881 Estimates of genetic parameters for infectious keratoconjunctivitis in beef calves before weaning.

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Bovine infectious keratoconjunctivitis (BIK, pinkeye) is an economically important illness affecting growth of calves. The primary objective of this study was to estimate genetic parameters for BIK in beef calves prior to weaning. Health records of 47,880 calves born at the Meat Animal Research Center, Clay Center, NE from 1983 through 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), and three composite breeds (MARC I, MARC II, and MARC III). Detection of BIK was by physical examination. If BIK was detected during the preweaning period a score of 100 was assigned and if not the score was 200. Overall average prevalence of BIK was 6.5%. Prevalence was significantly greater in Hereford (22.4%) compared to all other breeds. Pinzgauer and Braunvieh breeds had the lowest incidence rates of 1.3 and 1.8%, respectively. Infections began at approximately 45 d of age and frequency of infections increased until approximately 105 d of age. Variance components for each breed were estimated using REML. Fixed effects included year of birth, age of dam, sex of calf, and birth weight. Calf and dam of the calf (direct and maternal genetic) were random effects. Variance due to maternal permanent environmental effects was not significant. Heritability estimates for the direct effect of the calf ranged from 0.00 to 0.28. Hereford and Angus breeds had the highest heritability estimates, 0.28 and 0.25, respectively. Heritability estimates for the maternal effect were low and ranged from 0.00 to 0.11. Estimates of the direct-maternal genetic correlation were highly variable and ranged from -1.00 to 1.00. Within breed, response to selection to reduce the incidence of BIK in calves would be expected to be slow although breed differences suggest a potential to improve BIK resistance by selection, especially in the Hereford breed.

Key Words: Heritability, Disease, Maternal

882 Investigation of gestation length in *Bos indicus x Bos taurus* reciprocal backcross calves produced through embryo transfer.

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Gestation length (GL) was studied on 511 embryo transfer calves belonging to 28 full-sib families born 1990-1996. Calves were produced by backcross matings involving three distinct sire and dam types: Angus (A), *Bos indicus* (B) (Brahman), and F_1 Angus-*Bos indicus* (Brahman or Nellore). Resulting progeny were 3/4 A-1/4 B, or 3/4 B-1/4 A. Calves were born to recipients that were approximately 1/2 Brahman and 1/2 British. Data were studied through analysis of covariance with independent variables of sex, sire-type x dam-type interaction (ST x DT), family nested within ST x DT, sex x ST x DT, embryo quality (EQ), embryo stage (ES), and the regression on birth date within season-year combination. Family nested within ST x DT was considered a random effect, and was the error term to test for differences due to ST x DT. Calf sex, EQ, regression on birth date, and the ST x DT interaction accounted for variation ($P < .05$) in GL. The three-way interaction involving calf sex, ST and DT was not significant as is typically seen for birth weight in these reciprocal cross calves. Male calves averaged 291.2 d and female calves averaged 288.5 d. For A backcross calves, GL averaged 286.8 d from A x F_1 matings, but averaged 289.3 d from F_1 x A matings. For B backcross calves GL averaged 293.8 d from B x F_1 matings, but averaged 289.5 d from F_1 x B matings. Additionally, type of F_1 parent (AB or BA, sire breed first) was found to account for significant differences in GL. Among calves from A sires and F_1 dams, GL was 5 d longer in calves from BA dams (289.6) as compared to those from AB dams (284.5). Among calves from F_1 sires and A dams, GL was 2 d longer in calves from BA sires (290.8) than in calves from AB sires (288.4). For calves from B sires and F_1 dams, GL was 4 d longer in calves from BA dams (296.1) as compared to those from AB dams (292.4). For calves from F_1 sires and B dams, GL was 3 d longer in calves from BA sires (291.1) than calves from AB sires (288.3). In both the A and B backcross calves the trend was to have a longer GL when the F_1 parent was BA as opposed to AB.

Key Words: Reciprocal Cross, Embryo Transfer, Gestation Length

883 Genetic correlations between postweaning feed efficiency and cow traits.

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Postweaning records on 1781 bulls and heifers tested for feed efficiency at 267 d of age and cow records taken at 4 y of age on 751 of the same females were used to estimate genetic correlations between postweaning feed efficiency and cow traits. The study was conducted at NSW Agriculture Research Centre, Trangie. The postweaning feed efficiency traits used were residual feed intake (RFI) and feed conversion ratio (FCR). RFI was calculated as the difference between actual daily feed intake and that predicted from a model that included metabolic weight and ADG. FCR was calculated as daily feed intake per unit ADG. For both traits efficient animals will have lower values. The cow records were taken on non-pregnant cows after the weaning of their second calf. The cow traits were daily feed intake (COWFI), ultrasound measure of rump fat depth (COWFAT), longissimus muscle area (COWEMA) and weight at 4 y of age (4-yWT). Genetic parameters were estimated by REML using animal models. All analyses included pedigrees back to 3 generations of ancestors. Means for the traits were 0.04 kg, 7.56, 15.7 kg, 13.2 mm, 81.3 cm^2 and 498.3 kg, for RFI, FCR, COWFI, COWFAT, COWEMA and 4-yWT, respectively. Corresponding heritability estimates were 0.42, 0.28, 0.27, 0.47, 0.12 and 0.62. The genetic correlation between RFI and the cow traits were 0.74 (COWFI), 0.32 (COWFAT), 0.41 (COWEMA) and -0.03 (4-yWT). Corresponding values for FCR were 0.39 (COWFI), 0.32 (COWFAT), 0.12 (COWEMA) and -0.33 (4-yWT). The results indicate that when selection of young cattle for improved feed efficiency is based on FCR a weak correlated response in reduced cow feed intake and increased cow weight is expected. However, when selection of young cattle for improved feed efficiency is based on RFI a strong correlated response in reduced cow feed intake is expected with no response in cow weight.

Key Words: Cattle, Feed Efficiency, Body Composition

884 Investigation of birth weight in *Bos indicus x Bos taurus* reciprocal backcross calves produced through embryo transfer.

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Birth weight (BWT) was studied on 511 embryo transfer calves belonging to 28 full-sib families born 1990-1996. Calves were produced by backcross matings involving three distinct sire and dam types: Angus (A), *Bos indicus* (B) (Brahman), and F_1 Angus-*Bos indicus* (Brahman or Nellore). Resulting progeny were 3/4 A-1/4 B, or 3/4 B-1/4 A. All calves were born to recipient dams that were approximately 1/2 Brahman and 1/2 British. Data were studied through analysis of covariance that included independent variables of sex, sire-type x dam-type interaction (ST x DT), family nested within ST x DT, sex x ST x DT, embryo quality (EQ), embryo stage (ES), and the regression on birth date within season-year combination. Family nested with ST x DT was considered a random effect, and was the error term to test for differences due to ST x DT. Calf sex, the regression on birth date, ES, and the three-way interaction sex x ST x DT accounted for variation in BWT ($P < .05$). Male calves averaged 38.2 kg, and female calves averaged 35.2 kg. Among A backcrosses, A x F_1 calves were 3.5 kg lighter ($P = .04$) than F_1 x A calves (34.9 vs. 38.4). Also, among B backcrosses, F_1 x B calves were 4.7 kg lighter than B x F_1 calves (34.4 vs. 39.1). Among A backcross calves from A sires and F_1 dams, the BWT difference was 1.8 kg between male (35.5) and female (34.3) calves, but when A backcross calves were produced from F_1 sires and A dams the difference in male vs. female BWT was 5.0 kg (40.9 vs. 35.9 kg, respectively). For B backcross calves produced from B sires and F_1 dams, male calves averaged 4.6 kg heavier than females (41.4 vs. 36.8 kg), whereas when B backcross calves were produced from F_1 sires and B dams, BWT of male calves (35.0 kg) averaged 1.2 kg heavier than female calves (33.8 kg). These *Bos indicus-Bos taurus* reciprocal differences have been widely reported in natural service calves, and these results are consistent with earlier reports in ET calves.

Key Words: Reciprocal Cross, Embryo Transfer, Birth Weight

885 Teat scores in first-parity Gelbvieh cows: Relationship with suspensory score and calf growth traits.

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Teat and suspensory scores from 9,418 first-parity Gelbvieh (GV) cows and growth records from 19,119 calves were used to estimate genetic and environmental parameters for teat and suspensory scores and to investigate the relationship of teat and suspensory scores with calf growth traits and maternal genetic growth effects. First-parity cows did not have multiple scores within 280 d, gave birth to one calf, were 4 yr of age or younger at first-calving, and were at least 50% GV. Producers scored cows within 24 h of parturition. Teat score (T), a subjective measure of teat size, ranged from 0 (very large) to 50 (very small) and suspensory score (S), a subjective score of udder support, ranged from 0 (very pendulous) to 50 (very tight). Unadjusted birth (BW), weaning and yearling weight of the calves, born in the first three parities to the first-parity cows, were used to calculate pre- (WG) and postweaning (YG) ADG. A mixed model was employed for the multiple trait analysis of T, S, BW, WG, and YG which included herd-yr, mo of calving, age of cow at calving and sex of calf (included only for BW, WG, and YG) as systematic effects; regression on percentage GV; and additive animal, maternal genetic and permanent environment of dam (included only for BW and WG), and residual as random effects. Heritability estimates were 0.27, 0.22, 0.39 (0.09), 0.27 (0.14) and 0.21 for T, S, direct (maternal) BW, (maternal) WG and YG, respectively. The genetic correlation between T and S was 0.95. The genetic correlations between T (S) with direct BW, WG and YG and with maternal BW ranged from -0.18 to 0.38. The genetic correlation between T (S) with maternal WG was -0.47 (-0.55) suggesting that cows with smaller teats and tighter udders produced less milk. Pearson correlations between EBV of T and S with maternal WG indicate that animals with extremely large or small EBV for T or S may have problems with accessibility of milk or adequate milk production. Therefore, it may be more beneficial for producers to select animals with intermediate EBV for T and S.

Key Words: Growth, Suspensory Score, Teat Score

886 Calving day and age at first calving in Angus heifers.

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Reproduction is one of most economically important traits in beef production. Due to difficulties in data collection and analysis, in most breeds there has been no objective way to evaluate fertility in females on a between-herd basis. The objective of this study was to determine if calving date (CD) and age at first calving (AFC) could be used to select for female fertility in beef cattle. Records (n = 2082) from a university research herd and a large purebred breeder were used. There were a total 147 sires with heifers represented in the CD data. CD was calculated for each heifer by subtracting the calving date of the first heifer to calve in that contemporary group from the calving date of the heifer. For example, within each contemporary group of heifers, heifers that calved on the first day of the calving season were given a calving day of one. Heifers that calved the next day had calving days of two, and so on. To avoid bias, non-calving heifers were assigned a CD of 30, 60, and 90 days after the last heifer in that contemporary group calved. These assigned CD were also used to give open heifers a predicted AFC. Data were analyzed by MTDFREML using a general linear animal model. Fixed effects included herd-year, service sire of the heifer, and age of dam. Covariates that were tested included adjusted yearling weight and age of the heifer at the start of the breeding season (for CD only). Heritabilities for CD for the 30, 60, and 90 day adjustments were 0.07 ± 0.04, 0.10 ± 0.05, and 0.11 ± 0.05, respectively. Average, minimum, and maximum estimated breeding values for sires of heifers were 0.7, -10.6, and 9.8 days for CD30; -1.1, -17.2, and 16.5 days for CD60; and 1.6, -22.6, and 19.5 days for CD90. The estimates for AFC30, AFC60, and AFC90 were 0.28 ± 0.06, 0.28 ± 0.06, and 0.28 ± 0.06, respectively. Average, minimum, and maximum estimated breeding values for sires of heifers were 0.6, -46.6, and 45.9 days for AFC30; -1.2, -50.1, and 51.6 days for AFC60; and 1.7, -52.9, and 56.7 days for AFC90. These results indicate that AFC may be more useful than CD in selecting for female fertility in beef cattle.

Key Words: Fertility, Calving Day, Age at First Calving

887 Genetic prediction for estimating mature cow maintenance energy requirements.

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Cow maintenance energy requirements are defined as the amount of dietary metabolizable energy required for maintenance. According to NRC (1996) nutrient requirements of beef cattle, maintenance requirements account for roughly 70% of the total metabolizable energy requirements of a beef cow. The goal of this project was to develop a selection tool to assist producers in improving beef production efficiency by simultaneously accounting for change in income (sale weight) and cost (cow maintenance). A genetic prediction for mature cow maintenance energy requirements was developed using equations from the 1996 NRC to predict the energy required for maintenance of a beef cow and Woods lactation function. These equations were modified so an animals genetic prediction for metabolic weight and weaning weight maternal could be used to predict its maintenance energy requirements through a non-linear combination of the two traits. Metabolic weight genetic predictions were calculated by random regression using Best Linear Unbiased Prediction (BLUP) procedures where metabolic weight (mature cow weight pre-adjusted to condition score 5 and raised to the power 0.75) was regressed on age to predict metabolic weight at 5 years of age. Weaning weight maternal genetic predictions were estimated by applying BLUP procedures to an animal model with birth weight and weaning weight as the dependent variables. A prediction error variance equation was developed using the algebra of variances and co-variances in concert with the genetic prediction equation. The prediction which is reported as a progeny difference in the units of mega-calories per month has been adopted by the Red Angus Association of America and will be published in their 2004 sire summary.

Key Words: Genetic Prediction, Cow Efficiency, Maintenance

888 Estimates of genetic correlations among carcass traits adjusted to different end points.

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Carcass measurements of 1,664 serially slaughtered steers from 12 breeds (Red Poll, Hereford, Angus, Limousin, Braunvieh, Pinzgauer, Gelbvieh, Simmental, Charolais, MARC I, MARC II, and MARC III) were used to estimate genetic correlations among carcass traits adjusted to slaughter age, carcass weight or backfat thickness end points. Traits were carcass weight (CW), dressing % (DP), fat thickness (FT), longissimus area (LA), kidney pelvic heart fat % (KF), marbling (MS), yield grade (YG), predicted % of retail product (ER), retail product wt (RW), fat wt (FW), bone wt (BW), retail product % (RP), fat % (FP), and bone % (BP). The model included breed group, feed energy level, age of dam, year of birth, significant interactions, number of days on feed, and end point nested within breed (except age) as fixed effects, and genetic effect of animal and total maternal effect of dam as random effects. Genetic correlations, estimated by REML, for CW LA, FT RW, LA-KF, LA YG, LA ER, LA FW, LA-BW, LA RP, LA FP, KF RW, KF BW, ER RW and ER RP at constant age, wt, or fat thickness, respectively, were .32, –, and .51; .26, .77, and ; -.01, -.10, and .25; .71, .89, and .66; .68, .85, and .63; .16, -.51, and .22; .24, -.19, and .30; .47, .57, and .27; .44, -.43, and .18; .02, .48, and .15; .08, .55, and .04; .26, .80, and .01; and .72, .73, and .32. The magnitude and the sign of the genetic correlation changed across end points for many pairs of traits. Correlated responses to selection would differ depending on end point. Regardless of end point, FT was highly correlated with YG (.86, .85; common age and wt) and ER (.85, .82; common age and wt), indicating that selection for reduced

FT would improve YG and ER. Carcass quality, however, would be affected negatively because of the moderate genetic correlations (.34, .35; common age and wt) between MS and FT.

Key Words: Carcass Traits, Genetic Correlations, Slaughter End Points

889 Genetic evaluation of beef cattle for growth using records across a wide range of ages.

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A simulation study was conducted to validate agreement between multitrait model (MT) and random regression model (RRM) estimates of growth in beef cattle. Secondary goal was to compare RRM with Legendre polynomials and RRM with splines. Four data sets were generated assuming RRM with cubic regression on Legendre polynomials of age for direct genetic and permanent environmental, maternal genetic and maternal permanent environmental effect. First data set contained records located exactly at 1, 205 and 365 days of age. Second data set consisted of records at 1, 205 ± 45 and 365 ± 45 days. Third data set was created by adding two extra records at 100 and 300 days to the first data set. Fourth data set contained birth weight and records located in an interval of 45 days around 100, 205, 300 and 365 days. Three models were fitted: 1) multitrait model with preadjustment to constant age and traits defined at 1, 205 and 365 days of age; 2) random regression model with Legendre polynomials; and 3) random regression model with linear splines. Variance components in all models were equivalent at 1, 205 and 365 days. Accuracies were calculated as correlation between simulated and predicted breeding values estimated at 1, 205 and 365 days of age. Multitrait and both random regression models showed excellent agreement in the first data set. RRMs were 1.4 %, 1.9 %, 2.0 % more accurate than MT at 1, 205 and 365 days of age, respectively, in the second data set. Accuracy of RRMs with the third data set was 0.5 %, 2.5 %, and 0.2 % higher at 1, 205 and 365 days of age, respectively, over the first data set. Accuracy of RRMs with the fourth data set was 0.5 %, 1.6 %, and 0.0 % higher at 1, 205 and 365 days of age, respectively, over the second data set. The gains in accuracy were small due to high genetic correlations between records. RRM with Legendre polynomials and RRM with linear splines gave almost identical results, however the model with splines converged six times faster. Random regression models were slightly more accurate than multitrait model. RRMs with linear splines were simpler than such models with Legendre polynomials.

Key Words: Beef Cattle, Growth, Random Regression Model

890 Examining the genetic diversity of Hereford cattle.

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This study characterized genetic diversity in the U.S. Hereford population by examining the level and rate of inbreeding and effective population size. The impact of breeding structure on inbreeding was evaluated. Pedigree records for 20,624,418 animals were obtained from the American Hereford Association. Inbreeding coefficients for 1900 to 2001 born animals and the mean annual inbreeding coefficients (Fm) were computed from the pedigree. The rate of inbreeding and effective population size were calculated for a subset of the pedigree using all animals born from 1990 to 2001. Inbreeding increased in a linear fashion reaching a maximum Fm of 0.115 in 1966. The rate of inbreeding was not constant over time and five periods were identified in which inbreeding was changing at different linear rates, including a decrease after 1966. Almost 95% of 2001 born individuals were inbred, and the maximum inbreeding coefficient was 0.759. For animals born between 1990 and 2001 inbreeding was less than 0.10 for 56% of the population and ranged from 0.10 to 0.199 for 34% of the population. The mean rate of inbreeding from 1990 to 2001 was estimated as 0.12%, equating to an effective population size of 85 animals. Influential sires and their contribution to the population were identified to help explain changes in the inbreeding trend. A potential explanation for the decrease in inbreeding levels from 1967 to 1986 may be a shift in the popularity of within breed lines leading to a decrease in coancestry among influential sires and selected dams. The fluctuation of inbreeding suggests that changing breeding objectives impacted sire selection, but further study of selection decisions contributing to inbreeding in successive generations is needed. Most of the population is inbred suggesting that inbreeding levels should be factored into future mating programs to minimize the effects of inbreeding depression and the loss of genetic diversity.

