

treated with antibiotic alone (control). Secondary objectives were to describe the effect of treatment on the prevalence of IMI and linear score (LS) after calving, and on the incidence of clinical mastitis between dry off and 60 DIM. The study enrolled 437 cows from two dairy farms in western WI. On the day of dry off all four quarters were sampled for bacteriological culture and SCC measures. After the final milking all four quarters were routinely infused with a commercially available long-acting antibiotic. Two contra-lateral quarters (LF/RH or RF/LH) were then randomly assigned the treatment of infusion with an inert internal teat sealant (Orbeseal, Pfizer Animal Health, Groton, CT). The teat sealant was stripped out at first milking after calving and the quarters re-sampled at both 1-3 DIM and 6-8 DIM for bacteriological culture and SCC analysis. The incidence of new IMI occurring between dry off

and 1-3 DIM was 25.9% and 20.6 % for control vs. treated quarters, respectively (odds ratio<sub>treated</sub> = 0.72, P < 0.05). The prevalence of IMI at 1-3 DIM was 29.5% and 23.3%, for control vs. treated quarters, respectively (odds ratio<sub>treated</sub> = 0.71, P < 0.05). Mean LS was significantly lower for control vs. treated quarters at 1-3 DIM (control = 5.5; treat = 5.2, P < 0.05) and at 6-8 DIM (control = 3.2; treat = 2.9, P < 0.05). Finally, there were significantly fewer clinical mastitis events between dry off and 60 DIM occurring in quarters treated with teat sealant and an antibiotic (5.9%) than in quarters treated with antibiotic alone (8.0%) (odds ratio<sub>treated</sub> = 0.72, P < 0.05).

**Key Words:** Internal teat sealant, Mastitis, Dry period

## Breeding & Genetics: Beef cattle breeding

**340 Factors to adjust birth and weaning weights of Red Angus calves for age of dam.** J. M. Rumph\*<sup>1</sup>, L. S. Gould<sup>2</sup>, R. L. Hough<sup>2</sup>, and L. D. Van Vleck<sup>3</sup>, <sup>1</sup>University of Nebraska, Lincoln, <sup>2</sup>Red Angus Association of America, Denton, Texas, <sup>3</sup>USDA, ARS, USMARC, Lincoln, Nebraska.

Age-of-dam adjustment factors now used by the Red Angus Association of America (RAAA) were evaluated to determine if they were still applicable for the current Red Angus population. After edits, 61,322 records were available for birth weight on bull calves, 64,056 for birth weight on heifer calves, 29,663 for weaning weight on bull calves, and 31,073 for weaning weight on heifer calves. Records of bulls and heifers were analyzed separately to estimate age-of-dam adjustment factors for bulls and heifers for each weight. Statistical models were similar to those used for national genetic evaluations by the Red Angus Association of America. Additive factors to adjust to a mature (5 – 10 yr old) dam basis for birth weight of bull calves were determined to be 3.13, 1.41, 0.41, and 1.13 kg for 2-, 3-, 4-, and 11-yr-old and older dams, respectively. For birth weight of heifer calves, adjustment factors were determined to be 3.08, 1.32, 0.45, and 1.04 kg for the same dam classifications. For weaning weight, adjustment factors for bull calves were 32.97, 17.19, 7.30, and 11.97 kg and for heifer calves were 25.80, 13.70, 4.90, and 10.48 kg. The adjustment factors currently used by the Red Angus Association of America under adjust birth weights at all ages for both sexes compared to these new estimates. For weaning weight, the adjustment factors currently used under adjust weaning weights for calves with 2-yr-old dams and with dams that are 11 yr of age or older. Weaning weights for calves out of 3- and 4-yr-old dams are slightly overadjusted with the adjustment factors now used for both sexes, but the magnitude of differences for bull calves is greater than for heifer calves. New adjustment factors for age-of-dam are recommended for use in RAAA genetic evaluations.

**Key Words:** Adjustment factors, Beef cattle, Genetic evaluations

**341 Effects of genetic groups to account for selection on estimates of genetic parameters for a line of Hereford cattle.** L. D. Van Vleck\*<sup>1</sup>, K. J. Hanford<sup>1</sup>, and M. D. MacNeil<sup>2</sup>, <sup>1</sup>USDA, ARS, USMARC, Lincoln, NE, <sup>2</sup>USDA, ARS, LARRL, Miles City, MT.

