Breeding and Genetics: Beef Cattle Breeding I–Production Traits

460   Incorporation of external EBV into the American Gelbvieh Association carcass national cattle evaluation. S. E. Speidel*[1], R. M. Enns[1], and S. Willmon[2], *[1]Colorado State University, Fort Collins, [2]American Gelbvieh Association, Westminster, CO.*

The goal of this project was to incorporate prior genetic knowledge on Angus and Red Angus sires whose progeny are being registered in the American Gelbvieh Association (AGA) to better account for selection on these sires and to improve carcass EBV prediction for their crossbred progeny. External EBV (EEBV) for carcass weight (CWT), rib eye area (REA) and marbling score (MARB) were obtained from the American Angus Association (n = 5,472) and Red Angus Association of America (n = 3,482). EEBV for CWT and REA were added to the AGA model containing actual CWT, REA, and ultrasound REA (UREA). EEBV for MARB were added to the AGA model containing actual MARB and percent intramuscular fat (IMF). Prior to their inclusion, EEBV were deregressed for accuracy. Models currently used by the AGA for the prediction of carcass EPD were preserved. Heritability of the EEBV and genetic correlations between the EEBV and traits in the existing models were the only parameters estimated. A simple mean was the sole EEBV fixed effect included. Heritability estimates for the EEBV were found to be 0.23 ± 0.01, 0.28 ± 0.01 and 0.18 ± 0.01 for CWT, REA and MARB, respectively. Genetic correlations between external CWT EBV and actual CWT, external REA EBV and actual REA, external REA EBV and UREA, external MARB EBV and actual MARB, external MARB EBV and IMF were found to be 0.35 ± 0.15, 0.33 ± 0.15, 0.39 ± 0.06, 0.53 ± 0.15 and 0.49 ± 0.05, respectively. Angus animal EPD correlations between models with EEBV and those without were 0.94, 0.95 and 0.78; Gelbvieh EPD correlations were 0.98, 0.996 and 0.98; EPD correlations for all animals were 0.95, 0.98 and 0.90 for CWT, REA and MARB, respectively. Inclusion of the EEBV resulted in an increased EPD spread for the suite of AGA carcass EPD. For Angus animals and their progeny, this spread was increased by 43%, 25% and 101%; EPD spread increase for all animals was 6.3%, 3.4% and 44.8% for CWT, REA and MARB, respectively. This procedure resulted in positive and moderately high genetic correlations between the EEBV and corresponding traits in the current evaluation. This procedure resulted in the models more appropriately evaluating external Angus sires in the AGA carcass evaluation.

Key Words: beef cattle, genetic evaluation

461   Across-population estimation of heritability of carcass traits in beef cattle: Meta- vs. mega-analyses. H. Okut*[1,3], X.-L. Wu[1], D. Gianola[1], G. J. M. Rosa[1], S. Bauck[2], and B. W. Woodward[2], *[1]University of Wisconsin, Madison, [2]Merial Limited, Duluth, GA, [3]University of Yuzuncu Yil, Van, Turkey.*

Across-population estimation of genetic parameters is a challenge because populations are heterogeneous and the distribution of individual estimates over populations may be multi-modal. Two types of statistical methods can be used to combine estimates from many populations. Meta-analysis combines summary results from populations, whereas mega-analysis pools data from multiple populations into a single data set. We compared these approaches in estimation of heritability of 6 carcass traits [marbling score (MBS), back fat thickness (BFAT) at 12th rib, hot carcass weight (HCW), ribeye area (REA), yield grade (YG) and Warner-Bratzler shear force (WBSF)] using 15,016 cattle (2,964 phenotyped) from 4 populations sired by Angus, Hereford, Limousin or Simmental. We fitted fixed-effects (FMA) and random-effects (RMA) meta-analytical models in a frequentist framework. FMA viewed populations as homogeneous for any of the traits; RMA postulated a normal distribution of heritability values across populations. Further, a Bayesian non-parametric model with a Dirichlet process prior (DPP) was fitted, to avoid the normality assumption implied in RMA. In the mega-analysis, heritability was estimated with an animal model, pooling data over the 4 populations. Heritability was 0.42 (MBS), 0.24 (BFAT), 0.35 (HCW), 0.28 (REA), 0.29 (YG), and 0.12 (WBSF) using mega-analysis, and 0.31 to 0.39 (MBS), 0.21 to 0.34 (BFAT), 0.33 to 0.39 (HCW), 0.27 to 0.41 (REA), 0.31 (YG), and 0.17 to 0.20 (WBSF) with the meta-analysis models. In general, heritability estimates from RMA and DPP models agreed, but differed slightly from those obtained with FMA for all traits, except YG. When population heterogeneity is evident, meta-analysis using FMA (possibly mega-analysis too) appears suboptimal, whereas RMA and DPP can potentially capture the distribution of heritability estimates over populations.

