the entire 240d feeding period and classified as a binary observation, 1 for treated and 0 for non-treated, respectively. Data included 796 morbidity records; 2,848 first; 2,682 s; and 2,444 third US measurements with a sire pedigree ( $n = 3,255$ ). (Co)Variance components were estimated for each individual processing period using a multivariate sire model and average information REML procedures to obtain estimates of heritability and genetic correlations. Model fixed effects included contemporary group for all traits and processing weight as a linear covariate for US traits. Contemporary groups were comprised of year, ranch of origin and feedlot pen. An additional factor of US date was added to the definition for each respective processing period. Heritability estimates of morbidity, UREA, UFAT and UIMF at first, second and third processing were 0.15, 0.10, 0.06, 0.20; 0.16, 0.11, 0.09, 0.12; and 0.15, 0.14, 0.11, 0.06 respectively. Morbidity had a negative genetic correlation with all US measurements. The genetic correlations with the greatest magnitude were between morbidity and UREA, UFAT, and UIMF taken at receiving of  $-0.15$ ,  $-0.58$ , and  $-0.11$  respectively. These results imply those individuals with smaller ribeye area and less backfat upon arrival to the feedlot have the highest probability of suffering from a BRD incidence.

**Key Words:** beef cattle, health, carcass ultrasound

**M87 Performance and live-ultrasound traits of beef cattle breeds associated with DNA commercial markers.** F. Loya-Olguín<sup>\*1</sup>, M. Encinias<sup>2</sup>, R. E. Kirksey<sup>2</sup>, L. Lauriault<sup>2</sup>, and L. Avenida-Reyes<sup>1</sup>,

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The commercially available DNA markers, such as GeneSTAR Markers, provide prediction of phenotypic performance of tested animals. The objective of the present study was to evaluate performance and live-ultrasound traits of 4 beef cattle breeds using commercial DNA markers. Seventy 2 bulls from breeds Angus ( $n = 30$ ), Charolais ( $n = 20$ ), Hereford ( $n = 8$ ), and Maine-Anjou ( $n = 15$ ) were utilized. Initial BW for Angus, Charolais, Hereford, Maine-Anjou were 326.31, 360.66, 306.94, and 330.48 kg, respectively. The performance test lasted 112 d. All bulls were live-ultrasound for rumpfat (RF), ribfat (RBF), rib-eye (RE), and intramuscular fat (IMF). Also, were recorded average daily gain (ADG), weight per day of age (WDA); and genetic progeny difference on feed efficiency (GPDDE), tenderness (GPDT) and quality grade (GPDQG). The Charolais bulls had higher average number of stars, RE, WDA and GPDDE ( $11.32 \pm 0.41$ ,  $14.73 \pm 0.28$  cm<sup>2</sup>,  $1.50 \pm 0.03$  kg,  $-3.44 \pm 0.11$  kg, respectively) than ( $P < 0.05$ ) Angus, Maine-Anjou and Hereford bulls. Average of stars, RE and WDA of Angus and Maine-Anjou ( $10.30 \pm 0.35$ ,  $13.37 \pm 0.24$  cm<sup>2</sup>,  $1.42 \pm 0.02$  kg and  $10.13 \pm 0.47$ ,  $13.25 \pm 0.32$  cm<sup>2</sup>,  $1.39 \pm 0.03$  kg, respectively) bulls were similar. Meanwhile, Angus bulls had higher ( $P < 0.05$ ) RF, RBF, IMF, ADG, and GPDT ( $0.36 \pm 0.01$  cm,  $0.28 \pm 0.009$  cm,  $4.56 \pm 0.12\%$ ,  $1.97 \pm 0.03$  kg, and  $-1.42 \pm 0.08$  kg, respectively) than the Charolais, Maine-Anjou and Hereford bulls. The use of ultrasound technology in live animals and commercial markers data can be useful tools to select a potential genetically superior breed, and within the breed, can sort and predict a potential bull.

**Key Words:** molecular value predictions, rib-eye area, Charolais

**M88 No evidence for association between leptin polymorphism C.73 C>T and bovine viral diarrhea virus (BVDV) vaccine response.** X. Fang<sup>\*1</sup>, L. A. Hoff<sup>1</sup>, J. A. Walker<sup>1</sup>, K. C. Olson<sup>1</sup>, G. A. Perry<sup>1</sup>, J. X. Wu<sup>1</sup>, C. Maltecca<sup>2</sup>, and M. G. Gonda<sup>1</sup>. <sup>1</sup>*South Dakota State University, Brookings*, <sup>2</sup>*North Carolina State University, Raleigh*.

We have previously reported that sire affected humoral Bovine Viral Diarrhea Virus (BVDV) vaccine response in beef calves, suggesting that genetics may contribute to BVDV vaccine variation. In this study, we hypothesized that a single nucleotide polymorphism (SNP) within the leptin gene (LEP C.73 C > T) may be associated with BVDV vaccine response. To test this hypothesis, humoral BVDV vaccine response was measured in 209 Angus and Angus-cross calves. Calves were born between February and May 2009 at the South Dakota State University Antelope, Cottonwood and Cow-calf research herds. All individuals were vaccinated with Bovi-Shield GOLD-10 or -5, which includes modified-live BVDV strains type 1 and 2 (Pfizer, Inc., Exton, PA). Blood samples were collected at time of vaccination (d = 0) and post-vaccination (d = 21). Samples collected on d 0 were used to measure maternal BVDV antibody and to test for persistently infected (PI) BVDV calves, while samples collected on d 21 were used to measure humoral BVDV response to the vaccine. Real-time RT-PCR for BVDV on RNA isolated from plasma samples (Qiagen, Valencia, CA) revealed that none of the calves were PI with BVDV. A BVDV antibody ELISA (Idexx, Inc., Westbrook, ME) was used to measure total BVDV-specific antibody present on d 0 and 21. Antibody concentrations were converted to sample-to-positive (S/P) ratios, and maternal antibody S/P ratios (d = 0) were subtracted from d = 21 S/P ratios to calculate vaccine response. A PCR-RFLP assay was used to genotype the leptin polymorphism. To investigate a possible effect of the leptin polymorphism on BVDV vaccine response, an ANOVA model including effects of leptin genotype, month of birth, gender, and herd was fitted. Herd was significantly associated with vaccine response ( $P < 0.05$ ) and gender approached significance ( $P < 0.10$ ). Leptin genotype and month of birth were not significantly associated with BVDV vaccine response. Our results suggest that selection on the leptin genotype to improve beef cattle carcass quality will not have a pleiotropic effect on BVDV vaccine response.

**Key Words:** BVDV, leptin, vaccine response

**M89 A genotype combination approach using  $\mu$ -calpain as a candidate gene for growth, carcass, and meat quality in bulls of Senepol and Charolais inheritance.** P. Rivera\*, J. Bosques, A. Casas, D. Cianzio, and M. Pagan, *University of Puerto Rico at Mayaguez, Mayaguez, PR*.

A cytosine/guanine transversion in the  $\mu$ -calpain regulatory subunit (CAPN1-316) and cytosine/ thymine transition in catalytic subunit (CAPN1-4751) were organized as combined genotypes to investigate its potential associations with growth, carcass, and meat quality traits. Senepol, Charolais, and Senepol  $\times$  Charolais bulls grown under grazing conditions were genotyped ( $n = 94$ ) for each individual single nucleotide polymorphisms and organized in a total of 9 combinations (CC/CC, CC/TT, CC/CT, GG/CC, GG/TT, GG/CT, CG/CC, CG/TT, and CG/CT). For growth traits, a subset of 36 animals were used for the correspondent statistical analyses using the more representative CG/CT ( $n = 16$ ), GG/CT ( $n = 10$ ), and GG/TT ( $n = 10$ ) bulls. CAPN1 was associated with heavier body weights: at birth, 205 d, 240 d, and daily weight gain at 205 and 240 d. At birth, animals with the GG/CT combination were heavier ( $P < 0.05$ ) than those with CG/CT. However, CG/CT bulls were heavier ( $P < 0.05$ ) at 205 d, and gain at both 205 and 240 d than the GG/TT.