Robin Thompson originated the idea of an accumulated groups model to account for prior selection. Robin Westell's rules made the coefficient matrix for group models as easy to compute as the A-inverse rules of Henderson and Quaas made use of the numerator relationship matrix for calculation of predicted breeding values given components of the phenotypic variance. The effects of groups in the model on estimates of variance components, however, seem to be unpredictable. Groups were assigned arbitrarily instead of sire identification for some or all of 3,884 weaning weight records of Line 1 Herefords. With usual sire identification, estimates of parameters were 0.20, -0.38, 0.16, 0.19, 0.52 for direct heritability, direct-maternal genetic correlation, maternal heritability, and proportions of variance due to maternal permanent environmental and residual environmental effects. With 22 groups (to replace about one sire for each intake of sires), estimates were 0.13, -0.23, 0.11, 0.20, and 0.58. With 49 groups (all sires of an intake group assigned to that group), estimates were 0.05, 0.41, 0.11, 0.20, and 0.61. With each sire (160) assigned as a group, estimates were 0.06, 1.00, 0.01, 0.24, and 0.67. As another extreme, all sires were coded as missing and were not grouped. Estimates were 0.30, -0.72, 0.08, 0.28, and 0.45. For birth

weight, usual estimates were 0.36, -0.06, 0.14, 0.03, and 0.49. With arbitrary groups, estimates were affected but less extremely than for weaning weight. With a dam effect replacing maternal genetic and permanent environmental effects in the model, substitution of group effects for sires had little effect on estimates of heritability for birth weight but did affect estimates of heritability for weaning weight (although less extremely than for the direct-maternal genetic models). More extensive analytical or simulation studies of effects of genetic groups on estimates of genetic parameters seem warranted.

**Key Words:** Beef cattle, Genetic correlation, Heritability

**342 Maternal performance of Hereford, Angus, Red Angus, Simmental, Gelbvieh, Limousin, and Charolais sired two-year-old crossbred females.** L. V. Cundiff\*, USDA, ARS, Roman L. Hruska U.S. Meat Animal Research Center.

The objective of this experiment was to characterize reproduction and maternal traits of F1 cross females calving at 2 years of age in cycle VII of the Germplasm Evaluation Program at the U.S. Meat Animal Research Center. The females were produced in the spring of 1999 and 2000 as a result of artificial insemination matings of Hereford (H, 21 sires), Angus (A, 22), Red Angus (Ra, 21), Simmental (S, 20), Gelbvieh (G, 23), Limousin (L, 20), and Charolais (C, 22) bulls to Hereford, Angus, and composite MARC III (1/4 each Angus, Hereford, Red Poll, and Pinzgauer) cows. Data were obtained on 681 females exposed, 565 calves born, and 489 calves weaned in the fall of 2001 and 2002 as a result of natural service multi-sire matings to MARC III bulls. Data on calf crop born (CB, %) and weaned (CW, %), calving difficulty score (CDS, score), unassisted births (UB, %), birth weight (BW, kg), survival to weaning (SW), and 200-d weaning weight of progeny (WW, kg) were analyzed by least squares procedures using a model that included random effects for maternal grandsire in maternal grandsire breed, and fixed effects for maternal grandsire breed, maternal granddam breed, sex of calf (for BW, SW, WW only), birth year, and maternal grandsire breed x maternal granddam breed. Effects of maternal grandsire breed were significant (P<.05) for WW but not for any other trait. The means for WW of progeny with H, A, Ra, S, G, L, and C maternal grandsires were 187.4, 192.2, 188.1, 200.3, 195.2, 194.7 and 195.2 kg for WW, respectively. The mean least significant difference among maternal grandsire breed means for WW was 9.5 kg (P<.05). Breed of maternal grand sire means for S and G differed significantly from H and Ra, but not from any other breeds. Breed of maternal grandsire effects did not differ among H, A, Ra, L, and C breeds. Results for WW indicate that contrasts between British (H and A) and Continental European breeds (S, G, L, and C) are less than half as great for direct (3.5 vs 9.5 kg) and maternal (4.8 vs. 11.5 kg) breed effects in the current evaluation (Cycle VII of the GPE Program) as they were 25 to 30 years ago (Cycle I and II of the GPE Program).

**Key Words:** Beef cattle, Breeds, Germplasm

**343 Genetic trends resulting from selection based on an index of birth weight and yearling weight.** M. D. MacNeil\*, USDA-ARS, Fort Keogh LARRL, Miles City, MT.

The CGC population is a stabilized composite of 1/2 Red Angus, 1/4 Charolais, and 1/4 Tarentaise germplasm. The objectives of this research were to estimate genetic parameters for weight traits of CGC and to evaluate genetic responses resulting from selection based on the

index:  $I = 365\text{-d weight} - 3.2(\text{birth weight})$ . In 1989, a randomly selected control line and a line selected for greater values of the index were established. Average generation intervals were  $3.16 \pm 0.04$  yr and  $3.90 \pm 0.08$  yr in the index and control lines, respectively. Over three generations, the index selection line ( $n = 950$ ) accumulated approximately 212 kg more selection differential than the control line ( $n = 912$ ). Derivative-free multiple-trait REML methods were used to estimate (co)variance components and to predict breeding values upon convergence of estimates of (co)variance components. Heritability estimates for direct effects were:  $0.32 \pm 0.04$ ,  $0.49 \pm 0.05$ ,  $0.49 \pm 0.05$ ,  $0.30 \pm 0.04$ , and  $0.70 \pm 0.04$  for the index, birth weight, 365-d weight, 200-d weight, and cow weight, respectively. Heritability estimates for maternal effects were:  $0.05 \pm 0.02$ ,  $0.11 \pm 0.03$ ,  $0.04 \pm 0.02$ , and  $0.19 \pm 0.04$  for the index, birth weight, 365-d weight, and 200-d weight, respectively. In the control line, direct genetic changes for the index and its components were small. For the index selection line, direct genetic changes for the index, birth weight, 365-d weight, 200-d weight, and cow weight were  $6.0 \pm 0.3$ ,  $0.45 \pm 0.09$ ,  $7.74 \pm 0.55$ ,  $3.42 \pm 0.25$ , and  $6.3 \pm 0.9$  kg/generation, respectively. Maternal genetic changes were generally small for both the control and index selection lines. Thus, selection for the index produced positive correlated responses for direct genetic effects on body weight traits at all ages with only minor effects on maternal genetic effects. Results demonstrate that despite a genetic antagonism that compromises selection response for reduced birth weight and increased postnatal growth, favorable genetic responses can be achieved.

**Key Words:** Beef Cattle, Genetic Gain, Selection Index

**344 Bayesian estimation of breed-specific and segregation genetic variances applied to a Nelore-Hereford population.** F. F. Cardoso\*<sup>1</sup> and R. J. Tempelman<sup>1</sup>, <sup>1</sup>Michigan State University.

The objectives of this study were to apply a hierarchical multiple-breed animal model (MBAM) to estimate breed-composition effects, breed-specific additive genetic variances and variance due to the segregation between breeds, and to compare the MBAM with a regular animal model (AM), by simulation and on a dataset on post-weaning gain (PWG) of crossbred beef calves. Phenotypic records were modeled as function of breed composition means and animal additive genetic effects using the variance-covariance specifications as proposed by Lo et al. Bayesian inference was based on MCMC. We validated the model on five simulated datasets derived from a population based on crosses of two breeds having a two-fold difference in genetic variance. In each of the five populations, true values of all variance components in the MBAM were always contained within the corresponding 95% posterior probability intervals (PPI). We also analyzed a dataset of 22,717 PWG records of a Nelore-Hereford population (40,082 animals in the pedigree). MBAM inference on Nelore and Hereford additive genetic variances (in  $\text{kg}^2$ ) differed substantially. Herefords had a posterior median genetic variance of 90.9 with a 95% PPI of [69.8, 114.5] whereas the corresponding values for the Nelore were 32.9 and [20.1, 50.1], respectively. The posterior median variance due to the segregation between these breeds was 13.1 with a 95% PPI of [5.0, 33.8]. The common residual variance posterior median was 333.0 with a 95% PPI of [317.6, 347.8] using MBAM; corresponding values using AM were 348.5 and [332.7, 360.8], respectively. Bayesian model choice criteria heavily favored the MBAM over the AM for both simulated and PWG data, thereby having important implications for improved precision on breeding value predictions.

**Key Words:** Multiple-breed, Crossbreeding, Genetic evaluation

**345 Feedlot performance and carcass traits of Bonsmara, Angus, and Brahman steers.** J. J. Cleere\*<sup>1</sup>, F. M. Rouquette, Jr.<sup>1</sup>, R. D. Randel<sup>1</sup>, T. H. Welsh<sup>2</sup>, J. W. Holloway<sup>3</sup>, and M. F. Miller<sup>4</sup>, <sup>1</sup>Texas Agricultural Experiment Station, Overton, <sup>2</sup>Texas A&M University, College Station, <sup>3</sup>Texas Agricultural Experiment Station, Uvalde, <sup>4</sup>Texas Tech University, Lubbock.

