199 Evaluation of lifetime production of top cows in different dairy breeds.

M. Horvai-Szabo[1], J. Dohy*[1], and G. Hollo[1], [1]*Szent Istvan University, Godollo, Hungary.*

Due to recent achievements of biotechnical methods, best animals might have an important role for being embryodonors or cell nucleus donors. For this purpose, top cows of different dairy breeds with high lifetime production have been analyzed, in order to find correlation breakers (high protein yield combined with moderate milk quantity). Yields from different breeds were analyzed as follows: Swiss Simmental (n=241), Brown Swiss (n=52), Osnabrck Holstein-Friesian (n=47), Hungarian Holstein-Friesian (n=22), German Black and White (n=15), German Red and White (n=9), and Danish Jersey (n=22). Lifetime milk production of all cows but Danish Jersey and Swiss Simmental ones, exceeded 100000 kg. Traits studied were as follows: total milk yield (kg), total milk protein and butterfat production (kg), milk protein and butterfat percentage. Cows were ranked on milk protein yield (kg). Ranking of Danish Jersey individuals was made on butterfat yield (kg) and rank correlations were calculated on milk and protein (in Jersey on milk and fat) yield. The probability of appearance of correlation breakers was also tested according to the deviation from the mean based on age, milk and protein production. For Swiss Simmental and Brown Swiss breeds it was found that the lower the protein production is, the lower is the correlation. In the first Osnabrck Holstein-Friesian subpopulation high coefficient of correlation (0.74) was calculated, which was not the case in the other two ones. The share of the correlation breakers in the three subpopulations was 12.5%, 33.3% and 56.3%, resp. In German Black & White and Red & White, similar and high coefficients of correlation were present (0.9 and 0.84, resp.). The share of the correlation breakers was 26.7% and 22.2%, resp. In the Hungarian Holstein population the coefficient of correlation was low (0.29). Consequently, the ratio of correlation breakers is relatively high. The value of the rank correlation coefficient between milk fat and milk yield of Jersey top cows was 0.26 that also means a weak relationship. The ratio of the correlation breakers was 36.4%. In conclusion is: the lower is the coefficient of rank correlation, the higher is the chance for appearance of correlation breakers.

Key Words: Lifetime milk production, Correlation breakers, Dairy breeds

200 Analysis of plasma IGF-I hormone levels in Holstein-Friesian heifers.

M. Horvai-Szabo[1], R. Renaville[2], and J. Dohy*[1], [1]*Szent Istvan University, Godollo, Hungary,* [2]*Faculté des Sciences Agronomiques, Gembloux, Belgique.*

Genetic progress in animal breeding is determined by efficiency of selection. In addition to small genetic progress to be expected problems may arise from the time factor. For this reason, analysis of one of the physiological-genetic parameters, which has an effect on performance traits would be needed in the early part of life. The aim of this experiment was to determine the IGF-I level in Holstein-Friesian heifers as a physiological-genetic parameter from birth until 14 months of age. For this purpose animals were kept under the same environmental conditions. They, however, had different genetic background. During the experiment blood samples (10 ml) were collected from 100 heifers every month. Due to losses statistical analysis was made only for 86 individuals. All samples were centrifuged at 2000 x g for 20 min. at 4°C, and stored at -20°C for subsequent analysis. Concentrations of IGF-I in plasma samples were determined by (^{125}I)RIA procedure according to Lemal et al. (1989). Findings reveal higher IGF-I concentrations in plasma (42.84 ng/ml) ($P<0.05$) at birth than two months later (15.44 ng/ml). The IGF-I hormone level, however, seemed to increase thereafter at 3, 4, and 5 months of age. Moreover, it exceeded even the initial value at 6th month of age (61.45 ng/ml) ($P<0.01$). Although, the IGF-I concentrations in plasma showed slight decrease by 7, 8 months with slight ascending phase at 13 and 14 months of age. But these values remained still above the initial value. Peak value at 6 month suggests average age at precocity. IGF-I concentrations in plasma reached their maximum at 12 month of age (82.25 ng/ml) an increase of 100 % in comparison to the initial value ($P<0.01$). Both sexual maturity, and precocity depends on the state of development of the individual. For this reason, blood collection and body weight of the animals were measured simultaneously. In order to be able to answer the question if there is any correlation between the variation of the hormone level and precocity, the IGF-I concentrations and the variation of body weight were analysed. It can be stated that, the type of the variation of IGF-I concentrations in plasma followed the tendency of the variation of age and body weight.

Key Words: IGF-I, Sexual maturity, Dairy heifers

201 Results of a simulated selection using markers in dairy cattle with respect to longevity traits.

G. Freyer*[1], L. Panicke[1], and G. Erhardt[2], [1]*Research Institute for the Biology of Farm Animals,* [2]*Justus Liebig University Giessen.*

A study where two Casein loci were used to be markers for improving milk yield, fat content and protein yield in a marker assisted selection experiment focused on side effects which possibly may happen on longevity traits. The traits of interest to be selected on are the milk traits. The influence on longevity traits is indirectly taken into account. Using the complete information on two samples of Black and White cows of 974 and 454 individuals a simulation on the data was carried out evaluating the selection differences in period of use, period of life and production of the whole life. The selection criteria were chosen flexible using one of the milk production traits each as well as marker information. During the investigated period no negative effect of simulated selection using EBV for milk yield, fat content and protein yield alone or in combination with the marker information on the longevity traits occured in the population. There are no significant differences caused by selection on pure EBV and MAS within a trait. Combinations of heterozygous genotypes at more than one Casein locus affect the longevity traits positively.

Key Words: Dairy cattle, marker assisted selection, longevity

202 Relationships between parameters of the glucose tolerance test (GTT) in young sires and their estimated breeding values (EBV).

L. Panicke*[1], R. Staufenbiel[2], O. Burkert[2], E. Fischer[3], and F. Reinhardt[4], [1]*Research Institute for the Biology of Farm Animals, Dummerstorf, Germany ,* [2]*Free University Berlin, Institute of Veterinary Physiology, Germany,* [3]*University of Rostock, Faculty of Agricultural and Environmental Siences, Germany,* [4]*United Datasystems for Animal Production, Verden, Germany.*

A high milk performance connected to a sound health regarding metabolism and a sufficient fertility in dairy cows depends on a well balanced distribution of energy in the body. Insulin plays an outstanding role based on its central position in energetic metabolism. The function of insulin may be recorded by means of the intravenous glucose tolerance test (GTT). The reaction of insulin and glucose was investigated after infusion of 1 g Glucose per $kg^{0.75}$ because of the probable genetic determination of the reactive ability. The coefficients of heritability range from $h^2 = 0.16 \pm 0.10$ to $h^2 = 0.28 \pm 0.16$. The relationship between GTT-parameters and estimated breeding values (EBV) depends on the age. Investigating 28 sires the correlation coefficients amount to $r = 0.5$ for parameters of GTT and estimated breeding values (EBV) which is closer than those between pedigree breeding value (PBV) and GTT. This is expecting additional information for young sires before the insert of the test.

Key Words: young sires, glucose,insulin, breeding value

203 Realized advantages of progeny testing young dairy bulls in multiple countries.

N.R. Zwald* and K.A. Weigel, *University of Wisconsin, Madison.*

The objective of this study was to determine the extent of multiple country progeny testing and to examine the effects on reliability and marketability of these bulls. Holstein Bulls born between 7/1/92 and 12/31/94 were used; giving a set of bulls that had only first crop daughters. August 1999 Interbull evaluations were used to examine reliabilities in sampled countries vs. non-sampled countries. For each bull, home country was the country of registration if he had daughters there; otherwise it was the country with the most daughters. From the initial set of 11,862 bulls, 563 were sampled in at least two countries. Canada, Germany, France, Netherlands, USA, New Zealand, and Australia had the most extensive multiple country progeny test programs. The USA, Canada, France, and Netherlands were the most common home countries, while Germany, New Zealand, Australia, and France were the most frequent countries of foreign sampling. Mean production reliabilities for multiple country sampled bulls were 0.905 in the "home" country, 0.891 in foreign countries were the bull was sampled, and 0.779 in countries with no daughters. Reliability for teat placement was 0.865 in countries where a bull was sampled, and 0.822 in countries with no daughters. Reliability for rear udder width was 0.828 in countries where a bull was sampled, compared to 0.683 in countries where a bull was not sampled. The advantages of multiple country progeny testing were realized to a larger extent for countries that had low genetic correlations between production systems (e.g. US and New Zealand), and for type traits that were measured differently between countries. Marketing advantages also existed for bulls with daughters in multiple countries and thus higher reliability values. International sampling is increasing in popularity, and this should improve the accuracy of international sire evaluations in the future.

Key Words: Progeny testing, International evaluation, Reliability

204 Early prediction of 305 days milk production using an empirical Bayes method.

J.A.C. Pereira*[1], M. Suzuki[1], K. Hagiya[1], and Y. Atagi[2], [1]*Obihiro University of A & VM., Obihiro, Japan*, [2]*National Livestock Breeding Center(Ministry of Agriculture Forestry and Fisheries), Fukushima, Japan.*

The objectives of this study were 1) to predict the future milk production from early records of the lactation using an empirical Bayes method (EBM), and 2) to compare the EBM against the Test Interval method (TIM), Best Predicted estimation (BPE), and Wood's model (WM). Daily milk yields were from 606 first lactation Japanese Holstein cows in three herds. From each file of 305 daily records, 10 random samples with an interval of one month approximately were taken. The accuracies of the methods were compared using the absolute difference (AD) and the standard deviation (SD) of the differences between the actual and the estimated 305-d milk production. The results showed that in the early stage of the lactation, EBM was superior in obtaining the prediction with high accuracy. When all the herds were analyzed jointly, the AD during the first 5 samples were on average 373, 590, 917, and 1042 kg for EBM, BPE, TIM, and WM, respectively. Corresponding SD for EBM, BPE, TIM, and WM were on average 488, 733, 747, and 1605 kg. When the herds were analyzed separately, the EBM predictions retained its high accuracy. In contrast, TIM and BPE exchanged the results of their predictions; TIM obtained better accuracies in one of the herds. When more information on the actual lactation was added to the prediction, TIM and WM gradually achieved better accuracies in the predictions. Finally, in the last period of the lactation, both of the methods overwhelmed EBM and BPM. The AD for the last 2 samples analyzing all the herds jointly were on average 141, 142, 164, and 214 kg for WM, TIM, EBM, and BPE, respectively. In the current practices of collecting monthly records in Japan, early prediction of the future milk production may be more accurate using EBM. Alternatively, if enough information of the actual lactation is accumulated, TIM may obtain better accuracy in the latter stage of lactation.

Key Words: Empirical Bayes method, Daily milk yields, Absolute difference

205 Heritability and genetic correlation for lifetime production and first lactation traits of Holstein cows in Japan.

K. Hagiya*[1], M. Suzuki[1], J. A. C. Pereira[1], and T. Kawahara[2], [1]*Obihiro University of A & VM, Obihiro, Japan*, [2]*Hokkaido Dairy Cattle Milk Recording and Testing Association, Sapporo, Japan.*

Heritabilities and genetic correlations for 33 traits in cows' lifetime and first lactation were estimated and compared. Data consisted of 132,096 animals in a pedigree sub-file and 58,352 records. Herd life and productive life for longevity traits; and milk, fat, solid nonfat, and protein for lifetime production traits; in 48 and 84 months each, were 12 of the traits. Milk, fat, solid nonfat, protein, and 17 type traits in the first lactation were also investigated. Variance components for all the traits were simultaneously estimated using EM-REML with a multiple-trait animal model. Inbreeding coefficients of parents were calculated from a pedigree file containing more than 2,000,000 animals. An additive relationship matrix with the inbreeding was used to account for bias in variances. For all traits, heritabilities were higher (0.01 to 0.08) when considering the inbreeding than when not considering it. Heritabilities of lifetime production traits (0.19 to 0.20) were higher than those of longevity traits (0.13 to 0.16). Genetic correlations between milk productions in the lifetime and first lactation were 0.69 and 0.53 for 48 and 84 months, respectively. Genetic correlations between 84-mo milk production and type traits in first lactation ranged from -0.28 (capacity and strength) to 0.33 (mammary system). These genetic correlations could be used to predict genetic values for lifetime production traits from records of milk production and type traits in first lactation. The selection for capacity or related traits may decrease lifetime production.

Key Words: Holstein cows, Lifetime production, Genetic parameters

206 Method R estimates of heritability and repeatability for milk, fat, and protein yields of Japanese Holstein cows.

M. Suzuki*[1], K. Hagiya[1], J. A. C. Pereira[1], and T. Yoshizawa[2], [1]*Obihiro University of A & VM, Obihiro, Japan*, [2]*National Livestock Breeding Center(Ministry of Agriculture Forestry and Fisheries), Fukushima, Japan.*

Estimates of heritability and repeatability for 305-d milk, fat, and protein yields were calculated from records of Holstein cows used for national sire genetic evaluations in Japan. Data included 5,772,159 records and 2,170,997 cows for milk and fat yields, and 3,745,913 records and 1,539,187 cows for protein yield. Data were adjusted to 26 months of age in the first calving. Variance components were estimated by Method R, which uses iteration on data and second-order Jacobi iteration for obtaining solutions to the mixed model equations. The whole data and ten different random subsets from the data were used for parameter estimation. Heritabilities estimated from the ten subsets were on average 0.34, 0.32, and 0.30 for milk, fat and protein yields, respectively. These heritabilities were higher by 0.01 than those estimated from the whole data. Repeatabilites were 0.53, 0.52, and 0.51 for milk, fat, and protein yields, respectively. The mean of approximate standard errors of heritabilities and repeatabilites ranged from 0.003 to 0.004, and from 0.001 to 0.002. When the analysis was performed by parity, the results were different among parities. Heritability estimates for all the traits were 0.40, 0.37, and 0.32 for milk, fat, and protein in the first lactation, respectively, and decreased in the following lactations. These estimates in the latter lactations were similar to the results obtained when the whole data set was used in this analysis. If genetic evaluations are performed without taking account of the disagreement among the first and following lactations, negative impact on the accuracy of the evaluations could be encountered. Now that more powerful computers are available, sire genetic evaluations may be more accurate if the first and following lactations are treated as different traits.

Key Words: Method R, Heritability, Repeatability

207 Analysis of breeding efficinecy in relation to dairy performance in Holstein cows.

E. Szücs*[1], K. Bódis[2], A. Gáspárdy[1], I. Györkös[3], J. Tözsér[1], and Gy. Látits[1], [1]*Szent István University, Gödöllö, Hungary* , [2]*Technische Universität München, Freising/Weihenstephan, Germany,* [3]*Research Institute for Animal Breeding and Nutrition, Herceghalom, Hungary.*

In order to be able to characterize reproductive performance in dairy cattle attempts have been made using the term Breeding Efficiency developed by Tomar (1965). Breeding efficiency was defined by the formula BE = [365(n-1)+740] X 100/(AC+CI), where n is the number of calving intervals, 365 is the desired calving interval in days, 740 is the desired age at first calving in days, AC is the actual age at first calving and CI is the sum of the actual calving intervals in days. Database of representative sample from an upgrading program with Holstein-Friesian was used in this study (N=28631). Statistical analysis was made by SAS PC-Version, Release 6.04. (1996) using GML Type III, ANOVA, and multivariate regression analysis (backwards stepwise procedure). LSMs for BE seemed to improve from first to sixth calvings. Values for subsequent parities were 91.8; 92.9; 94.6; 94.7 and 96.4 %, respectively. BE can be estimated with high precision and relatively low standard error. Coefficients of determination were $R^2 = 0.99$ or even higher with SE = 0.67-0.17 ($P<0.001$) for different parities. Medium and negative relationships of BE with CI were calculated. Coefficients of correlation seemed to decrease for subsequent calvings ($r = -0.50$ and $r = -0.36$, $P<0.001$). Closer and negative coefficients of correlation of BE with AC ($r = -0.87$ and $r = -0.96$, $P<0.001$) and relatively low and negative relationships of BE with actual lactation milk yield, butterfat yield and milk protein yield were established as follows: $r = -0.12$ ($P<0.05$); $r = 0.15$ ($P<0.01$) and $r = -0.16$ ($P<0.01$), respectively. Relationships of BE with butterfat as well as milk protein percentage seemed to be low and negative ($r = -0.08$, $P>0,05$ and $r = -0.17$, $P<0.05$). In conclusion,

the term "breeding efficiency" proved to be a useful tool for evaluation of reproductive performance in dairy cattle.

Key Words: Breeding Efficiency, Dairy and Reproductive Performance, Dairy cattle

208 Feet and leg structures associated with changes in productive life in dairy cows.

P. O. Boisot* and R. D. Shanks, *University of Illinois, Urbana.*

Feet and legs have an impact on productive life (PL), but only extreme scores for these traits should increase involuntary culling. The objective of our research was to identify ranges of feet and leg structures associated with greater or less expectancy in PL. Type score during first lactation, milk deviation and PL on 49,601 Illinois cows born from 1979 to 1993 were provided by Holstein Association and USDA. An analysis of variance on PL was carried out, adjusting for the fixed effects of herd-year of first calving, age at first calving, herd status and one of the three linear feet and leg traits (rear legs-side view (RLSV), rear legs-rear view (RLRV) or foot angle (FA)). Each feet and leg trait was pre-adjusted for age at first calving, classifier and stage of lactation before being divided into 10 groups of 5 point intervals (group 1 for scores 1 to 5, group 2 for scores 6 to 10, . . . , group 10 for scores 46 to 50). Milk deviation and PTA somatic cell score were fitted as covariates in order to adjust PL for voluntary culling and mastitis. For RLSV, cows scoring between 1 to 10 and 41 to 50 points had a decrease in PL of 2.32±0.41 mo compared to other cows, expected PL in interval 41 to 50 was lower by 1.91±0.80 mo compared to expected PL in interval 1 to 10. Cows scored in interval 1 to 30 had a decrease in expected PL of 2.67±0.44 mo for RLRV and of 2.50±0.34 mo for FA compared to other cows. The decrease in PL was accentuated in interval 1 to 10 with a difference of 3.68±0.39 mo for RLRV and 2.75±0.39 mo for FA compared to interval 11 to 30. Dairy producers should only consider feet and legs in their voluntary culling criteria when cows have scores below 11 points for RLSV, RLRV or FA or above 40 points for RLSV. Other feet and leg scores on first lactation were not justified as criteria in deciding whether or not a cow should be kept in the herd. Our conclusion assumed that differences in PL reflected the real biological relationship between feet and legs with longevity rather than culling practices based solely on scores for feet and legs.

Key Words: Culling, Feet and legs, Longevity

209 Predicting losses due to mastitis.

C.M. Wachter* and B.T. McDaniel, *North Carolina State University, Raleigh.*

Objectives were to evaluate number of cases of mastitis as a predictor of 1) deviation between predicted and actual production in first through fourth lactations, 2) difference between first and second lactation yield, and 3) first lactation performance for animals with only one lactation versus those with at least two lactations. Number of cases was determined by number of treatments. Treatments less than 30 days after a previous one were considered the same case. Case was adjusted for length of lactation. Cows leaving the herd for mastitis and not listed as treated were considered to have one case during that lactation. Data were on Holsteins calving between 1986 and 1997 from the NCSU Dairy Educational Unit and two NC Department of Agriculture herds. Calving month was divided into two seasons: summer (months 4-9) and winter (months 1-3, 10-12). First (1483), second (1029), third (654), and fourth (406) lactation cows were used to investigate deviations of predicted and actual yields. Predicted value was sire's PTA + .5*mgs's PTA + .25*mggs's PTA + 9479 kg (milk) or 346 kg (fat). Difference was predicted yield (milk or fat) minus mature equivalent yield. Model was difference = case + herd*year of calving + season. Case had a highly significant and negative effect on production in the first three lactations, with each case equivalent to a loss of 450 kg of milk and 14 kg of fat in first lactation. For predicting deviation between first and second lactation, 776 animals were used. Change was yield (second lactation) minus yield (first lactation). Model was change = $\text{case}^{secondlactation}$ + $\text{herd*year of calving}^{firstlactation}$. Case (second lactation) had a large, negative effect on difference between first and second lactation. First lactation data on animals that only had a first lactation (565) were compared with data on animals that had two or more lactations (772). Animals without a second lactation had lower milk production, fewer days in milk, and more cases in their first lactation than animals with a second lactation. Overall, mastitis resulted in significant current and future performance losses.

Key Words: Mastitis, Yields, Holsteins

210 Estimates of genetic parameters for milk yield of first lactation Holstein cows.

A. P. Márquez*[1], J. H. Herrera[2], A. Correa[1], F. J. Verdugo[1], H. C. Hernández[3], and H. G. González[1], [1]*Universidad Autonoma de Baja California*, [2]*Colegio de Postgraduados*, [3]*Universidad Autonoma de Baja California Sur, Mexico.*

First lactation records (n=330) for milk yield of Holstein cows, from 42 sires were analyzed by using least squares. The objective was to estimate genetic parameters. Environmental correlation value (c^2) was used as a component of the equation to estimate breeding values for milk yield due to sires. The model included: season of parturition as a fixed effect, sire, sire x season interaction and the residual as random effects. The average milk yield 305d 2x in first lactations cows was 8757.50±1,401.89 kg; the projected milk production to mature equivalent 11,012.20±1,735.62 kg. The averages for milk yield of first lactation cows grouped by season of parturition were: 9,028±124.34, 8,232.90±1,163.96 and 8,783±1,602.42 kg October to January, February to May and June to September, respectively. Significant differences ($P<.01$) in milk yield were found between cows where parturitions ocurred from February to May, but no difference($P>.05$) was found between cows where parturition ocurred from June to September. The average predicted milk difference was 65±130.14 kg. These estimates were different from the reported values in sires summaries. The estimated value of the correlation between milk yield 305d and projected milk yield to mature equivalent was($r=.93$). The estimated heritability value for milk yield was ($h^2=.36\pm0.33$). The variance component due to sire effect (209,865.28) was highly significant for milk yield.

Key Words: Heritability, Breeding values, First lactation

211 Estimates of genetic parameters and breeding values for milk yield in a Holstein dairy herd at north west of Mexico.

A. P. Márquez*[1], J. H. Herrera[2], G. H. Torres[2], A. Correa[1], and H.G. González[1], [1]*Universidad Autónoma de Baja California*, [2]*Colegio de Postgraduados, Mexico.*

An analysis was made of 722 Holstein cows, daughters of 55 sires in 1,077 lactations. Data came from a dairy herd in Mexicali, Baja California, México. Data was analyzed by using MIVQUE. It allowed to estimate the heritability value(h^2) to millk yield. Lactations were classified within cows and sires to estimate through the intraclass correlation among paternal half sibs, the heritability value for milk yield. The average milk yield 8,437 kg 305d suggest a reasonable high productivity by cow. The average values for length of lactation, dry period, open days, parturition interval and number of services per conception were (295.80, 59.17, 127.80, 437.80, and 2.9) respectively. The estimated heritability value for milk yield ($h^2=0.28\pm.05$) is similar to the reported values for the same index for this trait. The estimated repeatability value for the same trait was($R=0.33\pm.55$). The magnitude of this value suggest a very similar environment in the animals whose the heritability value was estimated.The results on the estimated breeding values can be considered as reasonable values. Although those estimated values were different to reported values of predicted difference for milk yield into sires summaries.

Key Words: Milk yield, Heritability, Repeteability

212 Collection, validation, and use of test-day data for genetic evaluations.

J.C. Philpot* and G.R. Wiggans, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

For the August 2000 implementation of the first phase of a test-day model for US genetic evaluations of yield traits of dairy cattle, test-day data have been collected by the Animal Improvement Programs Laboratory (AIPL) for cows that have calved since 1990. The database includes more than 185 million test-day records from 24 million lactations. About 3.5 million observations are added each month. Test- day information is stored on a cow and herd basis. Cow information includes cow identification, herd code, calving date, days in milk, milking frequency, milk yield, fat and protein percentages, and somatic cell score. Herd information includes information on milk recording, such as sampling frequency, supervision received, and averaging of milk weights. Data are subjected to extensive validation. Test dates for the cow must match test dates for the herd. Test-day milking characteristics for individual cows are compared with herd milking characteristics. Results of record editing are carefully monitored to allow detection of potential problems with incoming records, such as an unusually high number of records that were replaced, deleted, or rejected. Test-day data are available to industry cooperators at the AIPL web site (http://aipl.arsusda.gov). Authorized users can query by cow or herd identification numbers and obtain test-day information. Error records from rejected test- day data also are available by querying on cow, sire, or herd identification numbers. Although test-day data were acquired for most herds, some gaps remain, particularly for the early 1990s. Some cows with lactation data do not have test-day data. The date for using test-day rather than lactation data in the national genetic evaluation system will be determined for each herd and based on the amount of test- day data available for that herd. For Holsteins, test-day records will be used for 42% of 1990 calvings, 78% of 1995 calvings, and >99% of 1999 calvings.

Key Words: Test-day model, Data collection, Data validation

213 Effects of crossbreeding and season of calving on production of milk fat and protein of primiparous dairy cows.

K. E. Lesmeister*[1], D. W. Kellogg[1], A. H. Brown, Jr.[1], Z. B. Johnson[1], and A. G. Lane[2], [1]*University of Arkansas, Fayetteville,* [2]*Lane Ag Consultants, Stephenville, TX.*

Effects of crossbreeding and season on milk fat and milk protein production were analyzed using first lactation records of 1,003 Holstein (H), 60 Brown Swiss X H cows (BSH), and 52 Jersey X H cows (JH). Projected actual 305-d (PA) and mature equivalent 305-d (ME) records were used to develop groups of BSH and JH cows that were contemporaries of H cows calving within the same month or 4-mo period as the BSH or JH crosses, respectively. Effects analyzed were seasonal effect, breed effect, and a season by breed interaction effect. There was a significant seasonal difference in PA kg of fat in the JH group. Significant differences for PA percent fat were observed in both contemporary groups for all effects, except seasonal effect in the BSH group. Significant differences in PA protein yield were observed for seasonal effect in both contemporary groups and for breed effect in the JH contemporary group (JH, 253.4 ± 9.0 kg; H, 285.7 ± 1.7 kg). Seasonal effect, breed effect, and season by breed interaction effect were significant for PA percent protein and ME percent protein in both contemporary groups. The BSH group had significant differences for ME fat yield for seasonal and breed effects (BSH, 391.4 ± 9.4 kg; H, 338.7 ± 3.7 kg). Significant differences were observed in ME percentage of milk fat in the JH group for all effects and in the BSH group for breed effects (BSH, 3.70 ± .07%; H, 3.42 ± .03%). Significant differences were also observed in ME protein yield in both contemporary groups for seasonal and breed effects (BSH, 353.8 ± 8.4 kg; H, 317.2 ± 3.3 kg; JH, 295.7 ± 9.6 kg; H, 321.1 ± 1.8 kg). The data suggest that seasonal variations influenced actual kilograms of fat and protein produced by BSH cows and H cows similarly, but affected JH cows more than H cows. Actual fat and protein percentages were less affected by seasonal fluctuations in crossbreds than in Holsteins.

Key Words: Dairy Cows, Crossbreeding, Seasonal Production

214 Effects of crossbreeding and season of calving on milk production of primiparous dairy cows.

K. E. Lesmeister*[1], D. W. Kellogg[1], A. H. Brown, Jr.[1], Z. B. Johnson[1], and A. G. Lane[2], [1]*University of Arkansas, Fayetteville,* [2]*Lane Ag Consultants, Stephenville, TX.*

Effects of crossbreeding and season on milk production were analyzed using first lactation records of 1,003 Holstein (H), 60 Brown Swiss X H cows (BSH), and 52 Jersey X H (JH) cows of Norwood Dairy Farm near Goldthwaite, TX. Projected actual (PA) 305-d milk and mature equivalent (ME) 305-d milk yields were used to develop groups of BSH and JH that were contemporaries of H cows calving within the same month or 4-mo period as the BSH or JH crosses, respectively. Utilization of net energy for lactation (NE_L) was calculated for a sample of cows that were weighed during lactation. Effects analyzed were breed, season, and breed by season interaction. There was no significant difference in PA milk yield between BSH (7824 ± 232 kg) and H (8137 ± 92 kg) cows; however milk yield corrected for ME was higher ($P < .05$) for BSH (10,640 ± 276 kg) than H (10,019 ± 109 kg). The H cows produced more ($P < .01$) than JH cows (8688 ± 55 vs. 7360 ± 284 kg PA milk and 10,131 ± 60 vs. 8735 ± 314 kg ME milk, respectively). There were no differences in either PA or ME milk yield between BSH and H cows due to season. The JH cows produced less PA milk during summer than H cows and the interaction effect was significant, but ME milk yield was similar for JH and H cows. Based on metabolic body weights of 112, 98, and 106 kg (± 3 kg), the sample of cows used 67.8, 69.4, and 68.1% of NE_L for milk yield for BSH (n = 9), JH (n = 11), and H (n = 12), respectively. The data suggest that while JH cows produce less milk than BSH or H cows during the first lactation, JH cows are as efficient in use of NE_L as the larger cows. If crossbreeding improves longevity, it may be a viable option for breeding dairy cows.

Key Words: Dairy Cows, Crossbreeding, Milk Production

215 Milk production loss associated with mastitis and the efficacy of treatment protocols.

E.H. Shim*, D.E. Morin, and R.D. Shanks, *University of Illinois, Urbana.*

The recovery in milk yield associated with two treatment protocols for mastitis was used to gauge the efficacy of the protocols. Between January 1994 and December 1995, 104,825 daily milk (DM) records on 540 lactations were taken at the University of Illinois Dairy Unit. Clinical mastitis was associated with 2,903 DM records during 127 lactations. Based on examination, each cow with clinical mastitis was assigned a severity score of 1 (least severe) to 3 (most severe) and randomly assigned to one of two treatment groups: N (supportive treatment only) and A (antibiotics in addition to supportive treatment). Extent of antibiotic and supportive treatment varied according to protocols. A random regression test-day model was used to estimate daily milk yield differences between treatment groups (A and N), time of onset of clinical mastitis (=<150 and >150 in milk), and severity at onset of clinical mastitis (1, 2, or 3). All estimated milk yield losses were those losses associated with the period of clinical mastitis. The average milk loss was 3.65 ± .14 kg/day during the infection period. The addition of antibiotics to supportive therapy alone resulted in 2.31 ± .26 kg/day more milk. The loss in daily milk yield was also dependent on the severity score at onset of clinical mastitis. Cows with a severity score of 1 produced .86 ± .22 kg/day more milk than the average of cows with a severity score of 2 or 3. Cows with a severity score of 2 produced 1.80 ± .41 kg/day more than cows with a severity score of 3. Mastitis episodes that occurred during the first 150 days of lactation did not result in significantly more milk yield loss than episodes occurring after 150 days. Based on less severe milk yield losses, the efficacy of antibiotics in addition to supportive therapy was greater than supportive therapy alone.

Key Words: cow, mastitis, antibiotics

216 Effect of adjustment for herd test day on repeatability and heritability of 305-day milk, fat, and protein yields.

H.D. Norman*, J.R. Wright, and G.R. Wiggans, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

The impact on repeatability (R) and heritability (h^2) was examined for adjustment for effects of herd test day prior to the use of the best prediction method to calculate 305-d lactation records from test-day data. The purpose of adjusting for each herd test day is to remove its effect directly before test-day yields are combined to estimate 305-d yield. If herd test-day adjustments account for environmental effects more effectively, the genetic component of lactation records should contribute to higher R and h^2. Estimates of R and h^2 were compared with and without adjustment for herd test day. Test-day yields of milk, fat, and protein from US cows that calved after 1989 were analyzed for Ayrshires, Brown Swiss, Guernseys, Jerseys, and Milking Shorthorns; test-day records for Holsteins were limited to cows that calved in California, Pennsylvania, Texas, and Wisconsin. Because R varies with closeness of parity, separate estimates of R were calculated for each parity pair by calculating the regression of yield from the later parity on yield from the earlier parity within herd and calving year. Similar comparisons were made for the impact of herd test-day adjustments on h^2 by calculating the regression of daughter yield on dam yield within herd, dam calving year, and daughter calving year. Across breeds for all yield traits, R for second parity based on first parity was 0.53 to 0.64 regardless of adjustment for herd test day. For Jerseys and Brown Swiss, R was equal or slightly higher (0.01) after adjustment for herd test day; for Holsteins, R was 0.01 higher for all three yield traits. First-parity h^2 were equal or higher (≤ 0.03) for all breeds and yield traits after adjustment for herd test day. Some improvement in accuracy of genetic evaluations will be achieved when lactations are adjusted for effect of herd test day.

Key Words: Test-Day adjustment, Best Prediction, Heritability

217 Effects of inbreeding on reproductive and growth traits, and breeding values in a closed Brown Swiss herd.

A. S. Falcao[1], R. M. Filho[2], C.D.U. Magnabosco*[3], and R. Bozzi[4], [1]*Universidade Estadual de Maring, Brasil,* [2]*Universidade Federal do Cear, Fortaleza, Brasil,* [3]*Embrapa Cerrados, Planaltina, Brasil,* [4]*UNIFI,Firenze, Italia.*

Inbreeding effects on calving interval (CI), birth weight (BW), weaning weight (WW) and on the direct and maternal breeding values for BW were evaluated in a purebred Brown Swiss herd in northeast Brazil. Data were collected from 1946 to 1993. Inbreeding coefficients (F) were estimated according to method of Wright using the MTDFREML package. Breeding values were estimated using a BLUP animal model that included sex, month and year of birth and parity of dam as fixed effects, and direct and maternal inbreeding as covariates. The GLM procedure (SAS Institute, Cary, NC) was used to perform the statistical analyses. The relationship matrix included 1,209 animals and the average and maximum inbreeding were 12.5% and 38.3% respectively. In general, increases in inbreeding levels were followed by reductions on direct breeding value for BW. Of the total variance, direct effects for BW accounted for 47% and maternal effects for 40%. For CI, the effects of sire of dam, parity of dam and year of birth were significant ($P<0.01$), and the regression coefficient of CI on direct inbreeding was 1.4. For BW, the effects of sire, sex, month, age of dam and linear and quadratic direct inbreeding were significant ($P<0.01$). The effects of sire and sex were significant for WW ($P<0.05$). The regression coefficient of WW on maternal inbreeding was -0.51 ± 0.14 kg. These results indicate that direct inbreeding decreased individual breeding values for BW, possibly due to reduced additive genetic variance. However, these levels of inbreeding were not sufficient to affect the genetic merit of the dams.

Key Words: Inbreeding, Breeding values, Brown Swiss

218 Quality of reproductive event data for Dairy Herd Improvement herds in Wisconsin.

W. Zhang* and G. E. Shook, *University of Wisconsin, Madison.*

Accuracy of genetic evaluation for reproductive traits depends on accurate recording of reproductive events. The objective of this study was to develop criteria to measure the within herd quality of reproductive data. Because gestation length (GL) is biologically determined and has low variation, it was selected to judge herd performance in reporting reproductive events. Data from Holstein herds during 1987 to 1999 were provided by AgSource Cooperative. A total of 4,733 herds reported 590,799 parities with at least one breeding date and subsequent calving date; these were defined as complete records (CR). Gestation length was calculated as days from last breeding to calving. Records that ended in abortion or had calculated GL outside the range 265 to 308 d were omitted. The overall mean of GL was 280.4 d. A summary for each herd was computed that included herd average and SD of GL and number and percentage of cows in the herd with useable CR (UCR). The average within herd standard deviation (SD) was 6.2 d. The table below summarizes herds stratified by percentage of herd with UCR (PUCR). Herds with PUCR <40% have relatively high average and SD of GL. These herds appear less consistent in reporting reproductive information. When herds were stratified by average GL, those with >282.0 d had larger within herd SD (7.66 d). Similarly herds with SD >8.0 d had higher mean GL (282.1 d). Herds in these strata may have questionable data quality. Based on these criteria, more than 3,500 herds with nearly 490,000 parities reported breeding dates that appear to be sufficiently consistent with subsequent calving dates.

Herd PUCR	Average UCR per herd	Average total records per herds	Number of herds	Average GL	Average SD of GL
<40	39.9	101.5	410	281.01	7.24
41-50	65.3	142.3	1401	280.50	6.25
51-60	88.9	160.4	1316	280.29	6.01
61-70	81.8	126.6	675	280.30	6.17
>71	52.3	66.4	902	280.43	6.11

Key Words: Gestation Length, Reproductive Data Quality, Dairy Cattle

219 Impact of input data quality on national genetic evaluations.

H. Jorjani*, *Interbull Centre, Uppsala, Sweden.*

Individual test-day records of dairy cows go through a number of genetically motivated statistical treatments until they are summarized in a few estimated genetic parameters. Each of these statistical treatments contributes to what is commonly known as input data quality. Unfortunately, the concept of input data quality is not adequately well-defined. The objective of this study was to identify some structural and operational parameters that can contribute to a more precise definition of input data quality. For this purpose sire standard deviations for milk, fat and protein yields estimated in the Interbull Centre for 63 dairy cattle populations from 26 countries and six breeds were used. Apart from country of origin, breed and trait, the data set included information on 14 different parameters that are used in national genetic evaluations. Number of bulls in the progeny testing programs and number of lactations used in the evaluations had a significant effect ($p<0.05$) on sire standard deviations for all traits in the Holstein and Simmental populations, respectively. Extension of lactation records had a highly significant effect ($p<0.001$) across countries for all traits. Number of fixed effects included in the genetic evaluation model had a varying significant effect (from $p<0.05$ to $p<0.001$) depending on the trait, breed and model of analysis. The national genetic evaluation model had also a highly significant effect ($p<0.001$). However, length of production and pedigree data, number of lactations, weighting factors for lactations, number of effects used in pre-adjustments, number of random effects in the evaluation model, minimum required reliability for publication of proofs, and percentage of sire-identified records did not have any detectable significant effect. The same was true for days open. It should be emphasized that the data set used in the analyses was quite small and therefore it may have contributed to the inability of detecting significant effects for some of these parameters. One unexpected result was the absence of any significant effect ($p>0.05$) for breed within countries.

Key Words: Input data quality, national genetic evaluation

220 Comparison of genetic evaluations of culled and surviving cows.

T.A. Ferris*[1], H.D. Norman[2], and G.R. Wiggans[2], [1]*Department of Animal Science, Michigan State University, East Lansing, MI 48824,* [2]*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Nearly 2 million Holstein lactation records from calvings during 1990 through 1997 (a 10% sample of Holstein data) that were acceptable for USDA genetic evaluations were used to determine age and genetic differences in predicted transmitting ability for milk (PTAM) and productive life (PTAPL) between surviving and culled cows. Only records from cows in herds that remained on test long enough to provide those cows with an opportunity to calve again were included. Cows sold for dairy purposes were excluded. Annual mean PTAM and PTAPL by calving year are in the table below. Annual trends were 49 kg for PTAM and 0.09 mo for PTAPL for survivors versus 50 kg for PTAM and 0.10 mo for PTAPL for culls. Mean PTAM for grade cows across years (67 kg for survivors and -10 kg for culls) were higher than corresponding mean PTAM for registered cows (54 and -19 kg). Mean PTAPL for grade cows across years (0.23 mo for survivors and -0.18 mo for culls) were lower than corresponding mean PTAPL for registered cows (.69 and .32 mo). Mean age of cows that left the herd ranged from 65.2 mo for grade cows and 64.8 mo for registered cows during 1990 to 76.8 and 65.1 mo, respectively, during 1997. Trends for PTAM and PTAPL were similar for surviving and cull cows, and surviving cows were genetically superior for yield and longevity. Age of cows that left the herd increased for grade herds over time.

Trait	Group	1990	1991	1992	1993	1994	1995	1996	1997
PTAM (kg)	Survivors	-145	-91	-37	19	78	137	194	246
	Culls	-234	-179	-125	-73	-12	43	105	170
	Difference	89	88	88	92	90	94	89	76
PTAPL (mo)	Survivors	-0.01	0.10	0.20	0.31	0.44	0.56	0.65	0.74
	Culls	-0.44	-0.34	-0.23	-0.12	0.00	0.13	0.24	0.34
	Difference	0.43	0.44	0.43	0.43	0.44	0.43	0.41	0.40

Key Words: Genetic evaluation, Culling, Longevity

221 Growth, luteal activity, and pregnancy rates of three breed types of dairy heifers. A. H. Brown, Jr.*[1], D. W. Kellogg, Z. B. Johnson, R. W. Rorie, W. K. Coblentz, K. M. Lesmeister, and W. R. Jackson, *University of Arkansas, Fayetteville.*

Growth, luteal activity and pregnancy rates were evaluated for three breed types of dairy heifer replacements. Eighty-nine dairy heifers were obtained from the Norwood Dairy Farm near Goldthwaite, Texas and raised as contemporaries at the University of Arkansas Agricultural Experiment Station in Fayetteville. Heifers were born between May 20 and August 6, 1998, and breed types were Holstein (H, n = 35), Jersey x H (JH, n = 30) and Brown Swiss x H (BSH, n = 24). Heifers were developed on pasture with grain supplementation to ensure .9 kg of daily BW gain. Body hip height, chest depth, BW and body condition score (BCS) were obtained. Heifers were considered cycling by 12 mo of age if progesterone concentrations were $\geq$ 1 ng/ml in either of the two serum samples taken 10 days apart. Heifers were bred by AI on a synchronized estrus starting at about 14 mo of age. Pregnancy status for each heifer was determined ultrasonically after approximately 30 d of gestation. Data were analyzed by least squares ANOVA procedures to determine differences among trait means for the three breed types. Heifer age was included as a covariate in the analysis. The JH were lighter ($P < .05$) than the other two breed types, with BSH and H having similar ($P > .05$) weights. Brown Swiss x Holstein and H were similar for mean hip height (125 ± .9 and 126 ± .7 cm, $P >$. 05) and both breed types were taller ($P < .05$) than JH (120 ± .8 cm). There were no differences ($P > .05$) between breed types for mean depth of chest and mean BCS at 12 mo of age. The percentages of cyclic heifers were greater ($P < .05$) for JH (90%) than for BSH (75%) or H (47%). Mean pregnancy rates did not differ ($P < .05$) among the three breed types (BSH, 96%, JH, 87%, and H, 77%). These data suggest that the genetic effects of crossbreeding influence early growth and cyclicity at 12 mo of age for dairy heifers.

Key Words: Dairy Cattle, Crossbreeding, Growth

222 Metropolis-Hastings procedures to sample directly from the joint posterior distribution of dispersion parameters. R.A.A. Torres, Jr.* and R. L. Quaas, *Cornell University, Ithaca, NY.*

Gibbs Sampling (GS) has been a popular computing algorithm for posterior estimation of variance components (VC). Block updates have been proposed to reduce the dependency of consecutive samples. The extreme case is the version of GS that samples β's and u's from their joint distribution, conditional on the VC. Here, we propose a Metropolis-Hastings (MH) sampling scheme, in order to sample directly from the joint posterior of the VC. It uses the same sparse matrix tools used in the derivative-free REML packages, and samples directly from the joint posterior of the VC without ever sampling a β or a u. Two possible candidate generating functions are used. One borrows the idea from the way the GS procedure works and samples the candidate VC from an Inverted Wishart distribution whose mean is equal to their current value (this is close to what the GS does when little data is available). The degrees of freedom are chosen to balance out acceptance rate and size of each step in this random walk MH scheme (MHr). The other function is a multivariate normal (MVN), which describes the state of the knowledge about the VC's. This is an example of independence chain MH (MHi) and the mean and variance for the MVN can be chosen either based on previous tuning runs of MHr or based on a MVN approximation of the posterior around its mode. The procedures are tested using a simulated data set with 6019 test-day records of 711 cows, with a fifth degree polynomial random lactation curve for each cow and a constant residual variance. Two chains with 25,000 samples were run for the MHr and MHi procedures. The MHi method represented a clear improvement over the MHr method in terms of decay on the autocorrelation. MHi had long runs with no acceptance, showing the existence of highly under-sampled regions. The choice of the MVN distribution might be what caused this, but it was chosen for being easy to simulate and for allowing a flexible description of the covariance.

Key Words: Variance Components, Markov Chain Monte Carlo Methods, Covariance Function

223 Impact of lactation length adjustment procedures on accuracy and heritability of adjusted milk yield in buffaloes. M. S. Khan[1], H. Z. Chaudhry*[1], and S. H. Raza[1], [1]*Faculty of Animal Husbandry, University of Agriculture, Faisalabad, Pakistan.*

Data on 2704 lactations of Nili-Ravi buffaloes were analyzed to compare different procedures to adjust milk yield for lactation length. Differences between predicted and actual yield (bias), standard deviation of bias and heritability under an animal model were the criteria for comparison. Milk yield (±standard deviation) averaged 1984±773 kg with lactation length of 267±55 days. Fifty-nine percent of the lactations were shorter than 44 weeks. Lactations were short mostly due to reproductive problems, mastitis or culling because of poor production, old age and repeat breeding. However, in most cases animals with shorter lactations dried gradually. Lactation curves of first and later parity buffaloes were also different. Milk yield adjusted to 308 days increased from first parity (1731.8±78.86 kg) to third parity (1919.6±64.56 kg) but declined gradually thereafter. Yield predicted from a linear regression equation (having lactation length as the only predictor) or from the last record-day information was higher as compared to actual milk yield due to extrapolation to a higher base. Linear regression procedure tended to overestimate the yield in the later part of the lactation curve. The standard deviation of bias decreased and correlation between actual and predicted lactation milk yield improved with inclusion of average daily milk yield as a predictor along with the last record-day milk yield. Heritability estimates of milk yield improved as data set was restricted to include more completed lactations ($\geq$180 days). Heritability of unadjusted lactation milk yield was 9.1% while for 308-day lactation milk yield (adjusted by using last record-day information and average daily milk yield), it varied from 10.7 to 12.0%, depending on the model. Information on last recorded milk yield along with average daily milk yield of the recorded lactation period are suggested to be used as a basis for adjusting milk yield data in Nili-Ravi buffaloes.

Key Words: Buffalo, Pakistan, Lactation length, Adjusted Milk yield, Heritability

224 SIMBULL2: An instructional simulator for dairy cattle breeding and management. G. E. Shook*, E. D. Hailman, and M. R. Dentine, *University of Wisconsin, Madison.*

SIMBULL2 places students in the role of herd manager and provides experience in making decisions that create genetic improvement. The software runs on a personal computer with the Windows^{TM} operating system. Students make breeding, culling, and mating decisions for a simulated herd of lactating cows and herd replacements. The simulator manages a bull stud from which the student selects sires for herd replacements. Each run of the program represents one year of herd operation. The simulator enables students to practice and evaluate several years of breeding decisions within the scope of a few weeks. The program displays lactation performance records and genetic evaluations for six traits similar to information available in the industry. Also simulated are an appearance trait and a genetic lethal condition with single locus genotypes. An inbreeding coefficient is displayed for each animal and the performance model includes inbreeding depression. Performance records and breeding values are generated stochastically so each herd and bull stud is unique. The software is designed for flexibility in instructional goals and students level of experience. Level 1 provides for decisions related to conventional AI and generates performance reports and genetic evaluations for a standard complement of traits: yields of milk fat, and protein, final type score, mammary composite score, and calving difficulty. Level 2 allows user choice of performance traits, use of multiple ovulation and embryo transfer, progeny testing and selling bulls produced by the herd, and user defined selection indexes. An economic option generates semen costs and an annual operating statement that tracks revenues from sale of milk and animals as well as costs for breeding, feeding, and housing. Students confront problems similar to those encountered by commercial producers. These problems stimulate a higher level of thinking and analysis and create unanticipated learning opportunities in an active learning mode.

Key Words: Dairy Cattle Breeding, Simulation, Instruction

225 Preconditioned conjugate gradient method by iteration on data for solving mixed model equations.

S. Tsuruta*[1], I. Misztal[1], and I. Stranden[2], [1]*University of Georgia, Athens, GA,* [2]*Agriculture Research Centre, Jokioinen, Finland.*

Preconditioned conjugate gradient method (PCG) using iteration on data was compared with the successive-overrelaxation algorithm (SOR) in terms of convergence when solving mixed model equations. PCG with a diagonal preconditioner was implemented using single- and double-precision vectors. Sixteen different models were used in the comparison, with data on beef, dairy, and swine, and with data size ranging from small examples to national data sets. The models included single and multiple traits as well as maternal effects and random regressions, and having low and high genetic correlations. Convergence was based on relative differences between left- and right-hand sides. PCG implemented with double precision converged for all models with up to 30 times fewer rounds of iteration than SOR. PCG implemented in single precision did not converge for large models. Differences in convergence rate between single- and double-precision SOR were small. PCG with the iteration on data is very easy to implement for a large class of models while such an implementation is more difficult and model-specific for SOR. Also, SOR requires an adjustment of an iteration parameter while the PCG algorithm does not. For reliable implementation, PCG requires double precision storage of 4 out of 5 variables/equation. Only one single-precision variable/equation is required by SOR although efficient implementations may use more storage. The PCG algorithm with the diagonal preconditioner by iteration on data appears to be the method of choice for solving large mixed model equations when sufficient memory is available.

Key Words: Preconditioned conjugate gradient, Iteration on data, Convergence rate

226 Application of hierarchical models to analysis of test day yields.

J. Jamrozik* and L.R. Schaeffer, *University of Guelph, Ontario, Canada.*

First lactation test day milk yield records of Canadian Holstein cows from Ontario and Quebec were analysed by three Bayesian hierarchical models. Wilmink's function for the lactation curve for each cow was included in the first stage for all three models. Herd-test date (HTD) subclasses were included in the first stage for models 1 and 2, but not 3. Residual effects of the first stage model were uncorrelated with constant variances within each of 29 DIM intervals. The observations for the second stage multiple trait model were the lactation curve parameters per cow. The second stage model included animal additive genetic and region-age-season effects in all three models, and herd-year-season (HYS) effects in models 2 and 3 only. Genetic parameters for lactation curve coefficients, daily yields, 305d yield, and persistency (the difference in yields between day 60 and 280) were estimated as posterior means of samples generated by the Gibbs sampling method. Models with HTD effects gave smaller estimates of residual variances over all 29 DIM intervals. Models with HYS in the second stage reduced the estimates of genetic variances for daily milk yields and their heritabilities, and gave higher genetic correlations between yields that were far apart in DIM. Heritability of persistency was 0.23 without HYS in the second stage and 0.16 with HYS effect. Inclusion of HYS effects gave estimates of genetic parameters that were closer to estimates from multiple trait models. Hierarchical models with linear trajectories are equivalent to random regression models.

Key Words: Test day yields, Hierarchical models, Genetic parameters

227 Modeling accuracy of final score observations at different ages.

L. Klei*[1], T.J. Lawlor[1], I. Misztal[2], and S. Tsuruta[2], [1]*Holstein Association USA, Inc., Brattleboro, VT.,* [2]*University of Georgia, Athens.*

It is a general belief among dairy farmers that conformation scores obtained on young cows are not as valuable in assessing the genetic potential of a sire as those obtained on older daughters. In the current genetic evaluation, age differences are accounted for through a fixed effect. This takes into account differences in the average effect of each age but does not address potential differences in the accuracy of scores or differences in components of variance due to age. The objective of this study was to investigate modeling solutions to differences in accuracy associated with age at classification. Final score observations on cows born since 1984 were obtained from Holstein Association USA. Cows had a first score between 25 and 36 months of age and a second score between 42 and 54 months of age. Data were categorized into four subsets. All subsets contained first scores on all animals, but only animals within each age subset (25-27, 28-30, 31-33, 34-36 months of age) were allowed to have a second score. Minimum contemporary group size was 10 and 5 for first and second score, respectively. Contemporary groups had at least one animal with a second score. For computational reasons one out every five herds was used. Number of animals with records were 24,005, 50,379, 53,492, and 43,292, respectively. Number of second scores were 3082, 16,073, 17,880, and 10,281, respectively. Data were analyzed with a model containing fixed effects for herd-year-classifier, age at classification, and stage of lactation at classification. Random effects were animal, permanent environment, herd by sire interaction, and residual. Variance components were estimated using average information REML. Phenotypic variance estimates ranged from 11.33 to 11.90, heritability from .24 to .25, permanent environment ratio from .33 to .44, and herd by sire interaction form .02 to .03. Repeatability was .61, .67, .70, and .71 for the four age groups, respectively. This shows that first scores given at a later age are a better indicator of an animal's score at maturity than those given at a young age. Results also show that the change in repeatability is fully accounted for by a change in permanent environment while the other components of variance remain constant over time. Other approaches of modeling this problem model will be discussed.

Key Words: Modeling, Precision, Conformation

228 Approximation of reliabilities for multiple-trait model with maternal effects.

T. Strabel*, I. Misztal, and J. K. Bertrand, *University of Georgia, Athens.*

The purpose of this study was to design an inexpensive algorithm for computing accuracies of breeding values in multiple-trait models used for beef evaluation. Single trait accuracies were approximated by combining the effective number of records with pedigree information for each set of animal and parents separately. Supported models included additive and permanent environmental but not maternal effects. To support maternal effects, approximations were obtained separately for the direct and the maternal effect. For the direct effect, the maternal and permanent environmental variances were assigned to the residual. For the maternal effect, variance of the direct effect was assigned to the residual. Components of single-trait accuracies were used to create a multiple-trait mixed-model coefficient matrix for each animal, and approximate accuracy was obtained by inversion. Data included 10,550 birth weights (BW), 11,819 weaning weights (WW) and 3,617 postweaning gains (GA). Accuracies were computed by inversion of the complete mixed-model coefficient matrix and by multiple-trait approximations Some accuracies obtained by inversion were negative because inbreeding was ignored in creation of the inverse of the relationship matrix. The correlations between accuracies obtained by inversion and by approximation for the direct effect were .78 for BW, .90 for WW and .92 for GA. The correlations for maternal effects for BW and WW were .95 and -.97, respectively. When the formula used to calculate the effective number of daughters ignored the distribution of sires in contemporary groups, the approximation greatly overestimated accuracy of sires in single-sire contemporary groups. When the formula was revised to ignore such groups, the approximation became better for high accuracy but worse for low accuracy animals. The importance of the formula diminishes in larger data sets where contemporary groups are generally larger. The proposed approximation is applicable to national cattle evaluations.

Key Words: accuracy of evaluation, maternal effect, beef cattle

229 Bayesian variable selection for describing growth data using a random regression model.

F. E. Grignola* and J. P. Steibel, *Facultad de Agronomia, Universidad de Buenos Aires, Argentina.*

Growth data can be considered as consecutive measurements on one variable for the same individual, or group of individuals, over a period of time. The multiple linear regression model can be used to approximate almost any function or shape, and many methods are available for selecting an appropriate subset of regressors. Random regression models fitting a linear function of a set of covariates have been proposed for genetic evaluation purposes in many species. However, how to choose the most suitable function, in terms of the number of covariates to be included, still remains unclear. In this study, a random regression animal model containing polynomials with fixed and random regression coefficients is used to describe body weight-age relationships in beef cattle. A Bayesian method for subset selection of promising regressors for the systematic effects using the Gibbs sampler is implemented. The method consists of including, in the regression models, vectors containing indicator variables for each regressor and then computing their posterior distribution. Therefore, the submodels associated with vectors that have high posterior probability can be selected. Of all possible $2^{predictors}$ submodels for each contemporary group, only a few showed high posterior probability, and their probabilities were affected by the priors chosen. For any linear function of covariates proposed to model growth data, the method provides an alternative for subset selecting the covariates to be considered.

Key Words: Random regression, Variable selection, Gibbs sampler

230 Covariance estimation with Method-R.

T. Druet*[1,4], I. Misztal[2], M. Duangjinda[2], A. Reverter[3], and N. Gengler[1,4], [1]*National Fund for Scientific Research, Brussels, Belgium,* [2]*Department of Animal and Dairy Science, University of Georgia, Athens,* [3]*Animal Genetics and Breeding Unit, University of New England, Armidale, Australia,* [4]*Animal Science Unit, Gembloux Agricultural University, Gembloux.*

The objective of the study was to develop algorithms based on Method-R that allow estimation of (co)variance components with large data sets for complex single trait models, e.g., with correlated additive animal effects and/or with dominance effects. Theoretical Method-R formulas were developed for simplified single and bi-variate models. In single trait, the curve of the regression of Method-R was continuous and monotonic, as is described in the literature, and its slope depended on the amount of information on one animal. The curve was flatter as the number of records per animal increased possibly indicating numerical problems with the sire model. For covariance, the curve of the regression was not always monotonic and it had a discontinuity; a regression factor of 1 still corresponded to the correct covariance. Similar curves were observed in analyses of simulated data sets. Due to the observed discontinuity, algorithms implementing Method-R that require continuous regression curve would not work in models with covariances. An alternative algorithm was based on a transformation matrix obtained by multiplying a matrix of numerators with the inverse of a matrix of denominators of the regression factors. This algorithm always converged in models with covariances, but was slow, requiring as many as 1000 rounds to converge. Convergence, faster by 3-10 times, was achieved by applying over-relaxation. Analyses of several simulated and real data sets by Method-R showed that sampling variance of (co)variance estimates with Method-R was higher for covariances or dominance effects than for additive effects. Therefore, larger number of samples is necessary for more complex models to obtain reliable estimates by Method-R.

Key Words: Method-R, covariance, estimation

231 Genetic variation of lactation curves in dairy sheep: Wood's model versus a quadratic function.

Y. M. Chang*[1], R. Rekaya[2], D. Gianola[1], and D. L. Thomas[1], [1]*Department of Animal Sciences, University of Wisconsin, Madison,* [2]*Department of Dairy Science, University of Wisconsin, Madison.*

Daily milk yield records (1752) of 451 first-lactation ewes in 4 flocks from Nebraska and Wisconsin were analyzed. Most ewes did not have test-day records prior to day 30, and milk yield was recorded more frequently in the second half of lactation. Objectives were to investigate genetic variation of features of lactation curves using a quadratic function (Q), and to compare this with non-linear Woods function (W). A 3-stage Bayesian hierarchical model was used. At stage 1, the function y=a+bt+ct^2+e represented within-ewe variation. Stage 2 model described variation in a, b and c between ewes. It had a linear structure with flock-year, age at lambing, type of lambing, length of suckling period and percentage of East Friesian origin genes as fixed effects, and additive genetic effects as random. Stage 3 had prior distributions for all parameters. A chain of 70,000 iterations (burn-in=12,000) was generated using Gibbs sampling. Posterior means of the residual variance were 0.0234 kg^2 for Q and 0.042 kg^2 for W. Heritabilities of a, b and c were 0.23, 0.15 and 0.17, respectively. Genetic correlations between parameters in Q ranged between -0.51 and -0.36. Q had an R^2=0.92, higher than the 0.74 found for W. The Bayes factor for Q relative to W was 11.64 in a log scale. Using 3 residual standard deviations as cut-off, the percentages of outliers were 0.2% and 0.4% with the Q and W models, respectively. Both models fitted well but Q failed to predict total milk yield accurately. Model W is more appealing than Q, especially because its parameters have a mechanistic interpretation.

Key Words: Lactation curves, Wood's function, quadratic function

232 Methodology to account for the effect of degree of non-linearity in breeding objectives on selection criteria.

G.E. Vander Voort* and G. Jansen, *University of Guelph, Canada.*

In animal breeding, when profit is a non-linear function of the traits in the breeding objective, a linear approximation to this function is usually made at the current population means, at the end of the planning horizon or in each generation within the planning horizon, depending on the goal. A linear selection index is used to select for this linearized goal. An optimal control method to obtain linear selection indexes for multiple stage objectives, based on a non-linear profit function has been developed. Numerical optimal control solutions can be difficult to obtain due to the complexity and degree of non-linearity of the model. To study these difficulties, the optimal control method was transformed into a recursive optimization problem. At each selection stage Adomian's decomposition method was used to derive series expansions of optimal selection index weights. These series are generalized Taylor series expansion about the base function. Numerical procedures to derive optimum indexes are outlined. The methodology was validated by calculating selection index correlations with Stratagey D for egg weight and rate of lay example of Dekkers et al. (Animal Science ,61:165-175). Average index correlation increased from 0.92 to 0.95 as series order was increased from 3 to 5. Potential use of series order and size to quantified degree of non-linearity are examined.

Key Words: degree of non-linearity, optimal control

233 Structuring the residual covariance matrix in the analysis of longitudinal binary data.

R. Rekaya*[1], K. A. Weigel[1], and D. Gianola[1], [1]*Department of Dairy Science, University of Wisconsin, Madison.*

Longitudinal binary responses measured repeatedly over time on the same individual tend to be correlated. For example, mastitis infection status of a cow at a given stage of lactation may depend on clinical episodes in preceding stages. Clinical mastitis data (3341 binary test-day records) from 329 first-lactation Holsteins were used to investigate 3 structures of the residual covariance matrix in a longitudinal Bayesian threshold model. Results were compared with those from a multivariate analysis for binary responses in four intervals during lactation. In structure 1, liabilities to mastitis were conditionally (given fixed effects and breeding values) independent. In structure 2, a serial dependence pattern was fitted; the correlation between liability at times and was: $\rho^{|ti-tj|}$. In structure 3, a constant correlation between periods was assumed. The multivariate analysis showed a decreasing pattern in the residual correlation as the time between intervals increased. Correlations were 0.29 between adjacent intervals and 0.07 between intervals 1 and 4. In the constant correlation structure (3), the posterior mean of ρ was 0.11. Structure 2 gave a pattern similar to that in the multivariate model, but with a single parameter, as opposed to 6 in the latter. In Structure 2 the posterior mean of ρ was 0.22, and the correlation was 0.22 for adjacent test days, 0.05 when the interval between test days was 60 d, approaching 0 for longer intervals. Bayes factors supported Structure 2 for the residual covariance matrix, relative to the alternative parameterizations of ρ.