Key Words: Hereford Cattle, Inbreeding, Genetic Diversity

891 Evaluation of Angus field records: Using new sets of variances to estimate weaning weight EPDs and the effect on genetic trends.

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The objective of the current study was to evaluate the effect of using new sets of variance components on genetic trends and animal ranking for weaning weight (WWT) records. National Genetic Evaluation Programs for the Angus breed use heritability of 0.20 and 0.14 for weaning direct (WD) and weaning maternal (WM) effects, respectively. Current programs also assume zero covariances between WD and WM effects. In the present study, random samples of WWT records were used to estimate new sets of variance components. For each of the samples, covariances between WD and WM effects were negative and different from zero ($P < .01$). Means of variance estimates from the different samples were then used to calculate expected progeny differences. Weaning weight measures were analyzed together with postweaning gain (PWG) information using multiple trait animal model that included fixed effect of contemporary group (CG), random effects of direct genetic, maternal genetic, permanent environment, and an error term. Model for PWG included fixed effect of CG, random effects of direct genetic and residual. Mean trend for WD and WM effects based on currently used variances were 0.67 and 0.37 kg/yr, respectively. The corresponding values based on the new variance estimates were 0.72 and 0.28 kg/yr, respectively. Overall rank correlation between each of the new and currently published direct and maternal EPDs were 0.99 and 0.94, respectively. However, rank correlations were associated with the accuracy of EPDs. The relatively weaker rank correlations for groups of animals with low accuracy values may suggest that the use of negative covariances between WD and WM effects in cattle evaluation programs may influence the selection of young sires.

Key Words: Beef Cattle, Weaning Weight, Genetic Trend

892 Genetic evaluation of feedlot performance and efficiency in beef cattle marketed at a constant finish endpoint.

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Objectives were to estimate genetic parameters and calculate genetic evaluations in the form of across breed comparisons (ABC, across breed EPD) for post-weaning feedlot performance traits in crossbred beef steers. Feedlot feed intake, feed:gain ratio, and growth data from 941 crossbred steers fed at the University of Guelph's Elora Beef Research Centre from 1996 to 2002 were analyzed. Steers were fed either a high-energy diet from start to finish or a haylage-based diet for the first 112 days and then a high-energy diet to finish. All animals were targeted to a slaughter criterion of 8 mm backfat, as determined by ultrasound measurements taken every 28 days. Seventy sires were represented from 5 different breeds (Angus, Simmental, Charolais, Hereford, Limousin), averaging 13 progeny per sire, ranging from 2 to 38. Three feedlot traits, average daily gain, final live body weight, and days on feed were available on all 941 animals. Two additional traits, daily dry matter feed intake, and feed:gain ratio were available on 452 of the steers. A multiple trait animal model was used to estimate genetic parameters and calculate ABCs for all five traits simultaneously. Model effects included regression on breed proportion, age at feedlot entry as a covariate, fixed effects of contemporary group (herd of origin, year, nutritional treatment), and the random animal effect. Heritability estimates were 0.32, 0.44, 0.15, 0.56, and 0.48 for average daily gain, average daily dry matter feed intake, average feed:gain ratio, final live body weight, and days on feed, respectively. Genetic correlation estimates of days on feed with final live weight and feed:gain ratio were 0.72 and 0.56, respectively. Across breed comparisons were calculated from the individual animal effect and the breed covariate solutions. Results show that selection has potential to improve feedlot efficiency in terms of optimizing performance to reach a desired size at a constant level of fatness. Multiple trait selection for

feedlot traits based on economic considerations of the production system is important to achieving improved feedlot performance to constant finish.

