192 Genetic covariance functions for body weight, condition score, and dry matter intake in Holstein heifers measured at different lactation stages.

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Genetic parameters for body weight (BW), body condition score (BCS) and dry matter intake (DMI) of dairy heifers were estimated using covariance function (CF) methodology. Data were from 469 Holstein heifers of the Langhill Dairy Cattle Research Centre and included observations at calving and at 3, 5, 10, 20, and 25 weeks of lactation. The experiment comprised a selection line and a control line. Heifers were allocated to a high or to a low concentrate diet, which was offered as a complete mixed ration *ad libitum.* Compared to multivariate REML analyses the number of parameters to estimate variance components could be reduced when covariance functions (CFs) were used. Genetic variances for the traits clearly depended on the lactation stage. For all traits the genetic variance at all stages during lactation could adequately be described by a second order polynomial CF. Heritability estimates for observations measured at different stages of lactation ranged from 0.43 to 0.5 6 for BW and from 0.21 to 0.45 for BCS. For DMI heritabilities ranged from 0.17 to 0.32. The genetic correlation between repeated observations generally decreased with increasing time period between observations. The genetic correlation between repeated observations on BW and BCS ranged from 0.84 to 1.00. However, for repeated observations on DMI genetic correlations were lower. The genetic correlation between DMI in week 3 and week 25 was only 0.23. The eigenfunctions and their associated eigenvalues that were derived from the estimated CFs showed that repeated observations can be assumed to be observations on the same trait for BW and CS but not for DMI. The results imply that observations for DMI at multiple lactation stages are needed when the aim is to improve DMI during whole lactation.

Key Words: Body Weight, Body Condition Score, Dry Matter Intake

193 Effect of missing daily feed intake data on the estimate of average daily feed intake of growing pigs during the test period.

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Breeding organizations are using computerized feeding stations for recording *ad libitum* feed intake data of group-housed growing pigs. Average daily feed intake (DFI) during the test period is calculated per pig averaging all its records on feed intake per test day (day totals). DFI is usually calculated after correcting errors, which is time consuming and subjective. Instead of correcting, day totals with one or more incorrect visits could be treated as missing values. Objective of this study was to examine the effect of such missing values on the estimate of DFI by using polynomial functions. Data came from 192 pigs that were tested for on average 93 days. All animals had for each test day a record for day total. A first (1) and third (3) degree polynomial function was fitted per pig to the data on day totals. Both functions were used to estimate DFI (EDFI) per pig. Using all day totals, the Pearson correlation between DFI and EDFI equaled one for both functions. To examine the effect of missing values, records on day totals were set to missing before fitting both functions to the data. Setting randomly 70% of day totals per animal to missing reduced the Pearson correlation between DFI and EDFI to 0.96 for both (1) and (3). Setting randomly 90% of day totals to missing reduced the correlation to 0.84 for (1) and to 0.60 for (3). Setting 25 successive day totals to missing maximally reduced the correlation when it concerned the day totals of the first 25 test days for (1) and (3) or the last 25 test days for (3). Setting the first 25 day totals to missing reduced the correlation to 0.92 for (1) and to 0.59 for (3). The results imply that treating day totals containing incorrect visits as missing values is a good alternative for correcting data if polynomial functions are used for estimating DFI. Especially for (3), restrictions need to be set for allowed amount and position of missing day totals.

Key Words: Daily Feed Intake, Missing Values, Polynomial Functions

194 Genetic correlations among carcass traits adjusted for age, weight or fatness.

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Carcass traits of beef cattle can be expressed on age, weight, or fatness constant basis. These definitions imply that a measured trait could be considered as three traits with different heritabilities and with genetic correlations among the traits. Carcass measurements of 1,292 steers sired by 409 Shorthorn sires were analyzed with REML. The models and measurements for the three subtraits were the same (herd, year, kill group) except for the linear covariates of slaughter age (336 to 865 d), hot carcass weight (220 to 477 kg), and fat depth at 12th rib (0 to 28 mm) with the subtraits denoted in that order. The estimates of genetic correlations between subtraits 1 and 2, 1 and 3, and 2 and 3 were: dressing percent, .99, .63, .64; kidney-pelvic-heart fat percent, .81, .64, .97; marbling score, .80, .66, .98; and ribeye area (cm^2), 1.00, .97, .97. Heritability estimates were also different for the subtraits even though the measured records were the same: dressing percent, .60, .56, .70; KPH, .53, .39, .33; marbling, .53, .37, .32; and ribeye area, .55, .56, .33. Environmental correlations ranged from .49 to 1.00 depending on trait and subtraits. Phenotypic variances were the largest based on fat depth except for dressing percent. These results based on a relatively small sample suggest that some carcass traits when adjusted for age, weight, or fat thickness should be considered different traits. Conversion of estimated progeny differences from one basis to another can be done with estimates of genetic correlations and heritabilities for the subtraits.

Key Words: Beef Cattle, Dressing Percent, Marbling

195 Genetic variation in feed efficiency of beef cattle.

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Providing feed to cattle is a major cost in beef production, and therefore feed efficiency of beef production is economically important. In beef cattle breeding, much attention has been given to improving outputs, but there has been less consideration of inputs required for production. The objective of this study was to examine genetic variation in feed intake and efficiency of cattle post-weaning, and determine the potential of using postweaning feed efficiency as a selection criteria to improve profitability and efficiency of beef production. Feed intake and growth performance of 1345 Angus, Hereford, Poll Hereford and Shorthorn bulls and heifers were measured during 7 tests of 119 days duration, shortly after weaning at 7 to 9 months of age. A pre-test adjustment period of at least 21 days was allowed. A pelleted diet consisting of 70% lucerne hay and 30% wheat was fed (approximately 10 MJ ME/kg dry matter, and 16–18% crude protein), with feed intake being recorded using an automated electronic feeding system. Animals on test were weighed once per week, and a linear regression of weight against time was used to describe growth. Residual feed intake was used as the measure of feed efficiency, and calculated as the residual from the regression of feed intake against mid-weight$^{0.73}$ and growth rate. An animal model was used to estimate variance components using REML. Heritability of residual feed intake was 0.42 ± 0.07, and genetic correlations between residual feed intake and growth traits were very low, indicating that genetic variation in postweaning efficiency exists in Australian cattle. Following one generation of divergent selection for residual feed intake, the progeny of high efficiency parents consumed less feed for no reduction in growth performance during postweaning tests or when fed in a feedlot to 400 kg slaughter weights. Further work is in progress to examine genetic relationships of post-weaning feed intake and efficiency with reproductive performance and feed intake of cows, and with efficiency and carcass characteristics of steers in feedlots.

Key Words: Feed Intake, Efficiency, Beef Cattle

196 Genetic parameters for performance traits of boars in a population of Large White swine with primary selection emphasis on maternal traits.

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The purpose of this study was to estimate genetic parameters for gain and feed intake data for a population of purebred Large White swine from 1990 to 1997. Boars from half the litters were culled at weaning based on a maternal breeding value (index) of the dam and remaining boars grown to 100 d of age (n = 26,151). Selection of boars for individual pen testing was based on a combination of growth and maternal indices. Boars were fed a corn-soybean meal ration that was 1.14% lysine, 19% protein, and 3344 ME/kg for approximately 77 d. Boars were weighed at the beginning and end of the test and feed intake recorded. Feed and gain records were available for 7,722 boars. Feed to gain ratio (FG) was calculated, and residual feed (RF) was estimated as the difference between actual feed intake and that predicted from a model that included initial test age and weight and test ADG. Genetic parameters were estimated using an animal model and single or multiple-trait DFREML procedures (MTDFREML). All analyses included pedigrees back to 1990 (92,145 animals in the relationship matrix). Fixed effects were contemporary groups (defined by month test started and barn of origin) and initial test age as a covariate. Heritability estimates for weight at 100 d, test ADG, daily feed intake (DF), FG, and RF were .48, .36, .38, .29, and .30, respectively. Genetic correlations between ADG and DF, ADG and FG, ADG and RF, and DF and RF were .78, −.30, .10, and .67, respectively. Results of this study indicate that RF is moderately heritable and should respond to selection. Genetic correlations indicate that one would expect a correlated response in the other trait when selecting for either ADG or DF, but selection for reduced RF could be made without adversely affecting ADG.

Key Words: Genetic Parameters, Swine, Residual Feed

197 Evaluation of growth and carcass traits as related to breed composition.

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Pre and post weaning performance was evaluated on 292 Simmental, Angus and reciprocal crosses. Calves were fed to an average age of 17 months and slaughtered. Straightbred Simmentals revealed the heaviest liveweights (601kg) and straightbred Angus were the lowest at 524kg ($P<.05$). Significant differences were noted for carcass weight and ribeye area within each genotype ($P<.05$). Straightbred Simmental calves revealed hot carcass weights of 358kg with straightbred Angus and 75% Angus yielding the lowest hot carcass weights of 318kg, respectively. Straight bred Simmental calves averaged 34.5 square centimeters for ribeye area with Angus measuring 31.1 square centimeters ($P<.05$). Significant differences were noted for 12th rib fat thickness, KPH and yield grade for each calf genotype. Additional study of the data revealed Angus and high percentage Angus calves posting the greatest marbling scores when compared to Simmental-sired calves. Straightbred Angus calves revealed scores for marbling of 593.7 while 75% Simmental calves scored 488.4 ($P<.05$). Quality grades for calves proved to be similar to marbling scores. Straightbred Angus calves produced quality grade scores averaging 729.0 while 7/8 Simmentals were found to have the lowest quality grades averaging 669.1 ($P<.05$).Simmental were found to wean the heaviest calves at 205 days of age at 264.8kg while Angus calves were lightest at 215.9kg ($P<.05$). Calving ease was found to be not significant between reciprocal crosses ($P>.05$). Average daily gain was calculated for the period from weaning to slaughter. There were no significant differences noted for reciprocal genotype ($P>.05$). Sex of calf was found to be significant ($P<.05$) for liveweight; ribeye; KPH; yield grade; adjusted birth weight; and average daily gain. All calculations were performed with the General Linear Models procedures of SAS.

198 Genetic evaluation of mature weight, hip height and body condition score in an Angus herd.

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Records on mature weight (MW), hip height (HH) and body condition score (CS) collected at the CSU Beef Improvement Center, Saratoga, WY from 1986 to 1994 were analyzed to estimate genetic parameters. Measures were taken at weaning around October 1 on 850 Angus cows with 2,622 observations for each trait. Two multivariate least-squares, paternal half-sib models on repeated records were used to estimate heritabilities and repeatabilities, Model I without CS as a covariate and Model II with CS. Both models contained age of cow at measure (AAM, 2,3, —, 10+ years) and year of measure (YOM) as fixed effects. In both models, sire and cows within sire were included as random variables. Heritability and repeatability estimates from Model I were .51 and .87, .62 and .79, .45 and .39, respectively for MW, HH and CS. Estimated phenotypic correlations were .60, .71 and .23 between MW and HH, MW and CS, and HH and CS, respectively from Model I. Corresponding estimates of genetic and environmental correlations were .68 and .17, .76 and .59, .30 and .10. From Model II, heritability and repeatability estimates for MW were .46 and .76, and for HH were .63 and .78. Estimates of phenotypic, genetic and environmental correlations between MW and HH from Model II were .60, .73 and .14, respectively. HH remained constant over YOM while MW and CS tended to decrease. All three traits increased with AAM but at different maturing ages.

Key Words: Mature Weight, Hip Height, Body Condition Score

199 Effects of sire line on pig growth and carcass composition.

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A study of pig growth and carcass composition of three genotypes that have different rates of fat and lean growth was conducted. 120 barrows and gilts were randomly assigned (4 pigs/pen basis) to a 3 × 2 factorial arrangement with sire line and sex as main effects. The three genotypes consisted of different purebred sire lines, Duroc (**D**), Pietrain (**P**) and Large White (**LW**), each crossed with the same dam line (Large White × Large White - Landrace). Pigs were reared using segregated early weaning procedures and fed conventional corn-soybean meal diets on an *ad libitum* basis. Eight pigs from each sire line × sex combination were slaughtered at 120 kg live weight. From 75 to 120 kg live weight, D-sired pigs demonstrated greater average daily gain (.88 vs. .76 vs. .77 ± .02 kg/day, $P < .01$) and greater feed intake (2.87 vs. 2.54 vs. 2.53 ± .05 kg/day, $P < .01$) than did P and LW-sired pigs, respectively. D-sired pigs received higher marbling scores (1 = devoid to practically devoid, 5 = moderately abundant or greater) of the loin muscle at the 10^{th} rib (2.41 vs. 1.25 vs. 1.41 ± .14, $P < .01$), and had more middle layer (1.24 vs. .79 vs. 1.04 ± .08 cm, $P < .01$), inner layer (.69 vs. .41 vs. .43 ± .05 cm, $P < .01$) and total fat depth (2.84 vs. 1.98 vs. 2.44 ± .13 cm, $P < .01$) at the 10^{th} rib than did P and LW-sired pigs, respectively. P-sired pigs had larger loin-eye areas (48.97 vs. 44.13 vs. 43.74 ± 1.35 cm^2, $P < .05$) and less outer layer backfat (.79 vs. .94 vs. .91 ± .03 cm, $P < .01$) than did D or LW-sired pigs, respectively. Sire line did not affect feed efficiency, 24-h postmortem pH (*longissimus dorsi*), drip loss, loin color or loin firmness evaluations. In conclusion, the majority of variation in 10^{th} rib fat depth can be accounted for by variation in the amount of middle and inner backfat layers.

Key Words: Pigs, Sire Effects, Carcass Composition

200 Carcass characteristics of Landrace pigs from a line selected for loin eye area using real-time ultrasound technology.

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Real-time ultrasound technology has become available to the livestock industry to directly evaluate loin eye area and fat thickness on live animals. A line of Landrace pigs was selected (S) solely for increased real-time ultrasound loin eye area for four generations using an Aloka 500V ultrasound machine. A contemporary unselected control (C) line also was maintained. A total of 1142 pigs, sired by 78 sires and out of 187 dams, were scanned for loin eye area at the 10th rib. Difference between the lines (S − C) for ultrasound loin eye area in the 4th generation was 9.8 cm^2. Each generation one barrow per litter was evaluated for carcass length (LEN), 10th rib backfat thickness (BF10), loin eye area (LEA), percentage trimmed lean cuts (LEAN), and subjective color (COLOR; 1 = pale, 5 = dark) and marbling (MARB; 1 = practically devoid, 5 = moderately abundant) scores. Firmness (FIRM; 1 = very soft, 5 = very firm) scores were obtained in generations 3 and 4. A total of 155 carcasses were evaluated. Data were analyzed using the Mixed procedure of SAS with a model that included the fixed effects of line-generation (LG) and a regression on hot carcass weight, and the random effect of sires within LG. Differences in LEA between the lines (S − C) were 2.7, 5.2, 8.1, and 8.2 cm^2 in generations 1, 2, 3, and 4, respectively. For LEN, the (S − C) line differences were −1.2, −.6, −3.0, and −3.5 cm, for BF10, (S − C) line differences were −.17, −.53, −.37, and −.39 cm, and for LEAN, (S − C) line differences were .9, 2.2, 2.6, and 2.0% in generations 1, 2, 3, and 4, respectively. The (S − C) line differences for the subjective meat quality traits of COLOR were −.27, −.11, −.59, and −.54, and for MARB, (S − C) line differences were .27, .34, −.48, and −.55, in generations 1, 2, 3, and 4, respectively. FIRM (S-C) line differences were −.91, and −.95 in generations 3 and 4, respectively. These results suggest that selection for loin eye area using real-time ultrasound will result in desirable changes in carcass LEA, LEAN, and BF10. However, undesirable changes in LEN, COLOR, MARB, and FIRM may also occur.

Key Words: Pigs, Selection, Carcass Composition

201 Genetic correlations between genotypes for carcass traits and direct and maternal genotypes for weaning weight in beef cattle.

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Estimates of (co)variance components and genetic parameters were obtained for weaning weight and several carcass traits using a derivative-free REML algorithm with animal models. Hot carcass weight, retail product percentage, bone percentage, fat percentage, rib eye area, actual fat thickness and Warner-Bratzler shear force data were collected on 4071 two-breed cross steers. Weaning weight was recorded on these steers as well as on their paternal half-sib sisters and on the three-breed cross calves of those females (n=11,193 total records). Direct and maternal heritabilities for weaning weight were .25 ± .03 and .16 ± .03, respectively. The proportion of phenotypic variance of weaning weight due to maternal permanent environmental effects was .17 ± .03. Direct heritabilities for carcass traits were moderate to large in magnitude (.25 to .65). Correlation between direct and maternal additive genetic effects for weaning weight was negative (−.21 ± .14). Direct genetic correlations for weaning weight with carcass traits were of small magnitude (−.10 to .08) except with hot carcass weight (.69) and with rib eye area (.25). Correlations between maternal genetic effects for weaning weight and direct genetic effects for carcass traits were of small magnitude (−.05 to .12) except for bone percentage (.58), although estimates may be associated with large sampling variance. In general, maternal ability for weaning weight does not seem to be highly correlated with carcass traits in steers.

Key Words: Genetic Parameters, Heritability, Growth

202 Comparison of models to estimate maternal genetic effects for weaning weight.

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Weaning weights from nine sets of Angus field data with 8128 to 11675 observations were analyzed. Six animal models were compared. Model 1 included random direct, maternal genetic, permanent maternal environmental, and residual effects. Age at weaning was a covariate, and fixed effects fitted were age of dam and a combination of herd, year, management, and sex. Additional effects in other models were regression on maternal phenotype (β) in Model 2, sire by herd-year (SH) interaction (Model 3), β and SH interaction (Model 4), grandmaternal genetic and permanent grandmaternal environmental effects (Model 5), and the interaction and grandmaternal genetic and permanent grandmaternal environmental effects (Model 6). Estimates of β and of the (co)variances were obtained by REML using either a derivative-free or an average information method. Estimates from Model 1 ranged from .25 to .50 for direct heritability (h^2), from .11 to .17 for maternal heritability (m^2), and from −.07 to −.57 for the correlation between direct and maternal genetic effects (r_{am}). Small estimates of β from models 2 and 4 were obtained (−.003 to .014) and (co)variance estimates were similar to models 1 and 3. Estimates of the relative variance due to SH interaction were .02 to .10, and estimates of h^2 and m^2 were smaller and estimates of r_{am} were higher than in models without this interaction. Grandmaternal heritability estimates ranged from .02 to .07, and estimates of m^2 and r_{am} increased compared to Model 1. Based on likelihood values, SH interaction effects were more important than β and grandmaternal effects. Likelihood values were highest from Model 6 where estimates of h^2, m^2, and r_{am} ranged from .17 to .32, .11 to .24, and −.35 to .06, respectively. Results suggest that the often suspected downward bias in r_{am} may not be caused by assuming the dam-offspring correlation to be zero but by not including SH interaction effects and grandmaternal effects in the model.

Key Words: Beef Cattle, Growth, Genetic Correlations

203 Phenotypic associations among serial ultrasound and carcass measures of composite beef steers.

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Ultrasound and carcass records from steers (n-120) were used to estimate phenotypic correlations and usefulness of serial ultrasound to predict carcass merit. Composite steers in each of two years were fed following weaning in late October until slaughter (458 d of age) when live weight and backfat reached a minimum of 500 kg and 7 mm, respectively. Ultrasound measures recorded at a mean age of 371 d (YR) and prior to slaughter (SL) were used. Carcass traits included hot carcass weight (CW), backfat thickness (BF), rib eye area (REA), Warner-Bratzler shear (WBS) force, percent intramuscular fat (IMF) and marbling score (MAR). Also, percent lean yield (PLY) was estimated. Ultrasound measures included backfat thickness (YRF and SLF) and rib eye area (YRR and SLR). Percent lean yield at YR (YRY) and SL (SLY) was computed using live weight and ultrasound measures of BF and REA. Residual correlations were estimated from a linear model including the effects of year, nutritional treatment and their interaction. Correlations ($P < .03$) between YRF and SF with BF were .75 and .68, with IMF were .33 and .31, with MAR were 0 and .20 and with WBS were 0 and 0, respectively. Correlations between YRR and SLR and REA were .50 and .78, respectively. Correlations between YRR and SLR with MAR, IMF and WBS were not different from zero. Correlations between YRY and SLY and PLY were .59 and .76, with IMF were −.19 and −.20, respectively, but were near zero with MAR and WBS. Correlations between YRF and SLF, YRR and SLR and YRY with SLY were .66, .50 and .65, respectively. Ultrasound measures of BF had similar associations with BF at YR and SL. Correlations between ultrasound measures at YR and SL were moderate. All correlations between ultrasound and carcass quality traits were low to non-existent. Ultrasound measures taken near yearling ages must be interpreted with care when inferences about carcass traits are desired.

Key Words: Ultrasound, Carcass Traits, Beef Cattle

204 Genetic relationships between Insulin-like Growth Factor-1 and pig performance.

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Insulin-like Growth Factor - 1 (IGF-1) fulfils a number of criteria for potential inclusion as an indirect selection measure. It can be accurately and relatively inexpensively measured in the blood of young animals and has been shown to be significantly related to growth rate. However, there is little information on its heritability or genetic correlations with economically important traits in pigs. The aim of this study was to provide this information. The following traits were measured; plasma concentration of IGF-1 at 5 weeks of age, average daily gain from birth to 24 weeks of age (ADG) ultrasonic fat depth at the last rib (P2), feed intake and feed conversion efficiency from 19 to 24 weeks of age (FI and FCE) and drip loss of the LD muscle (DLP). Two breeds, Large White and Landrace were used. The heritability and correlations were obtained using DFREML with an average information (AI) algorithm. The heritability of IGF-1 was 0.22 ± 0.09. The number of observations, genetic (r_g) and phenotypic (r_p) correlations for IGF-1 and the performance traits are presented below. Contrary to our expectations, IGF-1 was negatively correlated with growth rate and positively correlated with P2 and feed conversion efficiency.

Trait	ADG	P2	FI	FCE	DLP
Number	3522	3575	3531	3500	2318
r_g	-0.47	0.29	0.37	0.84	-0.26
r_p	0.24	0.18	0.01	-0.08	-0.17

205 Selective DNA Pooling for QTL mapping and MAS in dairy cattle.

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A complete genome scan for QTL affecting milk protein percent was implemented in Israel Holstein cattle by Selective DNA Pooling, using milk samples. A total of 17,000 daughters, progeny of 7 A.I. sires, were examined with respect to 117 microsatellite markers (75 markers per sire), distributed among all autosomes. Twenty QTL were identified on 15 chromosomes, at a significance level of $P<.001$. In effect, 3250 pool genotypings provided the statistical power of 500,000 individual genotypings. Extended to six traits, this implies total mapping of dairy cattle ETL with a total of 20,000 genotypings. Because confidence interval (CI) of QTL map location stands in inverse linear proportion to $3000/N\alpha^2$ (N= number of daughters; α = allele substitution effect), fine mapping of dairy cattle QTL to 95% CI of 1 cM would require about 70000 daughters of one or more sires heterozygous for the QTL. These numbers are achievable for large national herds, or by international networking. Examination of the within-chromosome within-sire distribution of significant linkage effects obtained through selective DNA pooling, demonstrated the presence of two separate QTL affecting milk protein percent on Chromosome 6; the same methodology can be used as a general procedure for examining the number of QTL affecting a given trait on a given chromosome. Selective DNA pooling can also provide marker-QTL phase within individual A.I. sires. Accumulated over a small number of generations this will enable MAS of sire mothers and candidate bulls to make a major contribution to dairy cattle genetic improvement.

Key Words: QTL Mapping, Marker Assisted Selection, Milk Protein Percent

206 Effect of a mutation at the myostatin gene on early life weights and calving ease in a population of Piedmontese inheritance.

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Double-muscled Piedmontese animals have a guanine to adenine transition mutation in exon 3 of the myostatin gene (MSTN), that appears to be responsible for muscle hypertrophy. The objective of this study was to establish the effect of the mutation in the myostatin gene on early life weights and calving ease in a population segregating the Piedmontese allele. Calves of Piedmontese inheritance, born in 1995 (n=66 surviving to weaning; no DNA was obtained on calves that died before weaning) and 1996 (n=72; 13 not surviving to weaning), were evaluated for birth weight (BWT; kg), adjusted weaning (W200; kg), and yearling (W365; kg) weight, calving ease (CE), and survival (SUR). The number of copies of the Piedmontese allele was assessed by sequencing the MSTN exon 3 from each calf. Data were analyzed with a model that included the effects of year, sex, interaction between line of dam and sire, number of Piedmontese allele copies at MSTN nested within the interaction, and age of dam as covariate. Sex was a significant source of variation ($P<.01$) in all weights. Year was only significant ($P<.01$) for W365. The number of copies of the Piedmontese allele was a significant source of variation for BWT ($P<.05$). The means for individuals with zero, one, and two copies of the Piedmontese allele were 37.5 ± .7 kg, 41.1 ± .6 kg, and 42.8 ± 1.3 kg, respectively. A significant difference ($P=.005$) was observed between individuals inheriting zero and one copies of the Piedmontese allele (3.13 ± 1.1 kg), while the difference between one and two copies approached significance ($P=.1$). From 1996 calves not surviving to weaning, nine were homozygous for double muscling, three were heterozygous, and one had zero Piedmontese allele copies. There was no evidence of an effect of MSTN on CE with dams with two or more parities. Mating schemes that maximize production of animals with one copy of the Piedmontese MSTN allele would be expected to increase BWT without effecting CE.

Key Words: Myostatin, Double Muscling, Birth Weight

207 Mapping of conserved segments of synteny between human chromosomes 7 and 16 and bovine chromosome 25; toward a gene map of bovine chromosome 25.

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The comparative positional candidate approach for identifying genes of interest in cattle requires a reliable comparative gene map. Our objectives are to construct a map of bovine chromosome 25 (BTA 25) and to accurately define the boundaries of HSA 7 and 16 segments homologous to BTA 25. Bovine chromosome 25 is homologous to human chromosome 7 (HSA 7) and 16 (HSA16), as defined by zoo-fish experiments. Only three genes have been mapped by linkage analysis and therefore the comparative map of BTA 25 is very sparse. Seventeen genes already mapped on human chromosomes 7 (11 genes) and 16 (6 genes) were selected. PCR primers were designed, PCR reactions were optimized and all fragments were cloned and sequenced to confirm the specificity of targeting. Two somatic cell hybrid panels were used to assign six genes to BTA 25 (2) and BTA 5 (4). The new chromosomal assignments, together with 6 other previously known, show that human chromosome 16 p arm is homologous to BTA 25, from hPRM1 (19–21 cM) to hMTTUF1 (50–56 cM). HSA 7 conserved segments can be defined as follow: a segment homologous to BTA 4 between GIAR (94–98 cM) and PPT2 (109–111 cM), a 1 to 3 cM gap, a segment homologous to BTA 25 containing EPO (111–112 cM) followed by a segment homologous to BTA 4 between RL (114–119 cM) and CFTR (125–126 cM). A BAC library is being screened with primer pairs representing all genes in this study. To date, all pairs tested (14) have yielded positive superpools. In conclusion, the segment of HSA 7 conserved in BTA 25 is shorter than expected from the zoo-fish experiments, indicating that there might be more than one segment of HSA 7 homologous to BTA 25. Our data also confirm and extend the previously known segment of homology of HSA16 conserved in BTA 25.

Key Words: Comparative Mapping, Gene Mapping

208 Identification of the causative mutation in ovine hereditary chondrodysplasia.

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Ovine hereditary chondrodysplasia, commonly called Spider Lamb Syndrome (SLS), is a recessive genetic disorder causing skeletal deformities in young lambs. Common features include abnormally long, bent limbs and curvature of the spine. Since the late 1960's the disorder has spread to several black-faced sheep breeds within the U.S. as well as Suffolks in Canada, Australia and New Zealand. Genetic mapping of the SLS locus was performed by linkage analysis between microsatellite loci in two large pedigrees (n = 303 lambs) produced from matings between carrier individuals. Genetic linkage was detected between four microsatellite markers and SLS, mapping the locus to the distal end of ovine chromosome 6. Comparative analysis of Type I marker maps between sheep, cattle and humans combined with the results of knockout studies in mice identified fibroblast growth factor receptor 3 (FGFR3) as a positional candidate for the disorder. Single-strand conformational polymorphism analysis of ovine FGFR3 identified a polymorphism that co-segregated with the disease in both pedigrees. Genomic and cDNA sequencing of ovine FGFR3 has revealed a single-base mutation causing a non-conservative amino acid substitution in the tyrosine kinase domain of the receptor. Population studies including more than 1000 sheep of differing SLS genotypes demonstrates that this is the causative mutation in SLS. It is most likely that the mutation leads to loss of receptor function in homozygotes that results in poorly controlled chondrocyte differentiation.

Key Words: Ovine, Spider Lamb Syndrome

209 Characterization of the prion protein (PrP) gene in ten breeds of sheep.

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Transmissible spongiform encephalopathies (TSE) are neurodegenerative disorders characterized by a long generation time, spongy degeneration in the cerebral gray matter, neuronal loss and proliferation and hypertrophy of glial cells. An abnormal form of the prion protein (PrP) plays a major part in TSE pathogenesis and has been hypothesized to be the only component of the infectious agent. Some animals exposed to scrapie, the TSE affecting sheep and goats, seem to be resistant to development of the disease. Alleles encoding amino acid substitutions at codons 136 (A/V) and 171 (Q/R/H) have been associated with scrapie resistance. It may be possible to reduce the incidence of ovine scrapie by increasing the frequency of the resistant genotypes (AA-136, RR-171 or AA-136, QR-171). Thus, an important consideration is the frequency of these genotypes in different breeds of sheep. In this study, the genetic sequence for codons 104-175 was determined for at least ten animals of ten sheep breeds (n=207). Genotypes at codons 136, and 171 were determined. For codon 136, the frequency of the susceptible allele (V) was less than 0.20 in all breeds. In contrast, the frequency of the susceptible allele (Q) at codon 171 ranged from 0.27 (St. Croix) to 0.96 (Hampshire). In addition, a previously unreported substitution was found at codon 143 (H/R), with frequencies as high as 0.40.