Key Words: longitudinal data, binary, residual covariance

234 Methods for attenuating bias of variance component estimates in threshold models when herds are small.

R. Rekaya*[1], K. A. Weigel[1], D. Gianola[1], B. Heringstad[2], and G. Klemetsdal[2], [1]*Department of Dairy Science, University of Wisconsin, Madison,* [2]*Department of Animal Science, Agricultural University of Norway, Ås, Norway.*

With binary response data and low incidence rates, observations for some levels of contemporary groups, such as herds (β), can be all "successes" or "failures" (1 or 0). This creates the "extreme category problem" (ECP): in likelihood or Bayesian settings (even with proper priors for β), estimates of variance components are biased. ECP causes difficulties in countries such as Norway, where herds are small, and where selection programs emphasize health and fertility traits, these being categorical. The problem was studied with clinical mastitis records on 13,070 first-lactation daughters of 250 sires in 1868 Norwegian cattle herds. About 32% of herds had no cases of clinical mastitis. Data were analyzed with a threshold model with proper priors for all parameters, leading to a suspicious heritability of 0.18. A simulation using the same incidence structure was conducted. Three techniques for dealing with the ECP were investigated: 1) fuzzy classification of observations within herds according to some membership function. 2) Hierarchical prior for b with unknown mean and variance. 3) Grouping observations from ECP herds with those from low mastitis incidence herds. Technique 2 had the least bias. With the actual data, the posterior mean of heritability of liability to mastitis dropped from 0.18 to 0.07 using technique 2.

Key Words: binary data, variance components, bias

235 Genetic parameters and response to selection in proportional hazard models.

M.H. Yazdi*[1], P. Visscher[1], V. Ducrocq[2], and R. Thompson[3], [1]*IERM, University of Edinburgh, UK*, [2]*Institut National de la Recherche,Agronomique, Jous-en-Josas, France*, [3]*Institute of Arable Crops Research, Harpenden, Hertfordshire, UK*.

Three methods of estimating genetic parameters and response to selection were examined using Weibull proportional hazard models. A new and simple equation for the estimation of heritability of survival time was proposed which does not depend on the Weibull parameters. Theoretical derivations for the heritability and reliability of sire proofs were validated using simulation studies with balanced sire designs. Simulated continuous and discretised data were analysed using (i) a Weibull frailty model, (ii) a linear model on binary observations, and (iii) a proportional hazards model for discrete data. Observed reliabilities were estimated from simulated repeated progeny groups. The expected reliability was calculated using the proposed formula for estimation of heritability. There was very good agreement between observed and expected reliabilities. The estimates of reliabilities from the Weibull model, discrete hazards model and from the linear analysis on binary data were related using simple transformations. For the linear model (binary data analysis) the genetic variation among the sires increased with an increased proportion of uncensored progeny per sire, reaching at maximum at the average proportion of 0.7. The observed and expected responses to selection from different combinations of sire variances and Weibull parameters were very similar. The expected response to selection of sires ranged between 3 to 8 months, depending on the shape of the survival curve and selection intensity.

Key Words: Survival analysis, Genetic parameters, Selection response

236 Beef genetic evaluation programs for carcass traits: current situation and future possibilities.

J. K. Bertrand*[1], D. W. Moser[2], and W. O. Herring[3], [1]*University of Georgia, Athens*, [2]*Kansas State University, Manhattan*, [3]*University of Missouri, Columbia*.

The implementation of grid pricing systems in the U.S. beef industry, where the value of carcasses is based on quality and red meat yield, has put increased emphasis on the development of genetic values to enhance selection for carcass traits. Five U.S. breed associations provide sire EPD for carcass traits based on carcass information from finished steer and heifer progeny. However, the amount of carcass data for most breeds is small compared to other traits such as birth weight, weaning weight, yearling weight, scrotal circumference and calving ease due to the time consuming nature, cost and difficulty of gathering useful carcass information on finished steers and heifers. Ultrasound technology has been explored as a vehicle for the seedstock industry to collect large amounts of data at a reasonable cost, with the potential result that more animals would have genetic values for carcass traits than are currently available. Two U.S. breed associations use yearling seedstock ultrasould measures to predict EPD. Genetic correlations between carcass measures from slaughter animals and yearling ultrasound measures from seedstock cattle were estimated using a Brangus field data set containing 2036 steer and heifer carcass measures and 3583 bull and heifer ultrasound measures. The genetic correlation estimates between yearling seedstock and finished cattle for ribeye and external fat thickness measures were .89 and .69, respectively. The genetic correlation between yearling seedstock measures of percent intramuscular fat with marbling scores in finished cattle was estimated at .70. The results of this study indicated that ultrasound measures from breeding animals can be used to predict genetic values for carcass traits. However, more research is needed to better quantify the genetic relationships between slaughter and live animal ultrasound measures of carcass traits across steers, bulls and heifers of various breeds to develop models that use any combination of carcass and ultrasound information available for the prediction of carcass trait genetic values. Research is also needed for the development of genetic values for tenderness and edible retail product coupled with multi-trait selection tools that allow producers to genetically identify animals that are profitable in grid pricing systems.

Key Words: Genetic Values, Carcass Traits

237 Terminal sire value (TSV): a selection index targeted to improve growth and carcass traits.

N. Caron* and R.A. Kemp, *Lethbridge Research Centre, Agriculture & Agri-Food Canada*.

A selection index was developed to compare and select sires for production of market calves. A total of six different selection objectives were compared and each included five economically important traits from birth to slaughter: birth weight (BW), weaning gain (WG), postweaning gain (PWG), marbling score (MARB) and lean yield (LY). Relative economic values (REV) were based on a review of recent studies. The selection objective chosen as most preferable had REV of 1, 1.5, 1.5, 2 and 3 for BW, WG, PWG, MARB and LY, respectively. The chosen objective was tested for sensitivity to variation in genetic parameters and relative economic values by independently varying each of them by 50% for each trait. For all traits, selection efficiency was higher than 95% with the exception of LY. Selection based on this objective will result in higher WG, PWG, MARB and LY but lower BW. On average, 6.9% of the economic gain will be from BW, 22.7% from growth traits (WG and PWG) and 70.4% from carcass traits (LY and MARB). A selection index, known as the Terminal Sire Value (TSV), has been developed for use in the Conception to Consumer program of the Canadian Charolais Association. The TSV uses EPD of the selection objective traits and is calculated as follows: $\text{TSV} = -8.17{*}\text{EPD}_{BW} + 2.63{*}\text{EPD}_{WG} + 3.11{*}\text{EPD}_{PWG} + 86.21{*}\text{EPD}_{LY} + 293.26{*}\text{EPD}_{MARB}$. The TSV is expressed such that the overall mean and standard deviation are 100 and 25, respectively.

Key Words: Beef Cattle, Selection index, Carcass traits

238 Genetic correlations between yearling bull ultrasound measurements and finished steer carcass measurements.

C.J.B. Devitt* and J.W. Wilton, *University of Guelph, Ontario, Canada*.

The objective of this study was to determine the genetic relationship between real-time ultrasound measurements on yearling bulls and actual carcass measurements on finished steers. Beef Improvement Ontario provided ultrasound measurements on 5654 purebred yearling bulls of 11 breeds measured at the end of Ontario's 112-day Bull Evaluation Program between 1995 and 1999. All bulls had ultrasound measurements of ribeye area (BREA), backfat thickness (BBFAT), as well as average daily gain (BADG). Ultrasound measured intramuscular fat percent (BIMF) was available on 3450 bulls. Actual carcass measurements were obtained from 843 crossbred steers raised between 1988 and 1998 in the University of Guelph's beef research herd. All steers had measurements of hot carcass weight (SHCW), ribeye area (SREA), backfat thickness (SBFAT), marbling score (SMAR), as well as average daily feedlot gain (SADG). Bulls were represented by 1535 sires averaging 3.7 bulls per sire and steers by 124 sires averaging 6.7 steers per sire. There were 20 sires with both bull and steer progeny, averaging 8.1 bulls, and 12.5 steers per sire. Genetic parameters for all traits were estimated simultaneously using a multiple trait animal model, which considered all genetic relationships between animals. Fixed effects for each trait were breed, management group, and age in days within breed as a covariate. Random effects were individual additive genetic animal effect and residual error. Heritability estimates for all traits were moderate to high. Additive genetic correlations between BREA and SREA, BBFAT and SBFAT, BIMF and SMAR, and BADG and SADG were .66, .80, .88 and .72, respectively. These strong, positive genetic correlation estimates between bull ultrasound measurements and corresponding steer carcass measurements suggest that genetic improvement for steer carcass traits can be achieved by using yearling bull ultrasound measurements as selection criteria.

Key Words: Beef cattle, Genetic parameters, Ultrasound

239 Associations among ultrasound measures of carcass yield from bulls and heifers and carcass traits of steers.

D.H. Crews, Jr., C. Gallivan, P.K. Charagu, and R.A. Kemp*, *AAFC Research Centre, Lethbridge, Alberta.*

Real time ultrasound (U) measures of ribeye area (R) and fat thickness (F) were taken at 12 and 14 months of age on composite bulls (B, n = 404) and heifers (H, n = 514). Carcass (C) R and F were measured on related steers (n = 235). Two (R and F) five-trait animal models, including traits expressed by B and H at 12 and 14 months of age and carcass traits separately, were used to estimate genetic parameters. Heritability estimates were between .64 and .68 for all ultrasonic measures of R. Heritability estimates were .32 for BUF12, .22 for BUF14, .56 for HUF12 and .55 for HUF14. Estimated genetic correlations between 12- and 14-month UR and UF within sex were above .88. The genetic correlation estimate between BUR12 and HUR12 was .67 and between BUF12 and HUF12 was .61. Estimates were similar at 14 months of age. Heritability estimates for CR (.58) and CF (.43) were similar to literature averages. Estimated genetic correlations of HUF12 with CF and HUR12 with CR were .73 and .71, and at 14 months, were .82 and .81, respectively. Estimated genetic correlations of BUF14 with CF, BUR14 with CR and BUR12 with CR were .38, .40 and .30, respectively. However, the estimated genetic correlation between BUF12 and CF was .07. These results indicate that the choice of age of measurement between yearling and 14 months may have little effect on ultrasound trait breeding value prediction. However, ultrasound measures on bulls and heifers, even at similar ages, may be considered different traits for genetic evaluation. Also, prediction of carcass merit breeding values should incorporate ultrasound and carcass data as separate but correlated traits. Genetic evaluation of carcass merit may be enhanced by including ultrasound data from replacement bulls and heifers and carcass data on siblings or progeny in a multi-trait model for each carcass trait of interest.

Key Words: beef carcass merit, ultrasound, genetic parameters

240 Carcass expected progeny differences using real-time ultrasound measures from developing Angus heifers.

D. E. Wilson*, G. H. Rouse, C. L. Hays, and A. Hassen, *Iowa State University, Ames.*

The objectives of this research were to determine genetic parameter estimates for real-time ultrasound (RTU) measured composition traits on developing Angus heifers and to compare sire expected progeny differences (EPD) based upon RTU measured traits to those based upon carcass measured traits of steer progeny. The RTU measures in this study were from 8,630 developing heifers. The heifers came from 402 contemporary groups as defined by herd and scan date. There were 851 sires represented in the data. RTU images were collected by technicians participating in a two-year research project at Iowa State University (ISU) and funded by the American Angus Association (AAA). ISU image-interpretation technicians made all RTU measurements at the ISU centralized ultrasound processing laboratory from images received from field RTU technicians. The measures included rump fat thickness (RFAT), 12-13th rib fat thickness (FAT), ribeye area (REA), and percentage intramuscular fat (%IMF). Measures were adjusted to a 390-d age end point. Genetic parameter estimates were made using restricted maximum likelihood procedures. The genetic prediction model was a multiple-trait sire model with sire and maternal grandsire additive genetic relationships. Carcass EPD used for comparison came from the Spring 2000 AAA Sire Evaluation Report. The h^2 estimates for RFAT, FAT, REA and %IMF were .56, .48, .40 and .42, respectively. Genetic correlation estimates for RFAT-FAT, FAT-%IMF, REA-%IMF and REA-FAT were .74, .09, -.04, and .23, respectively. Of the 851 sires with RTU-based EPD, 309 sires also had carcass-based EPD. Comparisons were made between EPD from the two sources of data using sire rank correlations. For RTU-EPD and carcass-EPD accuracy levels of .85 and higher, the rank correlations were .69, .76, and .72 for Marbling Score-%IMF, REA, and 12-13th rib fat thickness, respectively. These results indicate that breeders could use EPD based upon RTU measures from developing Angus heifers to predict the same genetic differences observed from steer progeny carcass measures.

Key Words: Beef Cattle, Composition, Ultrasound

241 Breed comparisons and genetic evaluation of carcass merit in *Bos indicus* x *Bos taurus* breed types in Australia.

A. Reverter[1] and S. Newman*[2], [1]*Animal Genetics and Breeding Unit, University of New England,* [2]*CRC for Cattle and Beef Quality, CSIRO Tropical Agriculture, Australia.*

Yield and quality data on 6789 purebred and 966 crossbred cattle were analyzed to perform breed comparisons and to estimate genetic correlations among purebred and crossbred performance (r_{PC}). Crossbred calves were produced using 9 Angus, 8 Hereford, 7 Shorthorn, 14 Belmont Red and 8 Santa Gertrudis sires bred to Brahman dams. These same sires produced progeny in the purebred data set. Purebred Brahman calves reared in the same environment as the crossbred individuals were also available. Cattle were managed under two finishing regimes (pasture and feedlot) to representative market weights of 400 (domestic), 520 (Korean), and 600 kg (Japanese). Care was taken to minimize pre-slaughter stress and all carcasses were electrically stimulated. Carcass measures included hot carcass weight (CWT, kg), retail beef yield (RBY, %), NIR-measured intramuscular fat (IMF, %), rump fat depth (P8, mm) and shear force (SF, kg) at the *l. dorsi* muscle. Breed rankings were based on least-squares means and the mean EBV of mixed model solutions estimated as deviations from their respective contemporary group (CG) means where CG did not include breed. Positive heterosis effects (1% to 19%) were estimated for CWT. Heterosis for RBY was negligible while heterosis for IMF and SF ranged from -18% to -1%. Crossbred steers and heifers out of Angus sires produced the heaviest and fattest carcasses with the smallest RBY and SF. In contrast, crossbred progeny out of Belmont Red sires expressed the lightest CWT with the highest RBY but an average performance in the remaining traits. Crossbred data yielded higher heritability estimates for all traits except RBY. Estimates of r_{PC} were .74, .78, .92, .59, and -.46 for CWT, RBY, IMF, P8, and SF, respectively. The negative correlation found for SF might point to overdominant genes for tenderness being recessive in tropically adapted breeds. Commercial breeders selecting sires for crossbreeding programs based on EBV developed from purebred analyses might encounter some re-ranking of sire's performance.

Key Words: Cattle, Crossbreeding, Genetic Evaluation

242 Effect of breed on carcass traits and fatty acid composition in longissimus muscle of finishing steers.

L. F. Laborde*, I. B. Mandell, J. J. Tosh, J. W. Wilton, and J. G. Buchanan-Smith, *University of Guelph, Ontario, Canada.*

One hundred and thirty six Simmental- or Angus-sired, crossbred steers were used to evaluate breed differences in carcass traits and fatty acid composition of total lipids and phospholipids from longissimus muscle. A multiple regression approach was applied to crossbreeding data to estimate genetic differences between Simmental (**SM**) and Red Angus (**RA**) at the same level of backfat finish (10-mm grade fat). SM needed more ($P < .001$) days on feed (+71.0 ± 18.9 d) to reach the backfat endpoint, with heavier ($P < .001$) slaughter weights (+154.1 ± 35.6 kg) and hot carcass weights (+111.4 ± 22.9 kg), larger ($P = .002$) longissimus muscle area (+19.4 ± 6.2 cm^2), and increased ($P = .023$) lean yield (+4.1 ± 1.8 %) when compared to RA. Breed did not affect ($P = .860$) subjective marbling score. For total lipids, SM had greater ($P < .01$) concentrations of myristoleic (+.28 ± .10 %), palmitoleic (+.87 ± .29 %), and vaccenic (+.29 ± .09 %) acids, and a larger ($P = .022$) omega-6 (ω**6**) to omega-3 (ω**3**) polyunsaturated fatty acid (**PUFA**) ratio (+.88 ± .38) than RA. In contrast, SM had lower ($P < .05$) concentrations of margaric acid (-.31 ± .12 %), eicosapentaenoic acid (-.08 ± .03 %), and total ω3 PUFA (-.29 ± .15 %) than RA. Activity of Δ^9-desaturase enzyme in the conversion of palmitic acid to palmitoleic acid was greater ($P = .001$) in SM (+2.93 ± .86) as compared to RA. Conjugated linoleic acid (**CLA**) concentration did not differ ($P = .864$) between breeds. For phospholipids, SM had lower ($P < .05$) amounts of eicosapentaenoic acid (-.55 ± .25 %), docosahexaenoic acid (-.19 ± .09 %), and ω3 PUFA (-1.23 ± .58 %), with a greater ($P = .017$) ω6:ω3 ratio (+1.40 ± .58) as compared to RA. Although breed differences in fatty acid composition were present, implications on human health need to be demonstrated.

Key Words: Beef Cattle, Breeds, Fatty Acids

243 Comparison of Warner-Bratzler shears of F_1 *Bos indicus* × British steers produced by one Nellore and 15 Brahman Bulls.

D. G. Riley*, L. B. Hager, J. O. Sanders, R. K. Miller, and D. K. Lunt, *Texas A&M University, College Station.*

Tenderness measures of 251 F_1 steers sired by one Nellore and 15 Brahman bulls and out of Hereford and Angus cows were evaluated. Calves were born from 1994 through 1998 at the Texas A&M University Research Center at McGregor, Texas. They were weaned at about 200 d of age, fed from about November through the end of May of the following year and slaughtered at about 13 mo of age. Carcasses were electrically stimulated and strip loins were stored at 1° C for aging periods. The most anterior steak from the left strip loin of each carcass was assigned to d 14 and steaks were randomized to the remaining aging periods, except that steaks were randomly assigned to all aging periods for carcasses of 1997 born steers. Warner-Bratzler shears (kg) were measured on six cores from steaks from each steer after 0, 7, 14, 21, 28 and 35 d of aging. Average shear force (SF) was analyzed by mixed model procedures with yr-dam breed combination and aging interval as fixed effects. Sire and calf within sire were included as random effects. Two contrasts of adjusted sire means were estimated: L_1 = d 0 SF minus d 14 SF and L_2 = d 14 SF minus d 35 SF. All L_1 estimates for the different sires were significant except one; estimates ranged from .334 ± .18 kg to 1.269 ± .389 kg with an average value of .868 ± .14. L_2 estimates ranged from -.537 ± .314 kg to .202 ± .39 kg. L_2 contrasts were significant for one sire and approached significance for three sires. Adjusted means for aging periods were 3.62, 3.21, 2.75, 2.97, 2.91 and 2.88 kg for d 0, 7, 14, 21, 28 and 35, respectively (SE were .05 kg for each). These data were also fit to the curve $\mathrm{SF} = \mathrm{G} + \mathrm{J}e^{-Hd}$, where G was asymptotic SF after an infinite aging period, H was estimated rate of change in SF over time, J was the estimated difference between initial SF and G, and d was aging period. Across the entire data set, the estimated G value was 2.96 ± .04, which was slightly larger than the adjusted mean for d 35. The estimated H value of .77 ± .07 was similar to the sum of the L_1 and the L_2 contrast, which was .744. Estimated G and H values were positively correlated (.68 in the overall data set). G and J estimates were negatively correlated (-.51 in the overall data set) and H and J estimates are less strongly negatively correlated (-.17).

Key Words: Warner-Bratzler Shear Force, *Bos indicus*

244 Heritability of Warner Bratzler shear force measures estimated from data on Simmental-sired calves.

Z. Zhang*[1], E. J. Pollak[1], R. L. Quaas[1], M. E. Dikeman[2], R. D. Green[3], J. Taylor[4], and S. Davis[4], [1]*Cornell University, Ithaca, NY,* [2]*Kansas State University, Manhattan,* [3]*Colorado State University, Fort Collins,* [4]*Texas A&M, College Station.*

Progeny of 27 Simmental bulls were scored using the Warner-Bratzler shear force measures done at Kansas State University. These data were collected as part of the National Cattlemen Beef Association's Carcass Merit Project. Along with bulls having progeny, additional animals without records or records on progeny but contributing to the pedigree structure were added to the analysis. A total of 113 pedigree animals were added. The model used to describe the observations contained the effect of age at slaughter (linear and quadratic), contemporary groups (defined as cohorts that were raised and managed together from birth to slaughter with the exception of separating individuals by sex), and an animal effect. A total of 310 progeny with shear force measures were used in the analysis with eight bulls having less than five progeny, eleven with 5 to 10 progeny, five with 11 to 20 progeny, and three with greater than 20 progeny. The additive genetic variance for shear force measures was 0.36kg^2 and the heritability was 0.48. The range in shear force EPDs for bulls with progeny was -.29 to 0.16 kg for a difference of .45 kg. The additive genetic correlation of shear force measure with marbling, carcass weight, rib-eye area were zero. The correlation with fat thickness, and yield grade were -0.11 and -0.37 respectively.

Key Words: Heritability, Shear Force, Simmental

245 Genetic parameters for intramuscular fat from beef cattle slaughtered at different market weights and finishing regimes.

D. J. Johnston*[1,2], A. Reverter[1,2], and J. M. Thompson[1,3], [1]*The Cooperative Research Centre for the Cattle and Beef Industry,* [2]*Animal Genetics and Breeding Unit, University of New England, Armidale, Australia,* [3]*Department of Animal Science, University of New England, Armidale, Australia.*

Genetic variances and covariances were estimated for chemically measured intramuscular fat percent (IMF) from 3,428 beef carcases. Cattle were from four British breeds (Angus, Hereford, Shorthorn and Murray Grey) that were slaughtered at different market weight endpoints. The domestic market group were finished to an average liveweight of 400kg and the export market group to either 520 or 600kg liveweight. Each market treatment group were separated after backgrounding and finished on either pasture or grain. Intramuscular fat percentage was predicted using NIR spectroscopy on a sample of m. longissimus dorsi taken between the 12 and 13th ribs. Export market carcases had on average 5.4% IMF compared to 3.3% for the domestic market carcases. Whereas the IMF from grain finished carcases was on average 5.3% compared to 4.1% from pasture finished carcases. Heritabilities by market were 0.38 and 0.43 for domestic and export markets, respectively, with a genetic correlation of 0.91 for IMF measured at the two market endpoints. The IMF additive genetic variance was 3.7 times larger for the export market compared to the domestic market carcases. Heritabilities by finishing regime were 0.30 and 0.46 for pasture and grain finishing, respectively, with a 1.0 genetic correlation between the traits. The additive genetic variance was 2.4 times larger for grain finishing compared to pasture finished cattle. Intramuscular fat can be improved by selection. The high genetic correlations suggest little evidence of a GxE for IMF across market weight or finishing regimes. However for effective selection the different variances observed will need to be taken into account.

Key Words: Intramuscular fat, Genetic correlation, GxE

246 Genetic parameters for carcass traits in Simmental cattle at different slaughter end-points.

B.C. Shanks*[1], M.W. Tess[1], D.D. Kress[1], B.E. Cunningham[2], and P.J. Burfening[1], [1]*Montana State University, Bozeman,* [2]*American Simmental Association, Bozeman, MT.*

Our objectives were to estimate genetic parameters for carcass traits and evaluate the influence of slaughter end-point on genetic parameters and estimated breeding values (BV). Data provided by the American Simmental Association were divided into three groups: 1) 9,604 records of hot carcass weight (CW) and percent retail cuts (PRC), 2) 6,429 records of CW, PRC, and marbling score (MS), and 3) 1,780 records of CW, PRC, MS, fat thickness (FT), and ribeye area (REA). Weaning weights (WW) from animals with carcass data plus their weaning contemporaries were also used. Data were analyzed with a multiple-trait animal model and REML procedures to estimate genetic parameters and BV at an age-, CW-, MS-, or FT-constant basis. The model for carcass traits included fixed contemporary group and covariates for breed, heterozygosity, and slaughter end-point, plus random additive direct genetic and residual effects. Weaning weight was pre-adjusted for founder effects, direct and maternal heterosis, age of dam, and age of calf. The model for WW included fixed contemporary group and random additive direct genetic, maternal genetic, maternal permanent environment, and residual effects. Within data group, slaughter end-point had only small effects on heritability estimates for all traits. However, differences in heritabilities were detected between groups. Genetic correlations among traits varied across groups and end-points, but suggested it should be possible to select for improved lean yield without sacrificing quality grade. Correlations were calculated among BV computed at different end-points. Adjustment to various end-points resulted in some changes in BV and reranking of sires; however, amount of information available had a larger influence than slaughter end-point.

Group	Slaughter end-point	CW	PRC	MS	REA	FT
Group 1	Age	.34	.25			
	CW	–	.25			
Group 2	Age	.35	.24	.36		
	CW	–	.25	.34		
	MS	.33	.25	–		
Group 3	Age	.32	.09	.12	.26	.10
	CW	–	.12	.12	.22	.14
	MS	.30	.09	–	.28	.10
	FT	.33	.17	.13	.29	–

Key Words: beef cattle, carcass, genetic parameters

247 Evaluation of genetic parameters and correlated responses for carcass traits in three lines of synthetic beef cattle.

A. Hassen*, R. L. Willham, and D. E. Wilson, *Iowa State University, Ames.*

Carcass information from steer progeny in small, medium, and large synthetic cattle were used to evaluate genetic parameters and genetic trends for carcass traits. Animals were born during 1978 through 1990 at Rhodes and McNay beef research farms. Traits included were hot carcass weight (HCW); longissimus muscle area (LMA); dressing percentage (DP); 12th - 13th rib fat thickness (FTK); and percentage of kidney, pelvic, and heart fat (KPH). All carcass traits were evaluated based on multiple-trait animal model. There were important ($P < .05$) differences in breed direct additive effects between Jersey, Angus, and the Simmental breeds. However, differences in breed maternal additive effects were not different from zero ($P > .05$). Effects of average individual and maternal heterosis were not important ($P > .05$). Heritabilities of HCW, DP, LMA, FTK, and KPH in the small line were .30, .09, .21, .34, and .15, respectively. The respective values in the medium line were .52, .35, .33, .29, and .07. In the large line, heritability values were .31, .18, .17, .31, and .18, respectively. There was an important ($P < .10$) change in mean phenotypic values of animals for HCW, DP, and KPH in all the three lines. However, these changes were largely due to an improvement in the management quality over the years. Sire selection based on weaning indices showed a significant ($P < .05$) genetic change for some of the carcass traits. It was concluded that breeding programs designed to improve carcasses traits need to incorporate carcass information in an index to speedup genetic progress. In this endeavor, evaluation of breeding cattle based on ultrasound measures provides a tremendous opportunity.

Key Words: Beef Cattle, Heritability, Composition

248 Examination of Calpastatin mRNA and Protein to Determine Tenderness in Brangus Cattle.

D.L. Wohlford*[1], S.M. Lonergan[2], J. Wower[1], W.H. McElhenney[1], and L.A. Kriese-Anderson[1], [1]*Auburn University, Auburn, AL,* [2]*Iowa State University, Ames.*

Defining factors that influence beef tenderness will play an important role in developing predictors of beef palatability. Using samples from top loin steaks of Brangus bulls ($n=10$) and steers ($n=20$) it has been shown calpastatin activity (CA) and Warner-Bratzler shear force (WBS) values were higher and sensory scores for tenderness (ST) were lower for bulls at 2 and 7 days (d) postmortem (PM) than steers. Also, there were differences in rate of tenderization from 2 to 7 d PM both within and between bulls and steers. Given these results, the purpose of this study was to determine if calpastatin mRNA or protein isoforms were related to 2 d CA, aknown predictor of WBS. Loin tissue samples from the Brangus bull and steer carcasses characterized for CA, WBS and ST were collected within 15 minutes PM and rapidly frozen in liquid nitrogen. Northern blot analysis was used to quantitate the relative amounts of the 3.8 and 3.0 kb isoforms of calpastatin mRNA. Western Blot analysis using two calpastatin antibodies was used to determine whether there were different isoforms of the protein produced by the different mRNA isoforms and the relative reaction of the calpastatin protein to the antibody. Densitometry was used to quantify the intensity of the signals produced. The GLM procedure of SAS was used to determine whether mRNA or immunoblot densitometry could predict CA, WBS or ST. Independent variables of sex and sire were also included in the model. There were 2 sexes and 11 sires represented in this data. Sires had 1 to 5 progeny each. From the analysis, sex contributed significantly ($P < .05$) in determining CA. Only the intensity of the 3.0 kb mRNA band contributed significantly in determining CA at 7 and 14 d. Likewise, only correlations for the intensity of the 3.0 kb band was significantly correlated with 7 and 14 d CA. Calpastatin mRNA isoforms and calpastatin protein levels were not useful predictors of tenderness of beef in this study.

Key Words: Beef tenderness, Calpastatin mRNA, Calpastatin protein

249 International genetic evaluation of dairy sires using individual performance records and herd clusters.

K. A. Weigel*, R. Rekaya, and D. Gianola, *University of Wisconsin, Madison.*

International dairy sire evaluations are presently calculated in a two-step process. Each country estimates national breeding values from local performance records, then these estimates are transformed to the genetic base and scale of other countries using a multiple-trait across-country procedure. However, differences between countries in national genetic evaluation procedures are ignored, and these can lead to biased international breeding values. Further, traits are defined according to country borders, but differences in climate and management within a large country (e.g., Vermont vs. California) can be larger than differences between small neighboring countries (e.g., Netherlands vs. Belgium). This study proposes a multiple-trait herd cluster model for international dairy sire evaluation. A profile of each herd is constructed using information regarding climate conditions, management practices, and the genetic composition of mates. Principal components are calculated from variables corresponding to each herd, and cluster analysis is used to group herds across country borders into unique production systems. The proposed model was applied to 4.6 million first lactation milk records from Austria, Belgium, Czech Republic, Denmark, Estonia, Finland, Israel, Switzerland, and five regions of the US. Descriptive variables included: herd size, calving interval, milking frequency, age at calving, milk yield, calving month, sire's genetic merit, sire's percentage of North American genes, latitude, altitude, temperature, rainfall, and percentage of arable land used for pasture. Five clusters were formed, each containing herds from 5-11 countries or regions. Genetic correlations between clusters ranged from 0.81-0.97. The proposed model is appealing because genetic merit is predicted for each unique production system, regardless of country boundaries. It is more parsimonious than the current model (the number of genetic correlations was reduced from 78 to 10), and it is computationally feasible.