Key Words: Feed Efficiency, Beef Cattle, Heritability

893 Predicting breeding values for feed intake from individual or pen-fed data.

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The objective of this study was to determine the reduction in accuracy of breeding values when pen-fed rather than individual observations on feed intake (FI) were used. The simulated data set consisted of 1,000 animals with true breeding values (BV) and phenotypes for FI (heritability of 0.34) representing 49 sires and 200 maternal grandsires (MGS). Three approaches were compared to predict breeding values for FI (EBV). The first approach was animal model BLUP (IAM) using 1,000 individual FI records. The second approach used 500, 250 or 100 combined FI observations on pens of i=2, 4 or 10 animals ($\mathrm{PAM_i}$). The residual variance was modified to account for the number of animals contributing to each pen FI observation. The third approach ($\mathrm{IPM_i}$) allocated each animal in the pen the average of the pen FI and incorrectly treated that as a unique FI observation in animal BLUP. Correlations were determined between the BV and EBV for each approach, separately for animals with data, sires and MGS. Correlations were 0.633 for animals, 0.767 for sires and 0.266 for MGS using IAM. These correlations are consistent with expectations based on the heritability and amount of information available. Correlations for animals reduced to 0.532 ($\mathrm{PAM_2}$), 0.470 ($\mathrm{PAM_4}$) and 0.371 ($\mathrm{PAM_{10}}$). Corresponding reductions were 0.774, 0.744, 0.619 for sires and 0.225, 0.107, 0.003 for MGS. When penned animals were treated as if they had individual FI the correlations were 0.531 ($\mathrm{IPM_2}$), 0.465 ($\mathrm{IPM_4}$), 0.365 ($\mathrm{IPM_{10}}$) for the animals, 0.776, 0.742, 0.624 for sires, and 0.218, 0.097, 0.002 for MGS. The reduction in accuracy with penning is consistent with the reduction in available data. The correlations were almost identical whether BLUP was correctly accounting for penning ($\mathrm{PAM_i}$) or allocating pen averages to each individual ($\mathrm{IPM_i}$). The apparent accuracy computed from the coefficient matrix was overstated in $\mathrm{IPM_i}$. Pen data can be effectively used in BLUP analyses when individual FI is not available. Correct account of pen information is recommended for reporting accuracy of EBV.

Key Words: BLUP, Accuracy, Animal Model

894 The use of ultrasound to evaluate growth and carcass quality in Nelore cattle.

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This study was carried out to support the development of expected progeny differences (EPD) for carcass traits in Nelore cattle raised under tropical grazing systems. Data from 1,721 bulls and heifers raised in central Brazil (Grupo OMB and Grupo HoRa) were collected at approximately 15, 18, 21 and 24 months of age. The animals were weighed (BW) and scanned for longissimus muscle area (ULMA); backfat thickness between the 12th and 13th ribs (UFAT); and fat thickness over the rump (URFAT), at the P8 site. Mean (and SD) scan data were: Age, 19 (SD = 2.6) months; BW, 321 (SD = 58) kg; ULMA, 47.80 (SD = 8.85) cm^2; UFAT, 1.5 (SD = 0.62) mm; URFAT 2.0 (SD = 0.97) mm. Data were analyzed using a mixed model. Fixed effects were age in months (AGEm), month of scanning (MONTH), contemporary group (including management group; CGxMG). The interaction between AGEm and MONTHSCAN was used to test the slopes for homogeneity, and the individual animal within contemporary and management group was included to account for repeated measures on the same animal. A large portion of observed variance in response variables was accounted for by GCxMG and AGEm ($P < 0.001$). Month of scanning (i.e., season) had no effect on BW or ULMA ($P > 0.05$) when the contemporary and management groups were properly accounted for. UFAT was not significantly influenced by MONTH or by AGEm ($P > 0.05$), nor was there any significant AGEm x MONTH interaction. By contrast, URFAT was significantly affected by AGEm ($P < 0.01$), indicating that it is a more sensitive fat deposit. The repeatabilities of measurements were very low for UFAT (0.035) but high for URFAT (0.62) and moderate for ULMA (0.44). Nelore cattle raised on tropical pastures exhibit growth patterns and carcass compositions that are very different from those observed in *Bos taurus* cattle raised on high-concentrate diets, but once the contemporary group and management were accounted for, seasonality had no effect on carcass traits and body weight.

