

**1695 Genetic parameters estimates for lean growth rate and its components in U.S. Yorkshire, Duroc, Hampshire, and Landrace pigs.** P. Chen\*, T.J. Baas, and J.W. Mabry, *Iowa State University, Ames, IA.*

Records on 361,300 Yorkshire, 154,833 Duroc, 99,311 Hampshire, and 71,097 Landrace pigs collected between 1985 and 1999 in herds on the National Swine Registry STAGES program were used to estimate additive genetic (animal), common environmental (litter) and residual variances and covariances for lean growth rate, days to 113 kg, backfat, and loin eye area. Analysis was by the REMLF90 program of I. Misztal using a multiple-trait animal model with fixed effects of contemporary group and sex and random effects of animal, litter, and residual. Estimates of heritabilities were 0.35, 0.40, 0.52, and 0.43 for lean growth rate, 0.43, 0.47, 0.57, and 0.46 for days to 113 kg, 0.35, 0.41, 0.55, and 0.49 for backfat, and 0.44, 0.43, 0.50, and 0.38 for loin eye area in Yorkshire, Duroc, Hampshire, and Landrace, respectively. Genetic correlations were -0.94, -0.86, -0.80, and -0.80 between lean growth rate and days to 113 kg, -0.32, -0.40, -0.25, and -0.41 between lean growth rate and backfat, and 0.40, 0.40, 0.36, and 0.36 between lean growth rate and loin eye area in Yorkshire, Duroc, Hampshire, and Landrace, respectively. Estimates for heritabilities and genetic correlations were consistent across breeds except for higher heritabilities for the Hampshire breed. Estimates for heritabilities across the four breeds for lean growth rate, days to 113 kg, backfat, and loin eye area were 0.43, 0.48, 0.45, and 0.44, respectively. Genetic correlations across the four breeds between lean growth rate and days to 113 kg, backfat, and loin eye area were -0.85, -0.35, and 0.38, respectively. Litter effects were generally small (< 0.1) except 0.12 for both days to 113 kg and loin eye area in the Yorkshire breed. The results indicate that lean growth rate should be used as an important selection criterion in genetic improvement of pigs.

**Key Words:** Lean Growth Rate, Heritability, Genetic Correlations

**1696 Evaluation of Duroc vs. Pietrain sired progeny for meat quality.** D. B. Edwards\*, R. O. Bates, and W. N. Osburn, *Michigan State University, E. Lansing, MI/USA.*

Novel swine populations may contribute beneficial genes to U.S. swine production systems. Crossbred progeny sired by either Duroc or ryanodine receptor gene normal Pietrain were used in this study. Boars from each breed were mated to Yorkshire or F1 Yorkshire-Landrace females. A total of 162 offspring were evaluated for meat quality. Measurements were taken on animals representative of each litter. Data were analyzed using an animal model with fixed effects of breed of sire, breed of dam, gender, slaughter group, the interaction of breed of sire and gender, and random effect of animal. An additional term of pig was included in the model to fit the within pig variation from sample to sample. Shear force measurements had six samples per pig, while other meat quality measures had two samples per pig. Meat quality measures were not different or favored Duroc sired progeny. Duroc progeny had better subjective meat quality scores (1-5 scale) for color (2.540 vs. 2.354,  $P < 0.05$ ), marbling (2.425 vs. 1.739,  $P < 0.001$ ), and firmness (2.615 vs. 2.295,  $P < 0.001$ ). Furthermore, Duroc progeny had higher 24-h pH (5.526 vs. 5.468,  $P < 0.001$ ) and less percent drip loss (2.892 vs. 3.893,  $P < 0.001$ ). No differences were detected between Duroc and Pietrain sired progeny for Minolta L\* (54.764 vs. 55.307), a\* (17.348 vs. 17.272), or b\* (7.581 vs. 7.441) objective color scores, percent cooking loss (28.629 vs. 29.187), or Warner-Bratzler shear force (6.942 vs. 7.095 kg). Both Duroc and Pietrain populations merit further study into the genetic control of these meat quality traits.

**Key Words:** pig, meat quality, breeds

**1697 Determining inbreeding levels for the Navajo-Churro sheep breed.** A. Maiwashe\*<sup>1</sup>, B. Tseveenjav<sup>1</sup>, B. Golden<sup>1</sup>, and H. Blackburn<sup>2</sup>, <sup>1</sup>Colorado State University, <sup>2</sup>USDA/ARS.

Maintaining genetic diversity in breeds and specifically breeds of small population size requires understanding genetic relationships among animals within a breed. Not knowing such information reduces breeder and association ability to correct situations of genetic erosion and inbreeding. The Navajo Churro is a sheep breed with a small population size and at one time was considered a rare or endangered breed. Therefore, pedigree records from the Navajo Churro Sheep Association were evaluated to determine inbreeding level, rate of inbreeding and the number of flocks with inbreeding. The breed society was formed in 1988; records

collected by the association from 1988 to 1999 were analyzed. There were 2,654 registrations in the analysis. Inbreeding level was calculated using the Animal Breeders Tool Kit. Information concerning inbreeding level and flock size was used as layers in a GIS analysis of the data. Since the formation of the breed society, there have been four generations produced. The average inbreeding for the fourth generation was calculated at 4.6 vs 1.3% for the third generation. Third generation registrations were 360 vs 95 hd for the fourth generation. As the breed moved from the third to the fourth generation, it appears that the rate of inbreeding increased exponentially. Flock inbreeding levels were calculated and it was determined that 32% of the breeders with generation 3 and 4 animals had flock inbreeding levels ranging from 3.1 to 10.5%. Inbreeding levels are increasing among sheep registered with the Navajo-Churro Sheep Association. If inbreeding is left unchecked, and is not intentional, this could develop into a significant problem for this breed.

**Key Words:** Navajo Churro sheep, Inbreeding, Genetic diversity

**1698 Genetic parameters for some growth traits of Local breed of goat in the United Arab Emirates.** Salih Al-Shorepy\*, