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

48   Population structure and identification of lineages in a Brazilian Guzerat metapopulation. J. C. C. Panetto*[1], M. G. C. D. Peixoto[1], G. G. Santos[1], F. A. T. Bruneli[1], R. S. Verneque[1], M. A. Machado[1], A. L. S. Azevedo[1], D. R. L. Reis[1], L. A. Silva[1], A. A. Egito[2], and M. R. S. Carvalho[3], *[1]Embrapa Gado de Leite, Juiz de Fora, MG, Brazil, [2]Embrapa Gado de Corte, Campo Grande, MS, Brazil, [3]Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil.*

Guzerat (*Bos primigenius indicus*) cattle was included in the FAO list of breeds to be conserved by means of management due to its beef and dairy potentials under various, especially harsh, environmental conditions. This study aimed to ascertain the population structure and the identification of distinct lineages in a metapopulation of the Guzerat breed in Brazil. Blood samples were collected from 664 animals in 15 seedstock herds in the country, including 5 herds with selection focused on beef, 9 herds in dual purpose systems and one closed herd with selection exclusively for dairy purposes. Genomic DNA was extracted from these samples and a panel of 21 microsatellites was selected for the Guzerat breed, according to their polymorphism information content (PIC). F-Statistics were used to estimate differentiation among subpopulations (F_{ST}) and the degree of reduction in heterozygosis due to non-random mating within subpopulations (F_{IS}). Lineages were determined by cluster analysis with a Bayesian approach with increasing numbers of inferred populations, assuming an admixture model based on the correlations between allelic frequencies. PICs ranged from 0.57 to 0.88, with a mean of 0.75. There was a large variation among herds on F_{IS} (values ranged between −0.109 and 0.061) indicating that some herds were more inbred than others. Average F_{ST} for this metapopulation was 0.034 ± 0.002. The closed dairy herd was the most differentiated among all (average pairwise $F_{ST} = 0.052$). The pairwise F_{ST} matrix demonstrated that, in general, the dual purpose herds were less differentiated within the entire metapopulation, when compared with the studied beef herds. Cluster analysis resulted in the identification of 6 lineages. Among them, 3 lineages included mostly animals from dual purpose herds, 2 lineages included mainly animals from beef herds, and one lineage included animals from dairy or dual purpose herds. One practical consideration is that the existence of herds with different purposes has contributed to the genetic structure of this breed. This project was supported by FAPEMIG.

Key Words: cluster analysis, genomic DNA, population structure

49   Genetic relationships among milk production and teat and udder scores in cows sired by seven prominent beef cattle breeds. L. A. Kuehn* and H. C. Freetly, *USDA-ARS, US Meat Animal Research Center, Clay Center, NE.*

Milk production and teat and udder quality are key components to lifetime cow productivity in commercial beef cattle. Our objective was to determine genetic relationships and breed differences for milk production and teat and udder quality in young and mature cows. Cows (n = 602) were crosses of F_1 cows and bulls ($F_1{}^2$) ; the F_1 parents resulted from matings of industry Angus, Hereford, Red Angus, Charolais, Gelbvieh, Limousin, and Simmental bulls with base Hereford, Angus, and MARC III composite cows. These $F_1{}^2$ cows were produced in 3 seasons and evaluated as 2 yr olds after their first calf and again as 5 yr olds. Milk production was measured approximately 100 d after parturition using the weigh-suckle-weigh method. Teat size and udder suspension were scored on a 9-point subjective scale in which 5 was considered an optimum. Genetic correlations and breed effects were derived from MTDFREML using a mixed model with fixed season, calf sex (for milk production), and breed and heterosis covariates and random effects of animal and error. Heritability estimates for 2 and 5 yr teat score, 2 and 5 yr udder score, and 2 and 5 yr milk production were 0.27, 0.31, 0.14, 0.32, 0.32 and 0.49. Genetic correlations among the same trait measured in different years were high (0.79 to 0.84). Similar to heritability estimates, correlations with udder score at 2 yr were lower than for other score traits likely indicating greater error in phenotyping udder suspension at 2 yr. Correlations between score traits and milk production were low and not significantly different than zero. Teat size was smallest in Charolais and largest in Simmental across years. Udder suspension was most optimal in Charolais. No breed effects were detected for milk production. This result is counter to breed effects generally observed on maternal effects for weaning weight in national cattle evaluation. Selection for these traits may lead to increased lifecycle productivity in beef cattle due to decreased culling on udder conformation.

Key Words: cow productivity, beef cattle, milk production

50   Genetic parameters for udder quality in Hereford cattle. H. L. Bradford*, D. W. Moser, J. M. Bormann, and R. L. Weaber, *Kansas State University, Manhattan.*

Udder quality is an important trait for beef producers because udders affect cow longevity and calf performance. The objective of this study was to estimate the genetic parameters for udder quality in Hereford cattle. The Beef Improvement Federation recommends collecting subjective scores on udder suspension and teat size. Prior to these guidelines, the American Hereford Association (AHA) recorded an overall score, which combines all udder characteristics into a single score. In all cases, scores ranged from 1 to 9 with a score of 9 considered ideal. Records on 78,556 animals and a 3-generation pedigree with 196,540 animals were obtained from the AHA, Kansas City, MO. These records contained repeated observations for overall score (n = 126,753), suspension (n = 61,758), and teat size (n = 61,765). Data were modeled using a multiple trait animal mixed model with random effects of additive genetic and permanent environment and with fixed effects of age and contemporary group (herd-year-season). Variances were estimated with ASREML 3.0. Heritability estimates (standard errors) of overall score, suspension, and teat size were 0.32 (0.01), 0.31 (0.01), and 0.28 (0.01), respectively. These results showed udder quality was moderately heritable, agreeing with previous research. The phenotypic correlations (standard errors) between teat size and suspension, overall score and teat size, and overall score and suspension were 0.64 (0.003), 0.31 (0.01), and 0.31 (0.01), respectively. Of the records for suspension and teat size, 57% had the same score for both traits. The genetic correlations (standard errors) between teat size and suspension, overall score and teat size, and overall score and suspension were 0.83 (0.01), 0.72 (0.02), and 0.70 (0.02), respectively. The genetic correlations between traits were extremely strong, indicating that these records were different measures of the same trait. In addition, differentiating between suspension and teat size might be difficult for producers.

Key Words: beef cattle, genetic parameter, udder score

51   Phenotypic relationships between docility and reproduction in Angus heifers. K. L. Otteman*[1], J. M. Bormann[1], K. C. Olson[1], J. R. Jaeger[1], S. Johnson[1], B. Downey[2], D. M. Grieger[1], J. W. Waggoner[1], D. W. Moser[1], and R. L. Weaber[1], [1]*Kansas State University, Manhattan, [2]Cowney Ranch Inc., Wamego, KS.*

Reproductive success is economically relevant in beef cattle operations, and may be influenced by temperament. The objective of this study was to elucidate the phenotypic relationships between docility and first service AI conception rate in heifers. Data (n = 337) collected from 3 cooperator herds in Kansas at the start of the synchronization protocol and included exit velocity (EV), chute score (CS), fecal cortisol (FC), and blood serum cortisol (BC). Statistical analysis was done using logistic regression with 30 d pregnancy rate as the dependent variable. The model included the fixed effect of contemporary group, and the covariates FC, BC, EV, CS, weight, and age. Correlation coefficients were also calculated between all continuous traits. Pregnancy rate ranged from 34% to 58% between herds. Blood cortisol positively correlated with EV (r = 0.22, $P < 0.01$), negatively correlated with age (r = −0.12, $P < 0.03$), and tended to be negatively correlated with weight (r = −0.10, $P = 0.09$). Exit velocity was positively correlated with CS (r = 0.24, $P < 0.01$) and negatively correlated with weight (r = −0.15, $P < 0.01$) and age (r = −0.12, $P < 0.03$). Chute score negatively correlated with age (r = −0.14, $P < 0.01$), and as expected, age and weight were moderately positively correlated (r = 0.42, $P < 0.01$). In general, older, heavier animals had better temperament, as indicated by lower BC, EB, and CS. The power of our test could not detect any significant predictors of 30 d pregnancy for the combined data from all ranches. When the data was divided by ranch, however, chute score ($P < 0.03$) and weight ($P < 0.01$) were both found to be significant predictors for 30 d pregnancy for ranch 1. Fertility is a complex trait that is dependent on many factors; our data suggest that docility is one factor that warrants further investigation.

Key Words: beef cattle, fertility, docility

52   Docility and heifer pregnancy heritability estimates in Angus heifers. K. L. Otteman*, J. M. Bormann, D. W. Moser, and R. L. Weaber, *Kansas State University, Manhattan.*

The objective of this study was to determine the genetic control of docility and reproduction in heifers as measured by pregnancy rate. Data included weaning contemporary group information, yearling contemporary group information, sex, docility score, yearling weigh date, age of dam, breeding contemporary group, age at first breeding, pregnancy check results, and first service sire. A subjective chute scoring system was used as the basis of their genetic evaluation for docility. Pedigree information included 508,015 animals over 30 generations. Contemporary groups were formed by the concatenation of weaning contemporary group, yearling contemporary group, and breeding contemporary group. Heritabilities were computed from estimates of genetic and residual variance components computed using ASReml 3.0 (VSN International, Hemel Hempstead, UK). Heifer pregnancy variance components were estimated from a univariate threshold model, with pregnancy outcome as the dependent variable, animal and contemporary group as random effects, and age at first breeding as a covariate. The heritability of heifer pregnancy was estimated to be 0.16 ± 0.02. Docility was fit as a univariate, linear animal model with docility score as the dependent variable, and animal and contemporary group modeled as random effects. The heritability for docility score was estimated to be 0.22 ± 0.03. Low to moderate heritability on these traits indicates that slow but definite genetic improvement can be made by selection on heifer pregnancy and docility.

Key Words: genetics, docility, reproduction

53   The effect of sire breed on birth weight, preweaning ADG, and adjusted 205-d weight of calves from commercial Angus dams mated to Angus, Braunvieh, and Hereford sires. C. L. Ferring*, G. A. Hansen, and J. P. Cassady, *North Carolina State University, Raleigh.*

The objective of this study was to assess the effects of breed of sire on birth weight, preweaning ADG, and adjusted 205-d weight. Angus (n = 58), Hereford (n = 37), and Braunvieh (n = 41) sires were randomly mated to commercial Angus cows (n = 184, 75% or greater Angus). Hereford and Braunvieh sired calves should express 100% heterosis. Data were available for 389 calves born from 2003 to 2011 at the Tidewater Research Station in Plymouth, NC. Male calves were castrated by 5 mo of age. Calves were not creep fed and never implanted. The GLM Procedure of SAS was used. The model included fixed effects of sire breed, age of dam, sex of calf, and calf birth year. Gestation length, calculated based on the day a cow was bred by AI and the day she calved, was included as a covariate. Age of dam and sex of calf affected birth weight, pre-weaning ADG, and adjusted 205-d weight ($P < 0.01$). Calf birth year affected preweaning ADG and adjusted 205-d weight ($P < 0.01$). A 1-d increase in gestation length increased birth weight by 0.19 kg ($P < 0.01$), increased preweaning ADG by 0.12 kg ($P < 0.05$), and decreased adjusted 205-d weight by 0.42 kg ($P < 0.06$). Sire breed affected birth weight ($P < 0.01$). Angus, Hereford, and Braunvieh sired calves had average birth weights of 34.6, 36.9, and 37.4 kg, respectively. Effects of sire breed on preweaning ADG and adjusted 205-d weight were not statistically significant. Birth weight, preweaning ADG, and adjusted 205-d weight increased as age of dam increased up to 5 years of age. In summary, breed of sire influenced birth weight but did not affect preweaning ADG and adjusted 205 d weight. These results are surprising in that heterosis did not result in significantly heavier calves at weaning.

Key Words: beef cattle, crossbreeding, growth

54   Breed × sex effects on birth weight in Brahman-Simmental embryo transfer calves. J. A. Dillon*[1], R. M. Thallman[2], J. O. Sanders[1], and D. G. Riley[1], [1]*Texas A&M AgriLife Research, College Station, [2]US Meat Animal Research Center, Clay Center, NE.*

Brahman cross calves exhibit unusual inheritance of birth weight: Brahman-sired crossbreds out of *Bos taurus* females are heavier with greater difference between sexes than calves of the reciprocal cross. The objective of this work was to compare birth weight in various crosses of Brahman, Simmental, and Simbrah. Embryo transfer (ET) calves (n = 2,486) were born in central Texas from 1984 – 1990 and were 1/4, 3/8, 1/2, 5/8, or 3/4 Brahman produced by multiple types of matings, dependent upon the breed group. Data were analyzed with an animal model, with 6,061 animals in the pedigree. Fixed effects investigated included contemporary group (n = 36; combinations of year, birth season, and location), sex of calf, breed group (n = 5), and linear covariates of direct expected breed heterozygosity (HET) and proportion of Brahman in the sire (BIS). Random effects included additive genetic and maternal permanent environmental (of the recipient dam); maternal genetic did not improve likelihood values and was not included in the final model. The regression coefficient for HET was 11.2 ± 3.52 kg ($P = 0.02$). The regression coefficient for BIS was 7.7 ± 1.04 kg ($P < 0.001$). There was a breed group by sex interaction detected ($P < 0.001$). Males were heavier ($P < 0.05$) than females in 1/4, 3/8, and 3/4 Brahman groups. Among females, 3/4 Brahman calves had lower ($P < 0.05$) birth weights than all other breed groups. In male calves, 1/2 and 3/4 Brahman calves had lower ($P < 0.05$) birth weights than all other groups. The estimate of heritability for birth weight from these data was 0.34 ± 0.05. Maternal permanent environmental variance as a proportion of phenotypic variance was 0.34 ± 0.09.

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Proportion Brahman in the sire relative to proportion Brahman in calf significantly influences birth weight in Brahman-Simmental crosses produced by ET. This effect is not consistent with standard models used in genetic evaluation, but is consistent with the mechanisms of genomic imprinting, early (before ET) embryonic maternal effects, and/or X chromosome effects.

Key Words: birth weight, Brahman, non-Mendelian inheritance

55   Phenotypic and genetic correlations as well as linear relationships of performance, carcass, feed efficiency, and economic characteristics of beef feedlot steers. K. M. Retallick*[1], D. B. Faulkner[2], S. L. Rodriguez-Zas[1], J. D. Nkrumah[3], and D. W. Shike[1], *[1]University of Illinois, Urbana, [2]University of Arizona, Tucson, [3]Pfizer Animal Genetics, Kalamazoo, MI.*

Several feed efficiency measures are being investigated including: feed conversion ratio in terms of feed:gain (FCR), residual feed intake (RFI), residual BW gain (RG), and residual intake and BW gain (RIG). These traits have production efficiency potential since they include feed intake inputs and production outputs. The objective of this study was to investigate 1) how these measures of efficiency affect one another and their heritability estimates and 2) relate measures of efficiency both genetically and phenotypically to feedlot cattle performance, carcass, and economic characteristics. All feed efficiency traits were favorably correlated genetically and phenotypically to each another. Heritability estimates were moderate ranging from 0.22 to 0.38 ± 0.10. Feed conversion ratio was genetically correlated to RG and RIG at -0.97 and -0.95, respectively. Feed conversion ratio was also highly correlated with growth traits therefore an increase in weight led to a more desirable FCR. A genetic increase in carcass value was associated with a more desirable FCR due to an increase in HCW. As expected due to genetic correlation to FCR, similar affects were shown for RG. A unit reduction in DMI yielded a 0.42 improvement in RFI and genetic results were similar. As designed, RIG reduced DMI similar to RFI and increased ADG similar to RG. Marbling was correlated phenotypically to RG and RIG at -0.08 and -0.09, respectively and correlated genetically to RFI and RIG at 0.59 and -0.59, respectively. This indicated that marbling decreased as measures of feed efficiency improved; however, the linear regression slope was small which indicated only a small decrease in marbling. As a result, carcass value was still favorably correlated with RG ($r = 0.15$) and RIG ($r = 0.10$) and not correlated to RFI. As profitability increased for steers, all feed efficiency measures improved.

Key Words: feedlot feed efficiency, genetic relationship, phenotypic relationship

56   Genotype by environment interaction effects on crossbred lambs at finishing. G. C. Márquez*[1], W. Haresign[2], M. H. Davies[3], R. Roehe[4], L. Bünger[4], G. Simm[4], and R. M. Lewis[1,4], *[1]Virginia Tech, Blacksburg, [2]Aberystwyth University, Aberystwyth, UK, [3]ADAS Rosemaund, Preston Wynne, UK, [4]Scottish Agricultural College, Edinburgh, UK.*

Accounting for genotype by environment interactions (GE) in genetic evaluations is important because animals may not perform predictably across environments. The purpose of this study was to investigate GE on full body weight (FWT), ultrasonic muscle (UMD) and fat (UFD) depth at finishing in crossbred lambs. Data on 6,325 lambs sired by Charollais, Suffolk, and Texel rams were obtained. The experiment was done between 1999 and 2002 on 3 farms in the UK. In total 89 sires (selected from the top or bottom 10% on a selection index that increased carcass lean weight while keeping fat constant) were mated to 1,984 ewes of 2 types (Bluefaced Leicester × 2 hill breeds). Most rams were used for 2 successive mating seasons, with some rotated among farms to create genetic links. Lambs were reared on pasture and assessed for fat cover until they reached a target of 11% subcutaneous fat, and then were weighed and ultrasonically scanned for fat and muscle depth. The UFD data were log-transformed to approach normality. All models included the fixed effects of sire index category, lamb sex and birth year, age of dam, and birth-rearing category. Subcutaneous fat at finishing was a covariate for FWT and UMD, and age at finishing for UFD. An additive genetic effect was fitted with a pedigree-based relationship matrix among lambs. Six genetic groups were fitted (3 sire breeds, 2 dam breed types, 1 maternal grandsire breed). For FWT a random rearing dam effect was fitted, which was unimportant for UFD or UMD ($P > 0.2$). The GE in the data was first investigated by fitting a random sire by farm interaction term. Likelihood ratio tests indicated that GE defined variation ($P < 0.001$). The ratio of interaction variance to total variance for FWT, UMD, and UFD was 0.07 ± 0.02, 0.11 ± 0.02, and 0.22 ± 0.03, respectively. Additionally, data from the 3 farms were fitted as separate but correlated traits. Heritabilities differed in the 3 farms ($P < 0.01$). Genetic correlations among farms were generally high, as were rank correlations of sire EBV (0.7–0.9). This indicates that, especially for scanning traits, GE should be considered in robust genetic evaluation programs.

Key Words: genetics by environment interaction, sheep