Key Words: heritability, mega-analysis, meta-analysis

462   Accuracies with different genomic models for traits with maternal effects. D. A. L. Lourenco*[1], I. Misztal[1], H. Wang[1], I. Aguilar[2], and S. Tsuruta[1], *[1]University of Georgia, Athens, [2]Instituto Nacional de Investigación Agropecuaria INIA, Las Brujas, Canelones, Uruguay.*

Several methods were compared for the accuracy of evaluation using phenotypic, pedigree and genomic information for a trait influenced by a maternal effect. A simulated population included 15,800 animals in 5 generations. Genotypes from 3k SNP were available for 1500 animals in the last 3 generations. All animals except 300 in the last generation had phenotypes. Simulations were by an animal model with direct (heritability 0.32) and maternal (heritability 0.13) effects, mimicking weaning weight in beef cattle. Models of analysis were regular BLUP, single-step GBLUP (ssGBLUP), BayesC with deregressed proofs (BayesC-D) and BayesC using phenotypes and ignoring the maternal effects (BayesC-ph). For all animals, the accuracies with ssGBLUP were 0.01 (0.04) higher than with BLUP. For genotyped animals, the direct (maternal) accuracies for males were 0.71 (0.43) for BLUP, 0.79 (0.60) for ssGBLUP, 0.70 (0.48) for BayesC-D, and 0.63 for BayesC-ph. For females, the same accuracies were 0.68 (0.54) for BLUP, 0.76 (0.65) for ssGBLUP, 0.69 (0.56) for BayesC-D, and 0.65 for BayesC-ph. For genotyped animals in the last generation, the direct (maternal) accuracies were similar for males and females and were 0.50 (0.38) for BLUP, 0.69 (0.58) for ssGBLUP, 0.62 (0.48) for BayesC-D, and 0.54 for BayesC-ph. Accuracies by BayesC-D were lower than those by ssGBLUP because of approximations involved in deregressions, lack of accounting for parental average that is done automatically by ssGBLUP, and by sequential rather than simultaneous fitting of genomic and nongenomic information. Low direct accuracies by BayesC-ph were additionally due to ignoring phenotypes on ungenotyped animals and ignoring the maternal effect. Highest accuracy of prediction with the genomic information occurs when the information on all ungenotyped but related individuals is included and when all sources of information (phenotypic, pedigree and genomic) are considered jointly. The accuracy with a procedure that uses simplified models and ignores information from ungenotyped animals can be lower than that by BLUP.