Key Words: Ovine, Scrapie

210 Optimal breeding values for quantitative loci with dominance.

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Use of identified quantitative trait loci (QTL) in selection requires integration of breeding values (BV) for the known QTL with estimates of polygenic BV. Selection then is on the sum of the BV for the QTL plus the polygenic EBV. For a QTL with two alleles, BV for the QTL are traditionally based on the allele substitution effect, $\alpha = \mathrm{a} + \mathrm{d}(1 - 2\mathrm{p})$, where a and d refer to additive and dominance effects, and p is the QTL gene frequency in the current generation. It is shown here that selection on BV for the QTL, thus defined, does not maximize response from the current to the next generation if the QTL exhibits dominance. BV for the QTL that maximize response from the current to the next generation with dominance are shown to be equal to $\alpha^* = \mathrm{a} + \mathrm{d}(1 - 2\mathrm{p}^*)$, where p^* is the frequency of the QTL among (selected) mates. Because the optimal BV for the QTL of, e.g. males, depends on selection among females, which in turn depends on selection among males, BV for the QTL must be derived numerically. Extra single generation response from selection on optimized BV for the QTL (α^*) versus selection on traditional BV (α) was evaluated for a range of additive and dominance effects at the QTL, gene frequencies, and selected fractions. Benefits of optimal selection were greatest for intermediate gene frequency and increased with the magnitude of additive and dominance effects at the QTL. Extra response was negligible for gene frequencies less than 0.05 or greater than 0.85. Extra response from optimal selection was greater than 8% for QTL with large effects and complete dominance and with the favourable allele at intermediate frequency. In conclusion, strategies for marker-assisted selection that aim to maximize short-term response must account for the effects of dominance and changes in gene frequency at the QTL on performance of future progeny.

Key Words: Marker-Assisted Selection, Dominance, Breeding Values

211 Quantitative trait loci mapping for disease traits in multi-family half-sib designs.

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This study considers mapping of Quantitative Trait Loci (QTL) affecting binary polygenic disease traits in a multi-family half-sib design. A Generalized Linear Model Interval Mapping (GLMIM) approach is developed based on threshold theory. Statistical power and bias of QTL mapping by GLMIM is compared with Regression Interval Mapping (RIM)using simulation. Data on 20 half-sib sire families with 100 or 500 progeny were simulated for a binary polygenic disease trait with 2 bi-allelic DNA markers (20 cM apart) that bracketed a bi-allelic QTL that was 5 and 15 cM from the marker loci. Additive QTL effects of 0.3 and 0.6 phenotypic SD were simulated. Heritability was 0.25 on the liability scale. Phenotypic values of progeny were first simulated on the Normally Distributed Liability (NDL) scale, based on the sire′s polygenic effect, the sire′s QTL allele substitution effect and a random residual. Phenotypic data were then transformed to binary data based on 3 thresholds, which corresponded to disease incidences of 15, 25, and 50%. RIM was also applied to phenotypic data on the NDL scale to evaluate the impact of the binary nature of data on power and bias. Simulations were replicated 1000 times. For binary data, GLMIM and RIM gave similar power and estimates of QTL location and effect. Estimates of location were biased toward the center of the marker bracket for both GLMIM and RIM by 1 to 1.5cM. QTL effects were overestimated by 3 to 15%. RIM for NDL data resulted in unbiased estimates of QTL effects and tended to give unbiased estimate of QTL location with larger family size. Analysis of binary instead of NDL data resulted in reduced accuracy of estimates of QTL location; power was reduced by 2 to 30% in many situations. Interval mapping for binary data had maximum power for intermediate incidence (50%). Larger family size and a larger effect of the QTL improved the power.

212 Implementation of an algorithm to estimate genotypic probabilities of protoporphyria in Limousin cattle.

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Protoporphyria is a simply inherited genetic disorder causing lesions on skin directly exposed to sunlight. A marker has been developed which is closely linked to the alleles involved. Our objective was to implement an algorithm for estimating genotypic probabilities of protoporphyria in Limousin cattle, given a large pedigree structure and known genotypes on a small percentage of the animals in the pedigree. The North American Limousin Foundation (NALF) supplied pedigree data for 1,259,770 animals born through 1995. Marker genotypes were available for 3,158 protoporphyria-free, 576 carrier, and 10 diseased animals. After removal of non-parent animals without a genotype that were born before 1994 the final pedigree included 582,829 animals. The algorithm calculated an animal's probability for having each genotype based on information from the animal, its parents, progeny, and collateral relatives. Using the algorithm, we identified an additional 15,261 protoporphyria-free animals and 78 carriers. We did not identify any diseased animals, but the probability of being diseased for four animals was greater than .62. Probabilities produced by the algorithm will be used by NALF to prioritize animals to be genotyped and will provide Limousin breeders with a low-cost tool to help eliminate protoporphyria in their herds.

Key Words: Limousin, Genotypes, Probability Analysis

213 Use of marker information on a subset of sires to follow segregation through a complex pedigree.

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The objective is to evaluate the feasibility of using DNA from a proportion of the sires in a population to track the flow of genetic material through the population. Twenty BTA 7 microsatellites were scored on 181 bulls which sired 63% of the 3748 females with records in the MARC twinning selection project. Nineteen of these bulls are ancestors of other bulls that were scored. A pedigree accounting for all relationships among these bulls was formed by adding 23 sires for which DNA was not available and 124 dams which were not scored. Two progeny of the same parent or two loci on the same meiosis have the same phase if they have identical grandparental origin. Phase is required to follow the segregation of a gene through a pedigree and in all forms of QTL mapping. The phase probabilities (PH) of the 542 meioses in the pedigree were computed by a multilocus approximation to iterative peeling. PH=1 or 0 indicates that phase is known with certainty while PH=0.5 indicates complete uncertainty. The distribution of PH (see table) describes the information content (pooled across loci) from different classes of parents and numbers of progeny per parent. In all classes except sires with few progeny and no DNA, the phases of the majority of meioses could be determined with near certainty (PH<.1 or PH>.9). The distribution of PH suggests that considerable segregation information can be obtained from experimental or commercial populations with deep pedigrees, provided an historical semen bank is available to supplement DNA from current animals.

Parent of Meiosis	#Meioses	PH<.01	.01–.1	.1–.9	.9–.99	PH>.99
Sires with DNA and 1–4 progeny	21	.23	.14	.34	.08	.21
Sires with DNA and >4 progeny	135	.30	.12	.20	.11	.27
Sires with no DNA and 1–4 progeny	28	.02	.07	.76	.12	.04
Sires with no DNA and >4 progeny	112	.20	.08	.43	.10	.20
Dams with no DNA and 1–4 progeny	185	.17	.08	.45	.13	.17
Dams with no DNA and >4 progeny	61	.29	.12	.35	.06	.17
Total	542	.21	.10	.38	.11	.20

Key Words: Genetics, DNA, Segregation

214 Selected chromosomal scan in a swine resource population for quantitative Trait loci.

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Four swine chromosomes (SSC1, 86.5cM; SSC8, 89.4cM; SSC12, 89.9cM; and SSC15, 60.4cM) were examined for the location (cM), magnitude (additive effects), and gene action (additive or dominant) of QTL using the interval mapping program of Knott and Haley, 1992. Eight growth and performance traits, 25 reproductive traits, and 15 meat quality traits were measured on F_2 pigs (n=260; 134 males, 126 females) in a Meishan x Yorkshire resource population at the University of Illinois, Urbana. A total of 36 polymorphic genetic markers (34 microsatellites, 1 RFLP, and 1 STARS) genotyped at the University of Illinois or Dalgety Food Technology Center in Cambridge, England were used in the analysis (8 on SSC1, 12 on SSC8, 8 on SSC12, and 8 on SSC15). A conservative probability statistic was computed for each QTL location using the likelihood ratio test statistic, the degrees of freedom for the likelihood test statistic (df=3), and the Chi Square distribution. Meat quality traits were measured only on barrows (n=118) and reproductive traits were measured only on females (n=123). Evidence of putative QTLs influencing 11 of the 48 traits measured were detected on single chromosome s ($P < .05$). Four traits had putative QTL on two chromosomes ($P < .05$) and putative QTL for two traits were detected on three chromosomes ($P < .05$). Finding QTL for the same trait on more than one chromosome was unexpected, although these chromosomes were chosen on the basis that they carried major genes or candidate genes influencing the traits measured.

Key Words: QTL, Interval Mapping, Swine

215 Evidence for major genes controlling beef carcass traits in Angus cattle.

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Carcass traits were measured on 28,980 Angus progeny records with known sires. Data for analysis were restricted to families with at least 10 progeny per contemporary group. The remaining 7,320 records were analyzed using FINDGENE, an iterative two-step method to examine segregation of major genes controlling hot carcass weight, longissimus muscle area, marbling score, fat thickness or percent cutability. Segregation analysis was used in the first step to determine genotype probabilities at a putative major gene with two alleles for each individual using phenotypic data. Single-trait mixed linear models were used in the second step for the regression of phenotype on genotype probabilities, fixed contemporary groups, slaughter age as a covariate, and residual polygenic breeding values. Results suggest segregation of major genes for hot carcass weight, longissimus muscle area, and marbling score. Estimated intraclass correlation coefficients for the effect of the putative major gene were .22, .29 and .52, respectively. Estimates for fat thickness and percent cutability were .015 and .038. Estimated difference between two homozygotes was 187.64 for hot carcass weight, 1.98 for marbling score, and 4.04 for longissimus muscle area. The analyses also provided genotype probabilities at the putative gene for each individual, which could help to identify heterozygous sires as candidates for marker-based quantitative trait loci (QTL) mapping. Such selection of family sires could improve experimental power of QTL detection using DNA markers.

Key Words: Segregation Analysis, Major Genes, Beef Carcass Traits

216 New advances in cloning and their impact on breeding programs.

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Cloning has advanced through the recent demonstrations that it is feasible to produce, in principle and with significant effort, an unlimited number of individuals of identical genotype from differentiated cell lines that have been frozen and thawed. Whilst the impact of the biological advance is immense for biomedical applications, the significance is less clear for livestock breeding. In our view the scientific issues for breeding programs (therefore sidestepping the important matters of ethics and cost!) lie in whether clones can increase genetic progress without a cost to biodiversity. Biodiversity may be categorized as: (i) genetic variation among parents within breeds; (ii) genetic variation among individuals within a farm; and (iii) between breed variation. For (i), genetic models are now sufficiently good to produce comparisons of breeding schemes, made at the same rates of inbreeding, of rates of genetic progress with and without the use of clones. The conclusions are that the judicious use of clones can give significantly faster rates of progress, and furthermore can help improve health traits which are at present less tractable than, say, yield. Item (ii) needs answers on how important genetic variation is within any one locality in buffering diseases, or ameliorating other management problems. There appear to be no good models for answering this question but experience from clonal forestry can be used to provide some clues. Finally in the face of a rapid global decline in breed diversity, cloning, in particular adult cloning, may be an important route to protect biodiversity. For many countries the technical requirements of effective cryoconservation using semen and embryos are very demanding, but those for cell collection and storage may be much more tractable. Consequently far more genetic variation may be available for new breed development in the future than practicable at present.

Key Words: Cloning, Breeding Programs, Genetics

217 Implications of cloning for breed improvement strategies: Are traditional methods of animal improvement obsolete?

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No!! Unless? Can the optimum animal be defined? Will that definition change over time, by location, by market demand? First, assume what may be impossible, that the perfect animal can be defined or only a limited number of definitions of "perfect" are needed! Then, can the "perfect" animal to match the definition be found? Suppose such an animal is found. "Is the animal perfect because of phenotype or genotype?" In other words, the P = G + E problem exists which requires traditional improvement methods to determine whether G, E or a combination leads to perfection. For most traits, additive genetic variance accounts for 10 to 50% of total variance. Cloning the "perfect" animal would eliminate that variance and could also capture optimum dominance and epistatic genetic effects that may account for additional variation. For some traits maternal effects are important. In that case, clones as breeding animals must be "perfect" for both direct and maternal genotypes. Use of clones to increase uniformity could be only partially successful. If heritability is 25%, then the standard deviation among clones would be 87% of that of uncloned animals. Fixing the genotype could increase susceptibility to failure if environment changes. Now limit the goal. Suppose an animal has a gene for low fat, well-marbled meat or same sex twins. Cloning would allow wide distribution of that gene but along with other genes of the designated animal. Again the P = G + E problem with the need to reduce the "bad stuff", save the desired gene, and increase the other "good stuff". Cloning, at best, is another tool for animal improvement that joins the list of previous biotechnological inventions, some of which have become cost-effective: artificial insemination; multiple ovulation and embryo transfer, sexing of semen, and in vitro fertilization. Cloning has a place in that inventory but, in the long-term, use of cloning will need to be managed to be cost effective for improvement of quantitative characters. Cloning, however, is "a natural" for distribution of fully expressed qualitative genetic characters.

Key Words: Genetics, Selection, Breeding

218 Ethical issues in livestock cloning.

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Although cloning may eventually become an important technology for livestock production, four ethical issues must be addressed before the practice becomes widespread. First, researchers must establish that the procedure is not detrimental to the health or well-being of affected animals. Second, animal research institutions should evaluate the net social benefit of cloning research by weighing the benefits to livestock producers against the opportunity cost of research capacity lost to biomedical projects. Third, a market structure for products of cloned animals must address key problems of consumer consent. Finally, scientists must consider the indirect effects of cloning research on the larger ethical questions surrounding human cloning.

Key Words: Cloning, Ethics, Public Acceptance

219 Comparison of test interval and best prediction methods for estimation of lactation yield from monthly, a.m.-p.m., and trimonthly testing.

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A method with best prediction (BP) properties that condenses information from many test days into lactation measures of yield and persistency has been proposed as a possible replacement for the test interval method (TIM), which currently is used in the US to estimate lactation yield. The BP method uses correlations between individual test days and requires inversion of a small matrix for each lactation. Milk weights from monthly (MO), a.m.-p.m. (AP), and trimonthly (TRI) test plans, which represent extreme differences in sampling methods, were examined to compare the effectiveness of BP and TIM for estimation of lactation yield. Individual weights were from 658 Canadian Holstein cows in 17 herds. Testing intervals were from 97,878 to 99,185 US Holstein cows enrolled in traditional MO test plans. Individual milk weights or daily yields of the Canadian cows were selected to correspond to test intervals of the US cows. For estimation of AP credits, the initial milk weight for the lactation was selected randomly from the morning or evening milking and alternated thereafter on the designated test day. For TRI credits, one of the first three designated test day weights was selected randomly, and each third designated test day weight was used thereafter. Correlations between actual and TIM-estimated 305-d lactation yields were 0.97, 0.96, and 0.93 for MO, AP, and TRI testing, respectively. Corresponding correlations for BP were 0.97, 0.97, and 0.93. Standard deviation of difference between estimated and actual lactation yields for MO, AP, and TRI testing were 388, 425, and 606 kg for TIM and 373, 400, and 546 kg for BP. Thus, BP had 4, 6, and 10% greater accuracy. Advantage of BP over TIM is minimal if two milk weights are recorded monthly but is substantial if testing is less frequent. Organizations that estimate lactation yield should consider replacing TIM with a more accurate procedure.

Key Words: Test Interval Method, Best Prediction, Lactation Yield

220 Analysing test day records of dairy sheep milk production by time series ARIMA models.

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Milk Test Day (TD) yields recorded at different time intervals along a lactation are usually analysed by two methods that disagree for some aspects yet being complementary for others. In the first approach, TD yields are treated as different values of the same trait, that can be linked by a lactation curve representing a regular function of time. In the second approach, each TD is viewed as a different trait related to the others TD by a correlation structure. The main limit of the first method is that the residual component of regression must necessarily be treated as a random noise; on the other hand, the multivariate methodology is not able to take account of the temporal dependence of covariance structure among different TD. Time series analysis models are able both to utilze the random component and to evalue the correlation between measurements as a function of the distance (in time) among them by using an autocorrelation function. In the present work, monthly milk TD yields of 1,307 dairy Sarda ewes were analysed by time series methodology. Global and partial autocorrelation functions were calculated for lactations within parity classes and altitude of location of flocks. Spectral analysis of the succession of data was developed by Fourier transform, and each series of values was fitted to different Box-Jenkins ARIMA models. The separation of deterministic and Stochastic components highlighted the Markov chain feature of milk production pattern. Previsional power of ARIMA models was tested by predicting total milk production for a standardised lactation length of 210 days from few TD. Results indicate higher previsional capacity in comparison to standard methods and suggest further development of time series analysis for studying lactation curves with more sophisticated methods, such as wavelet decomposition and neural network models.

Key Words: Test Day, Ewe Lactation, ARIMA Models

221 A random regression approach to estimate variance components for longitudinal records in beef cattle via Gibbs sampling.

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A single trait animal model, containing 5-th order Legendre polynomials with fixed and random regression coefficients, was used to describe body weight-age relationships in beef cattle. Using a Bayesian approach, covariance components were obtained from marginal posterior distributions via Gibbs sampling. Data were part of an ongoing crossbreeding experiment at the Agricultural University of Uruguay, and consisted of 9,020 weights from 478 crossbred females and castrated males. Animals were progeny of unrelated Hereford dams and 25 sires (7 Nellore, 7 Hereford, 7 Angus and 5 Salers). The records spanned from 0 to 1149 days of age, with animals being weighed every 45 days. The model included fixed regression coefficients for the year of birth∗sire breed∗sex effect, and random regression coefficients for additive animal and permanent environmental effects. Residuals were fit for every two months of age. Results showed that genetic variation changes over time for body weight. Daily weight heritabilities at days 0, 150, 300, 450, 600, 750, 900 and 1050 were .40, .18, .15, .24, .20, .21, .37 and .35, respectively. A plot of residual variance estimates suggested that fitting the residuals as a nonlinear function would describe the residual variance better than fitting discrete time intervals. Differences in individual EBV curves indicated that animals could be identified based on their weight genetic merit over time. This information can be useful (i) in designing breeding plans to match different breeding objectives. For instance, under extensive production systems selection of animals for which their genetic potential matches seasonal fluctuations in roughage availability would be desirable, and (ii) to maximize prediction of BV at a given age.

Key Words: Beef Cattle, Growth Curves, Random Regression

222 Bayesian procedure with an autoregressive prior for smoothing estimated time trends.

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In many linear models used in animal breeding, there is a fixed effect defined, at least in part, by time, e.g., contemporary groups or genetic groups partitioned by time. Motivating this work was the Simmental multibreed evaluation model wherein 'founders' are classified by breed and year of birth of progeny. There are two requirements for the proposed procedure to be useful. Firstly, there is limited information for estimating many of the effects, e.g., few founders in some years or small numbers per contemporary group (small herd size). Secondly, whatever the effect is, we do not, *a priori* expect large differences from one time to the next. The latter can be ensured in the estimates, unless the data are 'sufficient' to indicate otherwise, by adopting a Bayesian procedure with a prior that assumes an autoregressive process. For the founder effects in the multibreed model we wanted to incorporate estimates of breed differences from the literature, we wanted to allow trends in the founders without specifying a shape for the trends and we believed that these trends should be relatively smooth. This was accomplished by assuming a normal prior for the founder-year effects for the i-th breed, say $\mathbf{b}_i$, with constant mean μ_i and an autoregressive covariance structure $\mathbf{V}(\rho)\sigma^2$ where μ_i is taken from literature sources, ρ=0.95 implying adjacent effects are expected to be very similar and σ^2 is chosen to reflect belief in the literature values. The larger σ^2, the more emphasis given to the data. Implementation only requires augmentation of coefficient matrix with $\mathbf{V}^{-1}\sigma^{-2}$, (easily computed tridiagonal matrix) and RHS with $\mathbf{V}^{-1}\sigma^{-2}\mathbf{1}\mu_i$; the difficult part is choosing σ^2. The procedure is quite effective at 'smoothing' trends.

Key Words: Bayesian Analysis, Genetic Groups, Autoregressive Process

223 Approximate and empirical confidence intervals for heritability from Method R estimates.

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The objective of our study was to compare procedures for approximate confidence intervals to empirical confidence intervals for mean heritability using Method R estimates. We obtained Method R estimates from a purebred Hereford data set, which included observations on yearling bull scrotal circumference (SC) (N = 927) and yearling heifer pregnancy (HP) (N = 986). For SC, we estimated heritability using a univariate animal model with fixed effects of age of dam, contemporary group, and a covariate of Julian calendar day of year born. Random effects included random additive direct genetic effects of animal and residual error. Our estimates for HP were obtained using a maximum *a posteriori* probit threshold model with equivalent fixed and random effects. Empirical 95% confidence intervals (CI) were calculated from the distribution of the heritability estimates from Method R at the 2.5 and 97.5 percentiles. We normalized the distributions of heritability estimates for approximate 95% CI using a Box-Cox transformation procedure. We computed approximate 95% CI on the transformed distribution of estimates using CI = $\mu \pm (T \times \sigma)$, where μ = the mean, σ = the SE of transformed estimates, and T = the critical value of a T− distribution for a $1 - \alpha$ CI. However, we reported the CI on the original scale using a reverse Box-Cox transformation. For SC and HP, we obtained 6,000 and 975 Method R estimates each. The mean heritability estimate, SE, approximate 95% confidence interval, and empirical confidence interval for SC estimates were .73, .14, .47 to .99 and .46 to .99, respectively. The mean estimate, SE, approximate 95% confidence interval, and empirical confidence interval for HP were .13, .09, .005 to .35, and .004 to .32, respectively. For the continuously observed trait of SC the empirical and approximate CI were equally useful. Further study is required to understand the small differences between the two procedures for the categorical trait HP.

Key Words: Heritability, Confidence Interval

224 Comparison of heritability estimates for survival in crossbred cattle from linear and generalized linear mixed models.

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Heritabilities for female survival to seven specific ages were estimated with a linear model and a generalized linear mixed model. Data for animals born in years 1970–1976 were collected from Cycles I–III of the Germ Plasm Evaluation project at the U.S. Meat Animal Research Center. The females were two-breed crosses representing 16 breeds of sire. Records on a total of 2674 females from 372 sires were used. Survival was scored as 1 if the female survived from birth to a specific age and otherwise a 0. Each specified age (1 to 7 yr) was considered a different trait. For analyses assuming a linear model, variance components were estimated using MTDFREML (Boldman and Van Vleck 1991), for analyses with a generalized linear mixed model GLIMMIX (SAS, 1994) with a probit link and binomial distribution was used. In both cases a sire model with no relationships among the sires was assumed. Models included fixed effects of sire breed, dam breed, year of birth, sire-dam breed interaction and day of birth as a linear covariate. Estimates of heritability were obtained from single-trait analysis for each survival age for each of the three Cycles. Heritability estimates for survival to 1 to 7 yr for females of Cycle I were 0.106 vs 0.321, 0.075 vs 0.087, 0.074 vs 0.146, 0.016 vs 0.031, 0.020 vs 0.034, 0.034 vs 0.056, and 0.030 vs 0.052, for the linear and generalized linear mixed models, respectively. For females of Cycle II the only non-zero estimate of heritability was for survival from birth to one year (0.051 vs 0.820, for the linear and generalized linear mixed model, respectively). Heritability estimates for survival at 1 up to 7 years for females of Cycle III were 0.031 vs 0.0, 0.080 vs 0.0, 0.115 vs 0.0, 0.085 vs 0.025, 0.140 vs 0.088, 0.170 vs 0.183, and 0.375 vs 0.705, for the linear and generalized linear mixed models, respectively. Heritability estimates were greater for survival from birth to one year of age with both methods.

Key Words: Beef Cattle, Survival, Genetic Parameters

225 Effect of age, stage of lactation, milk yield and health events on length of productive life in Swedish Dairy Cattle.

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The effect of parity (1,2,3,4,>4), stage of lactation (0–30d, 31–60d, 61–150d, 151–270d and >270d), milk yield (FCM averaged for 2nd and 3rd test month after calving) and occurrence of diseases, all fixed effects, on length of productive life (LPL) was evaluated. Stage of lactation and diseases and their interaction were treated as time-dependent. Herd-seasons and sires were also included in the model and treated as random effects. Diseases considered were veterinary treated cases of dystocia, retained placenta, metritis, ketosis, milk fever, cystic ovaries, locomotor disorders and mastitis. Data consisted of 35,407 Swedish Red and White (SRB) cows in 1,647 herds and 27,598 Swedish Friesian (SLB) cows in 1,509 herds. A Weibull regression model was used to explain the effect of the diseases on LPL measured by the number of days from calving to culling. All diseases had a significant and similar effect on LPL for the two breeds. Time of culling was influenced by how each disease impacted the performance of a cow. Highest probability for culling was immediately after occurrence for diseases affecting cows' milk production (mastitis, locomotor disease, milk fever and ketosis) and delayed for diseases affecting cows' reproductive performance (cystic ovaries and metritis). Mastitis had the largest effect on LPL followed by locomotor disorders, dystocia and retained placenta. For SLB cows culling risk ratio for mastitis occurring in stage 1 to 5 of lactation was 2.3^{a}, 2.3^{a}, 1.9^{a}, 1.7^{a} and 1.3^{a} and for locomotor disorders was 1.5, 1.4, 1.8^{a}, 1.6^{a} and 1.6^{a}, respectively ($^{a}P<0.10$).

Key Words: Longevity, Diseases, Survival analysis

226 Applications in survival analysis.

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Survival or failure time traits such as herd life and days open are both important economically and pose a number a challenges to an analysis based on linear mixed models. The main features of a survival trait are that it is the time till some event occurs and some of the observations are censored. Survival models and the associated estimation procedures provide a flexible means of modeling survival traits. In this talk I will discuss the application of survival analysis based on the Weibull distribution. The components that make up a survival model will be presented along with their interpretation. Issues related to the model construction and estimation will be presented. The focus will be on the practical application of survival analysis.

Key Words: Survival, Failure Time, Mixed Model

227 Bayesian analysis of birth weight and calving difficulty with a joint linear-threshold and bivariate linear animal models.

L. Varona and I. Misztal, *University of Georgia, Athens.*

Birth weight and calving difficulty were analyzed with a joint threshold-linear and a bivariate linear animal models using Bayesian methods. Data included 26,006 first parity records from the American Gelbvieh population selected from larger herds; additionally 25,362 animals were included in the pedigree. The model of analysis included 8 sex-age of dam systematic effects, 75 herd effects, and animal and maternal effects of 51,368 each. Proper prior distributions were set to ensure a proper posterior distribution. The Gibbs sampler algorithm was used to obtain samples from the marginal posterior distribution, and the samples were used to derive marginal posterior mean and standard deviation for (co)variance components, heritabilities and correlations. Posterior mean (±SD) of direct heritability for Calving Difficulty was 0.52±0.04 and 0.35±0.03 for the bivariate linear-threshold and linear-linear model. Maternal heritabilities were 0.23±0.03 and 0.15±0.01 respectively. Direct heritability for birth weight was 0.47±0.04 for the linear-threshold model and 0.49±0.03 for the bivariate linear model. Maternal heritabilities were 0.15±0.02 for both models. Genetic correlation between direct genetic effects in both traits were 0.64±0.04 for both models, and residual correlation was 0.28±0.03 for bivariate linear model and 0.47±0.04 for the bivariate linear-threshold model. In a simulation study, the posterior mean estimates with the threshold-linear model were assumed as true values. The estimation procedure provided posterior marginal distributions that included the simulated values in the 99% Higher Posterior Density in all 5 replicates. Therefore, the posterior mean of marginal distribution can be regarded as an suitable point estimate for bivariate linear-threshold models. Analysis of birth weight and calving difficulty by a threshold/linear animal model is feasible with Bayesian techniques via Gibbs sampling.

Key Words: Calving Ease, Threshold Model, Bayesian Analysis

228 Comparison of univariate and bivariate models for genetic evaluation of calving ease. I. Misztal*, L. Varona, and J. K. Bertrand, *University of Georgia, Athens*.

Several models were evaluated in terms of predictive ability for calving ease (CE). Data included birth weight (BW) and CE records for 26,006 Gelbvieh cattle and for 5 simulated populations of 6,200 animals each. Distribution of CE scores was 71% in the first category, 21% in second, 7% in third and 2% in fourth. Included in the model were fixed age of dam x sex interaction effects, random management groups, and random animal direct and maternal effects. Bivariate linear-threshold (LT) and linear-linear (LL) models for BW/CE and univariate threshold (T) and linear (L) models for CE were applied to the data sets. For each data set and model, one half of CE records were discarded randomly. Predictive ability of the different models was defined by the MSE for the difference between a deleted CE score and its prediction obtained from the remaining data. For simulated data sets, the average MSE was .31 for LT, .33 for LL, .39 for T and .39 for L. For the field data set, the MSE was .32, .34,.41 and .40, respectively. Although the bivariate models for CE/BW were more accurate than univariate models, the threshold models showed an advantage only under the bivariate model. In the univariate model and field data, the L model was more accurate than the T model. One possible explanation why the theoretically more correct T model was less accurate for categorical data is that the underlying model for CE was simplified, e.g., by ignoring heterogeneity of variances, and that the L model is less sensitive to incorrect assumptions in the model. While the current evaluation for CE in beef cattle using LT seems justified, in dairy cattle either the T model should be refined or recording for birth weight added.

Key Words: Calving Ease, Threshold Model, Model Comparison

229 Genetic analysis of productive life with censored records. N. Vukasinovic*, J. Moll, and N. Kuenzi, *Swiss Federal Institute of Technology, Zurich, Switzerland*.

A simulation study was carried out to investigate impact of censoring on estimation of genetic parameters and accuracy of sire evaluation for the length of productive life by means of survival analysis. Data were simulated under a Weibull model with two fixed effects and a random sire effect with a sire variance of 0.034, assuming a data structure typical for dairy cattle populations. Two different family structures were investigated - 1000 sires with 10 daughters each and 200 sires with 50 daughters each. Sires were assumed related through the grandsires. The reference data were generated assuming no censoring. Sire variance and sire effects were estimated from the reference data with and without considering the relationships among sires. The impact of censoring was investigated by comparing variance estimates and by computing rank correlations among estimated sire effects from the reference data and from several different data files with increased proportion of censored records. Without considering the relationships among sires, the estimated sire variance was biased downwards, especially with increased proportions of censored records. Estimates of sire effects were generally more accurate with a large number of daughters. The rank correlations among sire effects decreased with increased proportion of censored records. With over 40% censored records, considering relationships among sires results in higher rank correlations. Similar results were obtained from the analysis of real dairy cattle data from the Swiss Braunvieh population.

230 Increasing the appeal of animal breeding programs for students. E. J. Pollak, *Cornell University, Ithaca, NY*.

Methods to increase appeal and interest in animal breeding for undergraduates will be discussed. Three problems will be addressed. First, animal science students are typically interested in veterinary medicine and in species other than production animals. They also have been exposed to biotechnology through newspapers, magazines, and TV, altering to a degree their motivation for learning genetics. Second, animal breeding is viewed as a statistical discipline that is abstract in nature. Third, there is a stigma of limited job opportunities in the field. Animal breeding has several strengths on which a strategy to overcome these problems should be built. Animal agriculture will be a major player in the application of technology, and it seems natural to capitalize on this by refining our curriculum to emphasis this component. Including disease characteristics and broadening the species discussed in courses has generated increased interest. Animal breeding is a quantitative field, which lends itself very well to computerized exercises. Computer labs allow students to graph equations, solve problems supported by simulated data, and do statistical manipulation of data using software such as Matlab. These activities not only enhance the learning experience but examples of interest to the students can be generated. This approach brings students in contact with computer technology, a skill they recognize as necessary, but also enables them to increase their quantitative and analytical skills. To address the wide scope of the application of genetics and job opportunities in the area, seminar courses are of great value. These, however, can be expensive to run and should be shared among institutions via distance education as is currently being done at Cornell, Pennsylvania State University, and the State University of New York at Cobleskill.

Key Words: Animal Breeding Curriculum, Teaching

231 Distance education in animal breeding: A Cornell experience. P. A. Oltenacu* and E. J. Pollak, *Cornell University, Ithaca, NY*.

In 1997 a one-credit weekly lecture course in Applied Animal Genetics was offered to Cornell students and to students at two remote sites, State University of New York at Cobleskill and Pennsylvania State University. An introductory genetics course was required as prerequisite. The course (http://www.ansci.cornell.edu/courses/as321/as321.html) presented topics related to genetic definition and control of qualitative and quantitative traits in various animal species. The topics were structured into three modules: 1) genetic implications of small breeding populations, 2) breeding programs for genetic improvement of animals, and 3) new developments in molecular genetics. The course was offered synchronously at all locations using a PictureTel Concord 4500 videoconferencing system with a speed of 384 kbps. As a backup for possible failure to connect, each site had a complete set of PowerPoint slides and a speakerphone, which allowed for “at least audio” connection if needed. Supporting reading materials were distributed to all students one week prior to lecture, and a handout of copies of each speaker’s slides with space for taking notes was available on the day of each lecture. Students at remote sites were encouraged to raise questions or contribute comments during the lectures. The facilitator at Penn State site assisted with student instruction. To provide Cobleskill students with a comparable opportunity without an instructor on site, they were asked to identify concepts that were unclear and formulate specific questions after each lecture. These were submitted electronically to Cornell within two days of the lecture and were discussed in a question and answer session later in the week via the videoconferencing system. Course evaluations were positive. The students’ comments indicated complete satisfaction with the content and format of the course. Students at Cornell indicated that the virtual presence of students at remote sites had a positive effect on the quality of the learning. We plan to offer this course to 2–3 more sites in the fall of 1998. Also, a computer-assisted lab that complements the course will be offered to one of the remote sites.

Key Words: Distance Education, Animal Breeding

232 Exploiting the potential of open learning in animal breeding.

M. M. Lohuis* and C. T. Lohuis, *University of Guelph, Canada*.

Animal breeding education is presently facing many challenges. These include rapid changes in breeding knowledge and technology, resource and funding restrictions and altering demographics of the learner and the animal breeding industry. The challenges can be met via the 'open learning' educational format. This non-traditional approach is based on the needs of individual learners, not the interests of the teacher or the institution. An important feature of open learning is its appropriateness for the professional development audience. Delivery methods include interactive WWW distance courses, computer-assisted learning and team-based study. In 1997, 1 in 6 U.S. adults (31 million) used the Internet on a regular basis. By the year 2005, 40% of all education and training in the U.S.A. will benefit executive, professional and technical personnel. Workforce training is increasingly being delivered by Internet and computer-based instruction. In Canada alone, annual expenditures for professional development reached $8.6 billion in 1996.

The Canadian dairy breeding industry (ie. A.I. companies, breed associations and milk recording organizations) has expressed the need for ongoing professional development to understand and adopt new animal breeding technologies. The University of Guelph responded by delivering a series of animal breeding short courses (Executive Certificate Program in Animal Breeding) to industry decision-makers in 1997. A version modified specifically for farmers and breeding industry personnel was offered in 1998. Through the collaboration of experts from various agricultural institutions and the use of a learner-centered format, this professional development initiative was a pedagogical and financial success. Animal breeding professionals and farmers have improved their access to information from educational and corporate web sites on the Internet. This paper will describe how the open learning approach differs from traditional university teaching. Using the University of Guelph example in animal breeding professional development, the framework for a successful open learning program will be examined. The best practices for effective adult education will also be identified and discussed within this case study.

Key Words: Animal Breeding, Open Learning, Professional Development

233 Analysis of genotype by bovine somatotropin interaction in commercial dairy herds.

K. A. Weigel and T. M. Fisher*, *University of Wisconsin, Madison*.

Milk yield data from 61 commercial dairy herds were analyzed to determine the presence or absence of genotype by bovine somatotropin (bST) interaction. A total of 36,223 completed lactation records from 19,914 cows calving since 1991 were used. Each herd was required to have a minimum of 5 cows receiving bST. Each sire was required to have at least one daughter receiving bST and one daughter not receiving bST, and 796 sires met these criteria. Traits included mature equivalent lactation milk yield, peak milk yield (milk at third test), late lactation milk yield (milk at ninth test) and persistency (difference between milk yield at ninth test and milk yield at third test, divided by number of days between tests). A linear model including effects of herd-year-season, bST, sire by bST interaction and residual was used for analysis of lactation yield. Parity, age and days in milk were also included in analysis of peak yield, late lactation yield and persistency. The estimated percentages of variation associated with each random effect are shown in the table below. Results indicate little evidence for interaction between genotype and bST.

Trait	Additive	Permanent Env.	Sire x bST	Residual
Lactation yield	21.8%	22.5%	0.9%	54.8%
Peak yield	11.4%	14.1%	0.5%	74.0%
Late lactation yield	12.6%	18.0%	0.8%	68.6%
Persistency	5.5%	7.6%	0.5%	86.4%

Key Words: Milk Yield, Bovine Somatotropin, Genotype Environment Interaction

234 Non return rate in Italian Holstein-Friesian cows.

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A total of 2,959,470 first inseminations from 1990 to '95 in 1,426,224 Italian Holstein-Friesian cows were analyzed. The effect of environmental factors on the non return rate at 56 days was investigated. The fixed model included the interaction effect of year by month of insemination, the age of the cow, the herd where the insemination was performed and the AI Center that handled the semen. All effects were statistically significant at $p<0.0001$. Overall, late spring and early summer months showed higher non return rate than other months. Non return rate was heavily affected by the age of the cow, with younger animals having higher percentage of non return than older cows. The effect of AI Centre was very small, suggesting that semen handling and preparation are quite homogeneous among AI Centres laboratories. The environmental factors identified will be included in the mixed model analysis for the genetic evaluation of service bulls, using a sire-maternal grand sire model.

Key Words: Dairy Cattle, Non Return Rate

235 Genotype by environment interactions for growth and milk traits in an international population of Charolais cattle.

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Our objective was to determine whether genotype by environment interactions were present for growth and milk traits in an international population of Charolais cattle. Charolais breed associations from the United States (US), Canada (CN), Australia (AU), and New Zealand (NZ) provided us with a total of 2,685,565 pedigree and 719,933 performance records. The breed association from the United Kingdom (UK) supplied an additional 189,154 pedigree records. We analyzed data from the US, CN, AU and NZ separately and then combined data from all sources, including the UK, for joint evaluation (JT). Contemporary groups and adjustment factors used in the within-country analyses were also used in JT, and variance components from the US were used in all analyses. We obtained EBV and approximate accuracies for birth weight, weaning weight (WW), milk (MI), 365-d weight, and 400-d weight from all analyses plus 600-d weight from the AU, NZ, and JT analyses. We computed correlations between predictions from within-country and JT analyses for all parents and for sires only. Observed correlations (r) were compared to expected correlations (E(r)), derived as the product of approximate accuracies between evaluations averaged over animals. For sires, r were generally higher than E(r) for US-JT, CN-JT, and AU-JT and lower than E(r) for NZ-JT. Observed and expected correlations agreed closely for WW and MI and for all traits among AU sires. For sires with weaning weight accuracies greater than or equal to .70 and sires registered in more than one country, r were well below E(r) for all traits, particularly MI. The large discrepancies between r and E(r) indicate that genotype by environment interactions exist in this population of Charolais. These interactions may be the result of different reporting policies across countries.

Key Words: Charolais, Genotype Environment Interaction, International Comparisons

236 Effect of herd environment level on the genetic and phenotypic relationship among milk yield, somatic cell score, and fertility.

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To evaluate genotype by environment interactions of mature equivalent milk yield (MY), somatic cell score (SCS), and conception rate at first service (CR), 248,230 first parity DHIA Holstein records from 588 sires in 3,042 herds were used. Herds were classified into low and high management levels using three criteria. Genetic parameters were estimated using multiple trait derivative free REML software (MTDFREML). Heritabilities and genetic and phenotypic correlations were consistent regardless of the classification criteria. For low level, heritabilities for MY, SCS, and CR averaged .232, .101, and .020, while for high level they averaged .283, .097, and .009. For low level, genetic (and phenotypic) correlations between MY and SCS, MY and CR, SCS and CR averaged .234, −.407, and −.228, (−.055, −.174, and −.037), while for high level they averaged .178, −.304, and −.139, (−.089, −.171, and −.034). The genetic correlation between low and high management levels for MY, SCS, and CR averaged .972, .972, and .949. The genetic correlation between pairs of traits were consistently lower in high than in low management groups, indicating a genotype by environment interaction. These changes are all in a positive direction, suggesting that differences of management between two levels reduces the genetic negative association between the traits considered.

Key Words: Genetic Parameters, Herd Management, Multiple Trait Linear Model

237 Acquisition of milk recording data classified by experts for machine learning.

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Every month, DHI provides dairy producers with a large number of test day values related to cows' milk yield, fat, protein and somatic cell count. While proper interpretation of these data may produce useful information to improve management, the process itself is generally time consuming. A knowledge-based system that could automate parts of this process and support dairy producers and their advisors would, therefore, be useful. Since traditional approaches to knowledge-based system development, based on interviews with domain experts, have also proven to be very time consuming and costly, alternative, machine learning techniques such as rule induction and case-based reasoning could be used to automate the process. This is achieved by learning how to classify new cases, based on sets of example cases that have been classified by domain experts. In this project, the use of machine learning to support the development of a knowledge-based system for the interpretation of lactation data was investigated. An important phase consisted of collecting example cases of the interpretation of mature equivalent milk production and lactation curves by domain experts. In consultation with domain experts, the different steps in the interpretation process were determined, such as removal of abnormal cases and classification of the performance of different groups of cows. In addition, the representations of example cases were determined for each of these steps. These include the average performance of a group, an indication of the variability of the data, reference values and class descriptions such as high peak or high persistency. A computer program was developed to show experts example cases and record their classification decisions. By use of this program, domain experts can classify test day records obtained from DHI and machine learning techniques can subsequently be used to transform the knowledge embedded in these example cases in a format that can later be used in a knowledge-based system.

Key Words: Milk Recording Data, Knowledge-based Systems, Machine Learning

238 Information technology via the Internet.

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As the Internet has grown in importance and in capabilities as a communication tool, so have our thoughts on how information technology might be used in dairy breeding. The two have acted synergistically. New applications are being developed for one, whenever additional capabilities are added in the other. The Internet was developed to allow for remote users to access programs and scientific data on large mainframe computers. Dairy producers and industry professionals are often in geographically remote areas due to their career, and they now have much greater access to dairy breeding information via the Internet. Some examples include sire summaries that are available at the same time to everyone on the Internet, as they are to the bull studs. Producers also have access to sire information from a variety of studs, where individual bulls can be compared and purchase decisions can be made without the influence of an on-site sales representative. The technologies have also allowed for the development of new businesses to provide facilitated computing environments via the Internet for this kind of cross-stud bull comparisons. Beyond just the distribution and sales of semen, dairy breeding is also a process, frequently a collaborative effort among individuals in various sectors of the dairy industry who are physically remote from each other. It is often difficult for these individuals to meet in person for committee or organizational meetings. There are a number of new information technologies available via the Internet that facilitate collaborative efforts. Some of those include immediate access to remote databases, software agents that can carry out assigned tasks, meeting room or desktop video-conferencing, whiteboard technologies and online expert systems. Examples of where these technologies might be useful in existing dairy breeding tasks include committees that need to meet to evaluate sire summaries, reporting of genetic abnormalities observed, service to remotely monitor semen supplies, and interpretation of records. The new technologies also may allow producers to market their cow information directly to bull studs, who might use it to calculate value-added information about proofs, bypassing the dairy herd record processing centers. Trends in information technologies concerning decision support systems with application to dairy breeding will be discussed. New technologies often have unanticipated impacts when used in new domains. Potential area where unanticipated impacts might develop will also be discussed.

Key Words: Internet, Breeding, Information Technologies

239 A genetic parameter estimate World Wide Web site.

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The primary consideration in the development of structured breeding programs is the breeding objective and its predictor, the selection index. The breeding objective is simply a statement (model) describing the relationship between various biological traits and income and expense. Genetic parameters like (co)variances, correlations and heritabilities are essential to their construction. Other uses of genetic parameters arise as a function of our ability to model larger and more complex systems and attempt to integrate information across herds (flocks), breeds, or enterprises. Examples include multi-breed EBV estimation and modelling of crossbreeding systems. Given that geneticists do not have access to the experimental populations they might require to estimate required genetic parameters (and the costs to maintain them), the ability to access one central source for these data will be a tremendous utility for all animal geneticists. A web site has the capability of: Tabulating and summarising genetic information from major farmed domestic species; Containing components including breed and heterosis estimates, genetic (co)variances, heritabilities and correlations; Containing auxiliary information including age at measurement, fixed effect adjustments, trait means and method of estimation; Having a nominated person (coordinator) responsible for each species; allowing electronic submission of parameters; Providing for older material to be loaded when electronically submitted by the author or nominee; Allowing access via hierarchical menus and search functions; Being cost effective.

Key Words: Genetic Parameters, World Wide Web

240 Dairybulls.com - an international genetic evaluation website.

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Dairy-sire genetic evaluation solutions for yield and type are released by different organizations across countries in varying formats. The emergence of global dairy genetics usage has prompted individuals and organizations to seek a dairy sire's genetic evaluation from the country of origin or the Interbull genetic evaluation. Dairybulls.com was established in February, 1997, using database technology and internet delivery for genetic evaluations across countries. Three countries, the United States, Canada, and the Netherlands authorized and provided data for inclusion on the website. These evaluations include the appropriate domestic and Interbull yield data, domestic selection indexes, and domestic type data in a searchable application. Several other countries are currently considering providing data. The timing and release of data by each country greatly influences website activity. After the August 1997 Interbull releases, over 7,000 user sessions averaging 16 minutes were recorded in a 24 hour period on the website. Internet access, database searches and delivery allows end users custom options for database information requests. This allows continous access to genetic evaluation data in a central repository for all interested parties.

Key Words: Genetic Evaluations, Internet

241 Use of the World Wide Web to distribute genetic evaluation information.

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The Animal Improvement Programs Laboratory (AIPL) has developed a web site (http://aipl.arsusda.gov) to allow worldwide access to information on genetic evaluation of US dairy cattle. The web pages contain quarterly reports, computer formats, documentation related to evaluations, links to related web sites, AIPL contact personnel, and recent AIPL publications. The primary goal in developing the web site was to allow access to information related to USDA-Dairy Herd Improvement Association (DHIA) genetic evaluations in an easy, timely manner. The AIPL web site was accessed nearly 10,000 times in 1997. All visitors have access to evaluation queries for single animals. Industry cooperators, including breed associations, dairy records processing centers, DHIA affiliates, and artificial insemination organizations have individualized pages that require passwords so that access to sensitive data is limited. Each organization-specific web page contains up to 18 applications for queries for both single and multiple animals. Examples of information that can be obtained are a four-generation pedigree, a list of a cow's contemporaries and their yields, and a list of evaluation information for a bull's daughters. Using a point-and-click interface, industry cooperators can upload a file of request information (e.g., animal identification numbers) to AIPL, process the request, and download the results to their local computer. The AIPL query system provides industry cooperators with a consistent, simple, and universally known user interface to obtain data. Future enhancements include cooperator access to error reports and checking records for errors on line. In addition to industry- specific web pages, cooperators also can access a file transfer protocol site that is password protected. This site allows receipt and distribution of sensitive data to appropriate cooperators while maintaining adequate security for the AIPL computing system.

Key Words: World Wide Web, Genetic Evaluation Information

242 Use of CowTemp^{TM} temperature monitoring system for automated estrus detection.

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CowTemp^{TM} is a new telemetric system in development that measures and transmits the core body temperature of a cow on a periodic basis (nominally every 30 minutes). The system consists of a 3.75″ x 1″ bolus transmitter that stays in the reticulum for the life of the cow, a receiver, and a computer program for displaying and analyzing the data. The bolus is inserted with a standard balling gun. It contains a temperature sensor, a microprocessor, and a transmitter. Each bolus is programmed with a unique ID number which is selected by the user on site. This ID is transmitted along with the temperature. The receiver captures the transmissions from the boli, displays them, and sends the data to a computer for further graphic display and analysis. Research is ongoing to determine the system's effectiveness in detecting core body temperature rise associated with estrus. In a preliminary study, five cows were induced to estrus using a protocol of GnRH and lutalyse and were not bred during the first estrus cycle. Three cows were then observed daily for visual evidence of standing heat for a twelve day period coinciding with the probable second estrus period. The CowTemp^{TM} system automatically recorded the temperatures of each cow at one minute intervals during this period. Two of the five cows were visually observed in standing heat. Two values were calculated to determine the correlation between the visual evidence and the rise in body temperature. A 5 day average temperature and a 1 day average temperature were calculated on an hourly basis. The difference between the one day average and five day average was used to determine the rise in temperature that is due to estrus. Data was grouped in sets of twelve hour intervals, the data point being the highest difference during the interval, resulting in 79 data points. Analysis of this data suggests that if the difference is greater than 0.5°C, then estrus is occurring. For the two data points coinciding with visual detection, the mean delta was 0.54°C ($P>0.10$). For the 77 data points where standing heat was not observed, the mean delta was 0.09°C ($P<0.0005$). Test results show the feasibility of automated estrus detection using core body temperature.

Key Words: Estrus Detection, Electronic ID, Temperature Monitoring

243 Supply of genetic information - amount, format and frequency.

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The volume and complexity of genetic information is increasing due to new traits being added in better defined breeding objectives and more complex and comprehensive evaluation models being used. New traits may include reproduction, health, and carcass traits. Examples of more comprehensive models include the test-day model in dairy cattle leading to evaluations for persistency or a growth model in beef cattle leading to evaluations for maturity rate. More complex models, such as, including nonadditive effects like inbreeding and dominance, also lead to additional information. The amount of information per animal may skyrocket if DNA marker typing becomes routine and QTL information is utilized. In many industries, evaluations are being performed more frequently. Such evaluations result in faster genetic progress and improved management and marketing opportunities but also in extra costs and extra information. Adopting new technology and making some organizational changes can help realize all the added benefits of the improvements to the genetic evaluation systems without incurring the excessive burdens. Going to continuous genetic evaluation, where an online system accepts new records all the time while continuously updating breeding values, will relieve time pressures. An online mating system with access to both genetic and marketing information can result in mating recommendations customized for each user and the delivery of the desired genetic products. Such a system could utilize inbreeding and dominance information (nicking) that cannot efficiently be acco mmodated in the current sire summaries or off-line mating programs. The new system will require a new organizational approach, where the task of scientists and technicians will not be simply running the evaluations but providing research, design, supervision and maintenance required in the entire evaluation, decision making and distribution system.

Key Words: Genetic Evaluation, Continuous Evaluation, Mating System

244 Assessment of estrus detection by observation and an electronic detection method in beef heifers.

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One hundred sixty-five-beef heifers (Angus, AN, Brahman, BH, Angus *times* Brahman, AB) were estrus synchronized following evaluation of weight, body condition score, and reproductive tract. Heifers were randomly assigned to one of two methods of estrous detection, either traditional observation for signs of standing estrus or a rump-mounted pressure-sensitive-detection- device. All heifers were bred by artificial insemination potentially three opportunities and subsequently by a bull). The effectiveness of estrus detection and timely insemination were evaluated by detection method, heifer breed-type and effective breeding event (that event leading to conception). At the end of three insemination opportunities, 60.5% of heifers observed were pregnant while only 45.8% of those detected by the mount detection device (p=0.04). Heifers categorized by effective breeding event, were different with respect to duration of estrus and time of insemination compared with the end of standing estrus. Heifers pregnant to the first service had a duration of estrus of 8 hours 58 minutes while at that same event the heifers that later became pregnant to the second or third estrus event and insemination were 11 hours 38 minutes and 19 hours 3 minutes, respectively (p=0.007) and the time of insemination relative to the end of estrus was 3 hours 8 minutes (-4 hours 34 minutes, -21 hours 13 minutes, respectively, p=0.03). Based on this data, the reduced first service conception rate in the detection device group suggests that insemination of detected heifers may have been earlier than was optimal for pregnancy. Breed differences were observed in estrus durations (AN 8 hr 31 min, BH 6 hr 44 min, AB 11 hr 51 min, p=0.03), number of mounts (AN 19, BH 26, AB 37, p=0.02) and gestation length (281, 291, 286 d, respectively, p=0.001).

Key Words: Estrus Detection, Estrus Synchronization, Estrus Detection Aids

245 The application of EDI in commercial pig breeding programmes.

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To enable a regular and standardised exchange of test data and derived breeding values between sow management systems and the databases of pig breeding organisations, a standard has been developed, introduced and experienced for already 10 years. By means of this standard EDI-PIGS, weekly exchange of test data, pedigree information and breeding values is currently in use by more than 500 breeding herds (80,000 purebred sows) and 4 breeding/A.I. organisations. The standard EDI-PIGS is based on the ADIS protocol (ISO 11787). Next to a description of data elements in a dynamic data dictionary, standard events and message decriptions are included. In addition to the standard for data exchange, an error recovery procedure is set up. Data exchange between herds and central computers is performed via electronic mail boxes and/or internet. The implementation of the standard for data exchange has decreased the costs of data entry enormously and moreover enabled a direct exchange of the latest data and breeding values between the different sow management systems of breeders and the computers of the breeding organisations.

Key Words: Electronic Data Exchange, Computers, Breeding Programmes

246 Dairy Herd Improvement records as replacements of technician breeding receipt database for routine estimates of non-return rates for AI bulls.

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The objective of this study was to find whether DHI data could be used to estimate sire non-return rates to replace current technician data estimates. Bull weighted least squares means for non-return rates were calculated separately for five overlapping 60–90 day service periods from each data source. Models included stud, sire, service number, and linear and quadratic form of breeding month for both data sources, service unit for technician and lactation for DHI data. Sire and lactation were not significant ($P > .10$). Technician differences ($P < .05$) were in service unit, stud, service number, and linear and quadratic service month in all but one service period. DHI differed ($P < .05$) for service number, month (linear and quadratic), and stud in two service periods. Technician R-square values were 0.23 to 0.28 versus 0.94 to 0.96 for DHI. Sire estimated non-return rates were weighted using the inverted estimator standard error squared and compared. Sire, stud, data source, service period, and appropriate interactions were modeled. Weighted bull non-returns differed ($P < .01$)in magnitude across data sources. Stud, data source by stud, and sire within stud by data source were significant ($P < .01$). Services per bull, service period and its interactions did not differ ($P > .10$). Four fertility categories based on mean and standard deviation of the weighted estimates were formed within the data sources across service periods. These categories were correlated ($.5 > r > .9$) and 52.9 to 87.4% congruent within data source for adjacent service periods and across data sources within service periods. With declining availability of technician data, DHI data was shown to be a reasonable substitute. Correlations and congruency of fertility categories suggest sire choices would be very similar.

Key Words: DHI, non-return rate, fertility estimate

247 A comparison of electronic management methods with conventional methods for managing sows.

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Osborne Industries Inc. (OII) operates a 300-sow Demonstration Farm for research, development, and demonstration of electronic animal management (EAM) methods. This facility demonstrates automatic data collection, analysis, and real-time control as part of the Electronic Animal Recognition Systems (EARS$^{\text{TM}}$) program at OII. Production evaluation during the first three years of operation compares sow performance under EAM with conventional management. Treatments include electronic gestation (EG), conventional gestation (CG), electronic farrowing (EF), and conventional farrowing (CF). Performance analyses for a three-year period show few significant differences between treatments. A significant difference was the time for return to estrus was less for sows under EG than CG for parities three through five (P 0.10). Other results may require further study. For example, the number of pigs born alive is higher in CG than EG on parity-3 sows, but lower in EG than CG for parity-four sows (P 0.10).

The reactions and adjustments of researchers, managers, and operations personnel to management differences between conventional and EAM methods also were observed. All sows are individually identified using radio frequency identification (RFID) EarButton$^{\text{TM}}$ transponders. Porcode® and Hunday® electronic sow feeding (ESF) stations automatically collect daily production data. Farm personnel use hand-held Osborne ID Loggers® to collect of data in a working database, which is later transferred directly to a PC farm management program. Data entry errors and tedium are eliminated, permitting more time for husbandry tasks with better at-hand information. EG and EF are compared with CG and CF on the basis of ability for individual feed control and for recognizing on-set of sow health problems. The success of automatic spray marking and automatic sorting combined with ESF was evaluated. The differences in observed behavior between EG and EF managed animals and CG and CF managed animals suggest lower stress in the electronically managed animals owing to disassociation of the care-giver from feed delivery.

Key Words: Electronic Feeding, Electronic ID System, Dataloggers

248 Inbreeding in populations with incomplete pedigrees.

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The objective of the study was to determine average inbreeding coefficient when pedigrees are incomplete. Current genetic evaluations usually involve animals with incomplete pedigrees. Unknown parents are assumed unrelated which may lead to underestimation of the levels of inbreeding. Van Raden developed an algorithm to calculate inbreeding coefficients for pedigrees with missing parents where the inbreeding coefficient of animals with unknown parents is assumed equal to the mean of animals with known parents born in the same year. Data included 2,251 Holsteins born between 1960–1996 with almost complete pedigrees and with sires identified. Mean inbreeding for animals born in 1996 was then computed using the regular algorithm and that of Van Raden, with 10%, 20%, 30%, 40% and 50% of dams randomly deleted. The results are presented in the table below. With missing dams, the mean inbreeding calculated using the regular algorithm was reduced by one half when the number of missing dams was around 25%, and was reduced nine times when 50% of dams were unknown. VanRaden's algorithm was able to recover most of the lost inbreeding for up to 30% of unknown dams. Incomplete pedigrees may lead to serious underestimation of inbreeding levels. Application of the algorithm by VanRaden may provide a good indication of the real level of inbreeding in a population.

Inbreeding average (%) for animals born in 1996

% Dams deleted	Regular algorithm	Van Raden's algorithm
0	3.5	3.9
10	2.8	3.6
20	2.1	3.6
30	1.5	3.2
40	1.0	2.5
50	0.4	1.6

Key Words: Inbreeding, Pedigree

249 Genetic and reproductive parameters in a Holstein dairy herd.

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348 first lactation records for milk yield of Holstein cows, daughters of 44 Holstein sires were analyzed by using least squares. The objective was to estimate genetic parameters and breeding values. The environmental correlation (c^2) used to estimate breeding values was .02. Cows were classified in three groups according to season of parturition. The model included: sire, sire-season interaction and the residual as random effects, and season as fixed effect. The average milk yield 305d 2x in first lactation cows was 8,724.5 ± 1,401.89 kg. The projected milk production to mature equivalent to those cows was 11,012.2 ± 1,735.62 kg. Open days and services per conception were 148 ± 103.23 and 2.84 ± 2.09 respectively. The averages for milk yield by season were: 9,028 ± 1,294.34, 8,232.9 ± 1,163.96 and 8,783 ± 1,602.42 kg to october–january, february–may and june to september, respectively. A significant difference ($P<.01$) in milk yield was found to cows which parturitions ocurred among october and january than cows which parturitions ocurred into february to may season, but not for cows which parturitions ocurred into june to september. The average predicted milk difference was 65 ± 130.14 kg. These estimates were different to reported values into sires summaries. The correlation between 305d milk yield and projected milk difference were ($r=.93$ and $r=.67$)respectively. The estimated value of heritability to milk yield was .36 ± .033. The variance component for milk due to sire (209,865.28) was highly significant ($P<.01$).

Key Words: Heritability, Breeding Values, First Lactation

250 Genetic parameters between litter weight weaned and fertility, growth and wool traits of Columbia, Polypay, Rambouillet and Targee breeds of sheep.

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The objective of this study was to estimate correlations for Columbia, Polypay, Rambouillet and Targeebreeds between the composite trait, litter weight weaned (4,609; 6,469; 5,101; 5,708 records), and fertility (1,941; 3,261; 2,268; 2,402), growth (7,750; 9,524; 9,530; 9,321) and wool (11,673; 34,746; 18,443; 15,014) traits. Data were from the U.S. Sheep Experiment Station. Fertility was recorded as litter size at birth. Growth traits included birth weight, and average daily gain from birth to weaning. Wool traits included greasy fleece weight, fleece grade and staple length. The bivariate analyses, using derivative-free restricted maximum likelihood with animal models, included a covariance between additive genetic effects of the two traits plus appropriate additional covariances. Growth traits included an additional maternal genetic effect with covariances between direct and maternal genetic effects. The ranges in estimates of direct genetic correlations were as follows between litter weight weaned and: litter size at birth, −.30 to .43; birth weight, −.03 to .44; average daily gain, .21 to .67; fleece weight, −.20 to .27; fleece grade, −.07 to .19; and staple length, −.11 to .04. These estimates suggest a moderate positive genetic correlation between direct genetic effects for litter weight weaned and litter size at birth, a small to moderate positive genetic correlation between direct genetic effects for litter weight weaned and growth traits, and a near zero genetic correlation between direct genetic effects for litter weight weaned and wool traits. These estimates of genetic parameters between litter weight weaned, and fertility, growth and wool traits can be used with appropriate economic values to construct multiple-trait selection indexes for dual-purpose sheep.

Key Words: Correlations, Genetics, Selection

251 Estimates of (co)variances for first lactation milk and fat yields of Holstein cows in the US and Brazil.

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Genetic relationships for milk and fat yields between the US and Brazilian Holstein cattle populations were studied with first-lactation 305-days mature equivalent adjusted records of 726,932 daughters of 701 sires in the US and 29,413 daughters of 704 sires in Brazil. There were 358 US sires with progeny in both US and Brazil data. Components of (co)variance, heritability, and genetic correlations for milk and fat yields within and between countries were estimated by between-country multivariate analysis simultaneously including milk and fat yields in both countries using a sire model with a REML derivative-free algorithm. Sire and residual variances for milk in Brazil were 57% and 80.5% as large as in the US. Corresponding figures for fat yield were respectively 39% and 65%. Genetic covariance between milk and fat in Brazil was 60% as large as in the US. Heritability estimates and genetic correlation for milk and fat yields were respectively .34, .35 and .62 in the US and .25, .22 and .79 in Brazil. Genetic correlations between countries were .85 for milk, .88 for fat, .67 for milk in the US and fat in Brazil, and .55 for fat in the US and milk in Brazil. Although these last two genetic correlation estimates appear different, the covariances used in their estimation differed by only 1%. Thus, the difference between these two correlations is due to the scale of variance components for milk and fat yields in different countries. These results suggest ranking of breeding values of sires (BV) do not change significantly between countries (rank correlation between BV were .92 for milk yield and .94 for fat yield), and differences among sires are smaller in Brazil than in the US. Estimates of the genetic covariances between traits in different countries allow between-country genetic evaluations and prediction of correlated response in Brazil from sire selection in the US.

Key Words: Genetic Correlation, Genetic Evaluation, Variance Components

252 Genetic parameters of litter mortality and 6 related characteristics.

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Still born and preweaning mortality in pigs sums to 15 to 20 % of total piglets born Genetic improvement in litter size might even further increase mortality. What are the possibilities of selection against mortality? Data on birth weight, crossfostering and mortality was collected on some 200.000 individual piglets in the breeding structure of Dalland, the Netherlands, in 2 boar lines and 2 sow lines. Piglets were born on 12 different farms and were pure line or crosses. This dataset was reduced to single litter records per sow for the calculation of heritabilities and genetic correlation's in a multitrait equal design animal model analysis, with a model including parity, HYS, line/cross and sow as the animal effect. Piglet mortality is addressed as a litter characteristic of the sow, mortality of crossfostered piglets is traced back to the biological mother. As potentially interesting other litter characteristics litter size, litter weight, average birth weight, variation in birth weight, gestation length and still born were taken. Heritabilities are in good agreement with literature. Genetic correlation's of litter mortality with litter size (0.26), average birth weight (-0.11) and variation (0.16) are not significantly different from zero and unexpectedly low in magnitude. It is concluded that adding piglet mortality to the selection index of a breeding program is worthwhile.

Table 1: Heritabilities (diagonal), genetic correlation's (below diagonal) and error correlation's (above diagonal) of litter mortality and 6 related litter characteristics.

Nr.	Trait	1	2	3	4	5	6	7
1	Litter size	0.10	0.89	-0.45	0.20	-0.18	0.18	0.06
2	Litter weight	0.54	0.12	-0.05	0.16	-0.11	0.11	-0.08
3	Average birth weight	-0.49	0.46	0.35	-0.17	0.20	-0.17	-0.29
4	Variation in birth weight	0.03	0.43	0.42	0.07	0.03	0.08	0.09
5	Gestation length	-0.19	-0.14	0.03	-0.13	0.36	-0.05	-0.07
6	Still bor	0.16	0.22	0.09	0.09	-0.08	0.04	0.49
7	Litter mortality	0.26	0.12	-0.11	0.16	-0.32	0.57	0.05

Key Words: Piglet Mortality, Genetic Parameters, Litter

253 Genetic and phenotypic correlations among measures of neutrophil oxidative metabolism in Holstein bulls.

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Relationships between measures of oxidative metabolism were determined using phenotypic data from 60 Holstein bulls. Measures of oxidative metabolism included opsonized-zymosan phagocytosis-associated native chemiluminescence activity, myeloperoxidase-catalyzed iodination, and superoxide generation. Bulls were tested in 5 groups of equal size and sampled within the context of a glucocorticoid-induced immunosuppression model. Dexamethasone was used as the immunologic stressor. Days relative to dexamethasone treatment defined period 1 (days −5, −4, and −3), period 2 (days 2, 3, 4, and 5), and period 3 (days 9, 10, and 11). Neutrophil function was assessed each day for treated and untreated control bulls. Results were expressed as a percent of controls. Parameter estimates were obtained with MTDFREML using a multiple-trait animal model. Separate analyses were conducted for periods 1, 2, and 3. The model for each assay within period contained a random animal effect and the fixed effects of group, day, and group-day interaction. Eosinophil contamination was included as a covariate in the model describing the neutrophil iodination assay. Genetic correlations between measures of oxidative metabolism in period 1 were moderately high (range .66 to .81), but lower in periods 2 and 3 (range −.30 to .66). Phenotypic correlations between measures of oxidative metabolism were positive in all periods (range .16 to .56). Heritability estimates were obtained for all neutrophil measures within period and ranged from .15 to .54. Genetic improvement of functional neutrophil traits appears possible. Furthermore, our results indicate that neutrophil function measured by the 3 assays of oxidative metabolism may be under similar genetic control. Selection for improved response in one facet of oxidative metabolism would likely result in improvement in all measures.

Key Words: Neutrophil, Parameter Estimation, Oxidative Metabolism

254 Variability in female fertility in 3-in-2 accelerated lambing system.

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The objective of this study was to estimate genetic and phenotypic variability of fertility of ewes on Ontario Lamb Improvement Breeding Scheme (OLIBS). This production system requires ewes to lamb 3 times in 2 years resulting in a biannual production cycle. For the 3-in-2 accelerated lambing system, breedings fall into spring (S1: March to June), fall (S2: July to September) and winter (S3: October to December) seasons. Not all ewes are able to breed in each season and the traits of fertility in each season appear to be different but correlated. Data included 16,558 lambing records on 5665 ewes in 18 flocks from year 1986 to 1997. There were 7853, 9906, and 7734 observations for S1, S2 and S3, respectively. Fertility in ewes was defined as their ability to conceive and was treated as a binary trait. The model used was the same for all the 3 seasons and included fixed effects of flock-year of calving, age and breed of ewe and its mate, and random animal (ewe) additive genetic, permanent environment and residual effects. Data were analyzed using VCE software package with fertility considered a separate trait in each season. The heritability of S1 and S3 fertility was same (.05), but a little higher (.08) for S2. However, the genetic variability was observed to be similar (and higher) for S1 and S2 than for S3. S1 had the highest environmental variance and S3 the lowest. The genetic correlations amongst the 3 fertility traits were positive: .39 between S1 and S2, .43 between S1 and S3, and .08 between S2 and S3. Evidence of sufficient genetic variability for seasonal fertility in OLIBS ewes justifies its consideration in the OLIBS programs. Selection of ewes with high genetic merit for seasonal fertility should result in improved productivity of Ontario sheep flocks.

Key Words: Fertility, Sheep, Parameters

255 Effect of dominance variation and population structure on estimation of additive genetic variance.

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The impact of ignoring dominance genetic variance (V_D)on the estimation of additive genetic variance (V_A)was studied. Six populations with varying percentages of animals in full sib families,(0,2,10,20,50, and 100 population, three different combinations of V_A and V_D were considered:(A) $V_A = 950$, $V_D = 50$, (B) $V_A = 800$, $V_D = 200$, and (C) $V_A = 500$, $V_D = 500$, thereby creating a total of 18 subpopulations, each with 10,000 animals. In all cases, the residual variance was 2000 such that the broad sense heritability was 33%. Variance components were estimated using the tilde-hat approximation to REML. Estimates of V_A under a full model, that included additive and dominance genetic effects were unbiased whereas estimates of V_A under a reduced model, that included only additive effects, were biased upwards by as much as 80%. The large bias in V_A was particularly pronounced in populations with large number of animals in full sib families. We conclude that even in populations where V_D is relatively small, it should not be ignored in variance component estimation if the percentage of animals in full sib families is 10% or greater.

Percentage of animals in fullsib families	Reduced Model A	B	C	Full Model A	B	C
0	951	790	508	950	790	508
2	979	830	557	949	800	497
10	1048*	920**	652**	959	837	485
20	995*	921**	826**	945	784	543
50	1012**	955**	896**	943	788	480
100	1010**	993**	905**	948	809	476

*Bias significant at $P<.05$

**Bias significant at $P<.01$

256 Variance component estimation of calving ease and stillbirth of canadian holstein using bayesian analysis.

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The objective of this study was to estimate genetic parameters of calving difficulty and stillbirth for precise evaluation of the current Holstein population in Canada. A total of 129,765 calving ease and stillbirth records of Canadian Holstein were used. Both calving ease and stillbirth were scored as ordered categories. Calving ease scores ranged from 1 to 4 (unassisted, easy pull, hard pull, and surgery needed). These scores were then transformed according to the SNELL scoring system to range from 1 to 100. Stillbirth was scored as 1 if calf was alive in 24 hours after birth or 2 if calf was dead. We applied Bayesian analysis to the mixed linear sire model and Gibbs Sampling was used to obtain posterior densities. The results confirmed that the heritabilities (both direct and maternal) for these two traits were very low. The heritablities for direct calving ease (DCE), maternal calving ease (MCE), direct stillbirth (DSB) and maternal stillbirth (MSB) were 0.05, 0.03, 0.03 and 0.06, respectively. Negative correlations were observed between direct and maternal components for both calving ease and stillbirth, but the relationship was greater for stillbirth. The genetic correlation between DCE and MCE was −0.16; DSB and MSB was −0.25. These negative correlations between direct and maternal genetic cause selection difficulties for both calving difficulty and stillbirth. Genetic correlation between DCE and DSB was high (−0.57). The phenotypic correlation between CE and SB was −0.19. The correlation between MCE and MSB was moderate (−0.34). The correlations between DCE and MSB, MCE and DSB were positive but very low (0.04).

Key Words: Calving Ease, Variance Components Estimation, Bayesian Analysis

257 Genetic parameters among preweaning and carcass traits of crossbred beef cattle.

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Preweaning and carcass trait records from crossbred steers (n = 1015) and heifers (n = 957) were used to estimate genetic parameters. Dams (n = 775) representing three F_1 and twelve back-cross types involving the Charolais, Hereford, Angus and Shorthorn breeds were mated over six years to Limousin bulls (n = 36) at two locations. Animal models were fitted to obtain estimates of direct and maternal heritabilities and genetic correlations among three preweaning and four carcass traits. Direct heritabilities were .28, .12 and .16 for birth weight, preweaning daily gain and 200 d weight, and .20, .35, .50 and .38 for hot carcass weight, fat thickness, ribeye area and percent lean yield, respectively. Maternal heritabilities were .21, .22 and .40 for birth weight, preweaning daily gain and 200 d weight. Estimated genetic correlations between percent lean yield and carcass weight, fat thickness and ribeye area were −.05, −.85 and .39, respectively, and .30 between carcass weight and ribeye area. Direct effects for birth weight had moderate (.51 to .54) correlations with direct effects for carcass weight, ribeye area and percent lean yield. Preweaning daily gain and 200 d weight direct effects had weaker (<.35) correlations with direct effects for ribeye area and percent lean yield. Direct effects of fat thickness were negatively correlated with direct effects for birth weight (−.44), preweaning daily gain (−.15) and 200 d weight (−.25). Maternal effects for preweaning traits had near zero correlations with direct effects for fat thickness and percent lean yield. Correlations between direct effects for carcass weight and maternal effects for birth weight, preweaning daily gain and 200 d weight were .44, −.05 and .64, respectively. Adding preweaning trait information to carcass trait evaluations slightly improved prediction error variances for breeding values and would be recommended only when information on carcass traits was limited.

Key Words: Genetic Evaluation, Carcass Traits, Beef Cattle

258 Comparison of models for the genetic evaluation of backfat depth and growth rate in pigs.

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Six single trait models were fitted to growth and backfat data of Duroc swine to investigate their suitability for evaluation of breeding values. The basic model included fixed test group and sex(herd), random direct genetic effects and residual. The five additional models were identical to the basic model but differed for combinations of random litter effect, maternal genetic effect, permanent environment and covariance between direct genetic and maternal genetic effects. Records of backfat depth and age in days adjusted to 113.4 kg for 44,223 Duroc pigs from 1677 test groups and 220 sex(herd) classifications were provided by the National Swine Registry. (Co)variance components were estimated using the MTDFREML computer programs and a single trait animal model. A likelihood ratio test was used for model comparison. Including the litter effect led to a better fit of the data and litter consistently accounted for 23 % of the phenotypic variance in days and 7 to 8 % of phenotypic variance for backfat. Permanent environmental effects were significant ($P < .001$) only for days and accounted for 1 % of the phenotypic variance. The model providing the best fit for days ($P < .001$) included all random effects while the model with the best fit for backfat ($P < .005$) did not include permanent environment. Heritability estimates from the best models were .45 for days and .43 for backfat depth. Estimates of the heritability for maternal genetic effects were .10 and .03 for days and backfat, respectively. Including the direct-maternal covariance did improve the fit of the model for both traits and the correlation was estimated as −.78 for days and −.53 for backfat. The selection of a suitable statistical model is an important step in the development of a genetic improvement program.

Key Words: Pigs, Variance Components, Linear Models

259 Estimates of genetic parameters for growth and meat quality traits in a pig sire line.

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Performance test data from 6,414 pigs out of a PIC line and meat quality data from 516 of these pigs were used to estimate genetic relationships between growth traits, carcass traits, and meat quality traits. Performance traits included legs score index (LEGS), days to 110 kg, real-time ultrasonic backfat measured 6 cm off midline at the last rib (P_2), average daily feed intake, loin muscle depth, and conformation score (MS). Longissimus muscle quality traits were ultimate pH measured at 30 hours post mortem (pH_u) and Minolta Chroma Meter lightness (L^*). Ultimate pH was measured on a homogenized sample of longissimus muscle. L^* was measured as the average of two measurements. The statistical package VCE (3.2, E. Groeneveld, 1996) was used to estimate (co)variance components with an animal model and full pedigrees. Genetic correlations between meat quality traits and production traits were small ($|r_g| < .12$). The genetic correlation between L^* and pH_u was moderate ($r_g = -.55$) indicating darker loins are genetically associated with higher ultimate pH. Heritability of performance traits ranged from .20 (LEGS) to .55 (P_2), and heritability of L^* and pH_u were .24 and .29, respectively. These estimates of genetic parameters are in agreement with previously published estimates from much smaller data sets. Small increases in accuracy are expected for breeding values of meat quality traits due to low genetic correlations with growth traits using multiple trait BLUP.

Key Words: Pigs, Grow-Finish Performance, Meat Quality

260 Factors affecting immunoglobulin G concentration and total solids percentage in ewe colostrum.

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This study was conducted to investigate sources of variation on ovine colostrum immunoglobulin G concentration (IgG) and total solids percentage (TS). We were also interested in determining whether TS is heritable and estimating the genetic, environmental, and phenotypic relationships between TS and lamb average birth weight (BW) and average weaning weight (WW). Nine hundred sixty colostrum samples from Columbia, Rambouillet, and Targhee ewes from the U.S. Sheep Experiment Station, Dubois, ID were used. Postpartum, presuckle IgG was assayed from 58 ewes using single radial immunodiffusion procedure. The freeze drying procedure was used to determine TS. Average IgG and TS were 76.5 mg/ml and 17.1%, respectively. We analyzed the effect of the different factors using ANOVA. Our linear model for the analysis of IgG included breed (B), age of ewe (AoE; 1 to 4 and 7 years), litter size (LS; single, twin, triplet), BW, and TS. Single birth data (N=25) were analyzed to evaluate the effect of lamb sex (SEX). The linear model for the analysis of TS included B, AoE (1 to 7 years), LS (single, twin, triplet, and quadruplet), BW, and sire of ewe within breed (SB). Lamb gender effect on TS was determined from single births (N=359). We obtained heritability (h^2) estimates for TS, BW, and WW using a single trait animal model and Method R. A multi-trait animal model was used to obtain correlations between traits. IgG was affected only by TS. Total solids percentage was significantly affected by LS ($P = 0.02$), SEX ($P = 0.06$), BW ($P = 0.08$), and SB ($P = 0.001$) but not B or AoE. The estimates of h^2 for TS, BW, and WW were .36 ± .10, .38 ± .11, and .29 ± .08, respectively. The heritability estimate for TS indicates that it should respond to selection. Assuming no dystocia, the genetic correlation between TS and BW (r = .17) is encouraging. To confirm these results, additional studies including more observations are necessary.

Key Words: Immunoglobulin-G, Heritability, Colostrum

261 Managing inbreeding and utilizing dominance effects in a herd mating program.

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The national data sets for 14 linear type traits and the overall measure of conformation called final score were analyzed with a model including fixed effects for management, age at calving and stage of lactation, a linear regression on inbreeding coefficient and random additive animal ($\mathrm{ADD}_{\mathrm{animal}}$), parental dominance ($\mathrm{DOM}_{\mathrm{sire,dam}}$) and permanent environment. A mating program, utilizing a linear programming algorithm, initially selects animals based upon additive genetic merit and then maximizes total genetic merit. Total genetic merit of an animal equals ($\mathrm{ADD}_{\mathrm{sire}} + \mathrm{ADD}_{\mathrm{dam}}$)/2 + $\mathrm{DOM}_{\mathrm{sire,dam}}$ + Inbreeding Depression. Different scenarios based on changing the herd's breeding objective and utilization of resources were examined to investigate their effect upon the improvement of total genetic merit versus randomly assigning mates. Applying constraints such as increasing number of sires used or limiting the usage of individual bulls increases the value of a mating program. Under realistic conditions, it is expected that a mating program should improve total genetic merit by .07 phenotypic s.d. and decrease average level of inbreeding by 1.5%. This improvement is worth approximately $28.00 per mating. Utilization of dominance effects and managing inbreeding through the use of a mating program will increase an individual herd's profitability by improving the total genetic merit over randomly assigning mates.

Key Words: Mating, Dominance, Inbreeding

262 Influence of genetic groups on estimates of genetic parameters and inbreeding depression in swine.

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The primary objective of this study was to evaluate the effects of dominance and inbreeding in a Yorkshire data set. The data set contained 118,603 records on 100-day weights. Initially, Method R was utilized for estimation of genetic parameters and inbreeding effects with a model that included the fixed effects of sex and contemporary group, a covariate for inbreeding depression, and the random effects of animal, dominance, and litter of birth. Results from these initial procedures revealed that the inbreeding depression was estimated as positive, which was counter-intuitive. Further inspection of the data set revealed a large number of import animals with little or no pedigree information. Subsequently, a second analysis was conducted that included the same effects initially described as well as unknown parent groups based upon birth year of the animal. The estimate of inbreeding depression from the second analysis was -1.3 kg / 10% of inbreeding, much closer to the expected range. Estimates of variances relative to the phenotypic variance were 24.5% for additive, 14.2% for dominance, and 12.7 for litter, which indicates relatively large dominance variation. Confounding between the inbreeding depression and unknown parent groups was due to generally lower 100-day weight of imported animals relative to nonimported ones. Because imported animals lacked pedigrees, the presence of inbreeding was an indicator of nonimported status. When the population contains a large number of imported animals, the use of current models which do not include unknown parent groups may result in confounding which decreases the accuracy of the estimation, and subsequently the prediction procedure. In general, the inclusion of dominance genetic effects, a covariate for inbreeding depression, and unknown parent groups may all contribute to an improvement in the accuracy of evaluation for growth traits in swine populations.

Key Words: Inbreeding, Unknown Parent Groups, Dominance

263 Calculation of expected inbreeding percentage of future progeny.

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Animals most related or least related to current members of their breed were identified by calculating expected inbreeding percentages for future progeny. Reference populations of potential mates were chosen by randomly selecting 300 males (if available) and 300 females from the most recent birth year (1996). Smaller samples of 100 and 200 animals of each gender were examined to determine effect of reference population size. The tabular method was used to compute inbreeding percentage and relationships among members and ancestors of reference populations. Although nearly 2 GB of memory were required for the maximum of 13,508 animals included in this step, computing times were just a few minutes. Mean relationship of other animals to the reference population was computed as the mean for their parents. To-Mar Blackstar-ET and Pawnee Farm Arlinda Chief were most related to the Holstein breed with expected inbreeding of 8.4 and 8.0%, respectively. Corresponding Jersey bulls were Highland Magic Duncan and Soldierboy Boomer Sooner of CJF with expected inbreeding of 11.6 and 9.8%, respectively. Among bulls with >100 daughters, highest expected inbreeding was 11.5% for Selwood Betty's Commander, 8.2% for Forest Lawn Simon Jetway, 10.1% for Dutch Mill Telestars Fayette, and 7.6% for Sunny View Princess' Promise for Ayrshire, Brown Swiss, Guernsey, and Milking Shorthorn breeds, respectively. Some bulls had few daughters but high expected inbreeding percentages. Their pedigrees almost always included one or more of the bulls above. Expected inbreeding percentages and rank changed little when reference populations included fewer animals. A regression on inbreeding in the genetic evaluation procedure would remove effects of past inbreeding, and information on expected inbreeding of future progeny could allow predicted transmitting abilities of bulls and cows to include expected future inbreeding depression.

Key Words: Inbreeding, Genetic Evaluation, Reference Population

264 Qualitative description of milk recording data using fuzzy sets. R. Lacroix* and K. M. Wade, *McGill University, Montreal, Canada*.

Dairy producers and their advisors can generate a large amount of useful information by analyzing test day data. This information can be used, in turn, to improve management decisions related to breeding, nutrition and health. However, the amount of data supplied by milk recording agencies is tremendous, and tools need to be developed to support analyzes of these data. Such tools can make use of many of the new techniques which have become available in the last two decades, resulting from research into artificial intelligence. One approach refers to fuzzy sets, which are helpful in manipulating data under qualitative terms, i.e., in a format which is natural to users. In order to help in the analysis of lactation data, a software system based on fuzzy sets was developed. The analyses were based on comparison of the data for individual cows with standard values determined as a function of their parity, days in lactation and herd average milk yield. An important step consisted of determining the membership functions which allowed the software to describe the numerical data qualitatively (i.e., in the same manner as experts). To establish the membership functions, 324 records were extracted randomly from a file containing 12,744 records, representing 36 herds and 1103 cows. The extracted data were then shown separately to two experts, who were asked to categorize each record into a maximum of two consecutive fuzzy sets out of five (very low, low, medium, high and very high). This information was then analyzed graphically and numerically, and a non-linear model was used to fit the data for each fuzzy set. The experts were relatively consistent in their analyses, but important differences were observed among them. The overall approach led to membership functions which differed considerably from those determined by the same experts prior to the project. Although the overall approach seems valid in establishing membership functions, research needs to be pursued to test alternative modeling approaches, such as neural nets, which would allow for the development of a multivariate non-linear model.

Key Words: Dairy Cattle, Milk Recording Data, Fuzzy Sets

265 Using blackboard-based decision-support software to determine genetic and management effects in dairy herds. A. A. Archer*, R. Lacroix, and K. M. Wade, *McGill University, Montreal, Canada*.

Animal breeding techniques have been quite successful at improving the genetic makeup of dairy cattle. However, on-farm management practices must also create an environment in which genetic superiority can be expressed. If management practices have a detrimental effect the producer will want to know which practices need improvement (in order of severity) and to what extent they can be improved. The objectives of this research were to determine the relative effect that farm management strategy has on a herd and to make recommendations for improvement to the manager, given the objectives, by using blackboard-based decision-support reasoning. Information comes from many organizations in the dairy industry. The difference between a herd's average genetic deviation from the national average, and its actual production gives an estimate of its management effect. To be as useful as possible the estimates are investigated at the individual cow level. From this, and the objectives of the producer, the system recommends a strategy to improve production efficiency. Processing relies on a blackboard methodology, multiple sources, and knowledge-based problem solving. This allows opportunistic techniques which means that the decision-support software does not require a set data pattern to function. Knowledge sources are developed from the expertise of organizations in the dairy industry (Genetic Evaluation Centers, DHI, AI Units, Breed Associations, etc.). Along with farm records, these organizations are also the source of the data. The system is designed to input data and information about a farm, process the information (using independently acting knowledge sources) and return a status report to the manager about his cows. The resulting report details the genetic superiority (or inferiority) of the herd and shows to what extent the management practices of that farm mitigate or enhance genetic expression. The report's recommendations, after proper interpretation, will be presented to the user in monetary terms that reflect improved efficiency.

Key Words: Decision-support Systems, Genetic Improvement, Management

266 Applying ActiveX technologies to create Internet-based decision-support systems for dairy cattle management. M. Strasser*, R. Lacroix, and K. M. Wade, *McGill University, Montreal, Canada*.

Advisory decision-support systems have long been available as management tools in the dairy community. Unfortunately, their degree of acceptance has not yet grown to expected levels. One of the reasons for this shortcoming is that they are used infrequently and, to some potential users, this might not justify the time and costs associated with acquiring, maintaining, and operating the software. Also, for decision-support systems to remain relevant they must be constantly updated and revised to reflect changes in their respective domains. However, distribution of software updates is usually infrequent, due to the associated costs, particularly when revisions are often relatively minor. One way to overcome these problems is to develop systems for distribution over the Internet. On its own, the programming language used to create HTML pages is not yet powerful enough for this kind of proposed system development since it allows for little more than the static presentation of text with relatively simple graphics. However, there exist many new tools that hold the promise of online system development. These tools include Java applets and Beans, as well as ActiveX controls, that can be embedded within HTML pages. The objective of this project was to investigate the applicability of using ActiveX controls for the development and distribution of a dairy decision-support system over the Internet, and to determine the effectiveness of the Internet as a media format for the distribution of expert knowledge to a large audience. The decision-support system was in the area of dairy cattle culling. ActiveX controls allow for rapid development, the ability to link controls to other sources of information (e.g., veterinary or milk recording agency databases), and the ability to interact with the user through a graphical interface. Once downloaded, it can run directly from the local computer and, every time the program is accessed, the control automatically retrieves any necessary update. These advantages make it extremely suitable for systems development in many on-farm situations.

Key Words: ActiveX, Decision-support Systems, Dairy Cattle Management

267 Relationships among age at the first race and racetrack performance traits in Brazilian Thoroughbred horses. M.D.S. Mota* and H. N. Oliveira, *Universidade Estadual Paulista*.

Racehorses beginning their careers at a precocius age can start more often, and may have better racing performance than animals beginning at older age. The aim of this study was to estimate the genetic and phenotypic correlations among age at first race (F) and following racetrack performance traits: number of victories (NV), number of placements in top 5 (N5), percentage of victories (PV), percentage of placements in top 5 (P5) and number of starts (NS). 1138 Brazilian Thoroughbred born between 1982 and 1989 were analyzed. Covariance components were estimated by a two traits model using MTDFREML, and the linear model considered the random effect of the animal and a set of fixed effects: birth month and year, and sex. Just the genetic correlations between F;NV and F;PV were positive (0.24 and 0.10, respectively), the others were negatives and close to zero (-0.03 to -0.06). In the same way, an only one phenotypic correlation, between F;PV, was positive (0.02). The higher phenotypic correlations were between F;N5 (-0.13) and F;NL (-0.15). This results indicates that horses with a high genetic merit for NV and PV were those with a low genetic potential for F. Phenotyipically, animals with greater NS and N5 were those with lower F.

Key Words: Racehorse, Thoroughbred, Genetic Correlations

268 Genetic parameter estimates for serum IGF-I concentration and carcass traits in Angus beef cattle.

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Divergent selection for blood serum IGF-I concentration was initiated in 1989 using 100 spring-calving (50 high and 50 low line) and in 1990 using 100 fall-calving (50 high and 50 low line) purebred Angus cows located at the Eastern Ohio Resource Development Center. Each year four bulls with the highest and four with the lowest IGF-I concentrations were saved for breeding within the selection lines. Bulls not saved for breeding were slaughtered at the conclusion of the 140-d postweaning performance test. The MTDFREML program (Boldman et al., 1993) was used to obtain genetic paramter estimates for serum IGF-I concentration at d 28, 42, and 56 of the postweaning period and for mean serum IGF-I concentration, as well as for carcass characteristics. The initial statistical model included fixed effects of year, season, selection line, sex of calf (omitted in the analysis of carcass traits), and age of dam, random animal, maternal, and permanent environmental effects, and a covariate for age of calf. Maternal and permanent environmental effects were deleted from the final model because they accounted for only a small proportion of the total variability. Included in the analysis were 1,910 animals in the A inverse matrix, 945 of which had valid records for IGF-I and 343 of which had valid carcass data records. Direct heritability was .42, .73, .42, and .50 for IGF-I at d 28, 42, and 56 of the postweaning period and for mean IGF-I, respectively. Additive genetic correlations of mean IGF-I with backfat thickness, ribeye area, KPH, hot carcass weight, marbling score, quality grade, and yield grade were −.18, .18, −.99, .43, .32, .21, and −.07, respectively. Environmental correlations of mean IGF-I with these carcass traits were .09, .03, .20, −.02, .10, .20, and ,09, respectively. Phenotypic correlations were .01, .07, .16, .11, .15, .19, and .04, respectively. Additive genetic correlations indicate that selection for increased serum IGF-I concentration in beef cattle should lead to genetically reduced carcass fat, increased lean yield, and increased carcass quality.

Key Words: Beef Cattle, Insulin-Like Growth Factor, Carcass Composition

269 Analysis of rams' testes for consistency, form and circumference of scrotum, libido and sperm quality.

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Consistency, form and circumference of scrotum (SC), libido and sperm quality of 20 mature and 65 inmature Hungarian Merino rams were examined in this study. The rams were classified into four categories according to the consistency of testes as follows: (1) compact and flexible, (2) loose and flexible, (3) compact and inflexible and (4) loose and inflexible, resp. Of mature and inmature rams 10, 7, 1 and 2, i. e. 30, 28, 2 and 5 were assigned into the four categories. Low variance with compact and flexible (1) or loose and flexible (2) categories were recorded for SC. On the contrary, a large variation has been found for SC in categories 3 and 4 in mature and inmature rams, as well. Low rank correlation between consistency and SC were present in both groups (r = 0.2 − 0.4). As for libido and sperm quality, the latter ram groups seemed to be inferior. The form of the scrotum was assessed as described by Coulter (1986) for bulls. Scrotum form was ideal, acceptable and undesirable in 43.8 and 50.3, 37.5 and 29.7, 18.7 and 20.0 % of cases for mature and inmature rams, resp. Rank correlation coefficients between form of scrotum and SC were r = 0.60 and r = 0.75 for mature and inmature rams, resp. Sperm quality in rams with undesirable form proved to be inferior. Findings reveal significant ($P\leq0.05$) seasonal differences in scrotum circumference for the Hungarian Merino breed (average for September, February and July records were 34.9, 33.6 and 32.6, resp.). For this reason, seasonal effects have to be taken into consideration in mature rams when assessing SC. Similar phenomenon has not been observed in inmature rams. Accelerated development of testes started at 3–4 months of age, with a slight rate of decrease at 7 months, attaining mature size at 1 and a half years. Intermediate relationship was found between body weight of inmature rams at 6 months of age and SC (r = 0.63). Rank correlation between libido and SC, libido and sperm quality and SC and sperm quality were r = 0.56, r = 0.45 and r = 0.26 − 0.52, resp.

Key Words: Ram, Testes, Scrotum

270 Influence of selection for greater yearling weight and smaller birth weight on the reproductive traits of scrotal circumference and age at puberty for purebred Hereford cattle.

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Beginning in 1975 and running through 1990, a selection program was initiated in a herd of closed line purebred Hereford cattle at the Northern Agricultural Research Center at Havre, MT. Selection of breeding males was based on the index of adjusted yearling weight minus 3.2 x adjusted birth weight. Direct response to the selection index was positive. By using the animal model and MTDFREML procedures, breeding values (BV) and genetic parameters were calculated for two traits relating to reproduction; scrotal circumference (SC) of the males and age at puberty (PUB) for the females. The model included year and age of dam with covariates of age at measurement for scrotal circumference and date of birth for age at puberty, individual inbreeding, and maternal inbreeding. The direct genetic, maternal genetic and permanent environment effects were initially included, but maternal genetic and permanent environment were not important. Single trait analysis showed heritabilities of .26 for SC and .24 for PUB. When run as a two-trait analysis, these values did not change, and the genetic correlation between their direct genetic effects was estimated at −.54. Yearly averages for BV for SC showed a slight increase of .03 cm per year. Breeding values for PUB also showed a slight increase of .27 d per year. Correlated responses in BV of SC and PUB were small when selection was for a selection index of greater yearling weight and smaller birth weight.

Key Words: Scrotal Circumference, Age at Puberty, Heterosis

271 Comparison of sperm metabolic rate with sperm motility between different sheep breeds using the resazurin reduction spectrophotometric assay.

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The metabolism is a basic process of biological activity and reproductive performance depends on metabolic processes. This study compared sperm metabolic rates with sperm motility between different breeds of sheep using the resazurin reduction spectrophotometric assay. Five breeds were tested: Polypay (n = 36), Columbia (n = 32), Rambouillet (n = 51), Targhee (n = 35) and Suffolk (n = 32). Semen from each ram was collected by electroejaculation, diluted 20 x with PBS and then exposed to resazurin dye (R7017, Sigma) at a final concentration of 7 µg/ml. The mixture was incubated at 37 °C for 60 min and then measured for specific absorbance at 600 nm wavelength. The concentration of motile spermatozoa was determined by a hemocytometer. One-way ANOVA and Fisher's LSD was used to determine differences between breeds. The relationship of absorbance values with sperm motility was analyzed by a simple linear correlation. The mean absorbance at 600 nm was .54, .56, .74, .66, and .70 for Polypay, Columbia, Rambouillet, Targhee and Suffolk, respectively. The metabolic rate for Rambouillet as measured by the specific absorbance was higher (P < .05) than those for Polypay and Columbia. The mean numbers of motile spermatozoa were 1.08, 1.06, 1.75, 1.31 and 1.28 x 10^9/ml for Polypay, Columbia, Rambouillet, Targhee and Suffolk, respectively. Sperm motility of Rambouillet was greater (P < .05) than those of the other breeds. Correlation analysis indicated that the absorbance at 600 nm was strongly ($r = .7626$, P < .01) associated with the numbers of motile spermatozoa in semen samples. We conclude that the resazurin reduction assay can provide pertinent information for quantitatively evaluating potential fertility of spermatozoa between different sheep breeds.

Key Words: Fertility, Metabolic Rate, Resazurin Reduction Spectrophotometric Assay

272 Method R estimates of heritability, repeatability, and dominance fraction of variance for milk, fat, and protein yields of Holstein dairy cattle.

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Fractions of variance accounted for by additive genetic, dominance genetic, and permanent environmental effects for milk, fat, and protein yields were estimated from Holstein data used for USDA-Dairy Herd Improvement Association genetic evaluations. Contemporary group assignments were determined with the procedure used for national evaluations. Data included 1,893,863 milk and fat records for 780,953 cows and 933,534 protein records for 426,125 cows. Data were selected to maximize the number of full-sibs in the analysis. Full-sibs were identified across herds, and data from herds with at least 15% full-sibs were used. All pedigree data in the USDA database were included. Unnecessary animals without records were removed from the pedigree. Because of computational limitations, a single level of recursion was used to build the inverse of the parental dominance relationship matrix. Those limitations resulted in the inclusion of full-sibs, three-quarter sibs, and some cousins in dominance relationships. Additive and dominance relationships included 1,402,810 (1,189,779) animals and 2,418,885 (1,321,325) dominance classes for milk and fat (protein) yields. Variance components were estimated with the JAADOM program, which uses iteration on data and second-order Jacobi iteration for obtaining solutions to the mixed model equations and Method R for estimation of variance components. Five different random subsets of the data were used for parameter estimation. Additive genetic, dominance genetic, and permanent environmental fractions of variance were 0.33, 0.05, and 0.11 for milk yield; 0.34, 0.06, and 0.10 for fat yield; and 0.32, 0.06, and 0.09 for protein yield. Mean approximate standard errors of additive genetic, dominance genetic, and permanent environmental variance fractions were 0.004, 0.009, and 0.008, respectively.

Key Words: Method R, Parameter Estimation, Dominance

273 Relationship between severity and duration of clinical mastitis and sire transmitting abilities for somatic cell score, yield, productive life, and udder type traits.

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The objective was to determine the relationship between severity and duration of clinical mastitis and sire transmitting abilities for somatic cell score (SCS), yield traits, productive life, and 7 udder linear type traits. A severity code of 1, 2, 3, 4, or 5 (1 = normal milk) was recorded daily for 30 days after detection of each clinical episode in 6 PA herds and 1 NE herd. Severity codes were recorded for 456 first lactation cows (1704 total first lactation cows) and 230 second lactation cows (1055 total second lactation cows). The first and second lactation cows with severity and duration data were sired by 168 and 100 Holstein bulls, respectively. Initial severity code, maximum severity code, log of the sum of all severity codes >1, and log of the total number of days the severity code was >1 in the 30 days following detection were regressed on herd, days in milk at clinical detection, and sire transmitting abilities taken one at a time. Linear or linear and quadratic effects for each transmitting ability were included in the models. In addition, logistic regression was used. Separate regression analyses were conducted for severity and duration of clinical mastitis from: (1) all cultured organisms (organism included as a covariate), (2) coagulase negative staphylococci, (3) coliform species, (4) streptococci other than *Streptococcus agalactiae*, and (5) all environmental organisms. Higher transmitting abilities for SCS were associated ($P<.10$) with higher initial severity codes and higher maximum severity codes for mastitis caused by coliform species and all environmental organisms in first lactation. Lower transmitting abilities for milk yield and higher transmitting abilities for protein % and fat % were associated ($P<.10$) with higher initial severity codes and higher maximum severity codes for mastitis caused by all organisms in first lactation. Results for other traits were mostly non-significant.

Key Words: Mastitis, Genetics, Somatic Cell Score

274 Confidence intervals for genetic parameters from method R estimates.

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Confidence Intervals (CI) for weaning weight direct (WWD) and weaning weight maternal (MAT) heritabilities, and the direct-maternal genetic correlation (DM) were obtained for simulated data using Method R estimates from a univariate, multiple random component, full animal model, with 50% subsampling. Twenty estimates of each parameter were used to obtain 80, 90, 95, and 99% CI for each of 500 data sets (N = 5000). Estimates of each parameter were transformed to normalize their distribution. Confidence intervals were computed as $\mathrm{CI} = \mu \pm \mathrm{T} \times \sigma$, where μ and σ were the mean and SD of a parameter's estimates, respectively, and T was the critical value from the T distribution for a 1-α CI, with N-1 df. Upper and lower CI bounds were converted back to the original scale by reversing the transformations. Percentages of CI containing the true value for 80, 90, 95, and 99% CI were 83.4, 92.2, 96.4, and 99.0% for WWD; 80.0, 89.2, 94.0, and 98.0% for MAT; and, 86.0, 94.2, 97.8, and 99.2% for DM. These percentages were significantly greater (or approached significance) than expected for 80, 90, and 95% CI for WWD and DM. Average limits of 95% CI for WWD and DM, respectively, were .01 and .05 further from the true value than CI that contained the true value at the expected frequency. These results suggested that Method R estimates can be used to obtain reliable CI for heritability and genetic correlation.

Key Words: Heritability, Confidence Intervals

275 Energy metabolism in early lactation of heifers selected for milk yield.

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Three genetic groups of heifers were fed ad libitum a complete diet (64 % DM and 6.9 MJ NE and 98 g dcp per kg DM). Genetic groups were: nucleus heifers (DD, n=50) selected as bull dams after 180 days of lactation, nucleus heifers (DN; n=309) not selected as bull dams and heifers (ID; n=126) from Dutch progeny tested sires. DD, DN and ID heifers consumed 134, 128 and 127 MJ NE per day, required for maintenance 33, 32 and 32 MJ NE per day and produced in milk 106, 93 and 86 MJ NE per day. NE-balance was −5, +3 and +9 for the genetic groups, respectively, while they gained −7, +11 and +18 kg of body weight in this period. Slight differences between the genetic groups were recorded for plasma concentrations of glucose, 3- Hydroxybutyrate, NEFA and Urea, which indicate the highest mobilization of body fat in DD heifers and a higher N-efficiency in this group. Heritability estimates were 0.5 for milk yield and body weight, 0.6 for feed intake and 0.2 for metabolites in plasma. Genetic correlations indicated that selection for milk yield will increase negative energy balance and increase body fat mobilization of heifers in the first 100 days of lactation. Selection for feed intake will yield favourable effects on energy metabolism in early lactation.

Key Words: Dairy Cows, Energy Balance, Genetics

276 Repeatability of endocrine response to intensive and simplified challenge test in juvenile dairy bulls.

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Fifty-five dairy bull calves were subjected to simplified challenge tests at 6.5, 8, and 10 months of age, and an intensive challenge test at 9 months of age. At each occasion two tests were performed on each calf: First, a growth hormone (bGH) release test using GRF to induce release (at 08.00 h), and next, a glucose tolerance test (at 14.00 h), where insulin was measured in plasma. Feeding was reduced for 4 days prior to testing and calves were fasted overnight before being tested. Blood was obtained through jugular vein cannulae at -15, -5, 0, 5, 10, 15, 20, 30, 45 and 60 minutes relative to infusions. In the simplified test, samples were taken at 0 and 15 minutes only. Plasma was stored frozen until assayed for bGH (RIA) and insulin (TR-FIA). Intraclass correlations (r) were estimated for concentrations in samples obtained at 0 and 15 minutes in both types of tests. The model included random effects of animal, testday, and residual, and fixed effects of age-class and age in days within age-class. Using a GRF challenge was efficient in increasing the repeatability of bGH measurements (r-before 0.09, r-after 0.23, s.e. 0.10). However, bGH response decreased with age, and results at 10 months were not correlated with response at younger ages. The repeatability of insulin response to glucose was not clearly increased by the test procedure (r-before 0.30, r-after 0.24, s.e. 0.13), and again responses at 10 months of age were more variable and showed lower repeatability. The results show that a simple challenge test can improve the repeatability of endocrine measurements in cattle. Application of simple endocrine tests as genetic indicator traits in selection programs may thereby become feasible.

Key Words: Repeatability, Endocrine Test, Indicator Trait

277 Genetic parameters for porc quality in a halothane- negative sire line breed.

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Genetic parameters for porc quality and production traits were estimated in the halothane-negative Stamboek Great Yorkshire sire line. The data-set consisted of 6,538 performance tested pigs, slaughtered between April 1988 and March 1997. Next to daily gain and ultrasonic backfat thickness, lean meat percentage after dissection and 7 meat quality traits were determined at the day after slaughtering. Genetic parameters were estimated in a multiple trait REML analysis. Heritabilities for meat quality traits varied between 0.11 for subjective colour score and 0.20 for pH value. The genetic cor- relations between meat quality traits and meat percentage were favourable for drip loss but unfavourable for meat colour. The analysis of results of boars versus gilts showed significant genotype × sex interactions for only pH value. Considering the genetic parameters estimated and the economic weights for the relevant traits, the inclusion of pH-value and meat percentage after dissection will improve genetic progress with 21 percent compared to selection based on only daily gain and ultrasonic backfat thickness. It was concluded that dissection and meat quality measurements are relevant for optimal selection in sire lines.

Key Words: Genetic Parameters, Pork Quality, Breeding Programs

278 Comparison between effects of restricted and non restricted reproductive traits on efficiency of selection indices for Hungarian Holstein Friesian populations.

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Maximum likelihood procedures were used to analyze the relationship between reproductive performance of Holstein Friesian and productive trait of daily milk yield performance. Genetic and phenotypic (co)variances were generated from this analysis to construct different multi-trait selection indices, and to study the effect of restriction of daily milk yield on efficiency of selection. Data structure was half-sib family of 281 sire groups, lactation records in each group ranged between 12 and 24 records. The reproductive index contained reproductive traits (number of services per conception (NOS), days open (DO), and age at first calving (AFC)). In productive index were involved productive traits (daily milk yield traits: average daily milk yield per lactation (AV), per calving interval (AVCI), and per life time production (AVLF)). In productive-reproductive Indices different combinations of productive and reproductive traits were involved. The highest expected genetic improvement in reproductive performance and the highest reduction in reproductive costs were (-7767 Ft/generation) achieved by a pure reproductive index (I1). The same trend can be seen in productive indices: in milk production an index (I2) contained only productive traits predicted the highest improvement: 0.36 kg milk/day/generation. Correlated responses connected to either productive or reproductive indices were very low. Incorporation of daily milk yield in the reproductive index reduced the expected improvement in reproductivity. Considerable decline was generated by restriction on AV in the expected reproductive costs.

Key Words: Correlated Response, Milk Yield, Reproductive Cost

279 Results of linkage analysis between QTL for milk production traits and Casein markers using multipoint analysis.

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Using the genetic values of 1258 Black and White dairy cattles QTL-effects for five milk production traits have been estimated. A maximum likelihood approach by Liu (1994) and Simianer (1993 and 1995) was applied for realizing linkage analysis underlying the model of mixed inheritance. The genotyping was carried out by isoelectric focusing. Two Casein markers each have been used in one treepoint analysis. The results of the analyses including β-CN suggest a close linkage to QTL for fat yield, protein yield and fat content indicated by estimated recombination fractions of 0 and LOD scores of 1.89, 1.17 and 1.09. The LOD scores were highest from analyses of α_{s1}-CN and κ-CN indicating a medium genetic linkage with map specific LOD score of 3.03. The recombination rate was estimated to be 0.26. The likelihood surface suggests the existence of more than one QTL in the region of the Casein locus on chromosome 6.

Key Words: Linkage Analysis, Casein Markers, Milk Production

280 Heterozygosity at the blood group loci in Jerseys.

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Objectives of this study were to 1) measure the heterozygosity of 10 blood group loci in Jersey bulls, 2) determine the effect of heterozygosity on predicted transmitting abilities (PTAs) for yields of milk, fat, and protein, somatic cell score, and productive life, and 3) determine if heterozygosity at the blood group loci agrees with increased homozygosity predicted from calculated inbreeding. Heterozygosity was determined as the number of heterozygous blood group loci for each bull. One model was PTA = number of heterozygous blood group loci (H) + birth year (BY); the other model was calculated inbreeding = H + BY. Only bulls with at least 10 daughters in five herds were included for each trait. Numbers of bulls used in each analysis varied from 1203 for somatic cell score to 3777 for inbreeding. Bulls were investigated as an entire group as well as divided into subsets for all traits except somatic cell score which had the fewest number of animals available. One subset included only bulls with odd registration numbers, while another included those with even registration numbers. A third subset consisted of bulls born in 1980 or later. Heterozygosity had strong ($P<0.05$), favorable linear relationships with PTAs for yields of milk, fat, and protein and length of productive life. Associations were remarkably consistent among subsets. Relationship of heterozygosity of blood group loci with somatic cell score was significant ($P<0.05$) and unfavorable. Heterozygosity showed no trends over time. Heterozygosity also showed no association to inbreeding levels of individual bulls as calculated by the USDA, indicating possible influence of natural selection maintaining diversity at blood group loci. Thus, alleles at blood group loci are not neutral. Results showed increased heterozygosity at blood group loci was favorable for yield traits and productive life and support efforts to maintain and expand genetic diversity in the Jersey breed.

Key Words: Jerseys, Blood Groups, Heterozygosity

281 Linkage relationships among polymorphic gene loci of milk protein of Xinong saanen dairy goat.

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The objective of this study was to investigate the genetic linkage relationships among polymorphic gene loci in milk proteins of the Xinong Saanen dairy goat, a high milk producing breed in China. 160 morning milk samples were collected from dairy herds of two Xinong Saanen dairy goat farms in Shaanxi province, China. Milk protein variants at α-casein (CN), β-CN, κ-CN and β-lactoglobulin (LG) locus were identified using continuous polyacrylamide Gel Electrophoresis. Linkage relation of milk protein loci were detailed and first analyzed using the Chi-square test and the sequential probability test with the data of dam-daughter pairs. Our results showed that there were significant linkages among three casein loci with a low probability of crossover for each pair observed. Genetic linkage existed between α-CN and β-CN and α-CN and κ-CN, but there was no obvious linkage between β-LG and κ-CN and the casein complex. The analysis for the frequency of casein genotype combinations (Haplotype) demonstrated a difference between observed and expected frequencies ($P<.01$). Observed frequency of casein haplotype BBB in this study significantly deviated from the expected frequency.

Key Words: Xinong Saanen Diary Goat, Milk Protein, Linkage Analysis

282 A simulation study to evaluate optimal strategies for selection on a quantitative trait using major gene information.

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Marker-Assisted Selection (MAS) based on a known major gene can increase response to selection in the short term but reduce longer-term response to selection (Gibson, 1994, 5WCGALP). Recently, Dekkers and van Arendonk (1998, 6WCGALP) developed methods to optimize the use of a known major gene in selection to maximize response over a planning horizon. Methods were based on a deterministic model with constant polygenic variance. The objective of this study was to use stochastic simulation to compare responses to phenotypic selection, standard MAS and optimal MAS, as derived by Dekkers and van Arendonk (1998), for a trait with a known major gene and unlinked polygenic effects. A population with discrete generations, fixed size and equal selection among males and females was considered. For MAS, animal i with major genotype j was ranked and selected based on the following index $I_ij = b_j g_j + h^2(P_{ij} - G_j)$, where b_j is an index weight on the major gene for major genotype j, g_j is the (known) breeding value for major genotype j, G_j is the average genotypic value for major genotype j, P_{ij} is phenotypic value of individual ij and h^2 is the heritability of the trait. Index weights b_j were equal to 1 for standard MAS and were derived from the deterministic model of Dekkers and van Arendonk (1998) for optimal selection. Alternative scenarios were considered by varying the additive effect of the major gene (.1, .25, .5, 1 phenotypic SD), degree of dominance, initial gene frequency (.05, .25, .5), and initial heritability (.1, .3, .5). Results confirmed that selection on a major gene using standard MAS increased response in the short-term, but may result in lower response in the long-term. A comparison with the optimal strategies of Dekkers and Arendonk (1998) confirmed the greater response for optimal MAS over standard MAS and mass selection for longer planning horizons, except for short planning horizons, which is likely due to the constant polygenic variance that was used to derive optimal strategies.

283 Multiple marker mapping of quantitative trait loci (QTL) for milk production traits on Chromosome 1 in Canadian Holstein bulls.

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Six Canadian Holstein sire families, with 70 to 72 unselected sons for each sire, were genotyped for eight microsatellite markers covering 116 cM of chromosome 1. Heterozygosity of the markers across sires ranged from 16.7% to 100% with an average heterozygosity of 58.3%. The traits analyzed were milk yield, fat yield, protein yield, fat percentage and protein percentage. Daughter Yield Deviations (DYD) of sons were analyzed across sire families and within individual sire families using weighted least square regression on probability of chromosome segment inheritance, based on marker genotype. Threshold values for the test statistics were derived empirically by permutation for across sire analysis and for each single sire family analysis. Results from the across sire family analysis provide evidence for a QTL affecting fat% at 17 cM ($p<.05$), a QTL affecting fat yield at 32 cM ($p<.01$) and a QTL affecting protein yield at 46 cM ($p<.01$). Individual sire analyses suggest that two sire families are heterozygous for a QTL affecting milk yield and protein yield located towards the centre of the chromosome, with a different QTL located at 10 cM being heterozygous in a 3rd sire. A 4th sire is heterozygous ($p<.01$) for QTL affecting fat yield and fat percentage at around 25 cM. Overall the results are consistent with at least 4 sires being heterozygous for one or more of at least 3 different QTL.

Key Words: Quantitative Trait Loci, Marker Mapping

284 Discovery and analysis of bovine liver and muscle cDNAs.

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Regulation of numerous genes affects expression of complex polygenic traits, such as milk yield. To help define the genes responsible for expressed phenotypes in cattle we have started to characterize expressed sequence tags (EST) from selected tissues. In these studies, adult muscle and liver mRNA from Holstein cows were isolated and used to create non-normalized plasmid cDNA libraries. The pSPORT plasmid was the host vector for directional insertion of muscle and liver cDNA sequences. Library titers were 8×10^5 and 5×10^6 clones for muscle and liver libraries, respectively. In both libraries cDNA insert presence was $> 95\%$ and average size was 1200 and 1700 bp for muscle and liver libraries, respectively. Individual clones for each library were nucleotide sequenced at the $5'$ end and compared to known genes within the Genebank database using a BLASTN analysis. The number of muscle sequences queried were 1158, which generated 150 clusters, 719 singletons and 480 unique clones. A cluster is defined as one or more matching clones within a library. Singletons are EST's which match a homolog in Genebank using a BLASTN cutoff score of 10^{-9}, while EST's were considered unique when no matching homologs were found in Genebank. For liver 6532 sequences were queried which generated 727 clusters, 3009 singletons and 1484 unique clones. Both libraries demonstrated good complexity based on cluster number relative to queried sequences. In liver the most abundant cDNA clones found were albumin, alpha-1-microglobulin, and beta or gamma-fibronectin. The muscle demonstrated a high level of mitochondrial content ($\sim$10%) for EST's characterized and type IIx myosin heavy chain was the most abundant EST. This approach will address a current deficiency in the availability of bovine ESTs needed to study multi-gene expression, mapping and chromosomal gene order. To further our understanding of various physiological states we will use small sets of these well annotated muscle and liver ESTs to study gene expression.

Key Words: Liver, Muscle, cDNA

285 Simple genetic test that supports marker assisted selection to increase retail product yield in cattle.

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Muscular hypertrophy (*mh*) is a heritable condition present in many cattle breeds. Homozygous *mh* animals display a dramatic increase in muscle mass resulting in more retail product per carcass. These animals also efficiently produce lean meat as the result of a marked decrease in body fat. The use of *mh* to increase production efficiency has been limited in the U.S. by problems associated with calving ease of homozygotes. In contrast, heterozygotes show a 7% increase in retail product yield without a significant effect on calving ease in mature cows. We recently determined that mutations in the myostatin gene underlie the *mh* phenotype. We have now developed a simple genetic test to allow for the detection of the myostatin alleles that have been identified in U.S. cattle populations. Data demonstrating the discriminatory power of a fluorescent primer based PCR assay is presented. Incorporating this assay into a breeding program permits exploitation of the positive aspects imparted by *mh* in heterozygotes, while neutralizing its negative effects by avoiding the production of homozygotes.

Key Words: Muscular Hypertrophy, Genetic Test, Breeding Program

286 Investigation of a quantitative trait locus for dairy form in one family of Holsteins.

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Preliminary analysis of quantitative trait loci (QTL) affecting conformation traits in seven large US Holstein grandsire families has been completed. Predicted transmitting abilities from Holstein Association USA were analyzed for association with marker genotypes using analysis of variance (ANOVA). Strong evidence ($P = 0.000021$) was found for a QTL associated with marker BM203 on chromosome 27 for dairy form in a single grandsire family. This grandsire had 79 sons represented in the dairy bull DNA repository (DBDR). The BM203 marker is the farthest marker from the centromere placed on the USDA Meat Animal Research Center (MARC) cattle linkage map for chromosome 27. Six additional microsatellite markers on the MARC map were genotyped for animals in this family. The grandsire was not heterozygous for two of these markers. Number of observations (i.e., sons), relative position from the MARC genetic map, and significance of marker are below for each marker. High levels of statistical significance provide further evidence of a QTL on chromosome 27. A more exact genetic location of the QTL is desired and will be the subject of further study.

Marker	Sons	Relative position	Significance
	(no.)	(cM)	
BM203	44	64.1	0.00002
BMS1675	0	64.1	...[1]
BMS17052	0	59.2	...[1]
INRA027	32	58.4	0.01658
BMS2116	51	55.4	0.00091
BM1857	42	52.7	0.00064
BMS2137	38	19.3	0.02072

[1] Grandsire not heterozygous for this marker.

Key Words: Quantitative Trait Locus, Dairy Form, Genetic Marker

287 Mapping of bovine and ovine genes with intronic single nucleotide polymorphisms.

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The stability of single nucleotide polymorphisms (SNPs) makes them superior to microsatellites for the establishment of chromosomal segment identity by descent. In order to assess the utility of this class of marker in placing genes from the human and/or mouse maps on the maps of livestock species, we have mapped several genes in the bovine and ovine genomes via SNPs. Polymorphisms were identified by comparing the sequence of introns amplified from founder animals of the MARC reference population using primers developed from exon sequences. All families of the population in which each polymorphism was informative were then genotyped by direct sequencing of the introns, and the data deposited in the MARC database for linkage analysis. In this way, the genes AKT, CAPN1, CKB, CHGA, MIP2, and IL8 were placed on the bovine maps of chromosomes 21, 29, 21, 21, 6, and 6, respectively. In addition, a systematic evaluation of the rate of polymorphism at the SNP level in bovine DNA is being conducted. The sequencing of a collection of random clones from three chromosome specific libraries and a directionally cloned muscle cDNA library has been undertaken to determine the frequency and distribution of SNPs in bovine genes and intergenic DNA. Early results indicate that SNPs provide reliable markers showing Mendelian inheritance, and are common enough to serve as useful positional makers. The theoretical ability to simultaneously assess hundreds of genetic loci using SNP markers in combination with high-density DNA array hybridization technology warrants the collection of SNPs informative across all U.S. cattle breeds to support QTL-driven genotyping efforts.

Key Words: SNPs, Genome Mapping

288 Epidermal growth factor maps to pig Chromosome 8.

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Epidermal growth factor (EGF) is a single polypeptide of 53 amino acid residues that is involved in the regulation of cell growth and cell differentiation. The objectives of this project were to identify polymorphisms at the pig EGF locus for linkage and physically mapping of the gene. Polymerase chain reaction (PCR) amplification resulted in allelic fragments of 1.5-kb and 655-bp of the porcine EGF gene. Sequence analysis revealed that the 655-bp fragment held 83.5% similarity to exons 3 and 4 in sheep EGF. Sequence analysis of the 1.5-kb fragment revealed that the ends of the fragment are identical to the 655-bp fragment with 870-bp inserted between the two ends. The 870-bp insertion contains 437-bp that hold a 93.2% similarity to a porcine L1 repeat sequence. Analysis of 71 unrelated animals from 8 breeds indicated overall allelic frequencies of 0.65 for the 655-bp allele and 0.35 for the 1.5-kb allele. The 1.5-kb allele was detected primarily in Chinese breeds. Autosomal Mendelian segregation of the polymorphic fragments was observed in two three-generation European PiGMaP families. Two point linkage analysis localized EGF to porcine chromosome 8 with significant linkages with the following markers: IL2, S0086, S0069, S0144, and S0225. Screening of a somatic cell hybrid panel (Yerle et al., 1996) by the PCR using EGF primers indicated that EGF is localized to the region 8q2.3–q2.7. Results of the linkage analysis supports the localization of this gene in close proximity to IL2. The EGF and IL2 loci are located in a homologous region on human chromosome 4.

Key Words: EGF, Pig, Mapping

289 Identification of a polymorphic microsatellite in the leptin gene of Angus cattle.

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The purpose of this study was to determine if a previously reported polymorphic microsatellite was present in Angus cattle and to determine allele frequency and the frequency of heterozygotes at this locus. A polymorphism in the leptin gene could serve as marker of important carcass traits including marbling, backfat thickness and tenderness. Leptin, the product of the obesity gene in adipocytes, is thought to play a role in regulating energy expenditure as well as serving as a messenger of the amount of fat stores within an animal. The physiological role that leptin plays in relaying information about fat stores makes it an excellent candidate gene for serving as a marker of carcass traits of beef cattle. The recent demonstration of a polymorphic site in the $5'$ UTR of the leptin gene from *Bos Indicus* and dairy cattle provided a basis for this study in Angus cattle. Using the microsatellite assay of Wilkens and Davey (Animal Genetics 28: 376), the microsatellite alleles were amplified and fractionated. The microsatellite sequence was $\mathrm{A}_n(\mathrm{TA})_n$. To date, 31 Angus cattle (steers and bulls) have been genotyped and it was determined that this polymorphism does exist. Six alleles were identified and designated as alleles one through six, with allele one being the largest fragment and allele six being the smallest. The preliminary frequencies for alleles one through six were 0.03, 0.11, 0.21, 0.08, 0.02, and 0.55 respectively. The frequency of heterozygotes was 0.68. The calculated polymorphism information content (PIC) was 0.59. The use of this information may aid in marker assisted selection of cattle for carcass quality traits.

Key Words: Leptin, Carcass Traits, Microsatellite

290 The effects of exogenous growth hormone (GH) on reproduction in oMt1a-oGH transgenic mice.

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Mice carrying a regulatable GH transgene ($oMt1a-oGH$) are sterile when the transgene is actively expressed. Pregnancy can be rescued, however, by withdrawal of the transgene stimulus prior to mating. The current study was designed to determine the minimum time needed for withdrawal of the transgene stimulus, thereby decreasing circulating levels of GH, to maintain pregnancy. For the experiment, 56 transgenic and 22 wild-type females were randomly allocated to one of four treatment groups at weaning: Group 1 - transgenic females always expressing the transgene, Group 2 - transgenic females never expressing the transgene, Group 3 - transgenic females expressing the transgene until 8 weeks of age, and Group 4 - wild-type females receiving the transgene stimulus until 8 weeks of age, after which the GH stimulus was withdrawn. At Day 17 of pregnancy, females were killed and the number of corpora lutea, fetuses, and resorption sites counted. Group 1 females had significantly ($p<.05$) lower pregnancy rates (21.4%) than Group 3 females (60.0%). Pregnancy rates of both of these groups, in turn, significantly differed ($p<.05$) from both Group 2 (93.3%) and Group 4 (100.0%). In addition, activation and then inactivation of the transgene resulted in an increased incidence of rematings leading to a significantly ($p<.05$) longer interval to pregnancy (7.89±0.58 days) in Group 3 animals compared with Group 1 (2.33±1.43 d), Group 2 (2.86±0.66 d), and Group 4 (2.50±0.51 d). At Day 17 of pregnancy, transgenic females in Groups 1 and 3 had a significantly ($p<.05$) higher ovulation rate (11.67±0.87 and 10.83±0.35 ovulations, respectively) compared with Group 2 (8.57±0.40 ov) and Group 4 (8.86±0.32 ov). However, Group 1 females produced significantly fewer ($p<.05$)live fetuses (2.82±1.09) at Day 17 than either Group 2 (7.33±0.93) or Group 4 (7.64± 0.77). These data suggest that the high GH environment impairs fertility in oMt1a-oGH mice, perhaps through modulation of the endocrine control of pregnancy and reproduction. The presence of elevated exogenous GH significantly decreases pregnancy rates. While these animals have an increased ovulation rate, they are unable to support most fetuses to term.

Key Words: Reproduction, Mice

291 Identification of a heparin-binding protein in bovine seminal fluid as tissue inhibitor of metalloproteinases-2 (TIMP-2).

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Sperm heparin binding protein (HBP) profiles determined by a monoclonal antibody are associated with bull fertility. The antibody recognizes multiple proteins which have not been previously characterized. We now report partial purification and characterization of a 24 kDa heparin binding protein from bovine seminal fluid. N-terminal amino acid sequence and partial cDNA sequence data identify this protein as a member of the family of tissue inhibitor of metalloproteinases (TIMP). Heparin binding proteins were isolated from seminal fluid by affinity chromatography followed by reversed-phase HPLC fractionation. A portion of each HPLC fraction was analyzed by SDS-PAGE and Western blotting. A 24 kDa protein recognized in immunoblots was prepared on PVDF membrane for amino acid sequencing. The N-terminal amino acid sequence matched with 17/20 residues reported for human TIMP-2 and 18/20 for a bovine metalloproteinase inhibitor (MI). RT-PCR analysis was performed using primers designed based on bovine MI cDNA. This analysis revealed the presence of TIMP-2 mRNA in bovine seminal vesicle, prostate, and bulbourethral glands. To our knowledge, this is the first report of TIMP-2 mRNA in bovine accessory sex glands. This corroborates previous reports of sites of production of heparin binding proteins related to fertility that are detected by a monoclonal antibody.

Key Words: Seminal fluid, TIMP-2, Fertility

292 Quantitative trait locus (QTL) analysis of the bovine butyrophilin gene.

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Bovine butyrophilin (bBTN) is a mammary specific protein that is expressed during late pregnancy and lactation. It localizes to the apical surface of secretory epithelial cells, and is enriched in the milk-fat-globule membrane. It possesses two exoplasmic Ig-like loops that share significant homology with the B7 immune molecules. Moreover, the gene encoding bBTN is found in the MHCI cluster. The cytoplasmic tail contains the conserved domain called B30.2 that is also found in other proteins. The tissue specificity of bBTN, the structural homology with other proteins, and the chromosomal localization of the gene point to possible roles for bBTN in lactation: in milk secretion and/or immunity. The allelic substitution effects of bBTN on milk production and udder health traits were investigated. Five intragenic molecular markers in the form of PCR restriction fragment length polymorphisms (RFLPs) were first identified: three within introns A and D, and two within exons 4 and 7. These markers were used to genotype grandsires and their sons from a granddaughter design. A QTL analysis was conducted to identify associations between bBTN and milk production and health traits as per the model described by Ashwell *et al.* (Ashwell, M. *et al.*, 1997, Anim. Genet., 28, 216–222). Three grandsire families with a minimum of 56 sons were used in the analysis. Seven traits were considered: milk yield, milk fat yield, protein yield, % fat, % protein, somatic cell score (SCS) and productive herd life. Most of the alleles showed no statistically significant effect ($P<0.05$) on the traits under consideration. In a single grandsire family however, a statistically significant effect was detected with a single trait, productive herd life. More grandsire families need to be analyzed in the future to improve the power of the QTL analysis.

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Key Words: Butyrophilin, QTL

293 Evaluating sire's heterozygosity for genes controlling a quantitative trait based on within-family additive genetic variance.

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Additive genetic variance of a paternal half-sib family was partitioned into two parts: 1) summation of variance of allelic average effects over loci controlling a quantitative trait, which is independent of sire genotype; and 2) sire's heterozygosity index that combines allele substitution effects, recombination fractions, and the genotype and linkage phase of the family sire. This index is nonnegative and measures an individual's heterozygosity at loci controlling a quantitative trait. With special family structures such as a grandsire with progeny-tested sons, the within-family additive genetic variance can potentially be accurately estimated. The difference in heterozygosity index between two individuals can be estimated as the difference between additive genetic variance of families produced from the two individuals. When all paternal alleles at loci of interest can be accurately traced with marker information, variance among marker genotypes of a half-sib family is equal to heterozygosity index of the family sire. Experimental power for mapping quantitative trait loci under half-sib designs could be greatly increased by identifying sires with higher heterozygosity indexes prior to the production of marker genotypes. Simulation results indicate that variance of heterozygosity index in a population increases quadratically as gene size increases linearly, suggesting that the index could be used in evaluating major gene segregation based on phenotypic data.

Key Words: Within-Family Additive Genetic Variance, Quantitative Trait Loci, Major Gene Segregation

294 Cloning and characterization of the bovine Somatostatin gene.

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Somatostatin(SRIF), a protein hormone is involved in regulating secretion of pituitary, pancreatic and gastrointestinal hormones including growth hormone. The objective of the study was to determine whether alternative alleles with different growth hormone release inhibiting potentials existed, bearing in mind that RFLPs in human somatostatin (hSRIF) gene have been reported. The gene(Genbank U97077), including the promoter region, exons 1 and 2, the single intron and 3' flanking region, was isolated using sequential PCR. The bovine SRIF (bSRIF) promoter is 91% homologous to the human promoter and 90% identical to the rat and mouse promoters, while the intron has 82, 84 and 80% identity with the human, rat and mouse somatostatin introns respectively. The promoter region contains an 8 nt palindromic, consensus CRE sequence (5'- TGACGTCA - 3') and two promoter proximal silencer sequences (5'- GCATG - 3'). Compared with hSRIF coding region, there is 95% homology among the 348 nt that code for 116 amino-acid pre-prosomatostatin. The bSRIF intron also has a consensus CRE sequence and a 7/8 nt consensus GAS, suggesting possible intron-based influence of gene transcription rates. Digestion of a 1,032 bp fragment including 96 bp of the first exon, the entire 832 bp intron and 104 bp of the second exon with BstXI, AluI, MspI and CfoI restriction enzymes revealed no polymorphisms among the DNA samples obtained from 100 bull calves enrolled in a progeny test program.

Key Words: Gene Transcription, cAMP-Responsive Element, Enhancer

295 Somatotropin MspI and AluI polymorphisms relative to indicators of the genetic merit of Holstein AI sires.

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Using RFLP analysis, the objective of the study was to identify different alleles in the bovine somatotropin (ST) gene in a group of 100 dairy sires, and to evaluate the relationship of the various alleles to two measures of genetic merit for milk production, Milk Fat Protein Dollars (MFPD) and Predictive Transmitting Ability for milk (PTA_M). Genomic DNA was extracted from leukocytes and PCR products of three separate regions of ST gene were digested with MspI, AluI and CfoI in separate reactions and resulting fragments were resolved by electrophoresis. No polymorphisms were detected in the promoter (from nt 2 to nt 849) region with any of the enzymes. MspI digestion of the second fragment (from nt 398 to nt 1597) detected three genotypes based on the intron 3 mutation. The 15% heterozygous MspI(+−), 1% homozygous mutated MspI(−−), 84% Msp(++) distribution frequency agrees with most previous reports. AluI digestion of the third fragment (nt 1388 to nt 2204) revealed 18% heterozygous, AluI(+−) sires. No homozygous mutated, AluI(−−), individuals were detected. Four animals were both MspI(+−) and AluI(+−). Sires were grouped based on their genotype in gr.1, MspI(−−)/AluI(−−), n=70; gr.2, MspI(+−)/AluI(−−), n=11; gr. 3, MspI(++)/AluI(−−), n=1; gr.4, MspI(−−)/AluI(+−), n=14 and gr.5, MspI(+−)/AluI(+−), n=4. There were no differences ($p>.05$) between MFPD or PTA_M values of the groups. Group 3 was excluded from analysis because only one individual had this haplotype. Even though the MspI site in intron 3 is located near a transcription factor binding site and the MspI (+−) is associated with a .9 kb insertion/deletion in the 3' flanking region, potentially carrying transcription regulator sites, neither this, nor the AluI(+−) or the presence of both MspI(+−)/AluI(+−) in the current study resulted in difference in indicators of genetic merit.

Key Words: Selection Marker, RFLP, Genetic Marker

296 Growth trait response to a selection index for greater yearling weight and smaller birth weight.

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Selection was conducted for 14 yr and 3.27 generations for the selection index (SI) of adjusted yearling weight minus 3.2 x adjusted birth weight in beef cattle. Approximately 100 linebred breeding females and four sires were used each year. Selection was applied only to the males. The animal model and REML procedures were used to estimate breeding values (BV) and genetic parameters. The model included year, age of dam, and sex with covariates age of animal, individual inbreeding and maternal inbreeding. Traits studied were birth weight (BW), wean weight (WW), yearling weight (YW) and SI. All traits included a direct genetic effect (DE), maternal genetic effect (ME) and permanent environmental effect. The BV for DE and ME, respectively were -0.002 kg/yr and -0.025 kg/yr for BW, 0.543 kg/yr and 0.142 kg/yr for WW, 1.378 kg/yr and 0.004 kg/yr for YW and 1.328 kg/yr and 0.247 kg/yr for SI. Direct heritabilities were 52%, 22%, 37% and 37% for BW, WW, YW and SI, respectively. Maternal heritabilities were 14%, 5%, 6% and 11% for BW, WW, YW and SI, respectively. The BV for BW and YW indicate SI was effective in increasing YW but not BW. BW had a high DE heritability with no genetic correlation to ME.

Key Words: Beef Cattle, Selection Index, Breeding Values

297 Comparison of growth and carcass characteristics of Hampshire sired progeny of Chinese (Meishan) and American three breed crossbred dams.

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The objective of this study was to investigate the growth and carcass characteristics of Hampshire sired progeny from three crossbred sow genotypes. The sow genotypes and total number of progeny tested from each genotype were Landrace × (Meishan × Yorkshire) (LMeY) (n=30), Duroc × (Meishan × Yorkshire) (DMeY) (n=25) and Landrace × (Duroc × Yorkshire) (LDY) (n=30), respectively. Animals were allotted to pens of five pigs on the basis of weight, sex and genotype, and managed according to standard commercial practices. Growth data was collected with pen as the experimental unit. The animals were fed from a start weight of 41.7 ± 1.41 kg. to an end weight of 106.8 ± 1.76 kg. A two-phase feeding program was used with the crude protein, lysine and metabolizable energy contents being 15%, 0.81% and 3300 kcal/kg, respectively, up to 75 kg and 13%, 0.63% and 3337 kcal/kg, respectively, to the end of the study. There were no significant genotype differences for average daily gain. However, DMeY progeny did have a higher average daily feed intake (2.94 ± .061 vs. 2.63 ± .055 and 2.74 ± .055 kg, $P<.05$) for DMeY, LMeY and LDY, respectively, with a corresponding lower gain:feed ($P< .05$). In addition, the barrows in this study had higher daily feed intakes than the gilts (2.8 ± .05 vs. 2.7 ± .05 kg, $P<.05$). At the end of the study (115.63 ± 1.19 kg), ultrasonic scans of backfat (BF) and loin eye depth (LED) were taken at 5 cm off the midline, at the last rib. There were no differences among genotypes for BF, LED and predicted percent lean. However, gilts had less BF (17.6 ± .85 vs. 21.3 ± .82 mm, $P<.01$) and a greater LED (54.4 ± .70 vs. 51.67 ± .67 mm, $P<.01$), with a significantly higher predicted percent lean (54.3 ± .54 vs 51.8 ± .52%, $P<.01$). In summary, progeny from one-quarter Meishan sows may be used commercially without significant decreases in growth rate and carcass characteristics in their offspring.

Key Words: Growth, Carcass, Meishan

298 Relationships among, and genetic trends of weights, degree of maturing and reproductive traits in a Guzera (Zebu) beef cattle.

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The purpose of this study was to determine the effects of selection for weaning and yearling weights on then degree of maturing at various stages of growth, and on the age at first calving (ACA) and at first conception (ACO). Data were obtained from 577 females of a Guzera beef cattle study herd that has been selected for weaning and yearling weights and for racial and functional traits along the period (1960–1986) covered by this study. A von Bertalanffy model was used to estimate mature weight (MW) individually to each cow, and the degree of maturing at a stage was obtained as the percentage of the mature weight achieved at that stage. According to the estimates of genetic parameters, selection for weights at fixed ages should result in increase of MW, ACA and ACO and in decrease of degree of maturing at various ages and at first calving and first conception. Genetic trends, shown little positive changes achieved in weights at the various ages (less than 0,2% of the mean) and negative changes in ACA and ACO. No substantial genetic changes were found on the degrees of maturing. These results suggest that little selection intensity was applied to weights and that some direct (voluntary or not) selection pressure was also applied to ACA or ACO.

Key Words: Growth, Degree of Maturing, Genetic Trends

299 Correlated responses in growth, feed consumption, feed efficiency and body composition to selection for large eight-week body weight in oMT1a-oGH transgenic mice.

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The sheep metallothionein 1a promoter-sheep growth hormone gene construct (oMT1a-oGH) is a closely regulated transgene in mice activated by increased levels of zinc ions in the drinking water. The objective of this study was to examine correlated responses in growth, feed consumption, feed efficiency and body composition to selection for large body size. Two replicates of four lines were selected for increased 8-week body weight: two transgenic lines, one with a high growth selected background (HGB) and one with a control line background (CB), and two nontransgenic lines, one from each of these genetic backgrounds. Two replicates of a fifth line served as a randomly selected control. At generation 0, all transgenic line mice were hemizygous, whereas the frequency of transgenic mice in generations 7 and 8 averaged .12 in the HGB line and .79 in the CB line. At weaning (3 weeks of age), males were randomly assigned within litters to receive 25mM zinc sulfate drinking water or plain tap water. Weekly body and feed intake weights were taken from weaning until 8 weeks of age. At 8 weeks, the mice were killed and fat pad weights measured. The HGB lines had larger body weights ($P<.01$) than the CB lines and nontransgenic lines showed larger body weights ($P<.01$) than the transgenic lines from 3 to 8 weeks. Feed intakes were larger in HGB lines ($P<.01$) compared to CB lines from weeks 4 to 8 and in nontransgenic lines ($P<.01$) compared to transgenic lines from weeks 4 to 7. Epididymal fat pad weights, a measure of total body fat, were a larger percentage of total body weight in the HGB versus CB lines ($P<.01$) and in transgenic versus nontransgenic lines ($P<.05$). These results indicate that HGB lines when compared to CB lines have larger body weights but at the expense of larger feed intakes and more fat, and that transgenic lines when compared to nontransgenic lines exhibit lower feed intakes but have lower body weights and more fat.

Key Words: Growth hormone, Transgene, Selection

300 Factors affecting birth weight and weaning weight in kids of Spanish and Boer-Spanish does.

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Birth weight and weaning weight data obtained from kids of Boer-Spanish (Bx) and Spanish (S) meat goat does in 1997 were analyzed using a mixed linear model with breed of doe, age of doe, sex of kid, and type of birth as fixed effects, birthdate of the kid as a linear covariate, and sire of kid and sire of doe as random effects. The 233 kids were by 8 different Boer sires. There were 16 Boer sires and 8 Spanish sires represented by the 171 does. Weights were taken at birth and at weaning (90 d of age). Birth weight of S kids ($n=98$) was not significantly different ($P=.33$) than Bx kids ($n=135$), 2.76 vs. 2.79; however S kids were .67 kg heavier at weaning ($P=.12$). Kids of 2 yr old does were .04 kg heavier at birth ($P=.12$) and 1.04 kg heavier at weaning ($P=.02$) than kids from yearling does, 2.80 vs. 2.76 kg and 16.29 vs. 15.25 kg, respectively. Buck kids were significantly heavier at birth (.05 kg, $P=.01$) and weaning (.89 kg, $P=.02$) than their female counterparts. Single kids were .21 kg heavier ($P<.01$) than twins at birth and 1.45 kg heavier at weaning ($P<.01$). Triplets were .22 kg lighter at birth than twins ($P<.01$), but weight at weaning did not differ ($P=.93$)between twins and triplets. These data suggest that, under typical range conditions, there were no significant differences in weights between kids from Bx does vs. S does for pre-weaning growth.

Key Words: Goat, Boer, Growth

301 Growth and carcass traits of F_1 steers and heifers fed for three markets at two locations in Australia.

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Brahman females were mated to sires of eight breeds (Angus, Belmont Red, Brahman, Charolais, Hereford, Limousin, Santa Gertrudis, and Shorthorn) to produce 450 F_1 calves fed to market specifications for the Australian domestic market (average slaughter weight = 400 kg) and the Korean (520 kg) Japanese (640 kg) export markets. Animals were born on two properties in tropical central Queensland and combined on one property at weaning (178 d). One-half of animals were sent to a feedlot in New South Wales, forming six groups (three markets × two locations). They entered the feedlot when the average weight of the cohort was 300 kg (domestic) or 400 kg (export). Slaughter ages were domestic north (562 d), domestic south (532 d), Korean north (711 d), Korean south (664 d), Japanese north (759 d), and Japanese south (705 d). Sample sizes ranged from 36 (Japanese north) to 102 (Korean north). One-half of northern steers for all markets were implanted with hormonal growth promotant. There were no heifers in the Japanese cohorts. The mixed model for analyses of hot carcass weight (HCWT), P8 fat depth (P8), and eye muscle area (EMA) included breed of sire, sex of calf, presence or absence of implants, location and two-factor interactions. Sires within breed (44) were used to test for breed differences. Analyses were done within market and all traits were adjusted to a common slaughter age within market. No interactions were important. Sire effects were unimportant for all traits, likely due to small numbers of progeny per sire ($P>.10$). Breed effects were important across all markets. Brahmans were 15% lighter than other breeds for HCWT. Within the domestic market, Hereford crosses were 42 kg heavier ($P<.01$). The large European breeds (Limousin, Charolais) were heaviest for the export markets (62 kg and 60 kg). Similar results were found for EMA, where the large European breeds expressed a 17% advantage over Brahman within all three markets. All carcasses are to be tested by consumer taste panel in the new Meat Standards Australia grading scheme based on eating quality, where percent *Bos indicus* may be a factor in determining quality grade.

Key Words: Beef cattle, Carcass traits

302 Age at first calving, calving weight and productive performance of straightbred Nellore and crossbred Charolais x Nellore cows in Brazil.

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The objective of this study was to compare age at first calving (AFC) and cow weight at calving (CWC) of straightbred Nellore and crossbred 1/4 Charolais + 3/4 Nellore (1CHA3NEL), and 5/8 Charolais + 3/8 Nellore (5CHA3NEL) cows, and the ratios birth weight of calf/CWC (BWR) and weaning weight of calf at 270 days/CWC (WWR) of straightbred Nellore and crossbred 1CHA3NEL, 5CHA3NEL, Canchim (5/8 Charolais + 3/8 Nellore) and 7/16 Charolais + 9/16 Nellore (7CHA9NEL) calves. Analyses of variance were carried out by the least squares method, with models that included the effects of year and season of birth, and genetic group of cow for AFC; year, season, and age of cow at calving, and genetic group of cow for CWC; and year, season, and age of cow at calving, and sex and genetic group of calf for BWR and WWR. Genetic group affected significantly all traits studied. The least square means for AFC and CWC were 1073.0 ± 9.0 days and 425.4 ± 1.4 kg for the Nellore, 1043.5 ± 3.6 days and 447.4 ± 1.7 kg for the 1CHA3NEL, and 966.1 ± 5.2 days and 486.4 ± 2.7 kg for the 5CHA3NEL cows, respectively. The least square means for BWR and WWR were 66.5 ± 0.9 and 438.3 ± 6.2 g/kg for the Nellore, 69.6 ± 0.4 and 415.4 ± 2.5 g/kg for the 1CHA3NEL, 75.1 ± 0.5 and 515.9 ± 3.3 g/kg for the 5CHA3NEL, 72.6 ± 0.7 and 469.0 ± 4.9 g/kg for the Canchim, and 73.9 ± 0.8 and 501.8 ± 5.8 g/kg for the 7CHA9NEL calves, respectively. The results show that the higher the percentage of Charolais genes in the cow, the smaller its AFC, the higher its weight at calving, and the smaller the weight ratios at birth and weaning; and the higher the expected heterozygosity in the cow, the smaller its AFC, and the higher the weight ratios at birth and at weaning.

Key Words: Beef cows, Cross breeding, Productive effciency

303 Evaluation of performance test of Limousin young bulls by principal component analysis.

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Performance test (PT) of Limousin sire candidates ($N = 194$) were made under field conditions at the ZIRC seedstock herd (Hungary). The data set covers a 3-year period between 1992 and 1994. Small groups of young bulls were housed in semi-covered yards and fed corn silage-based diets of high quality with concentrate and grass hay supplementation. Official evaluation of test results was made at 12 months of age. Figures obtained were analyzed by means of principal component analysis, and factors were rotated by VARIMAX procedure. Three factors were determined as follows: factor for type scores (I), factor for growth rate and weight gain (II) and factor for growth capacity (III). Their eigenvalues were 49.0, 22.1 and 21.8 %, respectively. Results reveal that (1) weight gain during performance tests might possibly be omitted from the selection index in the future, (2) omitting of live weights adjusted to 205 days from the evaluation index seems reasonable, since this trait significantly correlates with the live weight adjusted to 365 days ($r = 0.61$, $P \leq 0.001$), and (3) the index used at present has to be modified for optimum weighting of the traits involved.

Key Words: Limousin, Performance Test, Selection Index

304 Simultaneous estimation of genetic parameters for 38 traits of growth, carcass, meat quality and eating quality.

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Genetic evaluation of 38 traits was conducted by using REML for National Terminal Sire Lines Genetic Evaluation Program of National Pork Producers Council from 1991 to 1995. Among the 38 traits, there were 12 for growth and carcass, 13 for meat quality, and 13 for eating quality. There were 795 boars selected from 9 main terminal sire lines to produce 9000 doses of semen for mates in 188 different herds. The piglets were transported to 4 segmented early weaning stations at the age of 14 to 18 days. Pigs weaned at 20 kg were transported to 2 test stations for growth to 114 kg. After test, pigs were slaughtered in 2 slaughter houses to obtain carcass traits and loin muscle samples that were sent to the laboratory at Iowa State University for measuring meat and eating quality. There were 3261 pigs from 136 herds that finished the test. To estimate (co)variance components of the additive genetic, permanent environmental, and residual effects, canonical transformation and simultaneous diagonalization were used to transform correlations among the 38 traits to be nearly zero before each iteration of REML procedure. The memory and CPU time for this large analysis were far less than the usual requirements for (co)variance component estimation for multiple traits without using canonical transformation and simultaneous diagonalization. The heritability estimates of growth and carcass traits from this estimation procedure were close to .40. For meat quality traits, most heritability estimates were less than .20, except for meat color (.25 and .31), marbling (.31), and pH of loin sample (.38). In general, the eating quality traits, such as taste and cooking traits were difficult to measure, and also they were lowly heritable, except for lipid and cholesterol which were highly heritable. The genetic correlation estimates were similar to the corresponding phenotypic correlations, but it was not easy to classify them into different groups.

Key Words: Genetic Parameters, Growth, Swine

305 Deposition patterns of carcass yield traits measured using ultrasound in composite bulls versus heifers.

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Serial ultrasound measures were collected from composite bulls (n=150) and heifers (n=201) born in 1995 to examine the deposition of carcass yield traits from weaning in late October (229 d of age) to approximately 425 d of age. During the post-weaning period, animals were managed on a typical replacement regime (196 d) where bulls gained 1.15 kg per d and heifers gained .7 kg per d. Live weight (LWT) and ultrasound measures of back fat (FAT) and ribeye area (REA) were recorded every 28 d during the post-weaning period. Percent lean yield (PLY) was estimated using a constant dressing percent of .60 to scale LWT to an approximate carcass weight equivalent. To test for heterogeneity of slopes between sexes, a model including sex, linear and quadratic effects of age and the interaction of sex with linear and quadratic age was fit. Heterogeneity ($P < .01$) of slopes was detected for LWT, FAT and PLY, indicating the necessity to nest age coefficients within sex in the final model. No important ($P > .07$) sex by age interactions were detected for REA and therefore were removed from the final model. The main effects of sex were important ($P < .01$) for ultrasound traits and PLY. Sex-effect solutions indicated differences of 58.5 kg for LWT ($P < .27$), −10.1 mm for FAT ($P < .01$), 8.64 cm^2 for REA ($P < .01$) and 9.23 percent for PLY ($P < .01$), where bulls were heavier, had less FAT and larger REA. Linear coefficients for age differed ($P < .01$) between bulls and heifers for FAT and PLY. Quadratic coefficients for age differed ($P < .01$) between sexes for LWT, FAT and PLY. The quadratic effects of age in the final bull and heifer equations for LWT, FAT and REA were positive but were negative for PLY. Estimated lean yield differed by approximately two percent between bulls and heifers at 425 d of age. With the exception of REA, the deposition of carcass yield traits was different with respect to sex and age within sex during the post-weaning growth period of bulls and heifers.

Key Words: Ultrasound, Carcass, Beef Cattle

306 Correlations between linearized aAa codes and sire evaluations for diseases from Denmark and Sweden.

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Six linearized traits representing dairy, tall, open, strong, smooth, and style were derived from aAa codes on US and Canadian sires with daughters in Denmark (DK) and Sweden (SW). Trait values were determined based on the position of the trait in the six digit aAa code. For example, a trait was scored one if that trait's code appeared in the initial position of the overall code, through six if a trait's code appeared in the sixth position. These six linearized traits were correlated with sire evaluations for disease from DK and SW. In addition, residual correlations between disease traits and linearized aAa codes were calculated after adjustment for US PTA milk. Sire evaluations from SW included a composite trait of diseases other than mastitis. Sire evaluations from DK included separate evaluations for each of the first three lactations for: reproductive diseases, foot and leg diseases, digestive and metabolic diseases, and a composite trait of diseases other than mastitis. Correlations with sire evaluations for disease from DK were based on 99 bulls, and correlations with sire evaluations for disease from SW were based on 82 bulls. Correlations tended to be small and non-significant between the linearized traits and disease evaluations from both DK and SW. The largest correlations occurred between reproductive diseases in DK and dairy (.36 to .21), with more reproductive disease associated with dairy coded nearer the initial position. Correlations were nearly identical after adjustment for PTA milk. It appears that sires rated high for dairy have daughters with poorer reproductive health.

Key Words: Disease, Health, Breeding

307 On the relationship between two genetic evaluations of Holsteins in Uruguay.

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The relationship between two different genetic evaluations of Holsteins in Uruguay was studied. The data consisted of predicted breeding values of 3148 sires, obtained from two Uruguayan programs, Instituto Nacional para el Mejoramiento Lechero and Asociacion Rural del Uruguay; 401 bulls had proofs in both programs, whereas 770 and 1977 had proof only in the first and second organizations, respectively. Inferences about the correlation and regression between proofs were carried using maximum likelihood and Bayesian analyses assuming a bivariate normal distribution. Also, a t-distribution with known degrees of freedom (4, 6, 8, 10 and 20) was used as a robust alternative to the Gaussian approach. All analyses were performed using either only sires with both proofs or with all, including missing data. The maximum likelihood estimates were calculated by the EM algorithm, and the bootstrap was used to estimate the sampling distribution. The Bayesian approach employed flat prior for the location parameter and an inverse Wishart distribution as prior for the covariance matrix in each case; the Gibbs sampler was adopted for the posterior analysis. The results, in all of the cases, showed a weak association between the two proofs, with the correlation coefficient estimates varying from .22 to .25, in the case with only bulls with both evaluations, and from .18 to .21, with the whole data set, including missing values. The smaller values found for this last case probably denote a nonrandom pattern of missing data. The models employing t-distributions with small degrees of freedom seemed better supported by the data. The results from the frequentist and Bayesian analyses were very similar in the case with complete data, but showed some differences when the data include missing values.

Key Words: Correlation Coefficient, t-Distribution, Missing Data

308 Benefits from inclusion of MACE information into national genetic evaluations in Japanese Holsteins.

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Use of the information of Multiple Across-Country Evaluation(MACE) in Japanese(JPN) National Genetic Evaluations for Holstein was examined. The aims of this study were to improve consistency(or stability) across time, and compare Breeding Values(BV) among countries. The milking records were data files of Hokkaido Dairy Cattle Milk Recording Association, accumulated from 1975 to 1997. The records were 4,174,669 from 1,414,296 milking cows. MACE information of August 1997 for 14,388 US sires and 5,348 Canadian(CAN) sires were obtained through Internet. The following schemes were compared. Evaluation 1(E1) was domestic evaluation under ordinary conditions. Evaluation 2(E2) was the domestic evaluation adding MACE data by taking account the pedigree information and the number of daughters. Evaluations 3(E3) was the same as E2 but excluding records of daughters from imported semen, so as to avoid bias due to preferential treatment. Consistency was determined by the correlation between the proofs of 1995 and 1997, and the analysis of the Parent Average(PA) accuracy. The conversion formulas were obtained based on bull*s BV from this analysis and official US evaluation in order to compare the BV of cows from both countries. Best Linear Unbiased Equations(BLUE) were unchanged whether the MACE information was included or not. When the MACE information was taking into account(E2), the correlation between sire BVs from 1995 and 1997, and the correlation between the new BVs from 1997 and corresponding PA from 1995 evaluation were higher than those of E1. Little benefit were obtained in case of excluding records of foreign sires(E3). E2 was superior to other schemes in increasing consistency across time. The JPN sires were inferior to US sires in performance but the top JPN cows were comparable to the US elite cows.

Key Words: MACE, Japanese Holstein, BLUP

309 Correlations among US traits and calving traits in Denmark and Sweden.

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Sire genetic evaluations for productive life (PL) and selected type traits from the US (July 1995) were correlated with sire evaluations for calving traits from Denmark (DK) and Sweden (SW). Correlations were adjusted for accuracies to approximate genetic correlations. From SW, sire evaluations were available for direct and maternal calving difficulty and stillbirths based on first calvings. From DK, sire evaluations were available for direct and maternal calving ease, stillbirths, and calf size (separate evaluations were available based on first calvings and later calvings). Correlations involve data from 88 to 131 bulls. Higher values are favorable for DK and SW traits. Genetic correlations between US PL and direct effect stillbirths and calving ease from DK were favorable (.35 to .55). Genetic correlations between US PL and direct effect calf size from DK indicated higher PL was associated with smaller calf size (−.50 to −.54). Genetic correlations between US PL and direct effect stillbirths and calving difficulty from SW were near zero. Genetic correlations between US type traits that reflect body size and direct effect stillbirths and calving ease indicate that larger body size was associated with increased stillbirths and calving difficulty (−.24 to −.67). Genetic correlations between US type traits that reflect body size and direct effect calf size from DK were positive (.37 to .53). Genetic correlations between US PL and maternal effect stillbirths, calving ease, and calf size were small. Small body size as indicated by US traits tended to be associated with improved maternal effect stillbirths and calving ease (correlations were from .04 to −.40). Large size was unfavorable for both maternal and direct calving traits. Selection for steeper rump angles may improve maternal stillbirths and calving ease (correlations between rump angle and maternal traits were from .04 to .41) but have little effect on direct calving traits (correlations with direct effects were between −.10 and .09).

Key Words: Calving traits, Type traits, Productive life

310 Correlations among Jersey sire evaluations for productive life, somatic cell score, and udder type traits for the US and mastitis from Denmark.

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Genetic correlations among clinical mastitis (MST) and somatic cell count (SCC) from Denmark and US traits for type, somatic cell score (SCS), and productive life (PL) were calculated using data from 17 Jersey bulls. Genetic correlations were estimated by correlating Danish genetic evaluations and US genetic evaluations for SCS and PL (11/97 from USDA) and for type (8/97 from the American Jersey Cattle Association); these correlations were then adjusted for mean reliability. Unofficial sire evaluations (Fall 97) were used for the Danish MST and SCC. Bulls had averages of 278 and 385 daughters, respectively, for MST and SCC. Danish evaluations were from a single trait model; heritabilities were assumed to be .04 for MST and .11 for SCC. Danish MST was calculated based on binomial data so higher values indicate more mastitis. Because of the limited number of bulls involved, genetic correlations should be viewed cautiously. Genetic correlations between SCC and MST from Denmark and SCS from the US were large, .87 and .64, respectively. Genetic correlations were calculated between MST and the following US udder traits: rear udder width (.94), rear udder height (.86), teat placement (.53), udder cleft (.39), fore udder attachment (.09), teat length (−.13), and udder depth (−.46). The genetic correlation between MST and udder depth indicates that as the udder becomes more shallow the incidence of mastitis decreases. Correlations between MST and rear udder width and height are large and do not agree with data from Holsteins. Positive correlations between rear udder traits and MST may reflect the positive correlation between rear udder traits and yield and the positive correlation between yield and mastitis. Genetic correlations between US PL and Danish SCC and MST were .42 and −.18, respectively. The correlation between US PL and US SCS evaluations was .22.

Key Words: Type Traits, Mastitis, Udder Health

311 Correlation of international sire evaluations and genotypic values when an interaction exists between genotypes and environments.

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There may be a change in the order of merit of a series of genotypes when measured under different environments. Stochastic simulation was used to assess the effect of interaction between genotypes and environments on the correlation, rm between Multiple-Trait Across Country Evaluations (MACE) and genotypic value which are the total of breeding value (B) and interaction (I). The factors investigated were as follows: 1. Proportion of interaction variance to the total genetic variance (B+I), either 0.1 or 0.2. 2. Correlation of interaction between two countries, ri, from 0.9 to −0.9 at 0.1 interval. 3. Number of daughters per sire in two countries (C−D), 100−100, 100−50, 100−30, 50−50 and 30−30. 4. Situation of existence of sire proofs, all sires have proofs in both countries or 10 percents of sires have proofs in both countries with the remaining sires owning proofs only in each country. Two hundred replicates were conducted in each case. Ratio of total genetic variance (B+I) to the phenotypic variance was 0.25 throughout the replicates. The correlation, rm in one country increased by adding sire proofs in the other country when ri is 0.9 or 0.8 and 10 percents of sires have proofs in both countries. In particular, even in the case of the number of daughters per sire, 100−50,the size of rm in country D was almost the same as one in country C. When all sires have proofs in both countries and the number of daughters per sire are 100−30, 100−50 and 100−100, rm in country C remained in the small range from 0.92 to 0.96 despite the size of ri, while rm in country D decreased with the reduction of ri excepting the case, 100−100. When 10 percents of sires have proofs in both countries, rm decreased with the reduction of ri in all cases.

Key Words: Sire Evaluations, Interaction, Multiple Traits

312 Effects of breed type, feed environment, and interaction on beef production efficiency.

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The objective was to evaluate effects of cow rotation (Angus-Hereford, Simmental-Hereford, Tarentaise-Hereford), and environment (moderate versus restricted feed intake) on production efficiency of beef cattle. Cows were assigned randomly, by breed, to either a moderate (197 and 260 Kcal$*$BW$^{-.75}$ ME) or low (150 and 200 Kcal$*$BW$^{-.75}$ ME) pre- and post-calving intake level. Calves were allowed to nurse two times daily and had access to creep feed. Cumulative milk yields were estimated from nonlinear regression based on weigh-suckle-weigh measurements. Data (n=184 cow-calf pairs) were analyzed by least-squares accounting for cow rotation, phase of rotation (% Hereford), calf sire type (rotational versus terminal), year, sex, and treatment as fixed effects. Cow weight and condition score were significantly affected by rotation (P = .01) and treatment (P = .0001). At weaning, Tarentaise-Hereford calves weighed 8.4 (P = .07) and 11.5 (P = .05) kg less than calves from Angus-Hereford and Simmental-Hereford dams, respectively. Calves of moderate-intake cows were 22.2 (P = .0001) heavier than calves of restricted-intake cows. Low-intake cows were 14% (P = .0001) more efficient in calf production (calf weaning weight/ME intake) and 11% (P = .0001) more efficient in producing milk energy (milk energy/ME intake) but maintained lower weights and body condition than moderate-intake cows. When ME intake was adjusted for difference in cow weight change, low-intake cows were 3.9% (P = .03) more efficient than moderate-intake cows in weaning efficiency and there was no significant difference in milk efficiency. Cow rotation did not significantly affect milk or weaning efficiency, although cows of low percentage Hereford were more efficient for both endpoints than cows of high percentage Hereford. The interaction of treatment with cow rotation or phase of rotation was not significant for any of the traits evaluated.

Key Words: Production Efficiency, Environment, Breed Type

313 Comparison of three-breed cross females based on Chinese (Meishan) and American breeds of pigs for reproductive and pre-weaning productivity traits.

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The objective of this study was to compare the reproductive performance of one-quarter Meishan female lines with a three-breed cross female line based on conventional breeds. Three crossbred sow lines were evaluated, namely Landrace × (Meishan × Yorkshire) (LMeY) (n=45), Duroc × (Meishan × York) (DMeY) (n=41) and Landrace × (Duroc × York) (LDY) (n=53), respectively. Females were mated to Hampshire sires using artificial insemination and sows were maintained for a total of five parities within the same facility and were managed according to standard commercial practice. Data from a total of 142 LMeY, 153 DMeY, and 157 LDY litters were available for analysis which was performed using the GLM procedure of SAS. The model used included the effects of sow genotype, season, parity, litter sire, genotype x season, genotype x parity and dam nested within genotype, which was used as the error term for testing genotype effects. There were no significant differences between the sow genotypes for number of piglets born alive (10.5 ± .71, 10.1 ± .69, and 9.9 ± .54 for LMeY, DMeY, and LDY, respectively; P>.05). However, LMeY did have a significantly higher total litter birth weight than the other two sow lines (20.0 ± 1.24 vs. 18.3 ± .1.22, and 17.5 ± .89 for LMeY, DMeY, and LDY, respectively; P<.01). Gestation length was similar for the three genotypes, however, farrowing interval was shorter for the two Meishan lines (142.7 ± 3.17 and 144.2 ± 3.12 vs. 148.6 ± 2.53 for LMeY, DMeY, and LDY, respectively; P<.01). Number of pigs weaned per litter was higher (P<.05) for LMeY (10.2 ± .69) than LDY (9.1 ± .52) with DMeY being intermediate (9.6 ± .67) and not statistically different from the other lines. The percentage of sows culled prior to five parities was 53%, 41% and 60% for LMeY, DMeY, and LDY, respectively. In summary, this study suggests that LMeY females have improved reproductive performance compared to a conventional three-breed cross female line.

Key Words: Crossbred Comparison, Meishan, Reproductive Performance

314 Genetic performance of dairy cattle under management intensive grazing conditions.

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Production data from Wisconsin dairy herds which practice management intensive grazing were compared with data from three randomly chosen groups of control herds. All herds were required to participate in DHI milk recording programs, and lactation records of sire-identified cows calving from 1991 to 1995 were included. Management intensive grazing herds, which were identified via a farm financial survey, were defined as herds which derived at least 50% of annual feed intake from pasture during the past four years. Average phenotypic milk, fat and protein yield were similar in grazing and control herds, although fat percentage was slightly lower in grazing herds. Coefficients of regression of mature equivalent milk and protein yield on USDA sire PTA values were not statistically different in grazing versus control herds. Regression coefficients for fat yield were lower in grazing herds than in control herds, and this may be due to difficulties in maintaining fat percentage throughout the year as pasture quality varies. Results suggest that farmers which practice management intensive grazing will achieve predictable results when using dairy sires which are progeny tested in conventionally-managed herds.

Variable	Grazing	Control 1	Control 2	Control 3
Records	5621	6713	6238	5173
Cows	2762	3163	3227	2534
Herds	27	35	34	35
ME milk (kg)	8848	9100	9809	8659
ME fat (kg)	327	349	369	339
ME protein (kg)	286	289	316	275
Milk regression	0.97	0.90	0.88	0.95
Fat regression	0.76	0.98	1.01	0.98
Protein regression	0.95	0.76	0.96	0.94

315 Interactions of milk yield between Holstein cows in the US and México.

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To quantify genotype by environment interaction (GE) for milk yield (MY) of Holstein cows performing in northeastern US and México first lactation mature equivalent (ME) records of 55,162 cows from 1339 sires in México and 499,401 cows from 663 sires in US were used. There were 474 sires in common. Herd-year standard deviations (HYSD) were used to define high (> 1,600 kg) and low (< 1,300 kg) subsets from Mexican data and a low (< 1025 kg) subset from US data to evaluate if the US low HYSD subset is a better predictor of performance in Mexican herds. Genetic and phenotypic parameters and (co)variance components were estimated with multiple trait derivative free REML (MTDFREML) software. Likelihood ratio test was used to test whether the genetic correlation coefficients between pairs of traits in different environments differed from unity. Heritabilty for US All and US low was .21 and .18 and for Mexico all, low and high was .17, .18 and .20. Genetic correlation coefficients between MY in US all and MY in Mexico all, low and high were .63a, .60a and .71a while US low and Mexico low and high were .72a and .93 (a correlation coefficient significantly different from unity (p<.0001)). Regression coefficient of EBV for MY in México on the EBV in US was calculated to quantify the proportion of genetic superiority expressed in different Mexican environments. The regression coefficients for México low and high relative to US all were .620 and .401, while relative to US low were .828 and .567. The results indicate that, for a given sire, performance of its daughters in US low environment is a better predictor of the performance of its daughters in México.

316 Metabolic rate as an indication of fertilization capacity of cryopreserved ram semen.

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Biological activities involved in the fertilizing capability of spermatozoa depend on metabolic processes. This study investigated the metabolic activity of frozen-thawed ram spermatozoa and its association with fertilizing capability. Semen samples were collected from 9 reproductively proven rams and pellet-cryopreserved using an Aloe Vera gel-based diluent. Samples were also collected from a ram with epididymitis and a vasectomized ram and used as negative controls. Cryopreserved semen from each ram was thawed and then measured for metabolic activity using the resazurin reduction spectrophotometric assay (Wang *et al.*, 1998, Proceedings of the Society for Experimental Biology and Medicine Vol.217:197-202). The remainder of the thawed semen from the fertile ram group was used to inseminate synchronized ewes (n = 189) by laparoscopic artificial insemination. Eight to 33 ewes were assigned to each ram, respectively. The difference in metabolic rates between the fertile ram group and negative controls, and the differences in fertility and prolificacy between rams were examined by the *t*-test. The association of metabolic activity with fertility and prolificacy was analyzed by correlation statistics. Frozen semen from fertile rams had a relative absorbance at 600 nm between .17 to .42 with an average of .27, which was higher ($P < .05$) than the negative controls (absorbence less than .03). Within the fertile ram group, the average fertility was .58 and ranged from .55 to .61. The average prolificacy was 1.82 and ranged from 1.56 to 2.07. There was no difference ($P > .05$) in fertility and prolificacy between fertile rams, and correspondingly, there was no significant ($P > .05$) correlation between metabolic rate and fertilizing capacity. We conclude that assessment of metabolic rate by the resazurin reduction photospectrometric assay is informative in evaluating frozen semen quality.

Key Words: Fertility, Metabolic Rate, Resazurin Reduction Spectrophotometric Assay

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317 LDH isoenzyme peculiarity in different sheep tissue.

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LDH (Lactate dehydrogenase), an important enzyme in animal tissue, shows distinctly differently activity between animal species and among tissues. The objectives of our study were to investigate LDH distribution characteristics in tissues of sheep and provide information about LDH expression at the protein level. Seven 2-year-old Gansu mountain fine-wool sheep (4 does and 3 wethers) with average body weight of 50 kg were used in the experiment. Blood sample was collected before slaughter. Tissue samples including heart, liver, lung, spleen, crystalline lens, kidney, skeletal muscle were taken immediately after slaughtered and stored in freezer until analysis. Subsamples of all tissue were ground in a glass homogenizer at 4°C. Blood serum and tissue supernatant were separated by centrifuging for 10 min at 3,500 rpm and 4°C. The LDH isoenzyme distribution and its relative activity in heart, liver, lung, spleen, crystalline lens, kidney, skeletal muscle and serum of sheep were analyzed by polyacrylamide gel electrophoresis and electropherogram scanning techniques to compare the characteristics of electropherograms of LDH isoenzymes in different tissues. The results showed that there were no differences in LDH activity between wethers and does ($P>0.05$). The LDH isoenzyme distribution was different from that of other animal species, and its relative activity demonstrated a significant difference ($P<0.01$). LDH_5 activity in skeletal muscle was much higher than that of $LDH1_1$ with a higher percentage of M subunit than that of H subunit. The LDH_1 activity in heart and liver was the strongest.

Key Words: Sheep, Tissue, LDH Isoenzymes

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318 Relationship between grazing distribution patterns and performance of beef cows.

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A study was conducted in foothills rangeland to determine if grazing patterns differed among cow breeds and to determine if there was a relationship between individual grazing patterns and performance of beef cows. Hereford (HH), Tarentaise (TT), 3/4 Hereford 1/4 Tarentaise (3H1T), 1/2 Hereford 1/2 Tarentaise (1H1T) and 1/4 Hereford 3/4 Tarentaise (1H3T) cows (n=183) were observed at least two times per week during the summer in two pastures. Models included cow breed, age and nursing status. In the first pasture (160 ha, used June 1 to July 15), TT cows traveled further ($P<.05$) from water, both horizontally and vertically, than HH cows. Cows without calves used steeper slopes and areas higher above water than cows with calves ($P<.05$). Younger cows (3 yr) used steeper slopes ($P<.05$) and traveled further ($P<.05$) from water (horizontally and vertically) than older cows (5 + yr). In the second pasture (400 ha, used July 16 to September 8), TT and 1H3T cows used areas higher ($P<.05$) above water than HH cows. Cow age and nursing status did not affect ($P>.05$) grazing patterns. Using residual correlations, there were no relationships ($P>.05$) between grazing patterns and cow height, body condition score or milk production. In the second pasture, heavier cows used lower elevations ($r = -.22$, $P=.003$). Cows with earlier calving dates used steeper slopes ($r = -.20$, $P=.009$) and higher elevations ($r = -.16$, $P=.04$). Correspondingly, cows with higher actual weaning weights of their calves, not age adjusted weaning weights, used steeper slopes ($r = .15$, $P=.06$) and higher elevations ($r = .15$, $P=.05$). Grazing patterns in foothill rangeland varied among cow breeds. Performance of cows that used more rugged topography was similar to cows using gentler terrain.

Key Words: Cattle, Breed, Behavior

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319 Fecal ouput by calves from Hereford, Tarentaise, and crossbred cows under range conditions.

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Fecal output (FO) was estimated for calves raised on different biological types of cows under range conditions. Fecal samples were collected for calves from Tarentaise (TT), Hereford x Tarentaise (HT), and Hereford (HH) cows over three periods during the 1992 and 1993 grazing seasons. Fifty calves were evaluated each year. Collection periods were June (PI), September (PII), and October (PIII). Estimates of FO were obtained using constant release Cr_2O_3 intraruminal boluses. Data were analyzed by period using least squares GLM. Main effects were breed of dam, breed of sire, age of dam (AOD), year, and sex of calf. Calf days of age (DOA), dam weight, dam milk production, and calf weight were tested as covariates. Mean fecal outputs were 452, 1573, and 2159g/d, for PI, PII, and PIII, respectively. Breed of dam was important ($P<.05$) during PI and PIII with FO means for PI of 412, 512, and 493g/d for TT, HT, and HH, respectively. Tarentaise FO was less than HT ($P<.05$) and HH ($P=. 06$). Means for PIII were 1193, 2052, and 2960g/d, for TT, HT, and HH, respectively, with lower FO for TT then HH and HT ($P<.05$) and HT having less FO than HH ($P<.05$). For PIII AOD was significant ($P<.05$) and FO for calves from 2, 3, 4, and 5+ yr-old cows was 2474, 2746, 1611, and 1443g/d, respectively. Calves from 2-and 3-yr-old cows had more ($P<.05$) FO than calves of 4-and 5-yr-old cows. Mean calf weights for PI, PII, and PIII were 106, 202, and 226 kg at 76, 170, and 196 d, respectively. Regression of FO on calf weight was not important during PI ($P>.05$), approached significance ($P=.16$) for PII, and was 22.8 g/kg for PIII ($P<.05$). Calf age was important ($P<.05$) during P1. Calves in 1992 had higher FO ($P<.05$) than in 1993 for PI and PII. These results suggest there are differences in calf FO by biological type of dam and age of dam, and that calf weight becomes more important in determining calf FO as calves get older.

Key Words: Calves, Biological Type, Fecal Output

320 Effect of halothane genotype on carcass traits of swine.

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The halothane gene (HAL) when in recessive homozygosis (nn), is associated to the occurrence of the Porcine Stress Syndrome (PSS), whose major *post-mortem* manifestation is the occurrence of pale, soft and excudative pork (PSE). The HAL gene is also linked to occurrence of PSE when in heterozygosis (Nn), although there is a belief that this gene may be related to faster weight gain and thus higher carcass weight. This study characterized the genotype of HAL in a sample of 158 swine from a brazilian commercial farm, which were slaughtered in a commercial plant. For each animal, the following carcass traits were measured: hot carcass weight (Kg); backfat (mm); muscle deepness (mm); percent lean (%), muscle color (absorbance); and variation in carcass color (%). Genomic DNA was obtained by alkaline extraction from a plucked hair, a non-invasive and quick method to screen any animal in a farm. A polimerase chain reaction (PCR) was used to amplify a specific fragment of HAL gene. The PCR's product was digested by the HhaI restriction enzyme, followed by agarose gel electrophoresis. Among the 158 animals, 82 (52%) were identified as NN, 67 (43%) as Nn, and 9 (6%) as nn. Variation in carcass traits across genotypes was analyzed through analysis of variance, using the GLM procedure of SAS. The nn animals were excluded from the analysis, due to the small sample size. The NN and Nn animals did not differ ($P > .05$) as far as: hot carcass weight (73.8 and 74.4 Kg); backfat (21.3 and 20.1 mm), muscle deepness (48.6 and 49.4 mm); and percent lean (52.5 and 53.3%). However, variation in carcass color was lower ($P < .05$) for NN (40.8%) than for Nn animals (49.8%). These results indicate that the presence of HAL gene in heterozygosis was not associated with better carcass quality and higher carcass weight. Therefore, the intentional use of heterozygous animals should not be encouraged.

Key Words: Stress, PCR, Swine

321 Variation in percentage of female births over time in four breeds of registered beef cattle.

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Breed and sire effects for the percentage of female births over time in four breeds of registered beef cattle were studied. Cattle were in the purebred registered herds of the Arkansas Agricultural Experiment Station. Breed groups were managed separately. Matings were by artificial insemination and natural service. Sex ratio of progeny was not considered in sire selection. The percentage of female births was included in the study for sires which were used for at least 2 yr and sired at least seven progeny. Progeny of 48 Angus, 7 Charolais, 36 Hereford and 5 Red Poll sires were included in the study. The number of birth years by breed were 33 for Angus, 21 for Charolais, 31 for Hereford and 15 for Red Poll. Variances for breed and sire were partitioned for percentage female births using a nested random effects analysis of variance. Variance for breed effects was negligible. Sire effects accounted for approximately 9% of the total variation in the percentage of female births. Means for percentage of female births by breed were 49 ± 1 for Angus, 46 ±2 for Charolais, 49 ± 2 for Hereford and 48 ± 5 for Red Poll. Percent female births based on average of year means were for Angus 49 ± 1, for Charolais 4 ± 2, for Hereford 49 ± 2 and for Red Poll 49 ± 3. Although the overall means showed that the percentage of female births was slightly less than the percentage of male births and that sire differences were small, there were some sires that consistently produced a higher or lower number of females over time. These results suggest that more research is needed to determine the inheritance of sex ratio in cattle because it is of economic importance in the industry.

Key Words: Sex Ratio, Beef Cattle

322 Sex and breed differences in growth curves for two breeds of guide dogs.

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A desirable guide dog weighs 18–32 kilograms as an adult. Male and female German Shepherd Dogs and male and female Labrador Retrievers were weighed at least 11 times between birth and 16 months of age. Growth curves were constructed from 3805 observations on 301 dogs using the Gompertz function in the form W_t= Aex, where x= $-e^{(-(t-c)/b))}$, W_t is weight at time t, A is mature body weight, b is proportional to duration of growth, c is time at point of inflection, and t is age in days. Estimates for mature body weight were 2.9 ± 0.13 kg higher for Labrador Retrievers than German Shepherd Dogs and 4.9 ± 0.13 kg higher for males than females. Male Labrador Retrievers are closest to the upper limit for desirable weight, with an average estimated mature weight of 32.5 ± 0.16 kg. Duration of growth estimates, 4b, were 8.1 ± 2.5 days longer for Labrador Retrievers than German Shepherd Dogs and 11.6 ± 2.5 days longer for males than females. Male Labrador Retrievers had the longest estimate for growth at 253.7 ± 3.0 days. Time at point of inflection was not different between breeds, however the estimate for males was 5.8 ± 0.8 days longer than females. A better understanding of growth curves for guide dogs may aid in estimating mature weight at a young age, thus allowing earlier breeding and training decisions to be made and increasing genetic change per year.

Key Words: Growth Curves, Dogs, Body Weight

323 Suitability of Casein loci for genetic markers - effects of Casein genotypes on milk production and fertility.

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Using the data of 1721 Black and White cattle with 5765 kg milk in first lactation effects of α_{S1}-Casein, β-Casein and κ-Casein on milk production and fertility were estimated. The underlying model assumes besides fixed effects the effects of all Casein-genotypes simultaneously as well as the animal effect (PEST, Groeneveld 1992). Because of low heterozygosity the results from α_{S1}-Casein were meaningless. The differentiation between the homozygous genotypes β-Casein^{A2A2} and β-Casein^{A1A1} was 208 kg milk and 11.5 kg of fat and protein. β-Casein^{A2A2} was inferior in percentage of fat and protein. The differentiation between the homozygous genotypes was higher for κ-Casein regarding the latter traits favouring κ-CN^{BB}. The results show that high yield performances may go abead with sufficient fertility. The lowest days open were obtained by cows being heterozygous at all Casein loci.

Key Words: Dairy Cattle, Milk Production, Fertility

324 Effects of stressfull hot conditions on milk yield and reproductive traits of first lactation Holstein cows grouped by coat color.

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435 first lactation records for milk yield of Holstein cows of two dairy herds at north west of México were analyzed by using least squares. The objective was to evaluate the effects of stressful hot conditions on milk yield and reproductive traits of Holstein cows grouped by coat color. Cows were classified in three groups: (1=60% or more white color, 2=mixed coat color was 50% black and 50% white and 3=60% or greater black color). Cows were also grouped by season of freshening. The model included: coat color, season of freshening, coat color and season of freshening interaction as fixed effects, and the residual as random effect. The average milk yield to cows grouped by coat color (1, 2 and 3) were: 9071.67±1279.82, 8582.10±1386.21 and 8853.70±1587.38 and 6354.66±1312.51, 5774.44±1638.65 and 5896.67±1277.07 kg in herds 1 and 2, respectively. Milk yield in cows 60% or more white color was 4.06% higher ($P>.05$) than the average milk yield of the other coat color cows groups. The average estimates for open days to cows grouped by coat color (1, 2 and 3) were: 131.40±91.11, 143.75±94.76 and 149.56±87 and 113.25±86, 116.35±55 and 136.40±27d for herds 1 and 2 respectively. Estimates for services per conception were: 2.00±1.42, 2.29±1.5 and 2.89±1.78 and 2.68±1.66, 2.76±2.07 and 2.87±2.31 to cows grouped by coat color. The estimated averages values for services per conception in cows grouped by season of freshening (October to January, February to May and June to September) were: 2.37±1.59, 2.53±1.33 and 3.03±1.15 and 2.59±2.24, 2.86±2.01 and 3.23±2.27 in herds 1 and 2 respectively. The interaction between coat color and season of freshening was not significant ($P>.05$) on milk yield. It was found a significant effect ($P<.05$) of coat color and season of freshening interaction on the open days and services per conception.

Key Words: Coat color, Hot conditions, Milk yield

325 Genetic predisposition to heat stress in beef cattle caused by grazing endophyte-infected fescue.

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Sixty-nine beef cows (Angus, Simmental, and varying percentages of Simmental X Angus cross) were studied in order to locate/identify common ancestors that parented animals which were predisposed to heat stress caused by grazing endophyte-infected fescue grass. Susceptibility to the endophyte was determined by physical observation of the animal's coat, salivation, increased respiration rate, and desire to seek shade and pools of water. Susceptibility was also determined by blood collection to assay endocrine concentrations. The lactating females grazed endophyte-infected fescue and were observed for signs of heat stress in July 1996 and 1997, in an ambient temperature of 31°C. Forty-two cows exhibited signs of heat stress while 27 cows appeared unaffected by the heat. Six cows were randomly selected from each group to study differences in blood prolactin and cortisol levels. Blood samples were drawn at time=0 min., time=20 min., and time=40 min. At time=20 min. the non-stressed cows in 1997 expressed higher prolactin levels than they did in 1996 ($p<.05$). At time=20 min. the non-stressed cows in 1997 expressed higher levels of prolactin than the stressed cows in 1996. Stressed cows expressed significantly lower cortisol levels in 1996 at time=0 min. ($p<.05$). Stressed cows expressed higher levels of Cortisol in 1997 than they did in 1996 at time=0 min. ($p<.05$). Cortisol levels also showed a significant interaction affect over time ($p<.05$). Pedigree analysis of 4 generations failed to yield any statistically significant link between ancestors ($p>.05$).

Key Words: Beef Cattle, Endophyte, Fescue

326 Development of economic indexes for net merit, fluid merit, and cheese merit.

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Price formulas for fluid milk, protein yield, and cheese yield have been applied to US genetic evaluations since 1971, 1977, and 1984, respectively, to calculate the economic indexes of milk-fat dollars (MF$), milk-fat-protein dollars (MFP$), and cheese yield dollars (CY$). Since 1994, an index for net merit dollars (NM$) has combined economic values of productive life and somatic cell score with net economic value of milk, fat, and protein. Selection based on net prices results in higher profits than from selection based on gross prices if feed and other costs are not proportional to revenues. Feed costs were assumed to equal 30% of each component's value for NM$. New indexes for fluid merit dollars (FM$) and cheese merit dollars (CM$) were developed by substituting fluid milk and cheese yield prices for protein yield prices in NM$ and retaining original productive life, somatic cell score, and feed cost values. For FM$, protein value was negative because each kilogram of protein requires feed but yields no revenue. Alternatively, protein value could be set to 0 by assigning its feed cost to milk or fat. For CM$, a single formula for all breeds was used instead of the two current USDA breed formulas for CY$ based on high or low ratio of fat to protein. A group of 8514 Holstein bulls born since 1990 were used to compare indexes. Correlations between cheese and fluid pricing were lowest (0.92 between MF$ and CY$ and 0.86 between FM$ and CM$). Correlations between cheese and protein pricing were highest (0.99 between MFP$ and CY$ and 0.98 between NM$ and CM$). Correlations were 0.97 between MF$ and FM$, 0.98 between MFP$ and NM$, and 0.94 between CY$ and CM$; the lower correlation for cheese pricing reflects use of the breed-specific formula for CY$. The merit indexes could replace MF$, MFP$, and CY$. Commercial producers should choose an index that incorporates the net price formula that is closest to the price expected in about 5 yr. Suppliers of seed stock should select for long-term national or global demands instead of short-term local prices.

Key Words: Economic Index, Fluid Merit, Cheese Merit

327 Improved prediction of national genetic evaluations by including international information.

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The ability of national and international evaluations to predict later national evaluations for milk, fat, and protein yields was compared for Holstein bulls evaluated in Canada, Germany, Italy, The Netherlands, and the US. Data included national (N95) evaluations that were input data for February 1995 International Bull Evaluation Service (INTERBULL) evaluations, February 1995 INTERBULL (I95) evaluations on each country's scale recalculated using August 1997 methodology, and recent 1997 national (N97) evaluations. A bull was included only if the I95 evaluation included daughter information from at least one country in addition to the country for the national evaluation. If the use of foreign data is beneficial, I95 evaluations should be closer approximations of N97 evaluations than are N95 evaluations. However, strong part-whole relationships were recognized between N95 and N97 evaluations and between N95 and I95 evaluations. Therefore, results only for bulls with the largest increases in national and foreign daughter data relative to N95 evaluations were reported. Correlations between I95 and N97 evaluations were higher than between N95 and N97 evaluations by 0.01 to 0.04 except for the US. For the US, correlations with N97 evaluations were lower for I95 evaluations than for N95 evaluations by 0.01 for milk and protein yields and the same for fat yield. Standard deviations (SD) of differences of N97 evaluations from N95 and I95 evaluations showed a better agreement for I95 evaluations than for N95 evaluations except for US milk yield. Nearly all bulls originated from North America, particularly in the US, and reduction in SD of evaluation differences was less for Canada and the US than for the European countries. Addition of foreign data for daughters and relatives through the INTERBULL process generally improved prediction of later national evaluations, with the benefit greatest for importing countries.

Key Words: International Evaluation, National Evaluation

328 Factors Influencing Calving Difficulty and Stillbirth of Canadian Holstein.

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The objective of this study was to investigate factors that affected the degree of calving difficulty (CD) and stillbirth (SB) of Canadian Holsteins. Data were 2,848,590 CD and SB records of Canadian Holsteins from 1970 to 1995. Scores for CD ranged from 1 to 4 (unassisted, easy pull, hard pull and surgery needed). Stillbirth was scored as 1 if calf was alive in 24 hours after birth or 2 if calf was dead. The factors included in the model were herd (within three provinces), sex of calf, body size of calf, the interaction between sex and body size of the calf, lactation number of cow, calving year, calving season, and age of the cows at first calving. The GLM procedure of SAS was used to carry out ANOVA. Incidences of calving difficulty and stillbirth rate in three provinces were significantly different. Cows from Alberta had highest calving difficulty scores and stillbirth rate. Cows from Quebec had the lowest calving difficulty scores and stillbirth rate. The effects of lactation numbers on the CD and SB were divided into 4 groups: first lactation, lactations 2 to 3, 4 to 9, and 10 and above. Significant differences ($p < 0.05$) were observed among these lactation groups. First lactation and 10 and above groups have greater CD incidences and SB rate than that of other groups. Incidences of CD and SB were much greater for male than that in female calves. Body size of calf was another important factor affecting CD and SB in both sex groups. There were no significant differences between months of calving. The effect of age of cow at first calving was significant but no discernable pattern was observed, except that very young (under 22 month) and very old cows (over 36 month) had the greatest calving difficulties. Correlation analysis indicated that relationships among all of these environmental factors were very low (less than 0.2).

Key Words: Calving Difficulty, Stillbirth

329 Genetic parameters of mobility and body condition score.

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The objective of this study was to examine the relationships between mobility and body condition and their changes across lactation. Twenty-six registered Holstein herds in southern Ontario were visited twice, in October and December 1997. Approximately, 3000 dairy cows were scored for mobility and body condition. Mobility was scored on a scale from 1 to 5. A score of 1 indicated excellent mobility, whereas a score of 5 indicated a severely lame cow. Body condition was scored according to the standard 5-point system with intervals of 0.5. A score of 1 indicated an extremely thin cow, and a score of 5 indicated a very over-conditioned animal. Analysis controlled for the effect of time-of-visit, herd, parity, and stage of lactation. Herd accounted for 25 percent of the variability for both mobility and body condition. Stage of lactation had a significant effect on both traits, but its effects were more pronounced for body condition. In contrast, parity number had a greater effect on mobility than on condition score and cows with higher parity number had higher (poorer) scores for mobility. Repeatability of mobility and body condition score across rounds were 0.40 and 0.58, respectively. Descriptive analyses showed that cows with a mobility score of 5 were most likely to have a body condition score of 1. Whereas, cows with mobility scores 1, 2, 3, and 4 were most likely to receive body condition scores of 2.5, 2.5, 2, and 1.5, respectively. The phenotypic correlation between mobility and body condition score was -0.2, indicating that cows with poor mobility tended to have lower body condition. One interpretation of these results is that cows with sore feet and legs were less active, causing a decrease in feed intake, subsequently resulting in a decrease in body condition. Alternatively, lameness and low body condition may occur simultaneously as a result of certain disorders.

Key Words: Mobility, Body Condition Score, Genetic Parameters

330 Comparisons of cows and herds in two progeny test programs and two corresponding states.

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Data were USDA genetic evaluations on cows and DHI herd profiles from 4154 Holstein progeny test herds from two AI studs, 21st Century Genetics and Genex, and 6361 remaining herds from Minnesota and New York. We grouped herds into four categories, 21st Century Genetics and Genex progeny test herds, other Minnesota herds and other New York herds. Herds contributing less than 10 cows with birth dates from January 1989 to March 1995 with genetic evaluations were eliminated. Data included 83 % of 21st Century Genetics and 74 % of Genex's first crop daughters of progeny test bulls with genetic evaluations from January 1995 to February 1997. Herds were described by DHI profile and average cow evaluation data. Cows with extreme yield deviations (± 3 within herd standard deviations) were identified, as were daughters of progeny test bulls with extreme daughter performance relative to pedigree merit of the bull. Cows in progeny test herds were younger, sired by younger bulls, had higher PA's and produced more milk than cows in non progeny test herds. Genex and 21st Century Genetics appear to have on average selected the larger and genetically superior herds from within their appropriate regions. Also, we were not able to predict extreme performance of cows for yield deviation based on herd characteristics. We were not able to predict if a bull was going to exceed or fail to meet pedigree prediction by characteristics of the progeny test herds in which he was sampled. The difference between the parent average and daughter yield deviations for young sires appeared to result primarily from Mendelian segregation of genes.

Key Words: Progeny Testing, Genetic Evaluation, Yield Deviations

331 Multibreed data analysis: Genetic vs. gametic trends.

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Genetic trends are typically estimated as part of a genetic evaluation. For purebred animals, these are straightforward, being the average genetic merit of animals born by year (beef) or animals lactating for the first time by year (dairy). In the multibreed evaluation for Simmentals, options for reporting trends exist. Purebred averages as described above are computed. Trends in founders from other breeds can also be obtained; these, however, reflect the choice in animals selected from the population of a breed and are not necessarily analogous to the trends reported by that breed. This is because the Simmental multibreed evaluation is based on data reported to the Amer. Simmental Assoc. as opposed to incorporating all data from other breeds. Also of interest is the trend in average value of each breeds' genes in the Simmental data set. For this objective, a *gametic* trend is proposed. For each year of birth, EPDs are regressed on breed composition (by least squares) to partition the average EPD among sources of genes. Regression coefficients for each breed (for each year of birth) provide a gametic trend–the trend in merit of genes from each breed in all of the animals contributing to the evaluation. For example, purebred animals of a breed are weighted by one, F_1s by one-half, backcrosses by one or three-quarters, and so on. For this gametic trend, all individuals with a fraction of a particular breed contribute to the trend as opposed to selecting subgroups (e.g., all F_1s) to compute a trend. Gametic trend then reflects selection of founder animals (represented in their EPDs and EPDs in first crosses with these founders) and selection within the population from choice made among F_1s (and subsequent generations) as parents. It is interesting to note for weight that Simmental purebred genetic trend and Simmental gametic trend parallel each other, with gametic trend being higher. This is because most "purebred" Simmentals are a small fraction (one thirty-second or sixty-fourth) of another breed, typically smaller-sized.

Key Words: Multibreed Evaluation, Genetic Trends, Gametic Trends

332 Development of multitrait evaluation for linear traits and single-trait evaluation for final score of six dairy cattle breeds.

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A multitrait animal model was developed for genetic evaluation of final score and 15 linear type traits of US Ayrshires, Brown Swiss, Guernseys, Jerseys, and Milking Shorthorns; 14 linear traits were included for Red and Whites. An appraisal during first lactation was required. Variance components were estimated from appraisals since 1988 that had all linear traits scored. The model included fixed effects for interactions of herd, appraisal date, and parity group (first or later); parity and appraisal age groups; and parity group and lactation stage. Random effects were included for permanent environment, animal, and residual. A canonical transformation was used with approximate diagonalization. Solutions for variance components did not converge for linear traits of Red and Whites; therefore, previously estimated Holstein correlations among traits were used for computation of evaluations. Data for estimating breeding values included appraisals during 1980 and later, but data for some traits were missing. Effects for appraisal age group and lactation stage were defined within time interval (before 1988 or 1988 and later). A random effect of interaction between herd and sire was added to the model and assigned 40% of estimated (co)variance for permanent environment. Solutions for appraisal age groups from a preliminary analysis were smoothed with a quadratic curve to generate additive age adjustments by month of age at appraisal, parity group, and time interval (before 1988 or 1988 and later). Solutions from a previous evaluation were used as starting values. Fewer than 50 iterations were required to reach $<0.1\text{e}^{-8}$ for squared relative differences of solutions. For bulls with $\geq$20 daughters, correlations of solutions for linear traits with solutions from the current USDA sire model ranged from 0.69 to 0.91 for Ayrshires, 0.65 to 0.91 for Brown Swiss, 0.80 to 0.94 for Guernseys, and 0.80 to 0.91 for Jerseys.

Key Words: Animal Model, Linear Type, Final Score

333 Relationships of energy balance in early lactation with health and reproductive traits in Holstein cattle.

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The objective of this study was to examine relationships between feed intake and milk production in early lactation, and of the resulting energy balance, with subsequent health and reproductive performance. Data obtained from the Agriculture Canada Research and Development Centre in Lennoxville included over 42,000 daily records of dry matter intake and milk yield from an automated recording system from 1995 to 1997 on 235 multiparous Holstein cows, with a minimum of 20 days/cow. Cows were fed an ad-libitum total mixed ration grouped according to production, based on NRC requirements. A separate database contained all reproductive and health information, which was recorded by veterinarians and farm staff, and included dates of calving, estrous detection, inseminations, and confirmation of pregnancy. In addition, monthly percentages of fat and protein, monthly or biweekly body weights and condition scores, and body dimension scores from Holstein Linear Type Classification records (stature, size, body depth, chest width, and rump width) were available. Dry matter intake, milk yield and composition, cow age, weight and pregnancy status were used to estimate daily energy balance according to NRC guidelines. Three measures of negative energy balance, evaluated for each lactation, were: 1) number of days in negative energy balance 2) maximum daily energy deficit and 3) total energy deficit. Phenotypic relationships of each of these measures with health and reproductive traits were analyzed, as well as the relationship of feed intake with body dimension traits and the ability of body dimension traits to predict negative energy balance. The hypothesis was that a negative energy balance was associated with increased health problems and decreased reproductive performance.

Key Words: Energy Balance, Health, Body Dimension Traits

334 Docility EPD for Limousin Cattle.

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Our objectives were to determine whether docility is a heritable trait in Limousin beef cattle and, if so, produce EPD for cattle registered with the North American Limousin Foundation. The data set consisted of records on 65,097 animals with docility scores weaned from 1981 to 1995. Producers assigned a docility score at weaning on a scale from 1 to 6, where 1 was considered docile and 6 was considered very aggressive. We formed contemporary groups based on herd, year, and season of birth, weaning date, NALF weaning contemporary group, and creep feeding code. We combined animals with scores 4, 5, and 6 with category 3 due to the low frequencies of animals reported with scores of 4 or higher. Contemporary groups with no variation were removed, leaving 24,960 animal records and 4,147 contemporary groups in the data set. Fixed effects were contemporary group and sex, and random effects were additive direct genetic effect due to animal and error. Using Method R procedures, we estimated a heritability of .40 ± .034. We used a single-trait threshold model to calculate maximum *a posteriori* (MAP) predictions of genetic merit. After obtaining the MAP predictions, we converted them to EPD expressed as deviations from a 50% probability. Docility EPD ranged from -32.9% to 36.1% with mean 1.21% and SD 7.21%. Sire docility EPD ranged from -32.9% to 36.1% with mean 0.93% and SD 6.32%. Docility EPD may be used by Limousin breeders to select for favorable temperaments.

Key Words: Limousin, Temperament, Threshold Models

335 A practical method for estimating connectedness in large livestock populations with an application to Canadian swine herds.

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When genetic evaluations are carried out in large populations encompassing several herds, the real accuracy of comparisons between EBVs or EPDs of specific animals can be substantially lower than indicated by their reliability estimates, because of limited connectedness among herds or contemporary groups. A method for estimating the degree of connectedness in large livestock populations has been developed, which provides estimates of connectedness between each herd and every other herd in the population.

The method is based on the computation of prediction error variances and covariances among herd solutions. The resulting connectedness rating for two herds is the correlation between their herd solutions, which is an estimate of average PEV of all pairwise differences between the EBVs of the animals in the two herds adjusted for the effect of herd size and structure. A simple procedure is provided to obtain any required specific elements of the inverse of the coefficient matrix for a large set of mixed model equations. The method has been applied to national swine evaluations in Canada to the Yorkshire, Landrace, Duroc and Hampshire breeds, for production and litter size evaluations. Connectedness ratings between herds ranged between 0.1% and 80%. The standard error of the difference between herd effects, and consequently the standard error in the comparisons of specific EBVs from these herds, was substantially large for herds with connectedness rating lower than 3% or with a contemporary group size of less than 10 animals.

Breeders have now received average connectedness ratings for their herds, as well as individual connectedness ratings between their own herd and every other herd on the program. Guidelines on minimum connectedness levels, and on the use of AI sires to increase connectedness levels when required, have also been developed.

336 Multiple-trait genetic evaluation of carcass traits in swine.

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Multiple-trait genetic evaluations for carcass quality were computed in the Canadian swine population using two live animal measurements (backfat thickness, loin depth between the third and fourth ribs) and three carcass measurements (loin eye area, loin lean weight, and weight of lean in the 3 primal cuts). The Duroc, Yorkshire, Landrace and Hampshire breeds were evaluated separately. All data available on animals born after January 1, 1990 and their relatives were used in the evaluation. The effect of removing older backfat data was tested on the Hampshire breed, and found to be negligible as the correlation between evaluations for all and for restricted data exceeded 0.99 for all pigs born in the last two years. The number of animals evaluated in the Yorkshire, Landrace, Duroc and Hampshire breeds were 343517, 268430, 138301 and 43105, respectively. The evaluation model included fixed effects for herd, year, contemporary group, sex and probe or carcass weight and random effects for animal, litter and the residual. Variances and covariances were estimated based on the results of prior analysis and/or literature values. The heritabilities used in the analysis for backfat thickness, loin depth, loin eye area, loin lean and 3 primal lean were 0.52, 0.25, 0.47, 0.40 and 0.40 respectively. A large number of iterations (10,000 or more) was performed to ensure genetic trends had fully stabilized. For reporting purposes, the EBVs for 3 primal lean were converted to EBVs for % lean yield, and EBVs for % loin in the carcass were constructed using those for loin lean and 3 primal lean. Annual genetic trends for the Yorkshire and Duroc breeds were +0.23 for % lean yield, +0.05 for % loin in the carcass and +0.38 cm^2 for loin eye area. Estimates for the Landrace and Hampshire breeds were similar. Generally, to be in the top 5% of its breed, a pig should have an EBV of more than +1.2 for % lean yield, +0.4 for % loin and +2.3 cm^2 for loin eye area. National swine genetic evaluations for carcass traits will be produced routinely in Canada starting in 1998, on a quarterly and then on a monthly basis, with the resulting EBVs incorporated in both sire line and dam line indices.

Key Words: Carcass Traits, Multiple-Trait, Genetic Evaluation

337 Genetic evaluations of test day data with small size of contemporary groups.

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Test day data were used to estimate genetic parameters and breeding values for first lactation milk yields. Data comprised 170,937 test day records of 18,974 cows calved from July 1993 to June 1995. The linear model included the effect of contemporary group, linear and quadratic fixed effect of age at test day and four fixed regression coefficients describing lactation curves. Random effects were: permanent environment, additive genetic and residual. Models with different contemporary group definitions were studied: fixed herd-test-date effect (HTD - 31,856 levels), eight models with clustered herd-test-date groups (21,065 - 28,442 levels), herd-year-season (HYS - 2737 levels), herd production level - month of test (HLMT - 1633 levels), and additionally random herd-test-date effect (HTDR). The variance components were estimated via DFREML algorithm. Unitrait BLUP under an animal model was employed for genetic evaluation. Heritability of daily yield were: .48, .42-.49, .25, .20 and .38 for models with HTD, clustered HTD, HYS, HLMT and HTDR, respectively. Relatively high additive genetic variance and low permanent environmental variance estimates were obtained for models with HTD, clustered HTD and HTDR. This in consequence, led to high heritability estimates. A higher correlation between true and estimated breeding values was noted for models with HTD (.94) and clustered HTD effect (.90–.95) when compared to the remaining models with HYS, HTDR and HLMT (.86, .75 and .66 respectively). Herd-test-day clustering improved the reliability of cows evaluation and bulls having more than 25% of their daughters' records in single HTD classes while breeding values of bulls with more than 40 daughters remained almost unchanged (correlation between estimates for HTD models ranged between .98–.99). Relatively small correlation (.84) was found between estimates from HTD and HYS models. The lowest correlations were found for breeding values estimated from the model with random HTD effect and the other ones (0.55–0.64).

Key Words: Genetic Evaluations, Test Day Models, Contemporary Groups

338 Comparison of Hungarian and US Holstein-Frieisian bulls used in Hungary.

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The purpose of this study was to investigate if there were differences between Holstein-Friesian bulls of different geographical origin concerning production and reproduction traits. The results of 2163 daughters of 31 bulls were compared according to the sires' origin whether they were born in US (n = 15, number of daughters = 1047) or Hungary (n = 16, number of daughters = 1116). Data set covers recordings from the large scale Holstein-Friesian seedstock herd Enying (Hungary) over the period lasting from 1989 to 1997. From the data it can be concluded that concerning milk yield, butterfat and milk protein production in the first lactation (305 days) there are slight but significant differences between the two daughter groups in favor of the progeny group sired by bulls of Hungarian origin ($P<.01$). Mean values and standard deviations for first lactation milk yield, butterfat and milk protein yield of progeny groups sired by HF bulls from Hungary or US were 7252±1102, 252.8±61.3, 234.3±57.6, 6953±964, 235.0±52.4, 226.1±49.2 kg., respectively. In spite of superiority of the daughters sired by bulls of Hungarian origin in terms of first lactation performance the herd life performance and reproduction traits exceeded the results of their counterparts sired by bulls of US origin. Mean values and standard deviations for total milk yield, butterfat and milk protein yield as well as life span of progeny groups sired by bulls of Hungarian or US origin were 20354±10658, 758.6±314.3, 679.9±306.0 kg., 4.63±2.01 years and 24833±11025, 945.3±305.2, 785.7±358.3 kg., 5.73±1.95 years, respectively. The investigations are going on in order to promote the international integration of breeding work using top Holstein bulls in Hungary.

339 Impact of different methods of adjusting for heterogeneous variances on national and international evaluations.

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Three different methods to adjust for heterogeneous variances were applied to data used in Italy for official genetic evaluation and compared to results from unadjusted data. Data consisted of about 8,500,000 lactation records from 3,500,000 cows with first calving from 1974. Adjustment methods were: 1) the official preadjustment of data currently applied in Italy; 2) the preadjustment currently applied in Canada; 3) the adjustment in the model officially used in The Netherlands. Estimated Breeding Values were computed using the official Animal Model procedures. All methods had an impact on sire and cow genetic trend and on variability of proofs. The Italian method had the strongest effect in reducing both genetic trend and variability of estimated breeding values compared to unadjusted data results. Other comparison criteria were average difference between estimated breeding and Parent Average of Italian proven bulls and its variability and effect on estimated breeding values of cows in high and low variability herds. In addition the effect of each method on international evaluations was investigated with regards to genetic trend checks and to ranking of bulls. In general terms all adjustment methods for heterogeneity of variances across herds improved the accuracy of Estimated Breeding Values and reduced bias on bull dams. Impact on international evaluation was evident.

340 **Relationship between EPDs for Angus bulls evaluated in the Angus National Cattle Evaluation and the Simmental Multi-Breed International Cattle Evaluation systems.**

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In the ASA's Multi-Breed International Cattle Evaluation (MB-ICE) system, sires are evaluated together regardless of genotype. There were 107 Angus bulls in the MB-ICE system that were published in the Fall 1997 Angus Sire Evaluation Report. The average accuracies for the Angus EPDs were .98, .97, .96, and .93 for Birth Weight (BWT), Weaning Weight (WWT), Yearling Weight (YWT), and Maternal Milk (MMK). The average-BIF accuracies for the ASA EPDs were .38, .35, .35, and .30 for BWT, WWT, YWT, and MMK. The BIF accuracies were converted to r_{ti}. Individual expected correlations (E(r)) were calculated as the product of the Angus and ASA r_{ti}s. Sires were grouped into three groups based on individual E(r): High (> .75); Medium (.50–.74); and Low (< .50). Simple and rank correlations were calculated using the bulls' ASA and Angus EPDs. The results indicate the ASA sire rankings should move closer to the Angus sire rankings with additional progeny and daughter records.

Trait	Group	n	r^1_{pm}	r^2_{rank}
BWT	High	47	.60	.60
	Medium	52	.40	.42
	Low	8	.10	.23
WWT	High	41	.71	.71
	Medium	55	.39	.35
	Low	11	−.13	.00
YWT	High	41	.68	.59
	Medium	54	.37	.32
	Low	11	.00	.24
MMK	High	33	.59	.52
	Medium	54	.38	.33
	Low	20	.30	.44

[1] Rank Correlation [2] Product-Moment Correlation

Key Words: Expected Progeny Difference, Beef Cattle, Genetic Evaluation