Bonsmara cattle, a composite of Africander x Shorthorn x Hereford, have been recently introduced into the United States with a limited number of grazing-feeding trials conducted on half blood animals, but none with purebreds. To document performance from weaning to harvest, Bonsmara (BON) ( $n = 10$ ), BON x Angus (BOA) ( $n = 9$ ), Angus (ANG) ( $n = 8$ ), and Brahman (BRM) ( $n = 10$ ) steers grazed 'TAM 90' annual ryegrass (*Lolium multiflorum*) and 'Maton' rye (*Secale cereale*)

from January 4 to May 16, 2002 at TAMU-Overton. The BON, BOA, and ANG steers had similar ADG during the grazing period (0.92, 0.84, and 0.91 kg/d;  $P > 0.05$ ); whereas BRM had lower ADG (0.75 kg/d;  $P < 0.05$ ) during the grazing period than BON and ANG. At termination of grazing, steers were assigned to pens ( $n = 8$ ) by breed type and weight with 4 to 5 animals per pen at the Texas Tech University Alltech research feedlot on May 22, 2002. The BON and BRM steers entered the feedlot at lighter weights than BOA and ANG steers (292 and 285 vs. 351 and 360 kg, respectively;  $P < 0.10$ ). Feedlot ADG for BON steers (1.62 kg/d) was lower than ANG steers (1.87 kg/d;  $P = 0.02$ ), lower than BOA steers (1.77 kg/d;  $P = 0.08$ ), and greater than BRM steers (1.28 kg/d;  $P = 0.01$ ). Final feedlot weights of steers fed to estimated one cm back fat thickness were 504 (BON), 512 (BOA), 530 (ANG), and 489 kg (BRM) ( $P > 0.05$ ). Gain to feed ratios were similar among the four breed types. Also, adjusted fat thickness, kidney pelvic heart fat, and yield grades were similar among the four breed types. Hot carcass weights for the BON steers were similar to the BOA, ANG, and BRM steers (299 vs. 305, 314, and 296 kg). The BON steers had rib eye areas similar to the BOA, ANG, and BRM steers (79.7 vs. 78.3, 81.7, and 75.6  $\text{cm}^2$ , respectively). Marbling scores among the BON steers were similar to the BOA, ANG, and BRM steers (367 vs. 346, 413 and 352, respectively). This first U. S. grazing-feedlot study with BON steers revealed that they are intermediate in feedlot performance and carcass quality to ANG and BRM steers.

**Key Words:** Bonsmara, Feedlot, Carcass

**346 Redesigning beef cattle to have a more healthful fatty acid composition.** T. J. Knight\*, J. A. Minick, R. G. Tait, Jr., G. H. Rouse, D. E. Wilson, D. R. Strohbehn, J. M. Reecy, A. E. Wertz, A. H. Trenkle, and D. C. Beitz, Iowa State University, Ames.

Designing beef to meet the nutritional demands of consumers is essential for beef to compete in a market where a healthful product is emphasized. We initiated studies to evaluate the extent to which genetic variation controls beef fatty acid composition. Gas chromatography was used to determine fatty acid composition of the triacylglycerol and phospholipid fractions of the trimmed, edible portion of rib steak from 615 steers and bulls slaughtered at a typical market weight. Contemporary groups were based on year, farm of origin, feedlot, and harvest date. Restricted maximum likelihood (REML) with a sire-maternal grandsire relationship matrix was used to estimate variance components. There were 53 contemporary groups (1-59 cattle per group) and 63 sires (1-34 progeny per sire) represented in the data. In triacylglycerol, myristic acid (14:0) was highly heritable ( $h^2$  S.E.; 0.50 0.28) as was palmitoleic acid (16:1) (0.51 0.23) and oleic acid (18:1) (0.58 0.29). Heritability estimates for phospholipid fatty acids were nearly equal to the respective standard error. To evaluate enzyme systems (fatty acid desaturase and fatty acid elongase), ratios of product to precursor were evaluated. The fatty acid desaturase index (16:1+18:1/16:0+18:0) was heritable in triacylglycerol (0.49 0.28). In contrast, heritabilities of the indices of fatty acid elongase activity were nearly equal to the respective standard error. Finally, an overall health index of the fatty acid composition ( $[4*(14:0)+(16:0)]$  all other fatty acids excluding 18:0) was evaluated and was heritable in triacylglycerol (0.60 0.30). The most favorable EPD for overall health index was -0.045, which represents a >5.5% change from the average for this data set. EPDs for individual fatty acids, in some cases, represent a 5-12% improvement of the particular trait. We conclude that fatty acid composition of beef is in part an inherited trait and that the lipid composition of beef could be improved with respect to human health by genetic selection.

**Key Words:** Beef, Fatty acid, Heritability

**347 Genetic relationships of body condition score with carcass traits in Limousin cattle.** D. R. Eborn\* and D. W. Moser, Kansas State University, Manhattan, KS.

Body condition score (BCS,  $n=19,506$ ) on Limousin cows ( $n=12,439$ ) and carcass weight (CWT), longissimus muscle area (LMA) and fat thickness (FT) at the 12th rib, marbling score (MS), and % kidney, pelvic, and heart fat (KPH) on 4, 326 Limousin sired animals were used to estimate genetic parameters. Heritabilities (diagonal) and genetic correlations (below diagonal) were estimated by MTDFREML by single- and pair-wise analyses, respectively. The model for BCS included a fixed effect for contemporary group, covariates for age at measurement, and

random animal, permanent environment, and residual effects. Contemporary groups for BCS were defined by the cow's calf weaning weight contemporary group. The model for carcass traits included a fixed effect for contemporary group, covariate for age at slaughter, and random animal and residual effects. Estimates of heritabilities for carcass traits ranged from  $0.14 \pm 0.04$  for CWT to  $0.34 \pm 0.05$  for REA. Heritability of BCS was  $0.19 \pm 0.02$ . The genetic correlations between BCS and CWT, LMA, FT, MS and KPH were 0.28, 0.60, -0.04, -0.64, and 0.16, respectively. Our findings suggest that selection on LMA or MS may impact BCS in the cowherd. However, no significant correlation was found between FT and BCS.

	BCS	CWT	LMA	FT	MS	KPH
BCS	0.19 $\pm 0.02$					
CWT	0.28	0.14 $\pm 0.04$				
LMA	0.60	0.50	0.34 $\pm 0.05$			
FT	-0.04	0.09	-0.19	0.24 $\pm 0.05$		
MS	-0.64	-0.23	-0.40	-0.14	0.15 $\pm 0.04$	
KPH	0.16	-0.23	-0.51	0.53	-0.20	0.16 $\pm 0.04$

**Key Words:** Body condition score, Carcass, Genetic parameters

**348 Heritability and repeatability of back fat and rump fat thickness in Angus cattle.** A. Hassen\*, D. E. Wilson, and G. H. Rouse, *Iowa State University, Ames, IA.*

The current study included data from 912 purebred Angus bulls and heifers born during the spring of 1998 to 2001. Each year calves were serially measured for back fat thickness (BFT), rump fat thickness (RFT) and other ultrasound measures starting at weaning time and with 4 to 6 weeks interval between scans. The objective of this study was to compare trends in variance components, heritability and repeatability of BFT and RFT measures of Angus cattle measured between mean ages of 27 to 62 weeks. Initially BFT and RFT observations were analyzed by scan session across years using multiple trait animal model. Data pooled across years and scan sessions were then analyzed using random regression models (RRM) to produce general trends in genetic parameter estimates. Bull and heifer RFT measures showed higher heritability values than BFT for all scan sessions. Heritability of BFT increased from 0.13 at the 1st scan (mean age = 35 weeks) to 0.29 at the 5th scan (mean age = 53 weeks). Heritability of RFT increased from 0.33 at the 1st scan to 0.44 at the 6th scan (mean age = 56 weeks). Genetic correlation between yearling BFT (5th scan) and earlier RFT measures including scans one to four were 0.58, 0.62, 0.77, and 0.83, respectively. Results from RRM showed higher additive genetic variance values for RFT measures until 48 weeks followed by larger genetic variances for BFT during the rest of the ages. However, BFT measures showed larger direct permanent environmental variances than RFT for most measurement ages. Heritability of RFT ranged from 0.27 to 0.39, as compared to 0.24 to 0.34 for BFT measures. At a year of age heritability of BFT and RFT were 0.34 and 0.38, respectively. Both traits showed similar repeatability values ranging from 0.71 to 0.91. Repeatability of yearling BFT and RFT were 0.88 and 0.86, respectively. The relatively higher heritability values of early RFT measures and the strong genetic association with yearling BFT suggest that RFT measures could be considered as additional sources of information for earlier evaluation of Angus cattle for fat cover and other related traits.