Key Words: beef cattle, genomic selection, single-step procedure

463   Cumulative discounted gene expression for economically relevant traits for terminal and maternal purpose in cattle production system. X. Zeng,* B. W. Brigham, S. E. Speidel, D. H. Crews, and R. M. Enns, *Colorado State University, Fort Collins.*

The objective of the study was to estimate the cumulative discounted gene expressions (CDGE) for birth, slaughter, annual and end-of-cow-life traits in terminal and maternal purpose Angus cattle. CDEG were not calculated to annual and end-of-cow-life traits for terminal sire. The overarching goal of the project is to develop prototype producer-specific selection indexes based on production characteristics in the intermountain region of the US. The discounted gene-flow principle was used to estimate CDGEs. The parameters used in equations to calculate the CDGEs were estimated from 10,007 individual records and 27,165 pedigree records from the Angus herd at the John E. Rouse Beef Improvement Center of Colorado State University. There were 313 sires with generation interval of 3.30 years involved in the study, as well as 2,160 dams with generation interval of 5.32 years. The planning horizon, cull age of cow and discount rate were set as 20 years, 12 years old and 0.03 as the base situation to estimate CDGE. The result contained 14 CDGEs for 4 kinds of animals, each of which included different categorical traits. n the base situation, the CDGE of annual cow traits were 4.29, 6.93 and 29.01 for terminal female, self-replace female and sire breeding replacement females. The range of CDEG for slaughter traits is 20.39 to 35.00 from terminal sire to sire breeding replacement females, while 1.90 to 4.72 from terminal female to self-replacing female. For self-replacing female, the CDEGs of traits expressed at different time and frequency were 6.93, 6.15, 1.35 and 4.72 for annul, birth, end-of cow-life and slaughter traits, with a range of 1.35 to 6.93. Sensitivity analysis was adapted to test the effect of different levels of discount factors from 0 to 2.0. Results of the study indicated that different purpose of calves lead to large differences in gene expression. Thus, when adjustments are made to economic values, the relative economic importance may change for the economically relevant traits in a breeding objective.

Key Words: cumulative discounted gene expression, discounted gene-flow, economic value

464   Cluster and meta analyses of genetic parameters for feed intake traits in beef cattle. I. D. P. S. Diaz[1], D. H. Crews Jr.*[2], and R. M. Enns[2], [1]*Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil,* [2]*Colorado State University, Fort Collins.*

A lot of studies have been estimated genetics parameters for different measures of feed efficiency so it has becoming important to summarize all the different parameters found on publication and to get an average of these results. In this study feed efficiency data from 62 studies were used to estimate the pooled heritability and the pooled genetic correlation estimates among average daily gain (ADG); residual feed intake (RFI); metabolic body weight (MBW); feed conversion ratio (FCR) and dry matter intake (DMI) of beef cattle. A meta-analysis approach was applied following a cluster analysis of the heritability estimates. The total data sample had 177 heritability estimates and 149 genetic correlation estimates collected from studies published from 1961 to 2011. The cluster analysis was conducted using the Ward method within trait. Pooled heritability estimates were calculated for each cluster within each trait and for all the clusters together. For all traits 2 clusters were obtained, however for each trait the key variable that separated the groups was different. With this approach, the homogeneity between the studies could be evaluated and if present, a random model was chosen to calculate the variance between studies. In this study the variance was calculated using restricted maximum likelihood. Heterogeneity was found among the studies for all traits. Pooled heritability estimates for ADG, DMI, RFI, MBW and FCR were 0.32 ± 0.04; 0.39 ± 0.03; 0.31 ± 0.02; 0.31 ± 0.03 and 0.26 ± 0.03, respectively. Pooled genetic correlation estimates ranged from -0.15 to 0.67 among these traits. These pooled genetic parameter estimates could be used to solve genetic prediction equations in populations where data are insufficient for variance components estimation.

Key Words: feed efficiency, multivariate analysis

465   Marbling change patterns of rib eye area by slaughter age using random regression sire model. K. Kato,* Y. Nakahashi, and K. Kuchida, *Obihiro University of Agriculture & Veterinary Medicine, Obihiro, Japan.*