Moreover, at 240 d, CG/CT animals were heavier than GG/CT and GG/TT, and at slaughter CG/CT weighed more ( $P < 0.05$ ) than GG/CT only. For carcass and meat quality traits (CG/CT,  $n = 9$ ; GG/CT,  $n = 6$ ; GG/TT,  $n = 5$ ), CG/CT bulls presented greater tenderness ( $P < 0.05$ ) at 0 d (24 h aging period) than GG/CT, as determined by sensory evaluation of the loin. After 14 d of aging, beef from CG/CT was classified as moderately tender while GG/CT improved from moderately tough to slightly tender (hedonic scale; 1 = extremely tough/8 = extremely tender). In addition, in that same period, differences in sensory tenderness between CG/CT and GG/TT (less tender) were significant ( $P < 0.01$ ). However, the longissimus dorsi and bicep femoris muscle weights were lower ( $P < 0.05$ ) in the double heterozygous. The results of this study suggest that the double heterozygous for CAPN1 (316 = CG, 4751 = CT) presented more desirable growth, carcass, and meat quality traits. Therefore, the usefulness of these markers seems to be beyond its exclusive association with meat tenderness.

**Key Words:** CAPN1, growth, heterozygous

**M90 An insertion/deletion polymorphism at the bovine Calpastatin locus is associated with economically important traits.** N. Vega<sup>\*1</sup>, D. Velez<sup>1</sup>, A. Casas<sup>1</sup>, D. Cianzio<sup>1</sup>, C. W. Ernst<sup>2</sup>, and M. Pagan<sup>1</sup>,

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A total of 126 bulls (50% to purebred Senepol and Charolais) were genotyped for a cytosine insertion/deletion identified at intron 2 of the bovine Calpastatin locus to determine its segregation and potential associations with growth and meat quality traits. Overall, the frequency of the allele labeled as A (cytosine deletion) was higher (0.84) than the B (cytosine insertion) allele (0.16). In bulls of Senepol descent, allele frequencies were 0.90A/0.10B, whereas in those with Charolais blood, frequencies were 0.68A/0.32B. Genotypic frequencies were 0.82AA, 0.17AB, 0.01BB and 0.45AA, 0.47AB, 0.08BB for Senepol and Charolais bulls, respectively. Because the BB genotype was only observed in one Senepol bull and 3 Charolais bulls, it was excluded for corresponding statistical analyses ( $n = 55$  for growth;  $n = 24$  for meat quality traits). At birth, AB genotype bulls were heavier than AA bulls ( $P < 0.05$ ). However, the AA bulls presented higher body weights and weight gain at 205 and 240 d ( $P < 0.05$ ). After a 24 h aging period, lower Warner Bratzler shear force (WBS) was found in AA bulls (4.48 kg) than AB bulls (6.05 kg) in the longissimus dorsi muscle for a difference between genotypes of 1.57 kg ( $P < 0.01$ ). The difference in WBS after 14 d of aging was 0.60 kg (AA = 3.13 kg, AB = 3.73 kg;  $P > 0.05$ ). These results indicate that the Senepol breed has a higher AA genotype frequency than the Charolais breed, and may imply a tendency for Senepol animals to gain weight efficiently and produce tender beef. Therefore, this study suggests that this calpastatin polymorphism might be useful in animal selection due to its significant relationship with important beef traits.

**Key Words:** Calpastatin, Senepol, polymorphism

**M91 Partial characterization of bovine complement receptor-2 (CR2) in Angus cattle.** S. A. Olenich\*, X. Fang, L. A. Hoff, J. A. Walker, K. C. Olson, G. A. Perry, and M. G. Gonda, *South Dakota State University, Brookings*.

