

## 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<sup>1</sup>, M. G. C. D. Peixoto<sup>1</sup>, G. G. Santos<sup>1</sup>, F. A. T. Bruneli<sup>1</sup>, R. S. Vermeque<sup>1</sup>, M. A. Machado<sup>1</sup>, A. L. S. Azevedo<sup>1</sup>, D. R. L. Reis<sup>1</sup>, L. A. Silva<sup>1</sup>, A. A. Egito<sup>2</sup>, and M. R. S. Carvalho<sup>3</sup>, <sup>1</sup>Embrapa Gado de Leite, Juiz de Fora, MG, Brazil, <sup>2</sup>Embrapa Gado de Corte, Campo Grande, MS, Brazil, <sup>3</sup>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 heterozygosity 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. Freedly, *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. Weaver, *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



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To Whom It May Concern:

This is to certify that Joao Panetto was registered for the 2013 ADSA-ASAS Joint Annual Meeting held July 8-12, 2013 in Indianapolis, IN and presented the following research in the form of an oral presentations:

Wednesday, July 10, 2013

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Regards,

Debi Seymour

Joint Meeting Societies Representative