Japanese Black cattle (Wagyu) are the predominant beef breed due to high marbling. Degree of intramuscular marbling is measured at the 6th to 7th rib section, and graded according to the beef marbling standard (BMS, 1 to 12) in Japan. Currently the slaughter age of this breed is about 29 mo on average. However, it is required to shorten the length of fattening because of increasing the feeding costs. The objectives of this study were to investigate sire differences in marbling change patterns of rib eye area by slaughter age in Japanese Black cattle using regression within sire, and to find the appropriate slaughter age. Data were 18,350 carcass records (steer: 13,218, heifer: 5,132) collected between April in 2000 and December in 2010 in Hokkaido, Japan. Statistical analysis was performed using AI-REML procedure. The random regression model included year, month, sex and farm as fixed effects, slaughter age (linear and quadratic) as fixed regression, and random sire effects was fitted with a k-th ($k = 0, 1, 2$) order Legendre polynomials of slaughter age. The breeding value of sire for each age was predicted by BLUP of random regression coefficients. Estimated sires were totally 753. Estimated breeding value (EBV) of BMS increased with the age until the peak, and then decreased. The different regression curves and the peaks among sires were shown. For top 5 sires in service number, EBV of BMS ranged 1.0~1.4, 1.0~2.1, 1.0~1.2, 0.9~1.2 and 0.5~1.3, respectively Therefore, it is thought that fattening farmer can decide the slaughter age appropriately and carcasses can show their ability maximally.

Key Words: marbling, slaughter age, random regression

466   Estimation of heterotic effects on stayability in beef cattle. E. M. Huff*[1], B. W. Brigham[1], S. Willmon[2], and R. M. Enns[1], [1]*Department of Animal Science, University of Colorado, Fort Collins,* [2]*American Gelbvieh Association, Westminster, CO.*

Stayability in beef cattle is defined as the probability that a cow remains in the herd until age 6 given that she has calved as a heifer. In some breeds with total herd reporting, those cows are required to calve every year. Profitability of the herd is affected by stayability by decreasing the need for replacements by increasing the number of cows that reach the typical breakeven age of 6. Stayability is a binary trait on the observed scale and is considered a lowly heritable trait. General consensus is that lowly heritable traits should be subject to higher levels of heterosis in crossbreeding programs and has shown to have a large effect on cow longevity. Therefore, heterosis should have a positive effect on the cows' ability to remain in the herd until age 6. The objective was to estimate maternal and individual heterosis values for stayability. Data obtained from the American Gelbvieh Association and included a total of 103,022 animals, with 20,173 being purebred Angus, 6,223 purebred Red Angus, 47,549 purebred Gelbvieh, and the rest being a combination of crossbred animals. Variance components and fixed heterosis effects were estimated from an animal model using a probit threshold link function. The model

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included contemporary group as a fixed effect and breed percentage as a linear covariate. Contemporary groups were required to have variation within the group and to have at least 5 observations. After initial analysis Red Angus and Angus cattle were combined due to there not being a significant difference between the 2 breeds. Two models were run with different backcross covariates, model one included only individual backcross and model 2 included individual and maternal backcross. Heterosis was estimated to be 35.78% for the individual with the first model. For the second model individual heterosis was estimated to be 31.77% and 11.85% was the estimate for maternal heterosis. The results from this experiment indicate that stayability is affected by heterosis and that these effects should be accounted for in cattle evaluation using pure and crossbred data.

Key Words: heterosis, stayability, beef cattle

467 Comparison of single breed and admixed reference populations for across-breed prediction of direct genomic breeding values in Red Angus beef cattle. M. Saatchi*[1], R. D. Schnabel[2], J. F. Taylor[2], and D. J. Garrick[1,3], [1]*Department of Animal Science, Iowa State University, Ames,* [2]*Division of Animal Science, University of Missouri, Columbia,* [3]*Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand.*