**Key Words:** Composition, Ultrasound, Heritability

**349 Genetic parameter estimates of udder scores in Gelbvieh cattle.** R. L. Sapp\*, R. Rekaya, J. K. Bertrand, I. Misztal, and K. A. Donoghue, *The University of Georgia, Athens, GA.*

The objective of this study was to investigate genetic parameters for teat size score (T) and suspension (S) score in Gelbvieh (GV) cattle. Cows were scored, by the producer, within 24 hr of calving. The range of T and S is 0 (extremely large or very pendulous, respectively) to 50 (extremely small or extremely tight, respectively). Cows from sires that were at least 75 percent GV were retained for analysis. Bivariate analyses of

data from first parity (FP) animals ( $n = 11,997$ ) were performed. Second bivariate analyses of data with first and second parity (SP) records ( $n = 11,997$ ) were performed, where T and S were considered different traits (T1, T2, S1, S2, respectively) across the two parities. A first parity animal was considered to be four yr of age or younger at first calving. Contemporary grouping included herd, year, season, percent GV, and birth group identification for both data sets. The model included the fixed effect of contemporary group, a covariate for the age at measurement, and random additive genetic effect. AIREMLF90 was used to estimate variance components. Heritability estimates from FP data for T and S were 0.22 and 0.19, respectively; heritability estimates of 0.22, 0.18, 0.39, and 0.28 were found for T1, T2, S1, and S2, respectively, from SP data. The genetic correlation between T and S in FP data was 0.87. The genetic correlations between T1-S1, T1-T2, S1-S2, and T2-S2 were 0.86, 0.76, 0.73, and 0.98, respectively. The approximate SD for the genetic correlations were higher than we expected. The moderate heritability estimates suggest that selection for T and S is possible. It is interesting to note that the genetic correlations, estimated from SP data, is higher between T and S within a parity than the correlation between the same score across parities. This may suggest that producers consider T and S to be the same response instead of two separate measurements. Further research is needed to determine the relationship between udder scores and milk production.

**Key Words:** Udder score, Genetic parameters, Beef cattle

**350 Comparison of methods for handling missing fertility records in beef cattle data.** K. A. Donoghue\*<sup>1</sup>, R. Rekaya<sup>1</sup>, J. K. Bertrand<sup>1</sup>, D. J. Johnston<sup>2</sup>, and C. Teseling<sup>3</sup>, <sup>1</sup>*The University of Georgia, Athens GA, USA*, <sup>2</sup>*Animal Genetics and Breeding Unit, Armidale NSW, Australia*, <sup>3</sup>*The Angus Society of Australia, Armidale NSW, Australia.*

The purpose of this study was to compare methods for handling missing fertility records in beef cattle data. Data were days to calving records from natural service matings of 33,176 first-calf females in Australian Angus herds. Three methods for handling records from females that did not calve (missing records) were evaluated, with three separate data sets created for analysis. Non-calvers were assigned penalty values on a within contemporary group basis in the first data set (DCPEN). In the second data set, records for non-calvers were treated as censored, and were drawn from their respective truncated normal distribution (DCSIM), while records on non-calvers were deleted from the third data set (DCMISS). Bayesian approach via Gibbs sampling was used to estimate variance components and predict breeding values. Posterior means (PM) (SD) of additive genetic variance for DCPEN, DCSIM and DCMISS were 29.87 (4.69), 25.74 (3.89), and 13.2 (2.91), respectively. PM (SD) of residual variance for DCPEN, DCSIM and DCMISS were 435.3 (5.38), 371.7 (4.63), and 262.4 (3.43), respectively. PM (SD) of heritability for DCPEN, DCSIM and DCMISS were 0.06 (0.01), 0.06 (0.01), and 0.05 (0.01), respectively. Simulating trait records for non-calving females resulted in similar heritability to the penalty method, but lower residual variance. Pearson correlation between posterior means of animal effects in DCPEN-DCSIM was 0.98, and for sires with more than 20 daughters with records, correlations between DCPEN-DCSIM, DCPEN-DCMISS and DCSIM-DCMISS were 0.98, 0.80 and 0.84, respectively. Of the 424 sires ranked in top 10% of sires in DCPEN, 88% were also ranked in top 10% in DCSIM. These results indicate that although most sires ranked similarly, there were exceptions. Further research to understand the differences in ranking of animals under these methods is underway.