Key Words: Beef Cattle, Carcass, Ultrasound

Breeding and Genetics: Swine

895 Validation of QTL's in a swine population selected for ovulation rate.

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Variations in allele frequency of a four-breed, white composite population of swine selected for ovulation rate (OR) were evaluated. Animals were selected for 11 generations for increased OR and compared to unselected controls (CO). The selection line had an increase of 3.0 corpora lutea and an increase of 0.3 pigs in total litter size as compared to controls. DNA was collected from 146 CO and 156 OR gilts and boars at generations 10 and 11. A QTL analysis for OR identified loci on chromosomes 3, 8, and 10 in a Meishan-White composite population. Three microsatellite markers were selected for chromosomes 3 (17-42 cM) and 10 (85-96 cM) and six for chromosome 8 (1-13 cM) for utilization with selected and control lines. Allele frequencies of markers contained within QTL peaks were analyzed by logistic regression to ascertain any difference in allele frequency due to selection. All markers on chromosome 3 had significant ($P<0.01$) changes between lines in allele frequency. Odds ratio of the most significant marker ($P<0.0001$), SW2429 contained 7 distinct alleles, the 125 base allele was 530.2 times more likely to be present in homozygous OR animals than CO. Chromosome 8 had 3 of 6 markers with significant ($P<0.02$) changes in allele frequency. The marker SW2651, which contained 3 alleles, was most significant ($P<0.0001$) with an odds ratio of 2.6 for the 100 base allele in homozygous OR animals. Significant ($P<0.01$) changes in allele frequency were found on chromosome 10 with all markers. An odds ratio of 7.3 was calculated for the 107 base allele in homozygous OR animals for the most significant ($P<0.0001$) marker SWR1829 which had 8 alleles. Selection for OR has changed the allele frequency of markers from the three QTL regions studied. The QTL discovered in a Meishan cross population are likely segregating in occidental germplasm. The selection line will be useful to identify causative genes and genetic markers for use in the industry.

Key Words: Swine, Ovulation Rate, Allele Frequency

896 Identification of quantitative trait loci affecting reproduction and early growth in pigs.

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Quantitative trait loci (QTL) in a 3-generation population of a cross of low-indexing pigs of a randomly selected control line with high-indexing pigs of a line selected 10 generations for increased index of ovulation rate and embryonic survival were investigated. Birth weight (BWT, n = 428), weaning weight (WWT, n = 405), age at puberty (AP, n = 295), ovulation rate (OR, n = 423), number of fully formed pigs (FF, n = 370), number of pigs born alive (NBA, n = 370), number of mummified pigs (MUM, n = 370), and number of stillborn pigs (NSB, n = 370) were collected in F_2 females. Grandparent, F_1, and F_2 animals were genotyped for 151 microsatellite markers. Previous analyses with single Mendelian QTL models identified 16 putative QTL ($P < 0.10$). Data were reanalyzed with composite interval mapping (CIM) including models incorporating genomic imprinting. More QTL for reproductive traits than in the earlier scan (31 vs 16, $P < 0.10$) and two QTL for birth weight were identified. Mendelian QTL affected **FF** (C11, 52 cM, $P < 0.05$), **NBA** (C11, 71 cM, $P < 0.05$), **NSB** (C13, 100 cM, $P < 0.05$; C5, 131 cM, $P < 0.10$; C12, 37 cM, $P < 0.10$), **NN** (C11, 47 cM, $P < 0.05$; C8, 20 cM, $P < 0.05$; C7, 62 cM, $P < 0.05$), **AP** (C8, 172 cM, $P < 0.05$; C7, 1 cM, $P < 0.05$; C7, 58 cM, $P < 0.10$; C18, 40 cM,