The objective of this study was to derive and evaluate the accuracy of direct genomic breeding values (DGV) for Red Angus beef cattle using single breed and admixed reference populations. Seven traits (birth, weaning and yearling weights; calving ease direct and maternal; marbling; rib eye area) were evaluated using 2,359 Black Angus, 891 Hereford and 1,655 Limousin genotyped individuals as a reference population, separately and admixed. Genotyping used the Illumina BovineSNP50 assay. Deregressed estimated breeding values (DEBV) were used as observations in a weighted Bayesian analysis to estimate marker effects used in DGV calculation. Accuracy of DGV was the correlation between DEBV and DGV in a sample of 90 Red Angus sires. The single breed reference populations accuracies of DGV were, in general, higher for marker effects predicted in Black Angus, followed by Hereford, and finally Limousin, reflecting the genetic distances between the breeds. The use of admixed reference populations produced more accurate DGV (average accuracies over all traits were 0.24, 0.19, 0.13 and 0.06 when marker effects were predicted in admixed, Black Angus, Hereford and Limousin, respectively). Incorporating 86 additional Red Angus (different animals from validation individuals) and 102 Simmental individuals into the admixed training population dramatically increased the accuracies of DGV, averaging 0.43 over all studied traits. These DGV show promise for routine use by Red Angus breeders to predict the genetic merit of their animals at a young age. Red Angus breeders will benefit most from the use of an admixed reference population which includes Red Angus.

Key Words: admixed reference population, genomic breeding values, Red Angus

468 Adipose and muscle tissue expression of two genes (*NCAPG* and *LCORL*) located in a chromosomal region associated with cattle feed intake and gain. A. K. Lindholm-Perry,* A. K. Sexten, L. A. Kuehn, L. A. Rempel, J. R. Miles, R. A. Cushman, and H. C. Freetly, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

A region on bovine chromosome 6 has been implicated in cattle birth weight, growth, and length. Non-SMC conodensin I complex subunit G (*NCAPG*) and ligand dependent nuclear receptor corepressor-like protein (*LCORL*) are positional candidate genes within this region. We previously identified genetic markers in both genes that were associated with average daily gain and feed intake in a crossbred population of beef steers. Two markers within *LCORL* were validated in a second, unrelated population of steers. We also detected associations between these markers and hot carcass weight, adjusted fat thickness and ribeye area suggesting that one or both of these genes play a role in lean muscle growth and reduced fat deposition. The purpose of this study was to determine whether the transcript abundance of either of these genes in adipose and muscle tissues was associated with variation in beef cattle feed intake, residual feed intake and average daily gain phenotypes. Transcript abundance for *NCAPG* and *LCORL* in adipose and muscle tissue was measured by quantitative PCR from heifers (adipose only, n = 88), cows (n = 85 muscle, n = 18 adipose) and steers (n = 12). Phenotypic correlations among expression levels and measures of growth, feed intake, and efficiency were derived and tested for significance. The levels of *NCAPG* and *LCORL* gene expression in adipose tissue were not correlated to gain, feed intake or residual feed intake in steers, heifers or cows. However, transcript abundance of *NCAPG* in the muscle tissue of cows was correlated to BW gain (r = 0.31; P = 0.004) while muscle gene expression levels of *LCORL* were correlated with dry matter intake in steers (r = −0.57; P = 0.03). These data corroborate the genetic associations with gain and feed intake within this region and represent biological activity of these genes in the muscle tissue of cattle. The data also suggests that sex, age and/or nutrition-specific interactions may affect the expression of *NCAPG* and *LCORL* in beef cattle. USDA is an equal opportunity provider and employee.

Key Words: beef cattle, gene expression

469 Identification of single nucleotide polymorphisms for feed efficiency and performance in crossbred beef cattle. M. K. Abo-Ismail*[1], G. Vander Voort[1], E. J. Squires[1], K. C. Swanson[1,2], J. Thomson[3], B. Karisa[3], G. Plastow[3], S. Moore[3], and S. P. Miller[1,3], [1]*Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada,* [2]*Animal Sciences Department, North Dakota State University, Fargo,* [3]*Faculty of Agricultural, Life and Environmental Sciences, University of Alberta, Edmonton, AB, Canada.*