**Key Words:** Fertility, Genetic evaluation, Beef cattle

**351 Estimates of genetic parameters for respiratory disease in beef calves before weaning.** G. Snower\*, D. Van Vleck, L. Cundiff, K. Gregory, and G. Bennett, *USDA, ARS, Roman L. Hruska U.S. Meat Animal Research Center.*

Respiratory disease is one of the most economically important illnesses affecting growth and survival of calves. The primary objective of this study was to estimate genetic parameters for respiratory disease in beef calves prior to weaning. Health records of 31,000 calves produced at the U.S. Meat Animal Research Center, Clay Center, NE from 1983 to 2001 were evaluated. Cows and calves were monitored daily for health until weaning at approximately 194 d of age. Breed groups consisted of nine purebred breeds (Angus, Braunvieh, Charolais, Gelbvieh, Hereford, Limousin, Pinzgauer, Red Poll, and Simmental), two reciprocal crosses

between Angus and Herefords, and three composite populations (MARC I, MARC II, and MARC III). Respiratory disease was detected by physical examination, necropsy, or laboratory analyses. To avoid multiple incidence, records on the same calf which may be due to lingering respiratory disease, only the initial infection during the preweaning period was considered. Overall average incidence of recorded respiratory disease was 11.6%. Incidence was highest in Braunvieh (18.1%) and MARC I (17.8%), a composite breed with one fourth Braunvieh heritage. Herefords and the Hereford x Angus cross had the lowest incidence (4.6 to 7.8%). Incidence was highest after d 84. Variance components were estimated using REML. Fixed effects included year of birth, age of dam, sex of calf, and breed type. Calf and dam of the calf were considered random effects. Variance due to permanent environmental effects of the dams was not significant. Phenotypic variance for respiratory disease was 0.095. Heritability estimates for the calf direct and maternal effects were low,  $0.14 \pm 0.01$  and  $0.04 \pm 0.01$ , respectively. Estimate of the direct-maternal genetic correlation was large and negative,  $-0.93 \pm 0.04$ . Large and significant breed differences for respiratory disease were found. Within breed, response to selection to reduce the incidence of respiratory disease in calves would be expected to be slow although breed differences suggest a potential to improve resistance by selection or crossbreeding.

**Key Words:** Pneumonia, Lung, Health

**352 Simulation of net return using days to finish estimated breeding values in beef production.** M. A. Cleveland\*, R. M. Enns, W. J. Umberger, and B. L. Golden, *Colorado State University, Fort Collins, CO.*

The objective of this study was to determine if sire genotype and choice of finish endpoint for progeny interact to affect net return. A model was developed to determine the distribution of progeny for three carcass traits, carcass weight (CW), backfat thickness (BF) and marbling score (MS), when feeding to a CW, BF or MS endpoint. Days to finish carcass weight (DCW), backfat thickness (DBF) and marbling score (DMS) estimated breeding values (EBV) were used to simulate feeding costs, grid revenue, and net return. Three sire days to finish genotypes, high (H), medium (M) and low (L), as indicated by EBV, were considered for each trait. An H EBV suggests above average days to finish, while an L EBV indicates a shorter than average time on feed. All possible combinations of EBV resulted in 27 distinct sire genotypes for days to finish. Assuming an average of 130 days to each endpoint, results showed that progeny from sires with H EBV for days to finish needed an average of 142 days to reach a constant CW, and 148 days to reach constant BF and MS endpoints, while progeny from L EBV sires needed an average of only 118 days or less to reach each endpoint. The results from the model indicated that considerable re-ranking occurred among sires for net return, suggesting an interaction between genotype

and finish endpoint. Re-ranking resulted in changes of up to 20 positions at alternative endpoints for some sire genotypes. Net return was calculated using average yardage costs and grid revenue. When feeding to a constant CW or BF, the LHL sire (first character indicates the DCW, second, the DBF, and third, the DMS EBV) realized the highest return, while the LLL sire was most profitable at the BF endpoint. Progeny from sires with H EBV for DMS, when fed to the MS endpoint, were overall least profitable. With the inclusion of more precise costs of production, this type of model has the potential to become a selection and management tool using days to finish genetic predictions to assist producers in maximizing profitability.