Key Words: International evaluation, Dairy sires, Herd cluster

250 Estimation of sire variance in international genetic evaluation models with genetic groups.

W.F. Fikse*[1] and P.G. Sullivan[2], [1]*Interbull Centre, Uppsala, Sweden,* [2]*Centre for Genetic Improvement of Livestock, University of Guelph, Canada.*

International genetic evaluations of dairy bulls are currently computed with an across-country sire model based on national genetic evaluation results. The model includes a random effect for the genetic group of unknown parents, to account for genetic trend and different origin of bulls. The question has been raised how treatment of genetic groups affects estimation of sire variances. This study compared two procedures to estimate sire variances, and their impact on international genetic evaluations. A two-country progeny test scheme was simulated for ten generations, where semen was exchanged at a fixed rate from generation three onwards. True breeding values for both populations were sampled from a bivariate normal distribution. Each cow had a lactation record in one country only. All records were used in within population breeding value estimation. Breeding values of bulls were used to estimate sire variances and for international genetic evaluation. The first variance estimation procedure was based on both genetic group and known sire effects, whereas only sire effects were considered in the second procedure. Sire variances were estimated under different assumptions for the variance of genetic group effects, by modifying the constant added to the diagonals of the group effects of the mixed model equations. For a trivial constant, treating groups as fixed, the two procedures are equivalent and underestimated sire variances. When the constant was one, the first procedure yielded empirically unbiased estimates, and the second procedure resulted in slight underestimation. Estimated sire variance increased with higher values of the constant, and the maximum difference between both procedures was 10%. Estimation procedure had no effect on international breeding values, presumable because the ratio of sire variance between populations was unaffected. International breeding values are expected to be affected in situations where the procedures yield different ratios of sire variance between populations, and this is currently under investigation.

Key Words: International Genetic Evaluation, Genetic Groups, Variance Component Estimation

251 Characterization of data and proposed edits for the national calving ease genetic evaluation.

C.P. Van Tassell*[1] and C.G. Sattler[2], [1]*Animal Improvement Programs and Gene Evaluation and Mapping Laboratories, ARS, USDA, Beltsville, MD,* [2]*National Association of Animal Breeders, Columbia, MO.*

Distributions of scores for birth difficulty were examined for herds included in the national genetic evaluation for calving ease. This research was part of an investigation into unusual sire evaluations and was an effort to assess the impact of requiring an identified maternal grandsire (**MGS**). Birth difficulty scores ranged from 1, no problem, to 5, extreme difficulty. Data for this study were from the February, 2000 genetic evaluation and included scores from 8,296,832 calvings in 45,243 herds, with 25.7% for records from first parity calvings and 74.3% for second and later parity calvings. The fraction of birth difficulty scores 1 to 5 across herds were 0.65, 0.14, 0.14, 0.05, and 0.03 for first parity, and 0.82, 0.08, 0.06, 0.02, and 0.01 for second and later parities. Sires with suspicious evaluations tended to have a large fraction of records in a herd with an unusual birth difficulty score distribution. To determine useful edits for birth difficulty score distributions, frequencies of scores were summarized by herd-size and parity. Frequencies of observed scores (**OS**) and cumulative scores (**CS**) (5, $\geq$4, $\geq$3, and $\geq$2) were considered. Herds that exceeded the 95 to 99 percentiles were removed to test potential edits. Thresholds based on OS percentiles resulted in many fewer herds passing the edits than those based on the CS. For example, cutoffs based on the CS 95 percentile resulted in more records being retained than the OS 99-percentile cutoff. Elimination of records without MGS resulted in the loss of 46.1% of the data. For edits based on OS, 50.9% and 79.4% of the records were retained for 95- and 99-percentile cutoffs, respectively, when MGS was not required, and 24.6% and 40.6% when MGS was required. For edits based on CS, 82.4% and 92.6% of the records were retained for 95- and 99-percentile cutoffs when MGS was not required, and 42.5% and 49.1% when MGS was required. These edits were successful in removing 9 and 7 of 9 identified herds using 95- and 99-percentile cutoffs, respectively. A balance between data loss and data quality will need to be determined. Comparison of genetic evaluations from these different subsets of data will be compared to assess the impact of these edits. Based on these results, new edits will be proposed for the national evaluation system.

Key Words: Calving Ease, Genetic Evaluation

252 Prediction of breeding values for Finnish dairy cattle using random regression test day model.

E.A. Mantysaari, I. Stranden, and M. Lidauer, *Agricultural Research Center MTT, Jokioinen, Finland.*

A multitrait multilactation model was set up to describe daily observations of milk, protein and fat in all lactations. For each animal separate lactation curve functions were used to determine daily breeding values of traits in the first and the later lactations. In the later lactations the curve functions were treated as genetically repeated observations of the same trait. For each trait the breeding value function consisted of intercept, linear, quadratic and Wilmink terms. Residuals were modeled by intercept, linear and Wilmink terms plus a measurement error which were correlated across traits within test days. In addition, model for each later lactation included an extra lactation*cow curve function. Thus, a cow without observations received 6 breeding value curve functions, and a cow with data on 3 lactations another 12 functions for non-genetic animal effects. In the computational model, the dimension of each lactationwise group of functions, 12 or 9 equations, were reduced into 6 coefficients and their eigenfunctions were used as covariables. Environmental effects in model were: stage of lactation, year*month, herd*year, and days carried calf on the time of production and age*parity at calving, and a random effect of herd-test-day. A management auditing software is designed that displays herd-test-day solutions to herd owners.

Data consisted of all test days of cows with 1st calving after Jan 1988. In the February 2000 evaluations the number of animals was 1.51 million and number of observations 25.0 million. This lead into 58.5 million equations to be solved. For Ayrshire cows born 1994 the correlations between 305d yield indices derived from test day model and from the old official animal model were .85, .86, and .88, for milk, protein and fat, respectively. For active AI sires the correlations were .97, .95, and .96. The execution time for full evaluation with data preprocessing took 36 hours with a workstation running 4 processors parallel. When old solutions are utilized in a weekly evaluation the time drops to 15 hours.

Key Words: Breeding value prediction, Test day model, Random regression

253 Heterogeneity of (co)variance components for Jersey type traits.

N. Gengler*[1,2], T. Dusseldorf[2], G.R. Wiggans[3], and J.R. Wright[3], [1]*National Fund for Scientific Research, Brussels, Belgium,* [2]*Animal Science Unit, Gembloux Agricultural University, Gembloux, Belgium,* [3]*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Although a common assumption of genetic evaluation models is homogeneity of (co)variances, this assumption often may be incorrect across time or herds. Data can be adjusted to stabilize (co)variances by contemporary group before evaluation, and this strategy is used for some yield and type evaluations but not currently for US genetic evaluation of type traits for breeds other than Holstein. Most research on type traits has focused on phenotypic heterogeneity of (co)variances for final score. Heterogeneity of (co)variances for Jersey linear and final scores was investigated using February 2000 genetic evaluations. Only first appraisal scores during first lactation from records that included all traits were studied. Three classes of contemporary groups were created based on the number of cows for that herd and appraisal date: 5 to 15, 30 to 55, and 100 and more. In each class, contemporary groups were separated into high (above class mean) and low (below class mean) final score subclasses. The six data sets contained appraisal information from 21,024 to 23,692 cows. (Co)variance components were estimated using expectation-maximization REML and canonical transformation. Across all traits and independent of herd size, phenotypic variances tended to be higher in low-scoring contemporary groups; mean differences in variance were around 30%. Similar or even larger differences existed for genetic variances, but those differences were not as consistent across traits and contemporary group size. The variance differences led to differences in estimated heritabilities: large and high-scoring contemporary groups showed on average around 15% lower heritabilities compared with small and low-scoring groups. Results indicated that phenotypic and genetic (co)variances for Jersey type traits are heterogeneous.

Key Words: Genetic evaluation, Heterogeneous variance, Variance estimation

254 Reliability of progeny tests for reproductive traits computed from DHI data.

J. S. Clay*, B. T. McDaniel, and C. H. Brown, *North Carolina State University, Raleigh.*

Animal model methodology was used to compute yearly measures of relative fertility for lactating progeny groups by Holstein AI bulls. Estimates were based upon 70-day non-return (NR70) and days in milk (DIM) at first breeding as reported to DHIA during 1996 to 1998 and computed from breeding records of 1,157,129 daughters of 1,706 bulls with a minimum of 40 daughters. The models assumed heritabilities and repeatabilities of .02, .05 (NR70) and .04, .06 (DIM) and included fixed effects of herd-year-month bred and classes of lactation number, early lactation ECM and days in milk when bred (NR70 only). Valid dam identities were required. NR70s were expressed as differences of NR from average herdmates. DIMs were expressed as differences from herdmates for number of days postpartum of first AI inseminations. Values ranged from -27 to +25 (DIM) and -13 to +15 (NR70). For BVs computed from a minimum of 500 breedings, (78, DIM; 69, NR70)% were within 1 SD of zero and less than (3, DIM; 2, NR70)% were below -2 SD. DIMs computed from few breedings were tested for ability to predict DIMs computed from a minimum of 500 breedings in the same year from different herds. R^2 ranged from .60 ($p<.01$) to .83 ($p<.01$) for DIMs computed from minimum of 20 to 500 early breedings. NR70s were tested for ability to predict NR70s computed from a minimum of 500 breedings in the same year from different herds ($r^2=.43$ ($p<.01$)). Early BVs computed from few breedings were tested for ability to predict BVs computed from a minimum of 500 breedings in a later year. Betas ranged from .60 (DIM, $p<.05$) and .51 (NR70, $p<.05$) for BVs computed from 100-199 early breedings to .97 (DIM, $p<.01$) and .65 (NR70, $p<.01$) for BVs computed from a minimum of 500 breedings. For yearly estimates based upon a minimum of 500 breedings, only (9, DIM; 21, NR70)% changed by more than 1 SD units; (0, DIM; 10, NR70)% declined by more than 1 SD units. Since both traits were predictable and are important to daughter fertility, an appropriately constructed index could improve both traits.

Key Words: Non-return, Fertility, Reproduction

255 Relationships of PTA productive life of AI Holstein bulls with changes in yield traits from first to second lactation.

J.M. Abdallah*[1], B.T. McDaniel[1], and M.J. Tabbaa[2], [1] *North Carolina State University, Raleigh*, [2] *The University of Jordan, Amman, Jordan.*

The objective of this work was to investigate the relationships of PTA for productive life (PTAPL) of AI Holstein bulls with early sire evaluations for yield traits. Two data sets were analyzed. In the first, PDs for the difference in milk yield between second and first lactation (PDIFF21) were available from a previous study on AI Holstein bulls widely used in the southeastern US. These were correlated with PTAPLs from the August 1998 USDA sire summary (PTAPL988). Based on sires with at least 10 daughters (n=560) the correlation of PTAPL988 with PDIFF21 was 0.31. The correlation increased to 0.36 for sires with at least 50 daughters (n=319) and 0.41 for sires with at least 100 daughters (n=261). The second analysis included data from the USDA sire evaluations of August 1989 through August 1999. Data included only AI bulls with sampling status of "S" or "M" and for which first and second lactation PTAs were identified (n=3699). All PTAs were adjusted to the same base year. Linear regressions of PTAPL998 on PTAMK1 (first lactation PTA for milk) and PTAMK21 (difference between second and first lactation PTAs for milk) showed that R-square significantly increased from 0.07 for PTAMK1 to 0.12 for both. R-square was 0.09 for the regression of PTAPL998 on PTAPR1 (first lactation PTA for protein) and increased to 0.14 by adding PTAPR21 (difference between second and first lactation PTAs for protein). The regressions of PTAPL998 on PTAs for fat yield showed that fat was less important in predicting productive life than milk and protein. These results show that PDs or PTAs for the change in milk yield from first to second lactation should be useful predictors of productive life. Considering the difference between second and first lactation PTAs of milk and protein should improve the prediction of PTAs for productive life for little cost.

Key Words: Correlations, Productive life, PTAs

256 Stability of yield evaluation for Holstein bulls in artificial-insemination service.

R.L. Powell*, H.D. Norman, and G.R. Wiggans, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

The dairy industry has expressed concern that bull evaluations for yield traits decline too often. Although changes in genetic evaluations with additional data are accepted, earlier evaluations are expected to be unbiased; i.e., individual bull evaluations may increase or decrease, but means for any subset of bulls should remain the same. To examine evaluation stability, January 1995 genetic evaluations of yield traits for 540 Holstein bulls in active artificial-insemination (AI) service at that time were compared with their February 2000 evaluations. Mean changes in predicted transmitting ability (PTA) were small (-9 kg, milk; -1.4 kg, fat; -0.5 kg, protein), whereas mean reliability (REL) increased from 81.8 to 96.1%. Forty bulls with low ($<$70%) reliability in 1995 had much larger changes in PTA (-63 kg, milk; -2.4 kg, fat; -1.6 kg, protein) than did 97 bulls with high ($\geq$90%) REL in 1995 (+11 kg, -0.2 kg, +0.3 kg). Bulls in the top decile for PTA milk in 1995 had the largest declines in PTA (-50 kg, milk; -4.4 kg, fat; -2.5 kg, protein), whereas mean PTA for bulls in the lowest decile were nearly unchanged (+2 kg, -0.4 kg, +0.3 kg). Mean PTA of the 406 bulls from traditional AI organizations (a National Association of Animal Breeders controller number of $\leq$29) were fairly stable (-5 kg, milk; -1.3 kg, fat; -0.4 kg, protein), but declines in PTA for the other 134 bulls were larger (-23 kg, -1.8 kg, -0.8 kg). Changes in PTA were correlated positively with initial REL and negatively with change in REL over 5 yr. Similar results were found for active AI bulls in February 1997, except that PTA tended to decline more often overall. Thus, active AI bulls tended to decline in PTA, particularly for bulls with lower REL, higher PTA, and from less traditional AI organizations. Overevaluation of such bulls will be reexamined after implementation of model and base changes in the national system for genetic evaluations in August 2000.

Key Words: Genetic evaluation, Artificial insemination, Stability

257 A multivariate approach for analysing longevity in dairy cattle.

B. L. Harris[1] and A. M. Winkelman[1], [1] *Livestock Improvement Corporation, Hamilton, New Zealand.*

The objective of this study was to find a means for improving the timeliness and accuracy of the New Zealand's national genetic evaluation for survival. A new trait, longevity, was defined as days survived from birth until last known test day. Longevity was chosen because the trait better modelled the culling process that occur continuously over the milking season compared to the current binary survival indicators measured for each lactation until the fifth lactation. Survival analysis was used to assess the contribution of production and non-production traits in the prediction of longevity. The results of the survival analysis were used to extend incomplete longevity records (censored records) by using the mean residual life function. A multiple trait animal model with missing data was used to produce breeding value estimates for longevity. The multiple trait model had six traits; life expectancy recorded when the cohort group is completing the first lactation, life expectancy recorded when the cohort group is completing the second lactation and so on with trait 6 being life expectancy recorded when the cohort group is beyond the fifth lactation. The accuracy of the multiple trait method was compared with alternative approaches.

Key Words: Longevity, Multiple trait, Animal model

258 Genetic variations in milk somatic cell count in different age at calving within parity of Hungarian Holstein Friesian.

A. Amin*[1], [1] *Department of Animal Production, Faculty of Agriculture, Suez Canal University.*

Hungarian Holstein Friesian lactation records and sample test day of somatic cell count (SCC), daily milk yield (DY), fat % (F%), protein % (P%), lactose % (Lac%), and milk yield-305 (M-305) were examined and estimates of variance components were obtained. Sire-cow animal models by MTDFREML were used to compute estimates of heritability, genetic and phenotypic correlations for all studied traits. 255734 lactation records involved four parities were collected from five herds of 12 farms during the period from 1991 to 1993. Overall estimates of lactation heritability were 0.28, 0.23, 0.39, 0.40, 0.42, and 0.29 for SCC, DY, F%, P%, Lac% and M-305 respectively. The highest heritability estimates for all studied traits are presented in the 2^{nd} and 3^{rd} parity. Estimates of h^2 SCC increased steadily with monthly test day and ranged from (0.09 to 0.22). The highest h^2 of DY (0.31 in the 2^{nd} test day) associated with the moderate h^2 of SCC (0.12). Overall genetic and phenotypic correlation between SCC and DY were -0.29 and -0.31 respectively. The maximum genetic correlation between SCC and DY among calving age groups obtained at 20.1 to 24.0 mo (-0.30) and the corresponding maximum phenotypic association was -0.32 in calving group of '>= 44.0' mo. The highest phenotypic correlation between SCC and milk compositions was found for P% in the overall and the 2^{nd} parity estimates. Relationship between milk compositions was high and positive. Genetic and phenotypic (co)-variances generated by the suggested animal model indicated that SCC could play an important role in improving of milk production and in decreasing the possible rates of mastitis Incident by an appropriate selection index.

Key Words: Somatic cell, Genetic and phenotypic correlation, Fat, Protein, Lactose

259 Routine genetic evaluation for functional longevity in dairy cattle populations in Switzerland.

Natascha Vukasinovic*[1], J. Moll[2], and L. Casanova[2], [1] *Dept. of Mathematics & Statistics, Utah State University, Logan*, [2] *Swiss Brown Cattle Breeders Association, Zug, Switzerland.*

Genetic evaluation of sires for functional longevity of their daughters based on survival analysis has been implemented in the populations of Braunvieh, Simmental, and Holstein cattle in Switzerland. A Weibull mixed sire-maternal grandsire survival model was used to estimate breeding values of sires, using data on cows calved from April 1, 1980 onward. Data on Braunvieh and Simmental cows included over one million records, data on Holstein cows comprised about 250,000 records. The data contained approximately 20% censored records. Besides the random sire and maternal grandsire effect, the model included effects of herd-year-season, age at first calving, parity, stage of lactation, alpine pasturing (Braunvieh and Simmental), and relative milk yield and relative fat and protein percentage within herd to account for culling for

production. Heritabilities of functional longevity, estimated on a subset of data including approximately 150,000 animals, were .18, .20, and .18 for Braunvieh, Simmental, and Holstein, respectively. Breeding values were estimated for all sires having at least 6 daughters or 3 granddaughters in the data. Breeding values of sires can be expressed in genetic standard deviations or in days of functional productive life and published in sire catalogs along with breeding values for production traits.

Key Words: survival analysis, functional longevity, sire evaluation

260 Approximate ETA for lifetime production based on genetic evaluations for lactational production and herd life.

P.J. Boettcher[1] and F. Miglior*[2], [1]*University of Guelph, Canada*, [2]*Canadian Dairy Network, Guelph, Canada*.

Dairy cattle breeders in Canada have expressed an interest in a genetic evaluation of sires for lifetime production of their daughters. Lifetime production is a function of production per lactation and the number of lactations expressed. In Canada, genetic evaluations are currently available for lactational production and herd life (HL). The objective of this study was to use the existing genetic evaluations to develop approximate ETA for lifetime production. The approach taken was to multiply ETA for production in each lactation by their respective probabilities of expression and then sum across lactations. Direct application of this proposed approach was limited by three factors: 1) EBV for production are calculated for only the first three lactations, 2) ETA for HL are for functional HL rather than true HL, being adjusted for effects of production, and 3) ETA for HL are expressed as the expected total number of lactations survived. Selection index theory was used to develop EBV for lactations >3 based on EBV for lactations 1 to 3. Regression was used to convert ETA for functional HL to true HL. Survival analysis theory was used to convert ETA for HL into probabilities of expression for each lactation. The probability of culling was assumed to follow a Weibull distribution. The Weibull survivor function (probability of survival to lactation t = $\exp[-(\lambda t)^{r}]$) was fit to average survival rates in Canada to establish a base-line. The best fit occurred when λ=0.262 and r=2.0. The ETA for true HL of sires (expressed as a difference from the average of 3.0 lactations) were then fit as covariables with β= -0.617. Based on these parameters for the survivor function, the proportion of daughters from a given sire that survived to express lactation t was = $\exp[(-(0.262t)2.0]^{exp[-0.617(ETA-3.0)]}$. Production ETA and survival proportions were calculated within each lactation and their products were summed across lactations to yield the final ETA for lifetime production.

Key Words: Lifetime Production, Approximation

261 Genetic parameters for three experimental feet and leg traits for Canadian Holsteins.

P.J. Boettcher*[1], L.R. Schaeffer[1], J. Fatehi[1], and J.J. Shannon[2], [1]*University of Guelph, Canada*, [2]*Canadian Holstein Association, Brantford, Canada*.

In March 1998 the Canadian Holstein Association started to record three new feet and leg traits as part of their routine type classification. Traits were rear legs from the rear view, depth of heel, and claw uniformity. All traits were recorded on a nine-point scale, which is the standard for descriptive conformation traits evaluated by Holstein Canada. For rear legs-rear view, cows received lower scores if they hocked-in more severely. Cows with more depth of heel received greater scores. Cows with symmetric claws (right rear foot) received high scores and scores decreased as uniformity in shape and size of the claws decreased. More than 200,000 cows were scored over 15 months of classification. Due to expected increases in experience and precision of the classifiers, genetic parameters were estimated using 57,492 records from first lactation cows scored during the final 15 months of classification. Genetic parameters were estimated using a Bayesian procedure that employed Gibbs Sampling. Genetic relationships among the three traits and eight other conformation traits were estimated in a series of four 5-trait (3 experimental and 2 other) animal models. Factors in the model were herd*round*classifier, age and stage of lactation during classification, and animal. For each five-trait combination, six chains of 30,000 cycles were generated, discarding the first 5000 cycles in each chain. Means across chains were used as the point estimates of the parameters of interest. Heritabilities were 0.110, 0.096, and 0.045, for rear legs-rear view, depth of heel, and claw uniformity, respectively. Genetic correlations with rear legs-rear view were 0.34 and 0.55 for heel depth and claw uniformity. Genetic correlation between heel depth and claw uniformity was 0.66. Foot angle and overall feet and legs had high correlations (>0.65) with claw uniformity.

Key Words: Conformation, Feet and Legs, Genetic Parameters

262 Estimation of variance components for cow and parity effects from test-day yields.

J. Bormann*[1], G.R. Wiggans[2], J.C. Philpot[2], T. Druet[1,3], and N. Gengler[1,3], [1]*Animal Science Unit, Gembloux Agricultural University, Gembloux, Belgium*, [2]*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*, [3]*National Fund for Scientific Research, Brussels, Belgium*.

The initial step in implementation of a US test-day model includes estimation of cow and parity test-day variances needed to calculate lactation stage, age, and pregnancy effects. Single-trait repeatability models were fitted, and variance components were estimated for milk, fat, and protein test-day yields using Method R and a preconditioned conjugate gradient (PCG) equation solver because of large data sets (0.7 to 7.7 million records). Data were obtained for calvings since 1990 for Brown Swiss and Jerseys and for Holsteins from California, Pennsylvania, Texas, and Wisconsin. A minimum of three observations were required per subclass for herd test date and milking frequency. Three parity groups were defined: first, second, and later. Test-day data were adjusted for environmental effects of age, calving season, and milking frequency. Estimated breeding values (EBV) were expressed on a daily basis. To assess effect of adjustments, data also were analyzed without correction. For adjusted data, variance ratios (residual divided by variance of effect) within parity were similar across breeds, subpopulations, and samples: 1.5 to 1.8 for milk, 3.0 to 4.3 for fat, and 1.8 to 2.3 for protein. Variance ratios across parities ranged from 3.5 to 6.8 for milk, 8.7 to 17.6 for fat, and 5.5 to 9.4 for protein. Adjustment for EBV reduced both cow genetic and nongenetic variances. Variance ratios for permanent environment within parity from unadjusted data were nearly identical to those from adjusted data. For unadjusted data, heritabilities ranged from 0.19 to 0.30 for milk, 0.13 to 0.15 for fat, and 0.17 to 0.23 for protein. Although computations took several weeks, use of Method R and a PCG solver enabled estimation of the variance components that will be used for US evaluations based on a test-day model.

Key Words: Test-day model, Genetic evaluation, Variance estimation

263 Optimizing single-generation selection on QTL in crossbreeding programs.

J. C. M. Dekkers*[1] and R. Chakraborty[1], [1]*Iowa State University, Ames*.

Molecular genetics has enabled detection of quantitative trait loci (QTL) in livestock. The use of QTL in selection requires a balance between the QTL and other genes (polygenes). For non-additive QTL, standard QTL selection, in which selection is on the sum of the standard EBV for the QTL and an EBV for polygenes, does not maximize progeny performance, as illustrated by Dekkers (1999, Genet. Sel. Evol. 31:421) for purebred selection. Often, however, the aim is to maximize crossbred performance. Therefore, the objective here was to develop methods to optimize single-generation purebred QTL selection for a 2-breed terminal cross. A deterministic model for within-line selection on an index of the known breeding value for a QTL and a purebred EBV for polygenes was developed. For simplicity, crossbred progeny were produced by random mating of unselected male and female progeny from the sire and dam lines. Lagrange multiplier methods were used to develop iterative algorithms that maximized crossbred performance. Optimal QTL selection was compared to standard purebred QTL selection for a biallelic QTL with 30 and 40% frequencies in the male and female line and 10 and 25% selection of sires and dams within each line. Optimal QTL selection resulted in greater crossbred performance for dominant QTL. Extra responses were 1, 5, and 12% greater for QTL with partial, complete, and over-dominance for a QTL with an additive effect (a) of 1 polygenic EBV standard deviation, and 3, 11, and 37% greater for a QTL with a equal to 3 polygenic EBV standard deviations. Optimal selection strategies differed by line and resulted in opposite trends in QTL frequencies for over-dominant QTL. Pure-line responses under optimal selection were similar to standard QTL selection for the male line but substantially less for the female line. In conclusion, QTL information can be used to select for improved crossbred performance based on purebred data. The impact on multiple generation response requires further investigation. This research was funded by Pig Improvement Company.

Key Words: Marker Assisted Selection, Cross Breeding

264 Verifying the hypothesis of more than one QTL on chromosome 6 influencing the relation between both yield and percentage of milk protein and milk fat.

G. Freyer*[1], C. Kuehn[1], and I. Hoeschele[2], [1]*Research Institute for the Biology of Farm Animals*, [2]*Virginia Polytech Institute and State University, Blacksburg*.

Earlier studies, e.g. those involving data of 1721 Black and White cows, led to the hypothesis of the existence of more than one QTL on the bovine chromosome 6 for several milk production traits (Freyer et al. 1999, J Anim Breed and Genet 116:87-97). The Casein loci have been used as markers. These results suggested a QTL for fat yield, protein yield and fat percentage close to the Casein locus, while a QTL only moderately linked with the Casein locus affected fat percentage in the study mentioned. It has been shown that an adjustment of cows performances for the effects of their kappa and beta Casein genotypes reduced the genetic correlation coefficient between milk yield and fat percent from -.36 to -.31 and of milk yield and protein percent from -.33 to -.26. Here, we are using different statistical approaches fitting more than one QTL with the aim of comparing the results with respect to the number, locations and effects of the QTL involved. Methods compared are two different implementations of variance component analysis (REML) in the programs SOLAR and MQREML, and Least-Squares analysis. First results using data from a grand-daughter design in the German Holstein Friesian population provide evidence for two QTL and confirm a QTL for fat yield (Kuehn et al. Anim Genet 30(1999),33-340)). Results of the three statistical methods led to nearly equal inferences concerning the QTL location. Putative QTL for milk yield, fat yield and protein yield are located with a high probability between 40 - 68 cM and 88 - 105 cM. QTL for protein percentage are probably located between 7 - 66 cM and 75 - 95 cM, respectively, with map positions derived using Haldane's mapping function. The 95% confidence interval for yield traits cM is 1 to 89 cM and 40 to 102 cM, for protein percentage 0 to 76 cM and 43 to 102 cM. Because the Casein genes are located at 95 cM (Kosambi) there is a further support for the assumption of the hypothesis. For fat percentage, QTL appeared to be segregating only in a few families and did not attain significance.

Key Words: Dairy cattle, QTL detection, Trait relation

265 Accounting for uncertainty of QTL location in marker assisted selection in dairy cattle.

A. Stella*, J. Gibson, and G. Jansen, *University of Guelph, Ontario, Canada*.

The objective of this study was to evaluate whether the efficacy of marker assisted selection (MAS) could be improved by considering a confidence interval (CI) of QTL position. Specifically, MAS was applied for within-family selection in a stochastic simulation of a closed nucleus herd. The location and effect of the QTL were estimated by least squares interval mapping with a granddaughter design. Three generations were simulated. Nucleus size was 5 sires and 250 dams. Genotypes and EBV from the first two generations were used to identify probable QTL. This information was then used in the third generation to select bulls from within full-sib families for entry into a progeny testing program. Six markers on a single chromosome were evenly spaced around a QTL. Each marker had 6 alleles and the QTL had ten alleles, with normally distributed effects. The QTL explained 17 % of the total genetic variance. Heritability was either .10 or .30. Three approaches were used to select the best bull within fullsibships of 3 or 40 bulls. All three were based on the probability of inheriting the favorable allele from the grandsire (PROB). The first method selected the sib with the highest PROB at the location with the highest F-ratio (MAXF). The other two approaches were based on sums of estimated regression coefficients weighted by PROB at each cM within a 95 % CI based on either bootstrapping (BOOT) or approximate LOD scores (LOD). Selection criteria were compared with the following measures: 1) average BV of the selected bulls and 2) frequency of selected bulls inheriting the favorable allele. The average BV of the selected bulls was increased by 1.7, 2.3 and 2.5 % when MAS was applied using MAXF, BOOT and LOD, respectively compared to random selection ($h^2 = .30$). When heritability was .10, gains were reduced to 1.7, 2.0 and 2.0 %. Selected bulls carried the correct allele in 78, 71, 71 and 63 % of the cases for MAXF, BOOT, LOD and random selection respectively. Little advantage was observed when using a CI to account for uncertainty in QTL location.

Key Words: Marker-assisted selection, Confidence interval, Dairy cattle

266 Stochastic estimation of exclusion probabilities.

S. D. Kachman*[1] and G. B. Sherman[1], [1]*University of Nebraska, Lincoln*.

Microsatellites provide a powerful tool for paternity identification. However, the cost associated with obtaining microsatellite information can be high. Depending on a number of factors the probability of unambiguously identifying the sire of a calf in a breeding group can be small. A program to predict the exclusion probabilities and probabilities of unambiguous parentage based on the genotypes of the bulls has been developed. Using the genotypic information the program estimates, for each bull, the probability that his calves can be unambiguously assigned to him and the probability that each of the other bulls can be excluded as a sire of the calf. Genotypic information at 11 loci for 33 bulls was used to estimate the probability of unambiguous parentage. The program estimated an overall probability of unambiguous parentage of 73% for a group of 33 bulls that were co-pastured in a single large breeding group. The result agreed favorably with the observed frequency of 80% of the calves resulting from this breeding being assigned to a single bull.

Key Words: exclusion probability, microsatellite

267 Discovery of novel genes controlling feed intake in cattle.

D. R. Glimm*[1], F. Dong[1], P. K. Chelikani[1], E. K. Okine[2], G. R. Khorasani[1], and J. J. Kennelly[1], [1]*University of Alberta*, [2]*Western Forage/Beef Group, Lacombe Research Centre, Alberta, Canada*.

An experiment was conducted with five Holstein cattle fitted with duodenal cannulae to identify and characterize gastrointestinal genes that are differentially expressed during conditions of hunger or satiety. Intestinal tissue samples were obtained from the duodenum, approximately 50-cm distal of the abomasal sphincter, by endoscopy (Olympus CF type 1B) at five time points during fasting (48 h) and five time points during refeeding (24 h). Gastrointestinal genes that were differentially expressed over the course of fasting and refeeding were identified using expression genetics technology (differential display). So far, we have identified 60 genes that exhibit temporal patterns of expression during conditions of increasing hunger or satiety. The expression of some of the genes appeared to be turned off during conditions of extreme hunger that accompany prolonged fasting. In contrast, other genes were expressed only during conditions of extreme hunger. The expression of the remaining candidate genes was either substantially increased or decreased during fasting or refeeding. The 30 combinations of primers that we have used so far however, represent only about 30% of the theoretical number required to ensure statistically that all expressed genes are surveyed. The cDNA fragments corresponding to all candidate genes have been isolated and are at various stages of characterization. Comparison of sequence data from those that we have cloned with existing DNA sequence databases reveals that about 70% of our candidate genes have never before been identified or sequenced in any species. To confirm differential expression and further characterize candidate genes, we have generated antisense riboprobes from our clones and successfully used them to perform northern hybridization and ribonuclease protection assays. Our study demonstrates that expression genetics technology provides a powerful new experimental approach for the discovery of novel genes that encode proteins with key roles in regulating hunger and satiety in cattle.

Key Words: Feed Intake, Expression Genetics, Gastrointestinal Physiology

268 The National Animal Germplasm Program.

H. D. Blackburn*[1] and S. M. Kappes[2], [1]*USDA-ARS, Ft. Collins, CO*, [2]*USDA-ARS, Beltsville, MD*.

The National Animal Germplasm Program (NAGP) was established in 1999 to develop a national system for conserving and utilizing animal genetic resources. Within ARS the national system is comprised of a central repository and three satellite repositories. The repository system is responsible for the collection and maintenance of cryopreserved animal germplasm and tissue that represents the breadth of U.S. animal genetic resources. Germplasm is collected in conjunction with other research institutions and industry. In addition to preserving germplasm the program is to develop a database and decision support tools that assist in management of genetic resources. Much of the database and information system will be accessible on the NAGP website. For livestock species and aquaculture there are species committees comprised of research and industry members that assist in the identifying and collecting germplasm. Presently the system has stored three swine germplasm lines and 52 poultry lines. For small ruminants the Gulf Coast Native, Navajo-Curro, Myotonic Goat and Angora goat have been identified as potentially at risk populations. As a result conservation strategies are developed to monitor and collect germplasm from those breeds should conditions so dictate. The comprehensive approach taken in development of the NAGP should result in a national resource that allows preservation, utilization and characterization of animal genetic resources.

Key Words: Genetic conservation, Animal genetic resources, Cryopreservation

269 Reproductive and maternal performance of Angus-, Brangus-, Gelbvieh-, Gelbray-sired, and F$_1$ Brahman-Hereford cows.

S.M. DeRouen* and J.M. Turpin, *Louisiana State University Agricultural Center, Homer.*

A total of 738 reproductive and 485 calving records were collected from straightbred-sired, Brahman composite-sired, and F$_1$ Brahman-Hereford (BH) females from 1995 to 1999. Angus (A), Brangus (BA), Gelbvieh (G), and Gelbray (GB) bulls were randomly mated to BH cows to produce spring- and fall-born heifers. Contemporary weaning-aged BH heifers were purchased when other heifers were weaned. Percent Brahman inheritance was 25% in A- and G-sired females, 44% in BA- and GB-sired females, and 50% in BH females. After weaning, heifers were developed on a forage-based diet. Heifers were exposed to Red Poll bulls during a 60-d spring breeding season to first calve at 2.0 or 2.5 yr of age. Thereafter, cows were exposed to Simmental bulls during a 60-d spring breeding season. Calves were weaned in late September of each year at an average age of 210 d. Non-pregnant females were culled from the study. Separate analyses were conducted for first exposure, primi-, and multiparous females using a generalized linear mixed model procedure. Dam breed type affected ($P < .05$) pregnancy rate for first exposure and primiparous 2 yr old heifers with BA-sired females having rates that were 22 to 37% lower ($P < .05$) than A-, G-, GB-sired, and BH females. Dam breed type did not influence ($P = .27$) pregnancy rate (overall mean=93%) for multiparous cows. Dam breed type tended ($P < .08$) to affect calf 205-d weight from primiparous females with calves from BH cows being 11 kg heavier ($P < .05$) than calves from A-, BA-, G-, and GB-sired cows. Calf 205-d weight from multiparous cows tended ($P < .08$) to be influenced by dam breed type and were 233, 236, 235, 232, and 250 kg for A-, BA-, G-, GB-sired, and BH cows, respectively. These data suggest that lower reproductive performance was exhibited by BA-sired females during their first and second exposures, and improved maternal performance was achieved by BH females relative to the other dam breed types included in this study.

Key Words: Breed crosses, Reproduction, Maternal performance

270 Evaluation of body measurements of Charolais cows.

J. Tözsér[1], F. Szabo*[2], Z. Domokos[3], G. Tözsér[1], and E. Szuecs[1], [1]*Szent Istvan University, Godollo* , [2]*University of Veszprem, Georgikon Faculty, Keszthely,* [3]*National Association of Hungarian Charolais Cattle Breeders, Miskolc, Hungary.*

Charolais cows (n=311) of 6.8 years of average age and 600 kg average live weight were examined in summer grazing period in 1998. Live weight (LW), height at withers (HW), rump width 2 (RW), slanting body length (SBL) as well as chest girth (CG) were recorded simultaneously. The data were statistically analyzed using the SPSS 7.5 software package. Phenotypic correlation were computed by the covariance component and variance component estimates. Multiple relationship among traits listed above were investigated by principle component analysis after varimax rotation. Separated position of age was tested by cluster analysis. Means and SD for HW, RW, SBL and CG were 132.2±3.93; 52.1±2.74; 177.2±8.09 and 194.5±8.50 cm, respectively. Bivariate phenotypic correlation coefficents between traits reveal close relationship of body measurements on BW (BW vs. HW: r=0.54, $P<0.001$; BW vs. RW: r=0.63, $P<0.001$; BW vs. SBL: r=0.63, $P<0.001$; BW vs. CG: r=0.83, $P<0.001$). High multiple correlation coefficient (R = 0.88, $P<0.001$) was found among independent variables (RW, SBL, CG) and BW (dependent variable) by stepwise regression analysis. Relatively low relationship was shown between age of animals and body measurements (r = 0.04 - 0.26). Two factor loadings proved to be statistically significant, as follows: factor I for body weight - body measurements (variance: 3.2310 , ratio of variance: 53.8 %) and factor II of age (variance: 1.1032 , ratio of variance: 18.4 %). In conclusion, main role of SBL and CG (R=0.60; $P<0.001$) in HW of cows was elucidated by stepwise regression.

Key Words: Body measurements, Variance, Phenotypic correlation

271 Characterization of maternal productivity in the Hereford breed.

C. Gallivan, D. H. Crews, Jr., P. B. Mwansa*, and R. A. Kemp, *Lethbridge Research Centre, AAFC, Alberta, Canada.*

A review of the literature was conducted to characterize the Hereford breed for maternal productivity. Over 300 papers published since 1965 covering approximately 18 cattle breeds from Canada, the US, Australia, New Zealand and the UK were evaluated. For all traits, the model included the location of study, age of cow, % of inheritance from each of the cow breeds, and the heterozygosity of the cow. In addition, % of inheritance from each sire breed, and the heterozygosity of the calf were also included in the models for the following traits: % of cows exposed that calved (PCAL; n=27,290), calf birth weight (BWT; n=36,588), % of calves alive at weaning (PLWN; n=30,298), % of cows exposed that weaned a calf (PEWN; n=27,449), calf preweaning average daily gain (ADG1; n=31,071), calf age-adjusted weaning weight (WWTa; n=58,465), WWTa per cow exposed (WWTa:CE; n=28,855), and the ratio of the weight of the calf weaned to the weight of the cow at weaning (WWT:CWWT; n=457). The Hereford reaches puberty at an average age of 343.68±9.87 d and an average weight of 253.65±3.31 kg. With the exception of the Angus and the dairy breeds that reached puberty earlier, and the Charolais, which was heavier at puberty, the results for the Hereford were comparable to those of the rest of the breeds considered. It was shown that crossbred cows reached puberty 21.12±8.58 d earlier and 10.48±2.88 kg heavier than purebreds. The Hereford pregnancy rate of 81.37±0.99% was either similar or superior to all the other breeds considered, except for Red Poll, Brown Swiss and Shorthorn. An average BWT of 34.38±0.28 kg for the Hereford breed was lower ($P<.05$) than most of the other breeds. The Hereford was equal or superior to all the other breeds for PLWN. Average ADG1 and WWTa for the Hereford were lower than other breeds considered. Generally, no differences ($P>.05$) were observed for WWTa:CE among the breeds considered. Analysis of weight, height and condition score of cows tended to characterize the Hereford as a breed that is moderate in size and able to maintain condition relative to other breeds and types.

Key Words: Hereford, Maternal Productivity, Breed Effects

272 Genetic parameter for meat quality traits evaluated by image analysis method in Japanese Black.

K. Kuchida*, Y. Hamasaki, M. Suzuki, and S. Miyoshi, *Obihiro University of Agriculture and Veterinary Medicine, Japan.*

Carcass values are greatly influenced by marbling scores in Japan. Marbling scores assigned by graders (GRADE_MS) are comprehensively evaluated, considering the ratio of marbling area to ribeye area (FATPER), coarseness of marbling (COARSE), shape of marbling (SHAPE), dispersion of marbling particles in the ribeye area (DISP), etc. The purposes of this study were to calculate FATPER, COARSE, SHAPE, and DISP numerically by image analysis method and to estimate genetic parameters for meat quality traits involving these image analysis traits. Digital images of the ribeye area from the 6th to 7th rib cross section of 923 Japanese Black steers with GRADE_MS were used in this study. The image analysis traits were calculated using image analysis software programmed by authors. A marbling score (PRED_MS) was predicted using the multiple regression analysis with image analysis covariates by the STEPWISE method. Genetic parameters for carcass traits assigned by graders were estimated with an animal model using the multitrait REML program by canonical transformation. Genetic parameters for image analysis traits were predicted simultaneously. Heritability estimates of GRADE_MS, carcass weight (CWT), ribeye area (RIBEYE), and subcutaneous fat thickness (SFT) were 0.48, 0.57, 0.48, and 0.34, respectively. Those of FATPER, COARSE, SHAPE, DISP, and PRED_MS were 0.58, 0.27, 0.35, 0.47, and 0.52, respectively. Genetic correlations between GRADE_MS and FATPER, and GRADE_MS and PRED_MS were highly positive (0.98 and 0.97 respectively). Genetic correlations between PRED_MS and CWT, and PRED_MS and RIBEYE were 0.22 and 0.37, while those between GRADE_MS and CWT, and GRADE_MS and RIBEYE were slightly lower; 0.11 and 0.24. These results indicate that image analysis traits can be good indices of breeding improvement.

Key Words: Image analysis, Japanese Black, Genetic parameters

273 Evaluation of the heritability values of the most important traits of beef cattle.

F. Szabo*[1], Z. Lengyel[1], Z. Wagenhoffer[1], and J. Dohy[2], [1]*University of Veszprem, Georgikon Faculty of Agriculture, Department of Animal Husbandry* , [2]*Szent Istvan University Godolo, Department of Animal Science.*

Heritability values of the most important traits of beef cattle were evaluated on the basis of great number (n= 2691-7084) of animals in Hungary. Data for the evaluation were collected in straightbred and crossbred population of Hungarian Simmental and Hereford breeds in different farms. The statistical evaluation of the data was carried out using with analyses of variance of progeny groups using SAS Version 6, and the Last Square and Maximum Likelihood Computer Program (Harvey, 1990). As a results of the study, no statistical differences (P>0.05) were found as for the heritability values between the straightbred and crossbred population. During the study the averages of the heritability values (h2) were found as follows: gestation length 0,46, birth weight 0,39, calving difficulty 0,07, unassisted birth 0,11, caesarean section 0,10, calf loss or survival rate to weaning 0,07, weaning weight of the calves 0,29, 200-day weight of the calves 0,19, 400-day weight of the heifers 0,47, 550-day weight of the heifers 0,45, rate of the heifers showed oestrus at a given age 0,31, age at puberty of heifers 0,37, daily gain during the fattening period 0,50, final weight 0,43, carcass weight 0,39, carcass percentage 0,32, rib eye area 0,59, fat thickness 0,54, kidney, pelvic and heart fat percentage 0,68, marbling 0,37, tenderness 0,50, prime meat weight 0,50, prime meat percentage 0,64, fat trim weight 0,49, fat trim percentage 0,58, bone weight 0,49, bone percentage 0,46.

Key Words: reproduction, growth, carcass value

274 Genetic correlation estimates for weaning weight and postweaning gain across Hereford populations in four countries.

D. Lee* and J. Bertrand, *University of Georgia, Athens.*

Original data consisting of 45,831, 522,065, 116,232 and 2,367,857 weaning weight (WWT) records and approximately 40 to 55% less postweaning gain (PWG) records from the Hereford Associations of Argentina (AR), Canada (CA), Uruguay (UY) and the United States (US) were used to estimate genetic correlations across pairwise sets of countries treating WWT or PWG as a different trait in each country. The PWG in CA and US was an adjusted 160 day gain, and in AR and UY, PWG was adjusted to 247 days. A previous research study had found that the direct and maternal (in parenthesis) genetic correlations, treating WWT as a different trait in different countries in pairwise data sets, were estimated at .88 (.84), .86 (.82), .90 (.85), for CA-UY, CA- US and US-UY, respectively . An analysis of WWT in the present study for AR-CA and AR-US found genetic correlation estimates of .81 (.78) and .78 (.77), respectively. Based on these two studies, it appears that the four countries can be considered as a single population for the genetic evaluation of weaning weight. To examine the genetic correlations across countries for PWG, pairwise sample data sets were created by randomly sampling herds that had PWG records, had greater than 500 WWT records, had a herd average WWT contemporary group size that was greater than nine calves, and had progeny or grandprogeny from sires used across each pairwise set of countries. A multiple-trait animal model that considered WWT as the same trait in each country, but considered PWG as a different trait in each country was fit to the data in each pairwise analysis, using an EM-REML algorithm. The direct genetic correlations for PWG were .29, .35, .43, and .43 for AR-CA, AR-US, CA-UY and US-UY, respectively. The research to this point suggests that PWG should not be considered as the same trait for animals with progeny in both North American (CA and US) and South America (AR and UY) for the purposes of genetic evaluation.

Key Words: Genetic correlations, Across-country evaluation

275 Differences between optimum and actual feed intake of various pig genotypes, and consequences for selection.

E. Kanis*[1], J.J. Eissen[1], J.W.M. Merks[2], and K.H. de Greef[3], [1]*Wageningen Institute of Animal Sciences, Wageningen University, The Netherlands*, [2]*IPG, Institute for Pig Genetics BV, Beuningen, The Netherlands*, [3]*Institute for Animal Science and Health, ID-Lelystad, The Netherlands.*

Feed intake (FI) in growing and finishing pigs is a trait with an economic optimum (FIo). Therefore, the desired selection direction for ad libitum feed intake or feed intake capacity (FIC) in the purebred lines of a breeding program depends a.o. on the FIC of the commercial end products relative to their FIo. To estimate FIo in various pig genotypes, an experiment was carried out with five genotypes from two breeding companies during three phases of the growth period (25-65, 65-95 and 95-125 kg live weight). Per combination of genotype, growth phase and sex, FIo was defined as FI just sufficient to reach maximum protein deposition (PDmax), assuming a linear-plateau relationship between daily PD and daily FI. Pigs were housed in groups but feed intake was measured individually. The feed contained 15.1 MJ DE, 170-191 g crude protein and 9.0-10.6 g lysine per kg. The five genotypes consisted of two end product genotypes (gilts and barrows), two dam line genotypes (gilts) and one purebred genotype (gilts, barrows and boars). In total 1019 pigs, divided over three feeding levels (60, 75 and 100% of ad libitum) were tested and dissected. PD was estimated from dissection data using equations developed from a sample of 309 chemically analyzed pigs. Averaged over genotypes and sexes, estimated PDmax was 129, 138 and 100 g/d for the three weight ranges respectively, while the corresponding FIo's were 1.56, 2.20 and 2.29 kg/d. In general FIC was not much different from FIo. However, gilts from the end product genotypes tended to show a lower FIC than their FIo, particularly from 25-65 and from 95-125 kg. Because selection for production traits in the purebred lines should be aimed at improving the end product genotypes, it seems beneficial to select for a higher FIC in combination with selection for other traits, especially in sow lines.

Key Words: Feed intake capacity of growing pigs, Optimum feed intake, Protein deposition

276 A canonical correlation analysis of production traits in Large White swine.

Z. B. Johnson*[1] and R. A. Nugent, III[2], [1]*University of Arkansas, Fayetteville*, [2]*The Pork Group, Rogers, AR.*

A canonical correlation analysis was used to examine relationships between easily measured (EM) production traits and traits not so easily measured (NEM) for purebred Large White boars. Data were performance test records of 7,529 boars collected in a commercial swine operation from 1990 to 1997. Boars were individually pen tested for approximately 77 days (100 to 177 d of age). They were weighed at the beginning (WT100) and end of the test (WT177) and feed intake recorded. Daily feed intake (DFI) and feed:gain ratio (FG) were computed. Backfat (BF) and loin eye area (LEA) were measured at the 10th rib at the end of the test by ultrasound. Body length (LEN) was measured at this time. The traits WT100, DFI, and FG were adjusted to a beginning age of 100 d using regression coefficients obtained from previous analyses. Likewise WT177, BF, LEA, and LEN were adjusted to an ending age of 177 d. For the canonical correlation analysis, WT100, WT177, and LEN were one set of measurements (EM traits) and DFI, FG, BF, and LEA were the second set of measurements (NEM traits). Three canonical correlations were obtained (.96, .41, and .15; $P < .01$). Canonical variate 1 was most correlated to WT177 (.90) in the EM set and to DFI (.70) in the NEM set of traits indicating that a major portion of the variation observed contrasted heavier boars that ate more with lighter boars that ate less. Canonical variate 2 was most correlated to WT100 (.95) in the EM set and to FG (.73) in the NEM set of traits. Thus selecting for high values of this variate would choose boars that were heavier at 100 days and had poorer FG values. Canonical variate 3 was most correlated with LEN (-.70) in the EM set and to BF (.82) in the NEM set; therefore, selecting for high values of this variate would select shorter, fatter boars and selecting for low values of this variate would select for longer, leaner boars. Results of this analysis indicate strong relationships between the EM and NEM traits that may useful to producers in selection programs.

Key Words: Pigs, Body Lenght, Production Traits

277 Estimation of genetic effects for semen quality and quantity in AI boars.

S. H. Oh*[1], M. T. See[1], and R. Nugent[2], [1]*North Carolina State University, Raleigh,* [2]*The Pork Group - Tyson Foods Inc., Rogers, AR.*

The objective of this study is to estimate (co)variances and heritabilities for boar semen traits of motility, morphology and volume. Currently boars selected as "AI quality" are indexed and selected strictly on performance and carcass characteristics. By improving the accuracy of selection of AI sires using the amount and quality of semen it may be possible to reduce the numbers of boars required to service sows and improve overall productivity and profitability. The data of 23,970 animals and 306 AI boars were used to estimate genetic parameters and environmental effects of performance. For each trait, parameters were estimated from an animal model using MTDFREML procedures. Semen volume was described as the number of doses prepared from each ejaculate and motility and morphology scores were visually assigned by the processing technician. The analysis model included season, collector, age and number of collections as fixed effects and the random animal effect. The results obtained in this study are summarized as follows. Genetic variance components are 22.06 for volume, 0.30 for motility and 0.30 for morphology. In phenotypic variances, these are 53.36, 7.81, and 6.00, respectively. The heritabilities estimated from the variance components were 0.41 for volume, 0.04 for motility and 0.05 for morphology. These results would indicate that there is an opportunity to genetically select for increased semen volume but expected response to selection for improved semen motility and morphology would be less. The lower heritability for semen motility and morphology may be due in part to the subjective scores assigned by the processing technicians.

Key Words: semen, heritability, pigs

278 Genetic parameter estimates for real-time ultrasound traits obtained from a multi-breed sheep population.

T. Fernandes*, J.W. Wilton, and J.J. Tosh, *Centre for Genetic Improvement of Livestock, University of Guelph, Ontario.*

Variance components were estimated for three ultrasonic traits: loin depth (LD), loin width (LW), and average backfat thickness (AVFAT). Data were collected from purebred and crossbred flocks across Ontario between 1997 and 1999 (n=3483) using the Ultra Scan 50 (Alliance Medical, St. Laurent, Quebec). The population was comprised of 13 breeds (Rideau-Arcott, Canadian-Arcott, Suffolk, Texel, Polled Dorset, Hampshire, Newfoundland, Rambouillet, North-Country Cheviott, Charolais, Shropshire, Oxford, and Border Leicester). The data were analysed with a REML procedure in a multiple-trait animal model. Analyses of all traits included the additive genetic effect of lamb, sex, contemporary group, and breed-group. Covariates of either weight or age were included in two separate analyses. Direct additive heritabilities of 0.29, 0.26, and 0.29 were obtained for loin depth (LD), loin width (LW), and average backfat thickness (AVFAT) respectively, with genetic correlations of 0.43 between LD and LW, -0.17 between LD and AVFAT, and 0.23 between LW and AVFAT. When the data were analysed using age in the regression analysis, direct additive heritabilities were 0.38, 0.30, and 0.35 for LD, LW, and AVFAT respectively. The genetic correlation between traits were all positive, 0.61 between LD and LW, 0.29 between LD and AVFAT, and 0.44 between LW and AVFAT. The gentic variance for all traits was different from zero ($P<0.05$). Results indicate that it is possible to make genetic improvement if selection is based on ultrasound information.

Key Words: Real-time ultrasound, Genetic parameters, Heritability, Loin depth, Loin width, Backfat thickness, Sheep

279 Preweaning performance of DorperXColumbia, Columbia and SuffolkXWhiteface lambs.

H. D. Blackburn*, *USDA-ARS, Ft. Collins, CO.*

The Dorper breed is a new genetic resource that needs evaluation of survival and growth performance in extensive range environments. For two years F1 Dorper-Columbia (DC) lambs were compared to SuffolkxWhiteface [Whiteface ewes were Columbia, Rambouillet or Targhee; (SW)] and Columbia (C) lambs. SAS GLM procedures were used. The mortality model included: year, breed, age of dam and sex as main effects and birth weight as a covariate. Birth weight, average daily gain (ADG) and adjusted 120 d weight (120WT) were evaluated with models that included: year, breed, sex, type of birth or rearing, band, age of dam and appropriate interactions. Significant breed differences were found for the four traits evaluated and there were no significant interactions between breed and other main effects. Year effects were nonsignificant for birth weight, ADG and 120WT. Significantly lower mortality during the first 20 d of life was found for DC (7.7%) vs. C and SW lambs (12.9 and 15.3%, respectively). Compared to C and SW, DC lambs weighed significantly less at birth (5.2, 5.4 and 4.8 kg, respectively). By 120WT DC were intermediate to C and SW (37.9, 38.4 and 37.1 kg, respectively). For 120WT C were significantly heavier than SW and DC did not differ significantly from either breed. Breed ranking for ADG was C, DC and SW (.276, .269 and .263 kg, respectively) with C having a significantly faster ADG than SW while DC remained intermediate and non-significant. These results indicate the DC may have an advantage in reduced mortality and has no difference for growth characteristics compared to C and SW. The reduction in mortality rate with no difference in growth may infer an increase in bio-economic performance of DC lambs.

Key Words: Dorper, Growth rates, Mortality

280 Investigation of breeding strategies to increase the probability of dog guides attaining optimum size.

S. K. Helmink[1], R. D. Shanks*[1], and E. A. Leighton[2], [1]*University of Illinois, Urbana,* [2]*The Seeing Eye, Inc., Morristown, NJ.*

An optimum-sized dog guide weighs 18 to 32 kg and stands 53 to 64 cm at the withers when mature body size is attained. Effects of directional selection, stabilizing selection, negative assortative mating, selection index with and without restrictions, and independent trait selection were modeled using data from German Shepherd Dogs (GS) and Labrador Retrievers (LR) raised by The Seeing Eye, Inc., Morristown, NJ from 1979 to 1997. The goal of selection was to decrease mature weight and height in GS and decrease mature weight and increase height in LR. Mature weights were recorded for 1333 GS offspring and their 69 dams and 17 sires, and 1081 LR offspring and their 51 dams and 13 sires. Heights were also recorded for offspring and parents, including 871 GS from 70 dams and 15 sires, and 793 LR from 40 dams and 13 sires. Response to selection for one generation of directional selection for a single trait included a 0.50 kg decrease in mature weight for GS, a 0.59 kg decrease in mature weight for LR, a 0.18 cm decrease in height for GS and a 0.91 cm increase in height for LR. Selecting on mature weight alone produced the highest aggregate genetic-economic gain for GS compared to the selection indices, generating a decrease of 2.10 kg in mature weight and a correlated decrease of 0.36 cm in height. In LR, selecting for height alone produced the highest aggregate genetic-economic gain, but caused an increase in mature weight. Weighting the two traits equally but in the opposite direction without restrictions was the only index that produced the desired effect of decreasing weight and increasing height in LR. Increasing the percentage of dogs attaining optimum size may decrease cost of production for The Seeing Eye because fewer dogs would need to be raised and trained to provide assistance to the same number of blind individuals.

Key Words: Body Weight, Height, Selection

281 Genetic parameters for milk yield in Saanen, French Alpine, La Mancha, Toggenburg, and Nubian goats in a dairy goat herd north west of Mexico.

A. P. Márquez*[1], J. H. Herrera[2], A. Correa[1], F. J. Verdugo[1], H. C. Hernández[3], and H. G. González[1], [1]*Universidad Autonoma de Baja California,* [2]*Colegio de Postgraduados,* [3]*Universidad Autonoma de Baja California Sur, Mexico.*

Genetic parameters for milk yield were estimated. Data came from an experiment to characterize germplasm from different breeds of goats at northwest of Mexico. A total of 39 pair mother-daughter records were included. Data was analyzed by using least squares.The model (including relationships mother-daughter) consisted of fixed effects of breed group, year of birth and age of dam with date of birth included as a covariate to adjust a common age as well as random effects of animal's genetic value. The milk yield averages in two complete lactations evaluated was: 826.43 ±38.20, 806.66 ±44.00, 679.61 ±48.00, 821.79 ±39.00, and 775.45 ±43.00 kg to Saanen, French Alpine, La Mancha, Toggenburg and Nubian, respectively. Lactations ranged from 273 to 305d and standarized to 305d. The heritability values for milk yield were(h^2= 0.39 ±0.12), and the repeatability values for the same trait (R=0.68

±0.19) respectively. These results based in limited numbers suggest by themselves genetic differences in milk production among breeds.

Key Words: Milk yield, Heritability, Repeatability

282 Environmental factors affecting the racing time of Thoroughbred horses in Brazil.

M. Mota, R. Taveira*, and H. Oliveira, *Universidade Estadual Paulista, Sao Paulo, Brazil.*

The aim of this paper was to study environmental factors that affect the racing time of Thoroughbred horses that won races in the classical calendar at the Cidade Jardim race track, Sao Paulo, Brazil. The data used in this study were provided by the Study Book from the Association of Race Horse Breeders (ABCCC). Data included 2000 finishing times from 1110 animals that won 106 differents kinds of races held from 1974 to 1998. The analyses were conducted using the GLM procedure of the Statistical Analyses Systems (SAS,1996). Race year, track condition, grade, condition(sex and age combination) and distance were considered as fixed effects in the linear model. Light turf racing track, condition for 3 and 4 year old gelding and horse, and grade I racecourse (GP group I - considered the most important race), provided the best times. The worst times were on drenched turf track, with 2 years old males and in semiclassicals races. Linear regression of time on year of race showed an annual decrease of 0.0785 seconds (approximately 2 seconds in 25 years studied). This result is probably due to improvements in nutritional, veterinary, and training aspects, in addition to correlated response to selection (p.e. earnings, rank at the final race) since time is not a trait selected for by the Brazilian Thoroughbred breeders. The quadratic regression of time on distance showed increases in average speed of 0.75 m/s, when racing distance goes from 1000 m (16.80 m/s) to 2000 m (16.05 m/s), and 0.47 m/s from 2000 m to 3000 m (15.58 m/s).

Key Words: horse, race, time

283 Optimization of pig breeding programs by implementing the Optimal Genetic Contribution Theory.

E.H.A.T. Hanenberg*[1] and J.W.M. Merks[1], [1]*IPG, Institute for Pig Genetics BV, The Netherlands.*

Commercial pig breeding programmes are mainly focussed on genetic gain. In the present Dutch breeding programmes different methods are used to restrict the rate of inbreeding. A new method was derived by Meuwissen (JAS, 1997) to optimise genetic gain on a restricted level of inbreeding (OGC-theory). The objective of this study was to evaluate the realised inbreeding rates in different commercial breeding lines over the last decade and to study the possibilities for implementation of the new OGC-theory into the breeding programmes. Breeding lines included in this study varied from 100 to 5.000 sows. The number of boars used per generation varied from 29 to 80. The rate of inbreeding, calculated over the last decade, varied from 0.15% to 0.43% per year. Generation intervals varied from 1.5 to 2.3 years. Inbreeding levels per generation varied from 0.31% to 0.89%. In comparison with studies in other breeds inbreeding levels were relatively low. With the OGC-theory optimal contributions of male and female selection candidates to the next generation can be calculated. Information needed is limited to estimated breeding values of, and relationships between selection candidates and a predefined desired maximum rate of inbreeding. In this study the OGC-theory was implemented for male selection only for two selection moments: (1) selection of boars after own-performance-testing and (2) culling of AI-boars which have reached there optimal contribution. Change of the culling strategy of AI-boars from a fixed amount of inseminations per boar to a variable amount of inseminations based on the OGC-theory gave a 10% to 20% higher genetic improvement under an equal rate of inbreeding. The OGC-theory can also be implemented for female selection and for selection of testing candidates for an optimal use of testing capacity. It is concluded that rates of inbreeding are relatively low in commercial pig breeding programmes. Application of the OGC-theory will improve genetic progress with at least 10 to 20% under restriction of the same level of inbreeding.

Key Words: Inbreeding, Pigs, Selection Methods

284 Direct and correlated responses to selection for ovulation rate or uterine capacity in swine.

K. A. Leymaster* and R. K. Christenson, *USDA-ARS; U.S. Meat Animal Research Center; Clay Center, NE.*

The objective was to estimate responses of ovulation rate (OR), uterine capacity (UC), and litter size (LS) to selection for either OR or UC in a four-breed composite population of swine. A replicate of each OR, UC, and control (CO) line was established in two seasons (A and B). During the selection phase of the experiment, OR at the estrus of conception was recorded on dams of line OR. In line UC, UC per uterine horn was measured as number of fully-formed pigs born to unilaterally hysterectomized-ovariectomized (UHO) dams. Boars and gilts from OR and UC dams with the greatest records were selected for 11 generations. Then, to remove accumulated inbreeding effects prior to evaluation of responses, generation 11 replicate A gilts were mated to generation 10 replicate B boars and generation 11 replicate B gilts to generation 11 replicate A boars. Resulting littermate gilts of each line were randomly assigned to either remain intact for observation of OR and LS or to undergo UHO surgery for observation of OR and UC. At least 134, 62, and 62 observations for OR, UC, and LS, respectively, were collected within each line. Responses to selection were estimated as differences between means of selected and control lines and SE of differences included terms for drift variance. Direct selection for OR was effective (3.21 ova, $P <$ .001), however, correlated responses in UC (-.11 pigs per uterine horn) and LS (.70 pigs) were not detected. Likewise, direct selection for UC increased UC by 1.11 pigs per uterine horn ($P <$ .01), although correlated responses in OR (-.01 ova) and LS (.92 pigs) were not detected. These responses established that OR and UC were heritable and genetically independent of one another. Using published equations based on the OR-UC model of LS, observed and predicted LS means were 10.62 and 10.50 pigs for line CO, 11.32 and 11.69 pigs for line OR, and 11.54 and 11.04 pigs for line UC. Simultaneous increases in both OR and UC are necessary to produce a substantial increase in LS.

Key Words: Swine, Selection Responses, Reproductive Traits

285 Bayesian analysis of lifetime performance and prolificacy in Landrace sows using a linear mixed model with censoring.

S. Guo*[1], D. Gianola[1], and T. Short[2], [1]*University of Wisconsin-Madison*, [2]*PIC USA.*

Factors affecting variation of length of productive life (LPL), and lifetime prolificacy (LTP) in Landrace sows were investigated. Data were herd life and prolificacy records from 2616 daughters of 343 sires born in a nucleus herd between 1990 and 1996. Records from sows sold to other farms for production were treated as censored. Factors studied were year-season of entry in the breeding herd, age at herd entry, litter size at first parity (for LPL) and sire of the sow. Additional censoring rates of 25% and 35% were created to assess influence of censoring on fixed effects, variance components and sire evaluation. LPL, log(LPL) and LTP were analyzed using a linear mixed model with censoring. Age of entry into the breeding herd did not affect the traits studied. Sows with smaller litters at first parity had a higher risk of being culled than more prolific gilts. Posterior means of heritability of LTP, LPL and log-LPL were 0.22-0.25. Intra-trait correlations between sire evaluations at the 3 censoring rates ranged between 0.69 and 0.96. The rank correlation between sire evaluations for LPL and LTP (actual data set) was 0.85, suggesting a strong genetic correlation. Estimates of sire effects with censored records removed from the analysis were in less agreement with evaluations obtained with the actual data set than those found with the artificial censoring rates.

Key Words: Herd-life, Linear model, Swine

286 Genetic parameter estimates from joint evaluation of purebreds and crossbreds in swine.

E. Lutaaya[1], I. Misztal*[1], J. W. Mabry[1], T. Short[2], H. H. Timm[2], and R. Holzabauer[2], [1]*University of Georgia, Athens*, [2]*PIC USA, Franklin, KY.*

Data on two purebred lines A (n = 6,022), B (n = 24,170), and their reciprocal cross C (n = 6,135) obtained from a commercial swine company was used to estimate genetic parameters using a crossbred model of Lo, Fernando, and Grossman. Genetic parameters were also estimated from within lines, as a check on procedure. The traits investigated were lifetime daily gain (LDG) and backfat. The models fitted included fixed (contemporary group and sex), random additive, random dominance, and random litter effects. For backfat, end weight was included as a covariable and the dominance effect was not fitted. Heritability estimates for LDG were .26, .29, and .23 for lines A, B, and C respectively, for within line models and .26, .30, and .29 for the crossbred model. For backfat the heritability estimates were .53, .38, and .27 from within line and .51, .38, and .32 from the crossbred model, for lines A, B, and C, respectively. Similarity of heritabilities across lines suggests that purebred and F1 data can be combined to improve accuracy of parameter estimates. The genetic correlations between purebreds and crossbreds (r_{pc}) for LDG were .62 (A-C), .80 (B-C); for backfat the r_{pc} estimates were .75 (A-C) and .71 (B-C). The estimated genetic correlations were $\leq$ .8 suggesting a possible benefit from combined evaluation of purebreds and crossbreds. The amount of dominance variance from the crossbred model expressed as a proportion of phenotypic variance for LDG was .21, .14, and .17 for lines A, B, and C, respectively. These estimates suggest mating systems can be designed to exploit non-additive genetic variation for LDG.

Key Words: Key Words: Multibreed Evaluation, Genetic Correlation, Crossbreds

287 **Joint evaluation of purebreds and crossbreds in swine: II. animal rankings.** E. Lutaaya[1], I. Misztal*[1], J. W. Mabry[1], T. Short[2], H. H. Timm[2], and R. Holzabauer[2], [1]*University of Georgia, Athens* , [2]*PIC USA, Franklin, KY.*

Data from two purebred swine lines A (n = 6,022), B (n = 24,170), and their reciprocal cross C (n = 6,135) was used to examine the gains in accuracy of combined purebred and crossbred evaluation using the crossbred model of Lo, Fernando, and Grossman over conventional within line evaluations. A second objective was to compare animal rankings from within line, approximate, and crossbred model evaluations. The traits in the evaluation were lifetime daily gain (LDG) and backfat. The gains in mean accuracy of predicted purebred breeding values for both traits ranged from 2 to 9% when crossbred information was included in evaluations using the crossbred model. Gains in mean accuracy of predicted breeding values of purebreds for crossbred performance ranged from 21 to 72% when crossbred data was used in genetic evaluations. Rank correlations of predicted breeding values from within line and crossbred models were high ($> .99$) for the purebreds, but were lower ($\leq .87$) for crossbreds. Rank correlations of predicted breeding values from approximate and crossbred models were high ($\geq .96$) and suggest that where variances are similar across lines, the approximate model can be used for genetic evaluation. It is concluded that the gains in accuracy of predicted purebred breeding values will be small with limited crossbred information. However, if the breeding goal is crossbred improvement, the gains in accuracy of predicted breeding values of purebreds for crossbred performance are substantial and warrant joint evaluation of purebreds and crossbreds, even with small amounts of crossbred data.

Key Words: Key Words: Multibreed Evaluation, Accuracy, Crossbreds

288 **Effects of recombination on weight from birth to 154 days of age in pigs.** J. P. Cassady* and K. A. Leymaster, *USDA-ARS; U.S. Meat Animal Research Center; Clay Center, NE.*

The objective was to determine the influence of nonadditive gene action on pig growth in two experiments. Experiment 1 (Exp1) included Yorkshire, Landrace, Large White, and Chester White pigs. Experiment 2 (Exp2) included Duroc, Hampshire, Pietrain, and Spot pigs. Data were recorded on purebred, two breed, and F_1 through F_6 generations, where F_1 pigs are the first generation of a four-breed cross. Pig weights were recorded at birth, 14, 28, 56, 70, 98, 126, and 154 d of age. Number of observations at birth and 154 d of age were 7,685 and 4,351 in Exp1 and 7,159 and 3,996 in Exp2, respectively. Data from each experiment were analyzed separately. A mixed-model analysis was done with fixed effects of year and sex and random effect of sire within year. Included as covariates in each model were effects of direct and maternal heterosis and an effect due to recombination in crossbred animals, which is the breakdown of epistatic effects present in purebreds. Models also included direct, maternal, and grandmaternal effects of each breed as covariates. Effects of direct heterosis increased ($P < .1$) weights at all ages in both experiments. In Exp1 effects due to recombination were negative ($P < .1$) for birth weight and positive ($P < .1$) for weight at 98 and 126 d of age. In Exp2 effects due to recombination were positive ($P < .1$) for weights at birth, 14, and 28 d of age. Recombination effects did influence pig weights at early ages in both experiments. Epistasis affects early pig growth and thus, may indirectly affect pig viability. Effects of recombination on birth weight were in opposite directions in the two experiments. Advances in molecular techniques may allow for selection of favorable epistatic effects.

Key Words: Pigs, Growth, Epistasis

289 **Predicting feed efficiency from associated traits in Duroc pigs selected for lean growth efficiency.** D. L. Kuhlers*, K. Nadarajah, and B. L. Anderson, *Auburn University, AL.*

Efficiency of feed utilization is an important economic concern in swine production but gathering individual feed consumption data for performance testing is a very expensive process. The objective of this study was to determine whether it is necessary to directly measure feed efficiency rather than only predicting it from genetic relationships with ultrasound backfat thickness (UBF) and 168 day weight (AWT168). The data used for this study were from six generations of selection in a line of Duroc pigs selected on an index giving equal weights to EBVs for UBF and predicted feed conversion (PFC) with a contemporary control line. In each generation, up to 40 randomly selected barrows from both lines (n=200, over six generations) were placed in individual pens at 35 kg BW and fed ad lib until they reached 105 kg BW. Information on feed intake, AWT168, F/G, days on feed (DOF) and real-time UBF at 10th rib were obtained. Performance of gilts and boars from both lines for 168d wt and UBF were also recorded. Data were analyzed using a multiple trait mixed model program (MTDFREML) applying genetic and residual (co)variances estimated from the data that included F/G on barrows to obtain EBVs for AWT168, UBF and F/G. The correlation between EBVs for PFC used in the selection index and EBVs computed for F/G from MTDFREML on 200 barrows was 0.93 (P<0.001). Compared to the control line pigs, the mean EBVs of select line pigs in the 6th generation showed a reduction in UBF by 0.71 cm and 23 kg less feed/100 kg of gain. A linear prediction of EBVs for F/G of barrows on test (R^2=0.77) showed significant influence of UBF (P<0.001), AWT168 (P<0.01) and DOF (P<0.05) whereas the actual individual F/G of barrows showed little influence (P=0.18) in predicting EBVs for feed efficiency. Correlation between EBVs for UBF and EBVs for F/G among the barrows was 0.89 (P<0.001), and a partial regression analysis (STEPWISE) indicated that UBF (R^2=0.61) had the largest single influence on F/G in pigs. It appears that direct measurement of F/G performance data contributes little to that already explained by UBF and AWT168.

Key Words: Pigs, Selection, Feed Efficiency

290 **Effect of IMF-level as affected by genotype, sex, slaughter weight and feeding level on pork quality and consumers'perception.** J.W.M. Merks*[1], P. Walstra[2], and E. Kanis[3], [1]*IPG, Institute for Pig Genetics B.V., Beuningen, The Netherlands,* [2]*Institute for Animal Science and Health, ID-Lelystad, The Netherlands,* [3]*Wageningen Institute of Animal Sciences, Wageningen University, The Netherlands.*

To test the effects of genotype (2 crossbred commercial types), sex (gilts and barrows), feeding level (ad libitum and restricted feeding) and slaughter weight (95 and 125 kg) on intramuscular fat percentage (IMF) in the loin meat and its consumers'appreciation, an experiment was set up with in total 470 pigs. Pigs were housed in groups of 8 per pen of only one genotype, sex and feeding level. All pigs in the pen were slaugtered when the average weight of 95 or 125 kg was reached. At 24 hours after slaughtering, carcasses were dissected into wholesale joints and measurements of pH and colour were taken. About 10 cm of the loin, next to the transition of ham and loin, of the left carcass half was used to measure drip loss and intramuscular fat (IMF). From in total 96 carcasses the left and right loin was classified according to level of IMF and used in a consumer test. In total 256 consumers were asked to give their opinion on various sensoric characteristics of 4 pieces of grilled loin. Statistical analyses showed significant (P< 0.05) effects of genotype, sex, slaughter weight and feeding level on IMF and pH. Drip loss and colour were only significantly affected by genotype and feeding level. The consumer appreciation test showed that variation in IMF had a significant effect on taste (especially for the characteristic 'real pork taste'), juiciness, tenderness and overall appreciation. Especially the low levels of IMF were evaluated as negative. Besides the level of IMF, the consumers' appreciation was affected by effects of genotype and feeding level but not by sex or weight. From these results it is concluded that the level of intramuscular fat is an important quality characteristic of pork which can be regulated by choice of genotype and feeding level during fattening. Especially low levels of IMF (below 1%) are a risk for the overall appreciation of pork.

Key Words: Intramuscular fat, Pork quality, Consumers' perception

291 Impact of measurement errors on predicting pork carcass composition. I. Within-sample evaluation.

D.L. Lofgren*, A.P. Schinckel, and T.S. Stewart, *Purdue University, West Lafayette, IN.*

Data were simulated for carcass weight (CW, mean=84 kg), fat depth (FD, mean=25 mm) and muscle depth (MD, mean=50 mm). Fat-free lean mass (FFLM, mean=38 kg) was calculated as FFLM = 4.64 + .459*CW - .442*FD + .117*MD + eij, where eij was a random deviation for the pig. Measurement errors for FD and MD were simulated for each pig: the deviation from the mean for FD and MD was reduced by 85, 70 and 55%, which reduced the covariance with FFLM; random error was added to maintain the level of variation in FD and MD. Random measurement errors for FD and MD had a correlation of -.50. The simulated data contained 900 lines, with 15 pigs/line from each of two sexes. The lines were divided into nine groups, based on line means for FD and MD. Subsets of the data were created by randomly selecting one line from each of the nine groups; 50 subsets were randomly chosen for analysis. Equations to predict FFLM from CW, FD and MD were derived for each subset. As the level of simulated measurement error increased, the R^2 of the prediction equations decreased, residual standard error increased, the intercept increased, and regression coefficients for CW, FD and MD became closer to zero. All of these statistics became more variable, and individual equations for a subset were very different. As errors increased, line and sex biases were seen, particularly with 70 and 55% measurement errors. Correlations between line means for actual and predicted FFLM decreased as errors increased. The equations were less able to detect true differences between lines and between sexes as measurement errors increased. Variance ratios (variance of predicted line means divided by variance in actual line means) averaged 1.00 for data without errors, and decreased to .55, .32 and .20 as measurement errors increased. Predicted differences between the sexes were 99% of the actual difference for data without errors, and decreased to 69, 46 and 30% as measurement errors increased.

Key Words: Measurement Errors, Pork, Carcass Composition

292 Impact of measurement errors on predicting pork carcass composition. II. Out-of-sample evaluation.

D.L. Lofgren, A.P. Schinckel, and T.S. Stewart*, *Purdue University, West Lafayette, IN.*

Data were simulated for carcass weight (CW), fat depth (FD) and muscle depth (MD). Fat-free lean mass (FFLM) was calculated. Measurement errors were simulated for each pig: the deviation from the mean for FD and MD was reduced by 85, 70 and 55%, which reduced the covariance with FFLM; random error was added to maintain the level of variation in FD and MD. Fifty subsets of nine lines, with 15 pigs/line from each of two sexes, were simulated. Prediction equations for FFLM were derived for each subset. A large dataset of slaughter pigs was simulated for an out-of-sample analysis to evaluate the efficacy of derived prediction equations. This had 40 lines, and 80 pigs/line for each of two sexes. Measurement errors were simulated for these pigs as they were for the estimation data. When the equations were developed using data without errors, and the slaughter pig data being evaluated was without errors, correlations between actual and predicted line means were .99, variance ratios (VR; variance of predicted line means divided by variance of actual line means) were close to 1, and the predicted difference between the sexes was 98% of the actual difference. With any measurement error, either in development of equations or in slaughter pig data evaluated, there were significant line and sex biases. Correlations between actual and predicted line means were high ($r>.81$). However, the equations were unable to predict the true line or sex differences. VR decreased approximately 30% with each increase in error level (in equation or pig data), so that with the highest level of errors, VR averaged .11. Sex differences decreased similarly, and predicted differences were 26% of actual differences when errors were highest. For a given level of measurement error in slaughter pig data, equations based on data with the least measurement error produced the least biases. Increased measurement error in the data used for equation development resulted in increased out-of-sample line and sex biases.

Key Words: Measurement Errors, Pork, Carcass Composition

293 Prediction of kilograms of boneless primal yield and standardized primal cuts in pigs.

H. Sellers*[1], T. J. Baas[2], and R. N. Goodwin[1], [1]*National Pork Producers Council, Ames, IA,* [2]*Iowa State University, Ames.*

Data from the National Pork Producers Council (NPPC) Quality Lean Growth Modeling project were used to develop prediction equations for estimation of the components of boneless primal yield (BPY) and total BPY, and standard primal cuts (SPY) and total SPY. Pigs representing six genetic types, four diet regimes, two sexes, three off test weight groups, and three test groups were included. Genetic types were chosen to represent high, medium, and low attributes of growth, feed intake, backfat, and meat quality. Pigs were evaluated with real-time ultrasound (SCAN) one week prior to slaughter at Quality Pork Processors in Austin, MN, where they were evaluated using four procedures: Fat-O-Meater developed by SFK Technologies (FOM); Carcass Value Technology system developed by Animal Ultrasound Services, Inc. (AUS); last rib midline ruler (RUL); and carcass measurement (CARC). Dissection data from 699 half carcasses were used and primals were cut according to the IMPS references. BPY is the sum of the following cuts: inside ham, outside ham, knuckle ham, loin, shoulder, belly, and spare ribs. SPY is the sum of Ham401, Loin410, Picnic405, Boston Butt406, Belly409, and Spare Ribs416. Prediction equations were developed for each cut and for total kilograms of lean. Model fixed effects were genetic type, diet, sex, and off test weight group. Model R^2 values ranged from .908 to .959 for SPY and .831 to .891 for BPY. The range in R^2 values for prediction equations for components of SPY was small. Best fitting equations for components of BPY were for FOM, CARC, and SCAN.

Key Words: Pigs, Prediction, Primal yield

294 Correlations among methods of estimation of kilograms of lean in pigs.

T. J. Baas*[1], H. Sellers[2], and R. N. Goodwin[2], [1]*Iowa State University, Ames,* [2]*National Pork Producers Council, Ames, IA.*

Data from the National Pork Producers Council (NPPC) Quality Lean Growth Modeling project were analyzed to determine correlations among four methods for estimation of kilograms of lean. Pigs representing six genetic types, four diet regimes, two sexes, three off test weight groups, and three test groups were included. Genetic types were chosen to represent high, medium, and low attributes of growth, feed intake, backfat, and meat quality. Pigs were slaughtered at Quality Pork Processors in Austin, MN, and evaluated using four evaluation procedures: Fat-O-Meater developed by SFK Technologies (FOM); Carcass Value Technology system developed by Animal Ultrasound Services, Inc. (AUS); last rib midline ruler (RUL); and carcass measurement (CARC). Dissection data from 699 half carcasses cut according to IMPS references were used to develop prediction equations for kilograms of standardized lean (SDLN), kilograms of standardized fat-free lean corrected for moisture content (FFLN), kilograms of boneless primal cuts (BLSP), and kilograms of standard primal cuts (SDSP). Model fixed effects were genetic type, diet, sex, and off test weight group. Ranges in Pearson correlation coefficients across the four prediction methods were: .857 to .994 (FOM); .933 to .996 (AUS); .927 to .997 (RUL); .831 to .993 (CARC). Prediction of SDLN was highly correlated to FFLN (FOM, .993; AUS, .996; RUL, .997; CARC, .993). Prediction of BLSP was highly correlated to SDSP (FOM, .994; AUS, .995; RUL, .997; CARC, .991). A strong relationship exists among the four prediction methods evaluated.

Key Words: Pigs, Lean, Prediction

295 Genetic parameter estimates for prolificacy, growth and fleece characteristics of Targhee sheep.

K. J. Hanford*[1], G. D. Snowder[2], and L. D. Van Vleck[3], [1]*University of Nebraska, Lincoln,* [2]*USDA, ARS, US Sheep Experimental Station, Dubois, ID,* [3]*USDA, ARS, US Meat Animal Research Center, Lincoln, NE.*

Heritabilities and genetic correlations for prolificacy, growth and fleece traits were estimated from Targhee data collected from 1950 to 1998. Number of records ranged from 33,978 to 38,625, 32,715 to 33,994, 3,341 to 36,807 for prolificacy, growth and fleece traits. Direct heritability estimates from single trait animal model analyses using REML were .10 for number lambs born (NB), .07 for number lambs weaned (NW), .10 for litter weight at weaning (LW), .25 for birth weight (BW), .22 for 120 d weight (WW), .41 for fleece grade (FG), .54 for fleece weight (FW) and .65 for staple length (SL). Maternal heritability estimates were .20 for BW and .11 for WW. Estimates of genetic correlations among prolificacy traits were positive (.77 for NB-NW, .72 for NB-LW, .94 for NW-LW). Between BW and WW both the direct and maternal genetic correlations were positive (.52 for direct and .35 for maternal). FG was negatively correlated with both FW (-.47) and SL (-.69), and FW was positively correlated with SL (.54). Estimates of genetic correlations were small between the prolificacy and growth traits, except for the correlation between LW and WW, which was moderately correlated (.00, .00, .18, .20, .15, .38 for NB-BW, NW-BW, LW-BW, NB-WW, NW-WW and LW-WW). Estimates of genetic correlations were small between fleece characteristics and prolificacy traits: for FW (-.19, -.19, .04), for FG (.09, .11, .00) and for SL (-.14, .05, .09) with NB, NW and LW, respectively. Growth traits were positively correlated with FW and SL (.24, .24, .10, .08 for BW-FW, WW-FW, BW-SL and WW-SL), and negatively correlated with FG (-.06, -.05 for BW and WW).

Key Words: Heritabilities, Genetic Correlations

296 Genetic parameter estimates for prolificacy, growth and fleece characteristics of Columbia sheep.

K. J. Hanford*[1], G. D. Snowder[2], and L. D. Van Vleck[3], [1]*University of Nebraska, Lincoln*, [2]*USDA, ARS, US Sheep Experimental Station, Dubois, ID*, [3]*USDA, ARS, US Meat Animal Research Center, Lincoln, NE.*

Heritabilities and genetic correlations for prolificacy, growth and fleece traits were estimated from Columbia data collected from 1950 to 1998. Number of records ranged from 27,009 to 31,401, 23,903 to 24,741, 2,449 to 29,572 for prolificacy, growth and fleece traits. Direct heritability estimates from single trait animal model analyses using REML were .09 for number lambs born (NB), .06 for number lambs weaned (NW), .07 for litter weight at weaning (LW), .27 for birth weight (BW), .16 for 120 d weight (WW), .41 for fleece grade (FG), .53 for fleece weight (FW) and .55 for staple length (SL). Maternal heritability estimates were .25 for BW and .08 for WW. Estimates of genetic correlations among prolificacy traits were positive (.84 for NB-NW, .79 for NB-LW, .94 for NW-LW). Between BW and WW both the direct and maternal genetic correlations were positive (.56 for direct and .58 for maternal). FG was negatively correlated with both FW (-.47) and SL (-.70); FW was positively correlated with SL (.55). Estimates of genetic correlations were low between BW and the prolificacy traits (.10, .00, .11 for NB, NW, and LW) and moderate between WW and the prolificacy traits (.33, .24, .73 for NB, NW, and LW). Estimated genetic correlations were small between fleece characteristics and prolificacy traits: for FW (-.13, -.14, .08), for FG (.17, .04, .00) and for SL (-.05, -.20, -.05) with NB, NW and LW, respectively. Growth traits were positively correlated with FW (.21, .18 for BW and WW); negatively correlated with FG (-.04, -.11 for BW and WW) and SL was positively correlated with BW (.05) and negatively correlated with WW (-.04).

Key Words: Heritabilities, Genetic Correlations

297 Genetic parameter estimates for growth characteristics in a local sheep flock in United Arab Emirates.

S. Al-Shorepy*[1], *United Arab Emirates University, Al Ain, united Arab Emirates.*

Variance and covariance components and associated genetic parameters were estimated for lamb birth weight (BWT), daily gain from birth to weaning (ADG) and weaning weights (WWT) using REML procedures and single- and two-trait animal models. Data in this study were the accumulated records over the years 1994 to 1999 obtained from the Faculty of Agricultural Sciences Experimental Station, United Arab Emirates. It consisted of weight registrations of local purebred and of crossbred (>87% local purebred) lambs. The analytical model included fixed effects of sex, year-season, type of rearing and (for the combined data set) breed. The most complete model also contained random additive, additive maternal, permanent environmental maternal and residual effects. The analyses were conducted for the three data sets. Estimates of additive direct, additive maternal, and permanent environmental maternal effects, respectively, as a proportion of phenotypic variance for combined data were .30, .19, .03 (BWT); .44, .04, .01 (ADG), and .40, .03, .01 (WWT). Estimates of genetic correlations were .25 (BWT with ADG); .46 (BWT with WWT); and .92 (ADG and WWT). Residual correlation estimates ranged from .12 (BWT with ADG) to .96 (ADG and WWT). Correlations between additive maternal effects and permanent environmental maternal effects for BWT and WWT were close to unity. It can be concluded that, additive maternal effects were more important for birth weight trait than for the other two traits. Additive and permanent environmental maternal effects on BWT and WWT were highly correlated, indicating that many of the same genes and factors are involved.

Key Words: Local Sheep, Genetic parameters, Growth traits

298 The genetic components of dietary selection for Mountain Big Sagebrush (*Artemisia tridentata ssp. vaseyana*) in Rambouillet sheep.

G. D. Snowder*[1], J. W. Walker[2], K. L. Launchbaugh[3], and L. D. Van Vleck[4], [1]*USDA, ARS, U.S.Sheep Experiment Station, Dubois, ID*, [2]*Texas A&M University Agricultural Research and Extension Center, San Angelo*, [3]*University of Idaho, Moscow*, [4]*USDA, ARS U.S. Meat Animal Research Center, Lincoln, NE.*

The heritability of diet selection for big sagebrush by grazing sheep was estimated from fecal samples from a total of 549 Rambouillet ewes. Fecal samples were collected in September and October during 1996 and 1997 from free-grazing ewes on intermountain sagebrush-bunchgrass rangelands at the U.S. Sheep Experiment Station in Idaho. The total number of fecal samples was 1,949. Fecal samples were evaluated for composition of big sagebrush by near-infrared spectroscopy. Big sagebrush consumption was less in September than October (21.6 vs 31.7%, respectively). Single trait and bivariate derivative-free REML analyses were performed to genetically compare big sagebrush consumption between September and October. Heritability estimates were similar between September and October sampling (.25 and .28, respectively). The genetic correlation between September and October diet preference was high (rG = .91), inferring that there is a strong genetic similarity between September and October measurements. These results contribute to a greater understanding of dietary preferences in free grazing sheep, and suggest opportunities to improve production efficiency and forage management through selection for dietary preferences.

Key Words: Diet Selection, Sheep, Grazing

299 Heritability estimates for electrical conductivity of milk and correlations with predicted transmitting abilities for somatic cell scores.

R.C. Goodling*[1], G.W. Rogers[1], J.B. Cooper[1], and B. Rune[2], [1]*Pennsylvania State University, University Park*, [2]*SAE Afikim, Kibbutz Afikim, Israel.*

Electrical conductivity of milk (EC) increases during mastitis and can be routinely measured during each milking of dairy cattle. The objectives of the study were to estimate heritabilities for EC and to examine the relationship between sire PTASCS and daughter means of EC in various lactation segments. The Afikim computerized milking and management system measures composite EC in millimho (mmho) during milking and records daily averages for EC. Analyses were performed on 3503 cows sired by 259 bulls in eight herds. Heritabilities for EC were determined using the PROC MIXED procedure of SAS® with a model that included herd-year-season, age at calving, and sire. Heritabilities for lactation 1 were moderate: 0.36 for the EC mean over the lactation, 0.38 for days in milk (DIM) 6 to 100, 0.39 for DIM 101 to 200, and 0.27 for DIM 201 to 365. Heritabilities for EC for lactation 2 were also moderate: 0.22 for the mean over the lactation, 0.22 for DIM 6 to 100, 0.23 for DIM 101 to 200, and 0.21 for DIM 201 to 365. Sire solutions for mean EC over lactations 1 and 2 were correlated with sire PTASCS from USDA; correlations based on sires with 20+ daughters were 0.30 (lactation 1) and 0.46 (lactation 2). In addition, daughter EC was regressed on sire PTASCS. Bulls with higher PTASCS had daughters with significantly higher EC. The positive correlations and moderate heritabilities from this study indicate that EC might be useful in selecting for mastitis resistance in dairy cattle.

Key Words: Conductivity of Milk, Heritability, Mastitis Resistance

300 Estimates of genetic parameters for linear type traits, yield traits, and somatic cell scores in Holsteins divergently selected on transmitting ability for type.

B. J. DeGroot*[1], J. F. Keown[1], and L. D. Van Vleck[2], [1]*University of Nebraska, Lincoln*, [2]*USDA, ARS, US Meat Animal Research Center, Lincoln, NE*.

For four generations, half of the university research Holstein herd was bred to Holstein sires with predicted transmitting ability for type (PTAT) > 1.50 and the remainder to sires with PTAT < 1.25, with nearly equal PTA for yield traits for both groups. Data on first lactation cows for 16 linear type traits, final score, and milk, fat, and protein lactation yields were collected from 1986 to 1999 and on somatic cell scores (SCS) from 1992 to 1999. Estimates of heritabilities, genetic correlations, and phenotypic correlations were obtained from REML estimates of (co)variance components. Fixed effects were date cows were classified, age in days at freshening as a linear covariate, and days in lactation at classification as linear and quadratic covariates in model for type and year-season in which a cow freshened in model for yield and SCS. Animal genetic and residual were random effects. Heritability estimates for linear type traits ranged from 0.04 to 0.47. Final score, and milk, fat, and protein yields had heritability estimates of 0.38, 0.13, 0.22 and 0.09, respectively. Heritability estimate of SCS was 0.38. Estimates of genetic correlations among linear type traits ranged from -0.79 to 1.00 and of phenotypic correlations ranged from -0.27 to 0.84. Estimates of genetic correlations of final score with SCS and milk, fat, and protein yields were -0.68, 0.04, -0.16, and 0.10, respectively. Phenotypic correlations of final score with SCS and milk, fat, and protein yields were -0.16, 0.17, 0.10, and 0.22, respectively. The genetic correlation between final score and SCS suggests that selection for increased final score would decrease SCS, whereas, the correlations between final score and yield traits suggests that selection for increased final score would result in little change in yield traits.

Key Words: Genetic Correlations, Heritability, Dairy Cattle

301 Prediction of breeding value for milk, fat and protein yield based on endocrine response profiles.

M.K. Soerensen*, P. Madsen, K. Sejrsen, M. Vestergaard, and P. Lovendahl, *Danish Institute of Agricultural Sciences, Denmark*.

The objective of the study was to relate a number of endocrine variables measured in juvenile cattle to their breeding value for yield. With the view to develop early selection criteria for improved dairy cattle breeding schemes. Dairy bull (N=452) and heifer (N=372) calves from the Danish MOET scheme were tested as juveniles (age 9 month) with a panel of endocrine challenge tests. Prior to testing, calves were fed at maintenance for 7 days and fasted overnight. On the day of testing blood plasma was sampled serially before and following intravenous administration of GRF, adrenaline and glucose. Response to GRF was measured as bovine GH before and following challenge, and as degradation rate. Likewise response to adrenaline was observed in glucose and free fatty acids; and for the glucose tolerance test, as glucose degradation rate, and insulin peak. Most heifers (N=316) from the program stayed in the MOET herd and had at least one lactation there. The data set for milk yield included these heifers plus 816 herd mates. Among the bull calves from the experiment, 142 were progeny tested in Denmark. Daughter yield deviations (DYD) from these bulls and 5200 contemporaries were evaluated. Genetic parameters were estimated using a multivariate animal model. The heritability of GH variables was already high (h2=0.76) in heifers before GRF but low (h2=0.10) in bulls. Following GRF, the heritability was high in both gender groups (heifers h2=0.57, bulls h2=0.41). Also GTT helped increasing heritability of insulin in both sexes. In general genetic correlations between variables measured in bulls and heifers approached unity. Correlations between endocrine variables and yield in the MOET herd and daughter yield deviations were largely in agreement. Based on these parameters it is possible to combine an ”endocrine” index with a correlation of 0.42 to yield traits. The experiment confirm that it is possible to speed up genetic progress for yield in advanced dairy nucleus breeding schemes using endocrine response profiles.

Key Words: Endocrine response, Dairy cattle, Genetic parameters

302 Value of bull fertility computed from many states: its effects in single states.

B.T. McDaniel*, J.S. Clay, and C.H. Brown, [1]*North Carolina State University, Raleigh*.

Objectives were to determine how well Estimated Relative Conception Rates (ERCR) computed from 1.4 million records reported by herds in over 30 states predicted non-return rates in lactating Holstein cow mates in various subsets. Bulls with ERCRs higher than 2.9 were coded as High and those lower than -2.9 were Low. Others were denoted as Average. Cow values were adjusted for herd-year, early lactation Energy Corrected Milk (ECM), parity and days in milk when inseminated for the first time. Subsets were cows only in NC and cows only in VA. Both were further subdivided by month bred. In 22 of the 24 subsets cows mated to High bulls had the highest non-return rate. Superiorities averaged 10 units over Low bulls (range 0 to 18) and three units over Average ones (range -2 to 10). Effects of cow ECM were significant but much less than those of mating bulls. Results show that ERCR computed from herds in many areas of the US is useful in predicting non-return rates in herds in a single state-month subclass. Most if not all producers will improve non-return rates of similar cows by breeding them to bulls with High ERCRs while use of Low ERCR bulls will result in lower non-return rates.

Key Words: Bull Fertility, Non-return Rate, Holsteins

303 Genetic parameters of udder, mastitis and milk traits in two different climatic area using animal model analysis.

A.A. Amin*[1] and T. Gere[2], [1]*Suez Canal University, Faculty of Agriculture, Department of Animal Production, Ismailia-Egypt*, [2]*Godollo University of Agriculture Sciences, Gyongyos College of Agriculture*.

Lactation records of 2567 Holstein-Friesian (HF) cows in Egypt (subtropical area) and Hungary (rainy area) were used to detect any effect of drought on changing genetic parameters. Traits studied were udder length and depth, teat length, attachment and placement and milk production traits (total milk, fat and protein yield). Variation in all studied traits due to random effects of sires groups was much higher in the rainy area than in the subtropical one. Change of all genetic (co) variances with advancing order of lactation were greater for subtropical animals. In subtropical heritability estimates of udder traits for HF were higher than estimates for milk production and the their differences were also higher than the corresponding estimates of cold rainy area. Low heritability estimate was computed for mastitis infection for Hungarian HF. Highest genetic and phenotypic correlation (-0.67 and -0.87, respectively) for mastitis with udder depth were recorded in subtropical area. Many details concerning genetic parameters, which could be taken into consideration during planning and carrying out phenotypic and genetic selection for improving total economic benefit of dairy farms were tabulated and discussed.

Key Words: Udder conformation, Mastitis and milk production, Genetic parameters

304 Studies on genetics of heat tolerance in dairy cattle with reduced weather information via cluster analysis.

O. Ravagnolo and I. Misztal, *The University of Georgia, Athens*.

One of the limiting factors in dairy production in hot climates is heat stress. Under heat, animals produce less and have lower reproduction rates. The genetic components of heat tolerance in Holstein cattle in Georgia were previously studied by combining test data and use of weather information from 21 weather stations throughout the state. The assignment of a weather station to each herd was done manually and was laborious. With data from multiple states, matching herds and weather stations may become even more difficult. The objective of this study was to explore the possibility of reducing the number of weather stations for studies on heat tolerance. Similarity of information from Georgia weather stations was analyzed by cluster analysis. Two major clusters have been found, separating Georgia into North and South along the NE-SW line. One weather station was selected for each of the clusters based on the minimal distance to all the remaining weather stations and completeness of the weather information. The final data set consisted of 114751 first-parity test-day records on 14297 Holsteins from 120 herds in Georgia. Analyses using a model for daily milk yield with temperature humidity index (THI) classes and several other fixed effects showed no increase in Error Sum of Squares when using only two

weather stations. Average daily production was relatively constant at 60 lb. The threshold point at which production started to decline was 72 THI with all weather stations, 72 THI with one station and data corresponding to northern Georgia, and 76 THI with one station and data corresponding to southern Georgia. The rate of decline after the threshold was about .27 kg/ unit THI in all cases. Studies on heat tolerance based on information from only a few weather stations can be done without a significant decrease of accuracy. An additional increase of accuracy can be obtained by accounting for a different onset of heat stress within each station.

Key Words: Heat Tolerance, Dairy cattle, THI

305 Overview of progeny-test programs of artificial-insemination organizations in the United States.

H.D. Norman*[1], R.L. Powell[1], J.R. Wright[1], and C.G. Sattler[2], [1]*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD* [2]*National Association of Animal Breeders, Columbia, MO.*

Characteristics of progeny-test (PT) programs of US artificial-insemination (AI) organizations were examined for changes since 1959 by breed and sampling year: 1) bull age at semen distribution, daughter birth, and daughter calving; 2) sire, dam, and maternal grandsire age at bull birth; and 3) numbers of PT daughters and herds. State trends were documented for 1) PT participation, 2) percentage of cows that were PT daughters, and 3) percentage of PT daughters that were enrolled in a breed registry herdbook. Mean number of bulls progeny tested by major AI organizations annually from 1996 through 1998 was 10 for Ayrshires, 21 for Brown Swiss, 20 for Guernseys, 1248 for Holsteins, 105 for Jerseys, and 3 for Milking Shorthorns. Mean ages of ancestors at bull birth decreased across time and were 85 mo for sire, 48 mo for dam, and 136 mo for maternal grandsire for Holsteins recently progeny tested; corresponding ancestor ages for Jerseys were 78, 49, and 131 mo. Mean bull age at semen distribution was 16 mo; mean bull ages at daughter birth and calving decreased across time and were 29 and 56 mo (Holsteins) and 32 and 58 mo (Jerseys) for 1992 through 1994, the most recent complete PT years. Mean numbers of PT daughters and herds were 65 and 44 for Holsteins and 48 and 30 for Jerseys. For Holstein bulls that entered AI service in 1994, 22% of PT daughters were in California, 13% in Wisconsin, 12% in New York, and 10% in Pennsylvania and Minnesota. Percentage of first-lactation cows that were PT daughters has increased over time; was 15% overall in 1994; and varied from 4 to 25% for states with >500 cows. Percentage of PT daughters enrolled in breed registry herdbooks was 24% for Holsteins and 78% for Jerseys in 1998. The dairy industry has been able to reduce the PT generation interval by selecting younger parents of PT bulls and by distributing and using semen more quickly.

Key Words: Artificial insemination, Progeny test, Sire sampling

306 Characterization of dairy production systems in Interbull member countries.

K.A. Weigel and N.R. Zwald*, *University of Wisconsin, Madison.*

The objective of the study was to examine and describe the characteristics of dairy productions systems in countries that participate in international sire evaluations, and to identify the factors that cause lactation performance of a sire's progeny to differ between countries. Test day data from first lactation Holstein cows in Canada, USA, Finland, Israel, Czech, Ireland, Switzerland, Belgium, Austria, and Estonia were used. These data included 95,149 herds, 6,824,413 cows, and 58,862,259 test day records from cows calving between 1/1/90 and 12/31/97. Average herd size ranged from 10 cows in Finland to 203 cows in Israel. Peak yield was highest in Israel at 35.6 kg and lowest in Estonia 16.9 kg. Days to peak yield were 85 days in Israel compared to 10 days in Estonia. Percentage of cows still in milk at 280 days varied from 78 percent in Belgium to 42 percent in Ireland. Median days in milk ranged from 271 days in Ireland to 317 days in Belgium. Persistency was defined as the ratio of average amount of milk at 260 days to average amount of milk at 60 days. It varied from 0.863 in Isreal to 0.627 in Ireland. Other factors, such as temperature, humidity, genetic composition of the mates, etc. also differs widely between countries and between herds within a country. Currently, differences in production systems between countries are taken into account in international sire evaluations. However, variation in management or climate within countries is ignored, and future research should focus on identifying and prioritizing the factors that cause genetic correlations to be less than one between environments. It may then be more reasonable to define traits based on knowledge of the production environment in each herd, as opposed to defining traits based on political boundaries.

Key Words: International evaluation, Interbull, Genotype by Environment interaction

307 A comparison of Holstein Friesian cows from the Northern Hemisphere and New Zealand grazing pasture or fed a total mixed ration.

E.S. Kolver*[1], A.R. Napper[1], and L.D. Muller[2], [1]*Dairying Research Corporation Ltd., Hamilton, New Zealand,* [2]*Pennsylvania State University, University Park.*

During the last decade the use of Northern Hemisphere (NH) Holstein Friesian (HF) genetics internationally has been high. Countries such as New Zealand (NZ) use a dairy production system which is different from that in which the United States/Netherlands HF genotype was originally selected. This study compared the performance of NH and NZ HF dairy cows on an all-pasture diet in a seasonal calving system. Genotype x diet interactions were investigated during the year-long study by comparing primiparous cows fed either an all-pasture diet (Grass) or a TMR of corn silage, grass silage, and concentrate. The four treatments in this 2 x 2 factorial experiment were NZ Grass (n=14); NH Grass (n=9); NZ TMR (n=15); and NH TMR (n=10). Each treatment represented eight sires and had the same genetic merit. Compared with NZ HF, NH HF had a higher body weight and produced more milk, but milksolids yield (fat + protein), efficiency of milksolids production, and persistency of lactation were not significantly different. Compared with HF fed Grass, HF fed TMR produced more milk and milksolids, were more efficient, had a greater persistency of lactation, and ended lactation with a greater body weight. An important result was the inability of NH Grass to gain body weight, despite a generous pasture allowance. NH Grass ended lactation weighing 77 kg less than at pre-calving, whereas NZ Grass weighed 5 kg less. Compared with the NZ HF genotype, the high genetic merit NH HF produced the same yield of milksolids, but failed to maintain body weight in an all-pasture system.

Genotype (G)	NZ	NZ	NH	NH		P<	
Diet (D)	Grass	TMR	Grass	TMR	G	D	G x D
Milk, kg	3317	5036	3597	5898	<0.01	<0.001	ns
Milksolids (MS), kg	281	380	271	401	ns	<0.001	ns
Efficiency, kg MS/ kg $BW^{0.75}$	3.11	4.0	2.74	3.82	ns	<0.001	ns
Decline in milk, %/ month	10.4	5.9	9.5	4.8	ns	<0.001	ns
Body weight at season end, kg	434	501	464	575	<0.001	<0.001	ns
Body weight change, kg	-5	61	-77	56	<0.01	<0.001	<0.01

Key Words: Holstein, Genotype, Diet

308 Associations between liability to clinical mastitis and culling in Norwegian cattle.

B Heringstad*[1], R Rekaya[2], D Gianola[2], G Klemetsdal[1], and K.A. Weigel[2], [1]*Department of Animal Science, Agricultural University of Norway, Ås, Norway,* [2]*Department of Dairy Science, University of Wisconsin, Madison.*

A Bayesian bivariate threshold model with Gibbs sampling was used to study associations between liability to mastitis and culling in Norwegian Cattle. The two traits were clinical mastitis (CM) and culling (CU), scored as binary, based on whether or not a cow had at least one case of CM during an "opportunity" period (OP), and whether or not the cow was culled before the end of the OP. Two OP were considered: from 30d before calving to either 120d or 300 d postpartum. Data were from 13,070 first-lactation daughters of 250 sires in 1868 herds. The bivariate linear model for liabilities to CM and CU included age x season of calving, herds (random), sires (random, 482 bulls in pedigree) and a residual. The posterior mean (SD) of heritability of CM was 0.08 (0.02) for both OP. Heritability of culling was 0.01 (0.01) for 120 d and 0.02 (0.01) for 300 d. Posterior means (SD) of genetic, herd and residual correlations between CM and CU were: 0.48 (0.24), -0.10 (0.07) and

0.19 (0.02), respectively, for 120d, and 0.53 (0.21), -0.22 (0.07) and 0.10 (0.02) for 300d. Estimates were similar when the correlation between herd effects on CM and CU was 0. Culling before the end of the OP may produce bias in analyses of CM, and a bivariate analysis of CM and CU is one way of taking this into account.

Key Words: Clinical mastitis, Dairy cattle, (Co)variance components

309 Genetic correlation between fertility and body condition score (change), scored during type classification.

R. F. Veerkamp*[1], E. P. C. Koenen[2], and G. de Jong[2], [1]*ID-Lelystad, The Netherlands*, [2]*NRS, The Netherlands.*

Twenty type classifiers have visually scored body condition (BCS) of over 150,000 first lactation heifers since Oct. 1998. The objective of this study is to estimate the genetic correlation between (change in) body condition score and fertility. Insemination records were retrieved for all heifers calving between Oct. 1997 and Jan. 1999 for 601 sires that had daughters with BCS in this period (n=70,010). Days till first service (DFS) and inter calving interval (CIV) were derived from calving and insemination dates (n=338,653 and 124,086, respectively). First service conception (FSC) was scored as zero when cows had more than one service, as one when cows had only 1 service and a next calving, and missing for al others (n= 238,825). Genetic correlations of DFS, CIV, and FSC with both level and change of BCS were estimated using a random regression sire model. Fixed effects included were for all traits: breed group, year-month of calving, herd, and a quadratic regression on age at calving; for BCS were added: classifier, and a cubic regression on DIM of scoring; for FSC DIM at first service was added. Heritability of BCS was 0.29. For DFS, CIV and FSC the heritabilities were 0.06, 0.06, and 0.03, and the genetic correlations with level of BCS were -0.49, -0.39 and 0.37, respectively. Correlations with the slope for BCS were 0.11, 0.15 and -0.26 for the fertility traits, respectively. Hence, body condition score is an easy to measure predictor of genetic merit for fertility, as a lower level of body condition score is genetically associated with poorer fertility.

Key Words: Body condition score, Fertility, Heritability

310 Genetic and phenotypic correlations between body condition scores and productive and reproductive performance.

C.D. Dechow*[1], G.W. Rogers[1], and J.S. Clay[2], [1]*Pennsylvania State University, University Park*, [2]*Dairy Record Management Systems, Raleigh, NC.*

The objectives of this study were to describe the genetic and phenotypic relationships among body condition scores (BCS), production traits and reproductive performance. Producer recorded BCS at calving, postpartum, pregnancy check, and at dry off were provided by Dairy Records Management Systems in Raleigh, NC through the PCDART program. After edits, 27,813 cows had BCS available at one or more periods in first lactation, while 20,952 cows had BCS available in second lactation. Mature equivalent (ME) milk, days to first service (DFS) and services per conception (SPC) were available. Genetic and phenotypic correlations were estimated assuming an animal model using Derivative Free REML. Herd-year-season effects and age at calving were included in all models. The prior calving interval was included in models for second lactation. Analyses that included reproductive traits were conducted with and without ME milk as a covariable. The genetic correlation between BCS at calving and ME milk was 0.02 in first lactation and 0.27 in second lactation. Genetic correlations between ME milk and BCS at periods other than calving ranged from 0.23 to 0.43. Phenotypic correlations between BCS and ME milk were near 0 at calving and were negative at all other periods. After adjustment for ME milk, genetic correlations between BCS and DFS ranged from 0.09 to 0.72. Phenotypic correlations were negative and small in both lactations. Genetic correlations between BCS and SPC at calving were positive. Genetic correlations between BCS at periods other than calving and SPC were near 0 in first lactation, and were negative in second lactation. Most phenotypic correlations were near 0, but were positive between BCS at dry off and SPC. Higher BCS during the lactation were negatively related to production both genetically and phenotypically, but the relationship was moderate. Higher BCS during the lactation were genetically associated with improved reproductive performance.

Key Words: Body Condition Score, Correlations, Reproduction

311 Impact on body weight of divergent selection for body size.

B.J. Heins*[1], L.B. Hansen[1], A.J. Seykora[1], and G.D. Marx[2], [1]*University of Minnesota, St. Paul, MN*, [2]*Univesity of Minnesota, Crookston ,MN.*

Body weights of Holstein cows selected for small and large body size from the Northwest Research and Outreach Center and Pedigree Indexes (three generations of sires) for standardized transmitting abilities (STA) of type traits from Holstein Association USA were compared. Body weights (kg), pre-adjusted for age at calving, were measured for 359 first-lactation cows (1983-1994). Correlations between body weight and a single or composite STA were: stature (.48), strength (.48), body depth (.48), udder depth (.39), stature + strength (.49), stature + body depth (.48), and Minnesota Index ((2*stature + strength + body depth)/4, .48). Body weights were regressed on each individual STA and each combination STA. R-squares were stature (.23), strength (.23), body depth (.23), udder depth (.15), stature + strength (.23), stature + body depth (.23), and Minnesota Index (.23). The regression coefficient for the Minnesota Index was 8.0 kg. Multiple regression coefficients for stature and strength were 2.26 kg (stature) and 5.83 kg (strength) and for stature, strength and body depth were 3.73 kg (stature), 11.09 kg (strength), and -7.20 kg (body depth). Alternative weights on stature and strength were examined: 1:1, 1:2, 1:3, 1:4, 1:5, and 1:2.5. The highest R-square (.236) was for 1(stature):2.5(strength), compared to .233 for the Minnesota Index. An increase of one STA for Pedigree Index for the Minnesota Index resulted in an increase of 8.0 kg of body weight for first-lactation cows immediately postpartum. Body size for lines differed by 52.2 kg immediately postpartum at first calving, 68.0 kg at second calving, and 79.4 kg at third calving. The regression analysis suggests that one STA for the Minnesota Index would equate to 8.0 kg difference for first lactation, 10.3 kg for second lactation, and 12.2 kg for third lactation; therefore, the mean of one STA for the first three lactations was about 11kg. Active AI sires have STA for the size traits that range from roughly -1.5 to +3.5, which is a range of 5 STA, and corresponds to a 55 kg difference in body size. The increase over time of Pedigree Index for size of the large line demonstates a trend of increased body size of US Holsteins.

Key Words: body size, genetics, STA

312 Smoothing splines estimation of genetic variation in glucocorticoid-induced down-regulation of adhesion molecules in bovine neutrophils.

R. J. Tempelman*[1], P. M. Saama[1], A. E. Freeman[2], S. C. Kelm[2], A. L. Kuck[3], M. E. Kehrli, Jr.[4], and J. L. Burton[1], [1]*Department of Animal Science, Michigan State University, East Lansing* [2]*Department of Animal Science, Iowa State University, Ames*, [3]*Genex, Inc., Shawano, WI*, [4]*USDA-ARS, National Animal Disease Center, Ames, IA.*

Neutrophils use a variety of leukocyte and endothelial cell adhesion molecules to contact the vascular endothelium and migrate through it into sites of infection and inflammation. Previous work has shown that neutrophil CD62L and CD18 expression are sensitive to glucocorticoids, stress hormones that impair neutrophil migration and increase disease susceptibility in cattle and other animals. Our current objective was to assess genetic variation for neutrophil sensitivity to glucocorticoids. Smoothing splines mixed effects models were used to estimate genetic and non-genetic sources of variation for neutrophil expression of CD62L and CD18 before, during, and after three consecutive days of dexamethasone administration (0.04 mg/kg/d) to 60 registered Holstein artificial insemination bulls. Dexamethasone generally caused the predicted down-regulation of both adhesion molecules in this study. Heritability estimates (h^2) for CD18 expression were not influenced by dexamethasone administration and were relatively moderate in size (0.12-0.34) across days. Heritability estimates for CD62L expression, however, were influenced by dexamethasone administration, which exposed substantially greater additive genetic variation ($h^2 = 0.20$) in this phenotype compared to pre-treatment responses ($h^2 = 0.02$). When CD62L expression was measured as the percentage of neutrophils with detectable CD62L, heritability estimates were as high as 0.61, but precipitously fell after dexamethasone treatment to a low of 0.03 during recovery from dexamethasone-induced down-regulation. These results imply that genetic selection for neutrophil expression of adhesion molecules and their sensitivity to glucocorticoids may be possible.

Key Words: Health, Heritability, Leukocyte adhesion molecules

313 Relationships among calfhood diseases and sire transmitting abilities for measures of immune function.

D. L. Nash*[1], A. E. Freeman[1], A. L. Kuck[2], S. A. Schnell[2], and M. E. Kehrli, Jr.[3], [1]*Iowa State University, Ames*, [2]*GENEX*, [3]*NADC-USDA-ARS, Ames, IA.*

The objectives of this study were to determine the relationships between daughter diseases recorded during calfhood and sire transmitting abilities for measures of immune function. Fifty-four post-pubertal Holstein bulls awaiting progeny test were treated with dexamethasone to allow their immune systems to mimic the periparturient immunosuppression experienced by dairy cows. Fifteen in vitro tests of immune function were performed on these 54 bulls the week before, during, and after dexamethasone induced immunosuppression. Transmitting abilities were estimated for each test of immune function. Disease incidences and treatment data were recorded from birth through one year of age on 2968 progeny test daughters (in 505 herds in Wisconsin, Minnesota, and Iowa) of these bulls. A total of 73 calves (3%) had scours and 43 calves (1%) had pneumonia. All diseases combined were experienced by 139 calves (5%). Incidence of scours, pneumonia, and all diseases (binary variables) were regressed on herd, season of birth, age (in days) when the disease occurred (measure of time at risk), and sire transmitting abilities for measures of immune function taken one at a time. Logistic regression was used to estimate odds ratios. Daughters of sires that transmit higher antibody dependent neutrophil cytotoxicity had higher incidence of all diseases (odds ratio was 6.3, P = 0.07). Other sire transmitting abilities for measures of immune function were not significantly associated with daughter diseases measured during the first year of life. However, disease incidences were low, making it difficult to detect relationships.

Key Words: disease, immune function, sire transmitting abilities

314 Genotype x environment interactions in milk yield and quality in Angus, Brahman, and reciprocal-cross cows on different forage systems.

M. A. Brown*[1], A. H. Brown, Jr.[2], W. G. Jackson[3], and J. R. Miesner[3], [1]*USDA-ARS, El Reno, OK*, [2]*University of Arkansas, Fayetteville*, [3]*USDA-ARS, Booneville, AR.*

Milk yield and quality were observed on 93 Angus, Brahman, and reciprocal-cross cows over three years to evaluate the interactions of direct and maternal breed effects and heterosis with forage environment. Forage environments were common bermudagrass (BG), endophyte-infected tall fescue (E+), and a rotational system of both forages where each forage (BG or E+) was grazed at appropriate times of the year (ROT). Milk yield (MY) was estimated each of six months (April-September) by method of milking machine and converted to a 24-h basis. Milk fat (MF), milk protein (PRO), and somatic cell count (SCC) were measured by a commercial laboratory. The natural log of SCC was used for analyses. Heterosis for 24-h MY was large and similar among forages, averaging 2.4 kg ($P<.01$). There was little evidence of maternal effects for MY for any forage. Direct effects for MY were similar among forages and averaged 2.2 kg in favor of Brahman ($P<.10$). There was little evidence of heterosis or maternal breed effects for MF. Direct breed effects for MF were similar across forages and averaged .86% in favor of Brahman ($P<.01$). There was little evidence of direct or maternal breed effects for PRO nor was there evidence of forage effects for this trait. Purebred cows exceeded crossbreds in PRO by .13% on ROT ($P<.10$). Crossbred cows had lower SCC than purebreds on E+ ($P<.10$) but heterosis on BG and ROT was not significant. Maternal breed effects for SCC favored the Brahman dam on BG ($P<.05$) but not on E+ or ROT. Direct breed effects for SCC were small and unimportant. These results suggest that direct and maternal breed effects and heterosis for milk yield and quality were relatively stable across the forage systems evaluated.

Key Words: Genotype x Environment, Crossbreeding, Beef Cattle

315 Analyses of cow weight in beef cattle with random regression models.

J. Arango*[1], L. V. Cundiff[2], and L. D. Van Vleck[3], [1]*University of Nebraska, Lincoln*, [2,3]*USDA, ARS, US Meat Animal Research Center*, [2]*Clay Center, NE*, [3]*Lincoln, NE.*

Data from the first four cycles of the Germplasm Evaluation Program were used to evaluate weights of Angus, Hereford, and F1 cows produced by crosses of 22 sire and two dam (Angus and Hereford) breeds. Four weights per cow-yr were available from two through eight yr of age (AY) with age coded in months (AM). Weights (n=61798) were analyzed with REML fitting a random regression model (RRM), regressing on orthogonal (Legendre) polynomials of AM. The models included fixed regression on AM and effects of cow line, age in years, season of measurement and their interactions, year of birth and pregnancy-lactation codes. The random part of the models fitted RRM coefficients for additive (a) and permanent environmental (c) effects. The resulting covariance functions were used to estimate covariances for all ages in the data. Temporary environmental effects were modeled to account for heterogeneity of variance for the AY. Quadratic fixed regression was sufficient to model population trajectory and was fitted in all analyses. Different sets of models varied the order of fit of a and c coefficients. Models were compared using likelihood ratio tests. The best model included linear and quartic regression coefficients for a and c respectively. Coefficients for c were highly correlated, so estimation with a reduced cubic order did not reduce likelihood significantly. Additive and phenotypic variances increased with cow age, especially for older cows. The surface of the plots of permanent environmental and phenotypic covariances were not smooth. Heritabilities for AM were in the range of .38 (36 mo) to .78 (94 mo) with some fluctuation especially for extreme ages. Genetic correlations were high for most age combinations, with the lowest value (.70) between extreme ages (19, 103 mo). Permanent environmental correlations were more erratic. Results showed that cow weights do not fit a repeatability model with constant variances.

Key Words: Growth, Genetic Parameters, Heritability

316 Parameterization of random regression models for beef cattle data.

L. A. Kuehn*, B. L. Golden, and R. M. Bourdon, *Colorado State University, Fort Collins.*

Random regression models have been used to analyze data with multiple records per animal. In most beef cattle data sets, each animal only has one record for the trait of interest. The objective of this study was to determine the number of records per animal required to parameterize a random regression model. We simulated five records for each of 20,000 animals for the following traits: days to slaughter (**CONTROL**; no random regression), days to reach a specific backfat thickness (**BF**; days were regressed on backfat depth), and days to reach a specific weight (**WT**; days were regressed on weight). Phenotypic observations were calculated as the sum of breeding values and environmental effects sampled from multivariate normal distributions. We simulated WT and BF phenotypes using a constant set of backfat or weight observations. Observations from the CONTROL model were simulated to be either 20% or 40% heritable. Records from WT and BF models were simulated at 20% and 40% heritability for each trait (at the highest level of backfat depth or weight), crossclassified with two proportions of additive variance in the intercept term vs. the linear regression term. Data for BF were simulated using a correlation between the intercept and linear coefficients of -.20. The corresponding correlation was zero for WT data. We evaluated parameterization of BF and WT relative to CONTROL by comparing average accuracy of intercept and regression genetic predictions as well as average accuracy of predicted breeding values at final backfat depth or weight endpoint. Breeding values were predicted using the same model used for simulation and incorporating 1, 3, or 5 records per animal. Average accuracy at final backfat depth or weight ranged from .67 to .90, .66 to .88, and .66 to .90 in the CONTROL, BF, and WT models, respectively. Results indicate that one record per animal is sufficient to obtain reliable estimates of breeding values using random regression models that include intercept and linear terms only.

Key Words: Regression, Genetic Models, Simulation

317 Comparison of models for estimation of genetic parameters of mature weight of Hereford cattle.

J. M. Rumph*[1], R. M. Koch[1], K. E. Gregory[2], L. V. Cundiff[2], and L. D. Van Vleck[3], [1]*University of Nebraska, Lincoln*, [2,3]*USDA, ARS, US Meat Animal Research Center*, [2]*Clay Center, NE*, [3]*Lincoln, NE.*

Three different models were used to analyze mature weight records from three selection lines, selected on weaning weight, yearling weight, and an index of yearling weight and muscle score, respectively, and one control line of Hereford cattle. Weights were measured a maximum of three times per year; at the time of brand clipping (BC, generally prior to calving), before breeding (BB), and at palpation (PA, as calves were weaned). All models included year x age x line, dam age x line, pregnancy status x line, and birth and method of rearing of calf x line as fixed

effects. Additionally, each model included a covariate for the interval between calving and when the weight was taken and a random permanent environmental effect of the cow. All models were used to analyze each of three weights separately in univariate analyses with REML. The full model also included maternal genetic and permanent environmental effects of the dam. The second model included an overall effect of the dam. The third model did not include any maternal effects. The three models were significantly different based on likelihood ratio tests. The best model was the full model. With the full model, parameter estimates for direct h^2 (SE) were .79 (.09), .74 (.08), and .67 (.08) for BC, BB, and PA weights, respectively. Estimates for maternal h^2 were .07 (.03), .12 (.03), and .11 (.03) and the correlations between direct and maternal genetic effects were -.72 (.12), -.67 (.07), and -.63 (.09). Estimates of fractional variance due to permanent environmental effects of the cow were .00 (.06), .00 (.05), and .00 (.05) and of permanent environmental effects of the dam of the cow were .03 (.02), .05 (.02), and .06 (.02). Fractional estimates of residual variance were .27 (.01), .29 (.01), and .33 (.01). Maternal effects appear to be of some importance for mature weight and therefore should be considered in models for genetic evaluation of mature weight.

Key Words: Heritability, Growth, Beef Cattle

318 Birth and weaning traits of progeny of Hereford, Angus, Norwegian Red-Swedish Red and White, Friesian and Wagyu sires.

L.V. Cundiff*[1], [1]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Data were obtained on 1,384 calves born and 1,285 calves weaned resulting from artificial insemination matings of Hereford (H, 32 sires), Angus (A, 30), Norwegian Red-Swedish Red and White (NS, 14 and 16, respectively, considered same breed because of open herd books), Friesian (F, 24 non-Holstein influenced), and Wagyu (W, 19) sires to Hereford, Angus, and composite MARC III (1/4 each Angus, Hereford, Red Poll, and Pinzgauer) dams. Data on gestation length (GL), unassisted calving percentage (CE), survival to weaning (SW), birth weight (BW) and 200-d weaning weight (WW) were analyzed by least squares procedures using a model that included random effects for sire in sire breed and fixed effects for sire breed, dam breed, sex of calf, age of dam (4,5,...10 yr), birth year (1997 and 1998), sire breed x dam breed and any other two factor interactions that were significant ($P<.05$) for each trait. Effects of sire breed were significant ($P<.05$) for GL, CE, BW, and WW, but not for SW. The means for H, A, NS, F, and W sired progeny were 284.1, 282.3, 282.2, 281.4, and 286.9 d, respectively for GL with a mean least significant difference (LSD<.05) of 0.8 d. Corresponding sire breed means were 96.7, 96.8, 99.4, 99.2, and 99.3 % for CE (LSD<.05 = 2.4%); 41.9, 39.1, 38.6, 39.4, and 36.4 kg for BW (LSD<.05 = 0.8 kg); and 231.1, 229.1, 225.8, 221.1, and 208.0 kg for WW (LSD<.05 = 4.4 kg). In spite of significantly longer gestation length, progeny of W sires had lighter BW and greater CE than progeny of A or H sires. Progeny of W sires did not differ in CE from progeny of NS or F sires. At weaning, progeny of H and A sires were heavier than those of NS sires, which were in turn heavier than those of F sires. Progeny of W sires were significantly lighter than those of all other sire breeds at weaning.

Key Words: Beef Cattle, Breeds, Germplasm

319 Correlation amongst five body linear measurements of Zebu cattle.

O.T.F. Abanikannda*[1], A.O. Leigh[2], O. Olutogun[2], and O.Y. Apena[2], [1]*Lagos State University,* [2]*University of Ibadan.*

Linear measurements of five body dimensions of the Zebu cattle brought for slaughter at the cosmopolitan Abattoir and lairage in Lagos, Nigeria were taken and evaluated. 454 cattle comprising 362 male and 92 female were included in this study. The measurements taken includes Head to shoulder (HDS), Shoulder to drop (STD), Height at withers (HTW), Heart girth (HTG) and Body length (BLT). The mean values ± Standard error (cm) for the five measurements are 67.95±0.52, 126.47±0.80, 135.52±0.68, 186±1.67 and 197±1.21 respectively. In this study, HDS ranges from 33 - 92cm; STD, 49 - 168cm; HTW, 92 - 182cm; HTG 104 - 262cm and BLT, 102 - 255cm. With the exception of the correlation between HTG and HTW which was not significant ($P>0.05$) all other parameters studied were highly significant ($P<0.001$). In the analysis of variance, using BLT as the dependent variable and sex as a fixed factor, while the other four body dimensions are used as covariates, all factors studied except sex were highly significant($P<0.05$) on BLT. The coefficient of variation (CV) and coefficient of determination (R-squared) for this analysis was 5.72 and 0.81 respectively. The result of this study reveals that there are inter-relationships amongst the five body linear measurements of Zebu cattle

Key Words: cattle, linear measurement

320 Effects of the calpastatin system on growth of Angus bulls.

M. E. Davis*[1], H. Y. Chung[1], H. C. Hines[1], and D. M. Wulf[2], [1]*The Ohio State University, Columbus,* [2]*South Dakota State University, Brookings.*

Effects of the calpastatin system on growth and blood serum insulin-like growth factor I (IGF-I) concentration were examined in 47 purebred Angus bulls divergently selected for IGF-I at the Eastern Ohio Resource Development Center (EORDC). PCR-SSCP (single strand conformation polymorphism) analysis was conducted to search for genetic polymorphisms. The PCR primer selection was based on bovine calpastatin cDNA from domains L (CAST1) and IV (CAST28). The IGF-I concentration on d 28 (IGF28), 42 (IGF42), and 56 (IGF56) of the 140-d postweaning test was measured. Birth weight (BW), weaning weight (WW), on-test weight (ONW), weight on d 28 (W28), 42 (W42), and 56 (W56) of the postweaning test, and off-test weight (OFW) also were recorded. The statistical model included fixed effects of calpastatin genotypes, IGF-I selection line (high vs. low), age of dam, and age of bull as a covariate. Three genotypes (AA, AB, and BB) were detected for both loci. Significant influences of CAST1 genotypes on ONW, W28, W42, W56, and W140, and of CAST28 genotypes on W28 and W42 were observed. CAST1 and CAST28 genotypes did not explain significant variation in IGF28, IGF42, and IGF56, but CAST28 genotypes tended to influence mean IGF-I concentration ($P=.06$). The calpastatin polymorphisms reported here may provide useful information for marker assisted selection for weight traits in beef cattle.

Key Words: Calpastatin, IGF-I, PCR-SSCP

321 Effects of calpain and calpastatin genotypes on calpastatin activity and meat tenderness in Angus bulls.

H. Y. Chung*[1], M. E. Davis[1], H. C. Hines[1], and D. M. Wulf[2], [1]*The Ohio State University, Columbus,* [2]*South Dakota State University, Brookings.*

Effects of the calpain and calpastatin system on calpastatin activity, myofibril fragmentation index, pH, and meat tenderness were examined in 47 purebred Angus bulls reared at the Eastern Ohio Resource Development Center (EORDC). The bulls were divergently selected for blood serum insulin-like growth factor I (IGF-I) concentration. Genetic variants were found using PCR-RFLP and SSCP analysis of the u-calpain and calpastatin loci. PCR primers were selected based on the bovine cDNA sequence for calpastatin domain I, and the rat cDNA sequence for u-calpain domain II. Bulls were slaughtered at approximately 13 to 15 mo of age, and longissimus muscle samples were prepared for determination of calpastatin activity (CAC), Warner-Bratzler Shear Force (WBS), pH, and myofibril fragmentation index (MFI). The statistical model included calpastatin genotypes, calpain genotypes, age of dam, and IGF-I selection line as fixed effects, as well as age of bull as a covariate. Genetic polymorphisms were detected for calpastatin (AA, AB, AC, BB, BC and CC) and u-calpain (AA, AB, and BB). Calpastatin and u-calpain genotypes explained significant variation in calpastatin activity, but not in WBS. Least significant differences for CAC among calpastatin (AA > AB > BC > AC > CC > BB) and u-calpain genotypes (BB > AA > AB) were found. A strong positive residual correlation was detected between calpastatin activity and WBS ($r=.41$; $P<.05$), and a weak negative relationship was detected between CAC and MFI ($r=-.27$; $P=.12$). It may be possible to use calpastatin and u-calpain genotypes classified by PCR-RFLP and SSCP in marker assisted selection programs to decrease calpastatin activity.

Key Words: Calpastatin, Meat Tenderness, PCR-RFLP

322 Association of two Pit-1 gene polymorphisms with growth rate in beef cattle.

Qun Zhao*, M.E. Davis, and H.C. Hines, *The Ohio State University, Columbus.*

Growth rate, which is under the control of multiple genes, is an economically important trait in livestock. Pit-1 is a pituitary specific transcription factor that helps regulate the expression of growth hormone (GH). Therefore, the Pit-1 gene may be a good candidate gene for growth rate. Detecting genetic variations in the Pit-1 gene and relating them to growth rate could be helpful in development of marker-assisted selection (MAS) programs in animal breeding. A new SSCP polymorphism detected in intron 5 and a PCR-RFLP HinfI polymorphism in exon 6 were studied in Angus beef cattle, which were divergently selected for high or low blood serum IGF-I concentration. The intron 5 polymorphism was examined in 185 cattle and the exon 6 polymorphism in 416 cattle. For the intron 5 polymorphism we found genotypes AB and BB with frequencies of .09 and .91 respectively. No AA individual was found in this sample. For the exon 6 polymorphism, genotypic frequencies of .11, .45 and .44 were observed for AA, AB, and BB, respectively. The associations of the polymorphisms with growth rate were also analyzed using the GLM procedure in SAS. For the intron 5 polymorphism a linear model was fitted for birth weight, preweaning gain, weaning weight, on-test weight, off-test weight, and weight at d 56 of the 140-d postweaning test. No significant associations between the genotypes and these growth traits were found. A moderate association of genotypes with weight at d 56 was found (P=0.08), and genotype AB had a higher d 56 weight. Allele A could be associated with superior d 56 weight. For the exon 6 polymorphism a linear model was fitted for birth weight, pre-weaning gain, weaning weight, and off-test weight. Significant associations were found between exon 6 genotypes and birth weight (P=0.03) and preweaning gain (P=0.01). Therefore, this Pit-1 polymorphism appears to affect growth traits in Angus beef cattle and may be a candidate for use in MAS. Further study of these polymorphisms in a larger sample is warranted.

Key Words: Pit-1, Polymorphism, cattle

323 Identification of quantitative trait loci affecting meat quality in a Berkshire by Yorkshire 3 generation family.

M. Malek[1], J.C.M. Dekkers*[1], H.K. Lee[1], T.J. Baas[1], K.P. Prusa[1], E. Huff-Lonergan[1], and M.F. Rothschild[1], [1]*Departments of Animal Science, Food Science and Human Nutrition, Iowa State University, Ames.*

The techniques of molecular genetics and gene mapping have rapidly progressed. These methods, coupled with advances in human genetics, have opened new vistas for investigators wishing to identify genes that control quantitative traits (quantitative trait loci or QTL). A three-generation resource family was developed at Iowa State University to study individual effects of genes on meat quality traits in pigs. This family was developed using two Berkshire grand sires and ten Yorkshire grand dams. These F0 animals were mated to produce ten F1 litters. From the F1 litters a total of 65 matings were made in four seasons to produce a total of 525 F2 animals. All F2 animals were phenotyped for birth weight, 16 day weight, growth rate, backfat, loin eye area, drip loss, water holding capacity, firmness, color, marbling, percent cholesterol, ultimate pH, fiber type and several sensory panel and cooking traits. All animals were genotyped for nearly 120 microsatellite markers covering the entire porcine genome. Linkage analysis was performed using CRIMAP version 2.4 software (Green et al. 1990). The regression interval mapping method (Haley et al. 1994) was used to analyze the data. Permutation tests were performed to determine chromosome and experiment-wise significance levels for hypothesis testing. Significant QTL at the chromosome wide 5% level were detected for growth (chromosomes 1, 4, 7, 15), backfat (chromosomes 1, 5, 6, 7, 13, 14) and meat quality traits (chromosomes 1, 2, 4, 5, 8, 10, 11, 13, 14, 15, 17, 18). Additional marker analysis and examination for positional candidate genes is underway. This work was supported by an industry consortium consisting of National Pork Producers Council, Iowa Pork Producers Association, Iowa Purebred Swine Council, Babcock Swine, Danbred USA, DEKALB Swine Breeders, PIC, Seghersgenetics USA, and Shamrock Breeders.

324 Accuracy of DNA pooling to estimate microsatellite allele frequency.

J. P. McElroy*[1], H. Zhou[1], J. C. M. Dekkers[1], and S. J. Lamont[1], [1]*Iowa State University, Ames.*

The use of pooled DNA to estimate allele frequencies in groups of individuals is commonly employed to detect Quantitative Trait Loci (QTL) in large populations to reduce the number of genotypings required. The objective here was to examine factors that might affect the accuracy of DNA pooling to estimate the frequency of microsatellite marker ADL0268 in chickens. Two genetically distant, highly inbred (>99%) lines (Leghorn and Fayoumi) were used to generate an F2 population of 159 females, approximating a large full-sibship. The F2 birds were evaluated for six antibody response traits. Equal amounts of DNA from the phenotypic extremes (15% per pool) of each trait were used to create DNA pools. Each pool was independently replicated, resulting in 24 pools. All pools were amplified in two replicates of the polymerase chain reaction (PCR), yielding 48 PCR products. Only the two parental alleles were detected. Allelic frequencies in a pool were estimated by dividing the Genescan peak height of each allele by the sum of the two peak heights. Correlations of frequency estimates between replicates were >0.9 for DNA pools and PCRs, indicating that little variation was due to the pooling or the PCR procedure. Actual allele frequencies in the pools, determined by individual genotyping, ranged from 0.35 to 0.57, but did not differ significantly (P>0.05) between the high and low groups for any trait. The intercept and slope of the linear regression of pool on actual frequencies were 0.18 and 0.75. Correlations of actual with estimated frequencies based on individual replicated PCRs per replicate pool (n=48), the average of 2 replicated PCRs per replicate pool (n=24), and the average of 2 pool replicates per phenotypic group (n=12) were 0.551, 0.560, and 0.577, indicating little improvement in allele frequency estimates from pool or PCR replication. Although this experiment only examined one microsatellite marker, the results show that large discrepancies may exist between actual and estimated frequencies, thereby decreasing the efficacy of the DNA pooling technique to detect QTL.

Key Words: QTL, Microsatellite, DNA Pooling

325 Maximizing cumulative discounted response with selection on an identified QTL.

R. Chakraborty*[1] and J. C. M. Dekkers[1], [1]*Iowa State University, Ames.*

The standard approach to marker-assisted selection is to select on the sum of the EBV for the quantitative trait locus (QTL) and an EBV for polygenes. Standard QTL selection has been shown to result in less than maximum response. Dekkers and Van Arendonk (1998, Genet. Res. 71:257) developed methods to optimize QTL selection by optimizing weights in an index of the QTL and polygenic EBV. Equal selection in males and females, an additive QTL, and maximization of response at the end of a planning horizon were assumed. The objectives here were to relax these assumptions and to compare multi-generation optimal and stepwise optimal QTL selection to standard QTL selection for maximizing cumulative discounted response. Stepwise optimal selection maximized single generation response each generation and is equivalent to standard QTL selection for additive QTL. Percent selected was 10 and 25% in males and females. Effects of the QTL were known, with the additive effect (a) ranging from 1 to 4 in standard deviations of polygenic EBV, which is equal to accuracy times the genetic standard deviation, and the dominance effect (d) ranging from 0 to 1.5a. QTL frequency was 10, 25 or 50%. Selection was for 10 generations and discount rate was 5 or 10%. For an additive QTL, benefits from multi-generation optimal over standard QTL selection were small; less than 2% greater response when a=1 and less than 4% when $a \geq 2$. Dominance increased the benefit of optimal selection; extra responses were up 3 and 6% greater for a=1 and $a \geq 2$ when d=.5a, up to 4 and 8% greater for a=1 and $a \geq 2$ when d=a, and up to 6 and 12% greater for a=1 and $a \geq 2$ when d=1.5a. Extra responses were similar for a=2, 3, or 4 and tended to decrease with increasing frequency and interest rate. For non-additive QTL, extra responses from stepwise optimal over standard QTL selection were about half as large as those from multi-generation optimal selection. Results show that optimization of QTL selection can result in greater responses, although benefits are small unless the QTL shows dominance. This research was funded by USDA-NRI and PIC.

Key Words: Marker Assisted Selection, Discounting

326 Genome scan for quantitative trait loci for growth and reproductive traits in female mice.

F. Siewerdt*[1,2], E. J. Eisen[1], and D. Pomp[3], [1]*North Carolina State University, Raleigh,* [2]*Universidade Federal de Pelotas,* [3]*University of Nebraska, Lincoln.*

The objective of this research was to identify QTL for growth and reproduction in female mice. Genotypic and phenotypic data were collected on 442 female progeny of *inter se* matings from an F_1 cross between line L6 (small BW) and line M16i (large BW), from two replications. Females were exposed to unrelated F_1 males B6C3F1/J until a copulatory plug was detected. BW were taken at 3, 6, 10 wk and at detection of the copulatory plug (PW); tail length was measured at 10 wk. Females were killed at d 16 of pregnancy to obtain counts on number of corpora lutea (TCL) and number of live (TF) and dead (TD) fetuses; embryo survival rates (ES) were calculated. Genotyping was done at 72 microsatellites in all F_2 females bearing a litter. Each of the 19 autosomes had at least three markers. A model with the effects of replication and litter within replication was fitted to the data. Residuals from this model were used in conjunction with a linkage map for the molecular markers in a composite interval mapping analysis. The putative QTL with largest additive effects ($P < .05$) on BW and tail length were found to be linked with markers in chromosomes (chr) 6, 8, 11, 12, 14, and 19. The major QTL for PW were found in chr 4, 5, 7, 11, 12, 14, and 18. QTL with additive effect on TCL were in chr 4, 11, and 14; significant associations between markers and putative QTL with additive effects were found in chr 9, 13, 14, 17, and 19 for TF and in chr 2, 4, 5, 6, 9, and 17 for TD. ES were affected mainly by QTL with additive effects linked to markers in chr 2, 9, 14, and 17. Putative QTL with the largest dominance effects ($P < .05$) were found for PW in chr 2 and 17, for BW in chr 10, 11, 12, and 17, for tail length in chr 6, 9, and 13, for TCL in chr 11, 17, and 18, for TF in chr 2 and 11, for TD in chr 9, and for ES in chr 2 and 11. There is definite indication of QTL for growth and reproduction. Some QTL may be pleiotropic due to detectable effects on several traits associated with the same markers.

Key Words: Mice, Quantitative Trait Loci, Growth, Reproduction

327 Comparison of approaches for determining significance threshold values for QTL detection.

H. K. Lee*[1], J. C. M. Dekkers[2], M. Malek[2], M. Soller[3], R. L. Fernando[2], and M. F. Rothschild[2], [1]*National Livestock Research Institute, Korea,* [2]*Iowa State University, Ames,* [3]*Hebrew University of Jerusalem.*

Setting critical values (CV) for significance tests for detecting quantitative trait loci (QTL) with interval mapping is much debated. Several methods have been proposed to derive CV to control Type I error at the chromosome, experiment, or genome level, accounting for the number and dependence of tests, including the analytical method of Lander and Kruglyak (1995) (LK) and the permutation test (PT) of Churchill and Doerge (1994). Weller et al. (1998) proposed controlling false discovery rate (FDR) as basis for an alternative CV. The goal here was to compare 5% CV based on these 3 methods, recognizing that Type I error rate and FDR have different interpretations and relevance. Phenotypes of 5 meat quality traits and genotypes of 41 markers on 8 chromosomes covering 9.1 M (0.75 to 1.3 M per chromosome) from 525 F2's from a swine breed cross were used. Data were analyzed by least squares regression interval mapping with a test every cM. The PT CV were based on 10,000 replicates and FDR CV on tests at every cM. The 5% CV for a single test was 3.1. Experimentwise CV were 9.4 for LK and ranged from 7.1 to 7.4 for PT and from 4.4 to 6.7 for FDR, depending on the trait. Chromosomewise CV ranged from 6.5 to 7.2 for LK, from 4.6 to 5.2 for PT, and from 3.2 to 4.3 for FDR. Chromosomewise FDR behaved erratic due to dependence among tests and could not be obtained for several chromosome-trait combinations, for which FDR was above 5% for all tests, indicating no trait QTL on that chromosome. In conclusion, CV differed substantially between methods, leading to different numbers of QTL detected. FDR resulted in the least stringent CV. This while an FDR of 5% will be conservative for most purposes. This work was supported by an industry consortium of the National Pork Producers Council, Iowa Pork Producers Association, Iowa Purebred Swine Council, Babcock Swine, Danbred USA, DEKALB Swine Breeders, PIC, Seghersgenetics USA, and Shamrock Breeders.

Key Words: QTL Mapping, Significance Test, Breed Cross

328 Fitness of sheep metallothionein 1-a sheep growth hormone (oMt1a-oGH) transgenic mice.

E. J. Eisen*[1] and J. D. Murray[2], [1]*North Carolina State University, Raleigh,* [2]*University of California, Davis.*

Objectives were to determine if the oMt1a-oGH transgene shows normal mendelian segregation and if oMt1a-oGH mice exhibit normal growth without the zinc supplementation required to increase plasma oGH levels and stimulate growth. Transgenic mice were reciprocally backcrossed for four generations to high growth and control lines to form lines GM and GR. In the fifth generation, hemizygous transgenic mice (T/-) were crossed within each line. Pooled across backcross generations, there was a deficit($P < .001$) of T/- progeny in GM (31.6%) and GR (22.2%) compared to expected (50%). In the T/- x T/- cross the combined percentage of homozygous (T/T) and hemizygous transgenic mice was less ($P < .001$) than expected (75%) in both GM (44.2%) and GR (38.5%). Backcross T/- mice had lower ($P < .05$) 3-wk body weights and lower ($P < .001$) 6-wk body weights and 3-6 wk postweaning gains than nontransgenic mice. Similar genotypic differences were found in the T/- x T/- cross. No significant growth differences were found between T/T and T/- progeny. Using segregation ratios from the T/- x T/- mating, the relative fitness estimate of T/T, T/- and -/- (nontransgenic) mice were .345, .223 and 1.0, respectively, in line GM and .218, .205 and 1.0 in line GR. Fitness estimates in the backcross for T/- and -/- were .463 and 1.0 in line GM and .285 and 1.0 in line GR. Abnormal segregation ratios may be due to germline mosaicism or reduced fitness due to differential embryo survival. Reduced growth of oMt1a-oGH transgenic mice when the transgene is switched off suggests a subtle developmental abnormality, which may contribute to a reduction in fitness.

Key Words: Transgene, Growth Hormone, Mice

329 Mutation in exon 5 of bovine prolactin gene is not associated with milk traits in Holstein bulls.

I. Parmentier[1], N. Gengler[1], P. Laliberte[2], W. Holtmann[2], C. Bertozzi[1], V. Haezebroeck[1], D. Portetelle[1], and R. Renaville*[1], [1]*Gembloux Agricultural University, Gembloux, Canada,* [2]*Semex Alliance, Guelph, Canada.*

The prolactin hormone, PRL, plays a critical role in lactation. This hormone is, primarily responsible for the synthesis of milk proteins, lactose, and lipids, all major components of milk. In addition, PRL has been shown to directly stimulate insulin-like growth factor-I binding proteins, epidermal growth factor, a glycolysated mucin, parathyroid-like peptide, and PRL-inducible proteins in normal and neoplasmic tissue. The objectives of this research were to identify mutation in exon 5 of bovine PRL gene and to establish association between observed mutation and milk traits in Holstein bulls DNA was extracted from semen of 1100 Holtsein bulls provided by Semex-Alliance (Guelph, Canada). A mixed model was used to study association between alleles and milk, protein and fat yields. In this model, herd, year, season, parity, lactation, age classes, month of lactation were fixed effects and permanent environment, animal and residual effects were considered as random effects. Using BESS-Scan Mutation Detection and localization Kit (Epicentre Technologies), a mutation was found in the fifth exon of the PRL gene. By DNA sequencing, a A to G transition was identified at the 718 amino acid of the protein. In our population, allelic frequencies of the A and G alleles were 0.34 and 0.66, respectively. Statistical analysis showed no significant effect of PRL polymorphism at the exon 5 on lactation traits. In conclusion, the PRL polymorphism found in the fifth exon was not associated with lactation traits of Holtein bulls. This polymorphism is, thus, not a tool of choice for using in breeding programs. This research was supported by Belgian Ministery of Agriculture grant 5859 and Semex Alliance, Guelph, Canada.

Key Words: Prolactin, Mutation, Lactation

330 Genetic analysis of candidate gene (RELN) for Weaver Syndrome in Brown Swiss Cattle.

S. E. Speidel*[1], E. Oberg[1], M. B. Abdallah[1], and S. K. DeNise[1], *University of Arizona, Tucson.*

Weaver Syndrome or Bovine Progressive Degenerative Myeloencephalopathy (PDME) is a recessively inherited neurological disease described in Brown Swiss Cattle that has been mapped to bovine chromosome 4 (BTA4). To locate the PDME causative gene, human and murine candidate loci have been identified that map to homologous regions on

BTA4. The reelin gene (RELN) has been shown to control neuronal migration in the developing brain in mice; and mutations in the gene have shown similar symptoms to PDME. It maps to the long arm of human chromosome 7, which is homologous to BTA4. Primers developed from human studies were used to amplify a 159-bp fragment, which encompasses positions 1136-1295 of the human RELN sequence. After initial sequencing of direct PCR product, the fragment had a 90.06% homology score with human RELN. Sixteen animals representing nine breeds: Guernsey, Angus, Holstein, Jersey, Brown Swiss, Hereford, Gelbvieh, Limousin and Simmental, were PCR amplified and direct sequenced. Single nucleotide polymorphisms (SNP's) at positions 54 and 69 were identified. Using this information, we will develop either PCR restriction fragment polymorphisms (PCR-RFLP) or single strand conformational polymorphisms (SSCP) to map the gene by linkage analysis in the ARS Cattle Genome Mapping Project.

Key Words: Gene mapping, Dairy cattle, Genetic diseases

331 Genetic analysis of Bovine Progressive Degenerative Myeloencephalopathy (PDME) or Weaver Syndrome in Brown Swiss Cattle.

S.K. DeNise*[1] and E. Oberg[1], *University of Arizona, Tucson AZ USA.*

Eight bovine microsatellite markers have been used to develop haplotypes for carriers of PDME within the Brown Swiss Breed. These markers include TGLA116 (the original marker for PDME), BMS2172, BMS885, DIK8, BM1224, BM6437, BMS495 and INRA072, that encompass a 12.7 cM region of bovine chromosome 4. Haplotypes have been developed for all progeny-tested carrier sires, resulting in a high probability of determining carrier status of progeny from these sires. Using the haplotype test, we have identified a recombinant bull that is a known PDME heterozygote. This bull places the PDME locus telomeric of BM1224. Physical mapping of the region using bacterial artificial chromosome clones (BAC) has identified two human expressed sequence tags (ESTs) near BMS495. These sequences map to human chromosome 7 (Gene Map 98 (NCBI): D7S484-528, 55.6-58.9) and place these ESTs between GHRHR (7p14; 40.1-55.6) and IGFBP3 (7p13-12; 69.4-74.3). If the BAC clone is not chimeric, then these ESTs map centromeric to GHRHR in cattle with the linkage order as BMS495: 69.6; GHRHR: 74.8 and IGFBP3: 82.2 (ARS Cattle Genome Mapping Project). Thus, there may have been rearrangements between the bovine and human genomes in this region.

Key Words: Gene mapping, Dairy cattle

332 The effects of storage and preservative on genomic DNA extraction from bovine milk somatic cells.

G. Robitaille*[1], M. Britten[2], and D. Petitclerc[1], [1]*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada,* [2]*Food Research and Development Centre, Agriculture and Agri-Food Canada.*

Molecular approach of genotyping a huge amount of cow is complicated by the need of cells for genomic DNA extraction. An alternative approach to blood sampling is the use of milk somatic cells. The objective of the study was to define milk storage conditions for an efficient DNA isolation. Individual milk from 3 cows, having different somatic cell count, were processed immediately for DNA isolation or stored at -20, 4, 20, and 37^{o}C for up to 15 days, with or without bronopol or potassium dichromate as preservatives. DNA was extracted using InstaGene Matrix (BIORAD). Briefly, milk was diluted in a phosphate buffered saline and spun. Supernatant and excess of fat were removed, cells were resuspended in 20 μl of water and mixed to 200 μl of InstaGene Matrix (BIORAD). The suspension was incubated for 30 min at 56^{o}C and 100^{o}C for 8 min and kept frozen. PCR amplification (40 cycles : 94 ^{o}C - 30 sec, 55^{o}C - 30 sec, and 72^{o}C - 30 sec using Taq polymerase) was carried out on 10 μl of the supernatant in a reaction volume of 25 μl. Two sets of primers were tested on each sample, one that amplifies the bovine kappa-casein gene exon IV to discriminate genetic variants A and B (453 bp), and the other that amplifies the microsatellite region within intro III (246 bp). Results clearly demonstrated that, although fresh sample were more efficient as starting material, it is possible to isolate PCR-grade genomic DNA from milk that were stored up to 15 days at temperatures as high as 37^{o}C. This is particularly true when bronopol was added to milk. SSCP and RFLP of PCR fragments to genotype cows were carried out without problems. In conclusion, isolation of genomic DNA using InstaGene Matrix has proven to be effective with milk stored at various temperatures for up to 15 days. This means that individual milk samples, collected and forwarded to central testing laboratories within 15 days for milk composition analysis, can also be tested for gene polymorphism.

Key Words: Genotyping, DNA extraction, Somatic cells

CONTEMPORARY AND EMERGING ISSUES

333 Proposed new regional project on animal ethics.

S. L. Davis*[1], J. R. Males[1], J. C. Swanson[2], and K. K. Schillo[3], [1]*Oregon State University, Corvallis,* [2]*Kansas State University, Manhattan,* [3]*University of Kentucky, Lexington.*

Writing about Science, Lubchenco (1998. Science 279:491-497) wrote "Part of our collective responsibility to society must include a scientific community-wide re-examination of our goals and alteration of our course, if appropriate." The same is true for animal sciences of course, and with the increasing number of contentious social issues related to animal sciences it is becoming even more important that we conduct such a re-examination. This is basically what Thompson (1998. J. Animal Sci. 77:372-377) suggested in his presentation to ASAS at their 1997 meeting. Thompson (1998) also suggested that one approach to accomplish that re-examination would be to develop a new professional ethic, and one way to accomplish that would be the formation of a new Hatch regional project on Animal Bioethics. As a result, a group of 26 scientists have prepared a proposal to establish such a regional Hatch project titled Animal Bioethics. The objectives of this proposal are:

1. Create a forum in which animal scientists and non-animal scientists (philosophers, social scientists, etc.) may work together to examine and discuss contentious social issues.

2. Provide a means of encouraging the development and coordinating the activities of research projects dealing with bioethics of the animal sciences.

3. Develop mechanisms of outreach that would allow animal scientists to respond directly to consumers and our critics who may question our science and/or production methods.

4. Provide the means for ongoing critical analysis of the animal science professions in the context of their ability to address moral and sociopolitical issues.

Accomplishment of these objectives will require the participation and collaboration of animal scientists as well as philosophers and social scientists.

Key Words: Regional project, Animal ethics

334 The development and evaluation of Pennsylvania's Humane Society Police Officer Training Course: Animal Husbandry.

B.L. Coe*, E.P. Yoder, and D.E. Evans, *Pennsylvania State University, University Park.*

Recent Pennsylvania legislation (Act 1994-135) requires Humane Society Police Officers investigating animal abuse cases to receive training from a land-grant university regarding animal agriculture. A committee of Penn State specialists, humane society reps, farm organization reps, and PA Dept. of Ag. officials developed a relevant educational program. The program provides instruction in animal husbandry practices, animal behavior, handling, transportation, production systems, and investigation/evaluation of animal cruelty complaints. This project used an Instructional Systems Design framework for development and evaluation of the PA Humane Society Police Officer Training Program: Animal Husbandry. Data were collected from program participants, stakeholders, and a comparison group via detailed surveys. The program was conducted in PA from 1996-99 and 147 people completed the program. This study examined whether the new curriculum to train humane officers prepared them to adequately and reasonably enforce the