Novel genomics approaches offer opportunities to select for efficient cattle to reduce feed costs. The objectives of this study were to: (1) identify new SNPs for residual feed intake (RFI) and performance traits within the candidate genes identified in a genome wide association study (GWAS); (2) estimate the proportion of variation in feed efficiency traits explained by the detected SNPs; (3) estimate the effect of detected SNPs on carcass traits to avoid undesirable correlated effects on other economically important traits when selecting for feed efficiency; and (4) map the corresponding genes to biological mechanisms and pathways. A total number of 339 SNPs corresponding to 180 genes were tested for association with phenotypes using a single locus regression (SLRM) and genotypic model on 726 and 990 crossbred animals for feed efficiency and carcass traits, respectively. Strong evidence of associations for RFI were located on chromosomes 8, 15, 16, 18, 19, 21, and 28. The strongest association with RFI (P = 0.0017) was found with a newly discovered SNP located on BTA 8 within the ELP3 gene. In addition, SNPs rs41820824 and rs41821600 on BTA 16 within the gene HMCN1 showed strong evidence of association with RFI (P = 0.0064 and P = 0.0033, respectively). A newly identified SNP located on BTA 18 within the ZNF423 gene provided strong evidence for association with RFI (P = 0.0028). Several SNPs provided strong evidence of association with other feed efficiency, performance, and carcass traits using

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the SLRM and genotypic model. Genomic estimated breeding values (GEBV) from 98 significant SNPs were moderately correlated (0.47) to the estimated breeding values (EBVs) from a mixed animal model. The significant SNPs (98) explained 18.06% of the phenotypic variance of RFI. Functional analysis for the corresponding genes to significant SNP for feed efficiency traits suggested 35 and 39 biological processes and pathways respectively with majority in ion and cation transport, phosphorus metabolic process, and regulation of transcription. The newly discovered SNPs should be validated in another population before incorporation in a DNA testing panel to evaluate the genetic merit of beef cattle for feed efficiency industry-wide.

Key Words: single nucleotide polymorphisms, feed efficiency, beef cattle

470 Withdrawn by author

471 Genetic and environmental influences on movement patterns of beef cattle grazing foothill rangeland. D. Bailey*[1], D. Jensen[2], M. Thomas[3], D. Boss[2], and R. Welling[4], *[1]New Mexico State University, Las Cruces, [2]Montana State University, Havre, [3]Colorado State University, Fort Collins, [4]CashCattleBiz.com, Vaughn, MT.*

A study was conducted in foothill rangelands of Montana to evaluate the effects of genotype and environment (or early learning) on grazing distribution. Based on 5 years of observations, 5 of 180 cows that used the highest and steepest terrain (hill climbers) and 5 cows that used the most gentle terrain near water (bottom dwellers) were used as donor-dams for embryo transfer. A single unrelated Simmental sire was used in these matings. Recipient cows were classified as hill climbers (HC) and bottom dwellers (BD) based on 4 years of observation from a separate herd of 98 cows. This resulted in 2x2 factorial study with donor and recipient as factors and HC and BD as levels within each factor. During the summer of 2011, 18 of these cows (6 to 8 years of age) were tracked at 10-min intervals by global positioning system technologies in a 336 ha pasture. Distance to water, elevation, slope and a normalized average of these terrain attributes from recorded cow locations were averaged and evaluated using a statistical model that included donor, recipient and the donor*recipient interaction. A separate analysis compared breed groups irrespective of the donor and recipient classifications. We were unable to detect any differences between HC and BD recipients for any measure of grazing distribution. We observed a tendency ($P = 0.08$) for cows from HC donors (490 ± 13 m) to be farther from water than those from BD donors (456 ± 11 m), but we did not detect any differences ($P > 0.10$) between HC and BD donors for other measures of distribution. No interactions between donors and recipients were detected ($P > 0.10$). Tarentaise maternally influenced cows walked farther per day ($P = 0.03$) and were farther from water ($P = 0.01$) than Hereford maternally influenced cows. Grazing use of foothill rangeland appears to be affected to some degree by genetic factors, but the mechanism of this influence requires further study.

Key Words: genotype, early learning, behavior

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