**Key Words:** Beef cattle, Days to finish, Simulation

**353 Comparison of different selection criteria in populations simulated under growth curve parameters of Brazilian zebu cattle.** E. S. Sakaguti\*<sup>1</sup>, E. N. Martins<sup>1</sup>, and L.O.C. Silva<sup>2</sup>, <sup>1</sup>Universidade Estadual de Maringa, Maringa, Brazil, <sup>2</sup>Embrapa Gado de Corte, Campo Grande, Brazil.

Recently the Brazilian Association of Zebu Breeders started to report the EPDs for a new growth trait, the number of days that an animal would take to gain 240 kg in the postweaning period (D240). This new trait can be used as a substitute of the traditional postweaning average daily gain (ADG) and is calculated as  $D240 = 240/ADG$ . However, there is some uncertainty about the consequences of this change. Then the objective of the present work is to evaluate the response to selection when four different traits (ADG, D240, live weight at 205 (WW) and 550 (YW) days of age) were individually considered in populations generated by Monte Carlo simulations. A FORTRAN 90 program generated the parameters (A, B and K) of the Von Bertalanffy function for each animal. The parameters were implemented as biological traits with Medelian inheritance, polygenic effect and phenotypic and genetic correlations. Estimates of genetic parameters from live weight data of Tabapua breed were employed. Two levels of heritability (approximately .1 and .5) were considered and 10 base populations were generated for each level of heritability. Approximately 25,000 progenies of 200 sires and 10,000 dams composed a population in each generation. Simulations of a random mating system with single calf per parturition produced populations with half-sib family structure that were evaluated by 10 generations of BLUP selection on each trait. The selection for ADW and D240 produced similar results. Both showed the highest increases of the mature weight (A) and the lowest decreases of the maturing rate (K). In the other hand, the selection for WW had the lowest increases of A and the highest decreases of K. Intermediate results were found with the selection for YW. The selection for D240 produced the highest inbreeding increases that can be a consequence of the smallest estimates of heritability of this trait in the early generations.

**Key Words:** Monte Carlo simulation, Growth curve, Selection responses

## Companion Animals

**354 A new approach to testing nutraceuticals in animals: A placebo-controlled evaluation of a milk-based "immuno-nutritional" product in dogs.** D. A. Gingerich\* and J. D. Strobel, *SMBI, Cincinnati, OH, USA.*

Functional foods and dietary supplements with structure/function claims have become important in the health care system in USA, especially since the passage DSHEA in 1994. Pet owners are interested in the therapeutic value of such products for their pets. However, few dietary supplements have been rigorously evaluated in animals. Furthermore, it is FDA/CVM's position that DSHEA does not apply to animal products. Milk is a food with biological functions in addition to its nutritional value. A special milk protein concentrate (SMPC) prepared from the milk of hyperimmunized cows was shown to express anti-inflammatory and anti-arthritis activity in humans. To determine if SMPC is also beneficial to dogs, an 8-week, placebo-controlled clinical study was conducted in older dogs with osteoarthritis. The study was designed to test the product and also to evaluate an owner-based questionnaire designed specifically for dogs. Fifty dogs in 5 veterinary practices were enrolled, of which 35 completed the study. Significant ( $p < 0.05$ ) improvement in mean questionnaire scores and owner global assessments was detected in dogs in the SMPC group but not the placebo group. The treatment responses were significantly greater in the SMPC group than

in the placebo group ( $p < 0.005$ ). The effect sizes (treatment response - placebo response/SD placebo response) for case-specific and client global outcomes were 1.61 and 0.90 respectively, which are considered large. No treatment-related adverse effects or changes in serum chemistry findings were detected. Unlike many dietary supplements with no recognized nutritional value, SMPC contains high quality dairy protein. Because there is laboratory evidence that the anti-inflammatory activity in the milk from hyperimmunized cows is exerted through immunological mechanisms, we describe SMPC as an "immuno-nutritional". The results of this study also indicate that the individualized owner-based questionnaire is a valuable tool in testing nutraceuticals and can be adapted to evaluate a variety of new products in pets.

**Key Words:** Nutraceutical, Milk-based, Anti-inflammatory

**355 Measuring absorption of a purified, crystalline lutein additive in the canine.** L. B. Deffenbaugh\*, *Kemin Nutrition, Inc.*

Lutein is one of numerous carotenoids with potential health benefits for companion animals. Natural sources include green leafy vegetables, marigolds, and maize, in which lutein is present as a fatty acid ester.