Complement receptor-2 (CR2, or CD21), found on T-helper cells, assists in antigen recognition of B cells by reducing the threshold for antigen receptor stimulation. Antigen receptor stimulation is important for developing an effective vaccine response; therefore, CR2 is a candidate gene that could be associated with vaccine response in

cattle. Thus, our objective was to characterize genetic variation in CR2 among beef cattle using a DNA-pooling sequencing approach. Blood samples were collected from 300 Angus and Angus-cross calves from 3 research herds in South Dakota: the SDSU Cow-Calf Unit, Cottonwood Research Station, and Antelope Research Station. The DNA was extracted from white blood cells by phenol and chloroform extraction. Pools of equal amounts of DNA ( $n = 50$ ) were formed (6 pools total) and CR2 exon sequences were amplified using pooled DNA. Forward and reverse primers were designed in CR2 introns to ensure that the entire exon coding region would be amplified. Amplicons were sequenced in both the forward and reverse direction with the same primers used for amplification. Polymorphisms were identified by visually inspecting sequence traces. To date, we have characterized exons 1–4 and partial intron sequences flanking these exons. We have putatively identified a SNP in intron 1 (CR2 c.58+36 t > G) and an SSR within intron 2 (CR2 c.181–34T[12\_13]). We have not found any polymorphisms within exons 1–4. This study reports the identification of 2 novel, putative intronic CR2 polymorphisms in Angus influenced beef cattle. The polymorphisms discovered in this study will be used to test for association between CR2 polymorphisms and vaccine response in cattle.

**Key Words:** CR2, CD21, polymorphisms

**M92 Evaluation of insertion/deletion and single nucleotide polymorphisms identified at the bovine insulin like growth factor binding protein-2 locus.** D. Velez<sup>\*1</sup>, C. W. Ernst<sup>2</sup>, and M. Pagan<sup>1,1</sup>*University of Puerto Rico at Mayaguez, Mayaguez, Puerto Rico, Puerto Rico,  
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A total of 54 bulls of Senepol and Charolais inheritance were genotyped for 9 single nucleotide polymorphisms (SNPs) previously identified in

a 1,180 bp sequence tagged site of the insulin-like growth factor binding protein-2 (IGFBP-2) gene locus (GenBank Accession Number: BV680048). These SNPs have been identified as C/G (nt 162), G/A (nt 254), G/C (nt 259, 822) C/T (nt 345, 433, 448), A/G (nt 719), and T/C (nt 1109) substitutions. In addition, an insertion/deletion polymorphism creates an alternative allele that lacks the base at position 443 and has a GG insertion between bases 449 and 450. Additional genotyping was performed for a recently identified SNP located at position 245 (A/T) and a trinucleotide insertion/deletion (TGT) at nt 1103–1105. The presence of C at nt 443 was linked to the insertion of TGT at nt 1103 in these animals. The majority of animals genotyped exhibited deletions at both nt 443 and nt 1103–1105 (frequency 0.78), which were in linkage disequilibrium with homozygous SNP genotypes at nt 448 (TT/0.77), 433 (CC/0.85), 345 (TT/0.61), 259 (CC/0.83), 254 (AA/0.77), 245 (AA/0.62) and 162 (GG/0.73). A limited number of animals were heterozygous for the insertion/deletions (frequency 0.17 and 0.13 for nt 443 and nt 1103–1105, respectively). For these animals, because of different allele lengths, genotypes for SNP's at nt 822 and 719 could not be determined. Most of the IGFBP2 polymorphisms were segregating at very low frequencies in the purebred Senepol, purebred Charolais and crossbred Charolais animals. With the exception of SNPs at nt 245 (AT frequency 0.54) and 345 (CT frequency 0.62), most markers were also not segregating in the Senepol crossbred cattle. The SNPs at these 2 positions were associated with ribeye area (AA > AT for nt 245; TT > CT for nt 345;  $P < 0.05$ ). Therefore, further evaluation of these IGFBP2 polymorphisms and polymorphism combinations in additional animals is needed.

**Key Words:** IGFBP-2, SNP, bovine