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 (Orbesol, 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=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=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=0.72, P < 0.05).

Key Words: Internal teat sealant, Mastitis, Dry period

Bio Re-saving and Genetics: Beef cattle breeding


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, 3–4, 4–5, and 5–11 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 adjusted 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 Vleck1, K. J. Hanford2, and M. D. MacNeil2.

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 grand sire in maternal grandsire breed, and fixed effects for maternal grandsire breed, maternal grand dam breed, sex of calf (for BW, SW, WW only), birth year, and maternal grandsire breed x maternal grand dam breed. Effects of maternal grandsire breed were significant (P<0.05) 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 breeds for WW was 9.5 kg (P<0.05). Breed of maternal grandsire 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, Breed, Germplasm

343 Genetic trends resulting from selection based on an index of birth weight and yearling weight. M. D. MacNeil2, USDA-ARS, Fort Keogh LARRL, Miles City, MT.

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 grand sire in maternal grandsire breed, and fixed effects for maternal grandsire breed, maternal grand dam breed, sex of calf (for BW, SW, WW only), birth year, and maternal grandsire breed x maternal grand dam breed. Effects of maternal grandsire breed were significant (P<0.05) 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 breeds for WW was 9.5 kg (P<0.05). Breed of maternal grandsire 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, Breed, Germplasm

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 (1-50 cattle per pen) and 63 sires (1-34 progeny per sire) represented in the data. In triacylglycerol, myristic acid (14:0) was highly heritable (h² 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 ([(14:0+16:0)/36:0] 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 part of 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 between BCS and each of LMA, FT, MS, and KPH were estimated by MTDPREML 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 \(0.28 \pm 0.14\), \(0.60 \pm 0.50\), \(0.34 \pm 0.05\), \(-0.04 \pm 0.09\), \(-0.19 \pm 0.24\), \(-0.64 \pm 0.23\), \(-0.40 \pm 0.14\), \(0.15 \pm 0.04\), \(0.16 \pm 0.23\), \(-0.51 \pm 0.53\), \(-0.20 \pm 0.16\), \(0.24 \pm 0.05\), 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. 

### 348 Heritability and repeatability of back fat and rump fat thickness in Angus cattle

A. Hassen*, D. E. Wilson, 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 when 48 weeks and beyond, while larger residual 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: Body condition score, Carcass, Genetic parameters

### 350 Comparison of methods for handling missing fertility records in beef cattle data


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, DCNSSIM and DCNSSS 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 \(455.3 (5.38)\), \(371.7 (4.63)\), and \(262.4 (3.43)\), respectively. PM (SD) of heritability for DCPEN, DCNSSIM and DCNSSS were \(0.06 (0.01)\), \(0.06 (0.01)\), \(0.06 (0.01)\), 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-DCNSSIM was \(0.98\), and for sires with more than \(20\) daughters with records, correlations between DCPEN-DCNSSIM, DCPEN-DCNSSS 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 DCNSSS. 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


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 days of age. Herd groups consisted of nine purebred breeds (Angus, Brauneck, 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 ± 0.01 and 0.04 ± 0.01, respectively. Estimate of the direct-maternal genetic correlation was large and negative, -0.93 ± 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

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 carcase traits, carcase weight (CW), backfat thickness (BF) and marbling score (MS), when feeding to a CW, BF or MS endpoint. Days to finish carcase 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 yardenage 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

Comparison of different selection criteria in populations simulated under growth curve parameters of Brazilian zebu cattle. E. S. Sakaguti1, E. N. Martins1, and L.O.C. Silva2, 1Universidade Estadual de Maringá, Maringá, Brazil, 2Embrapa 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 mature rate (K). In the other hand, the selection for WW had the lowest increases of A and the highest decreases of K. Intermediate results where 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

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 use of dietary supplements in companion animals. 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

Measuring absorption of a purified, crystalline lutein additive in the canine. L. B. Defenbaugh*, Kemin Nutriscience, 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.

Key Words: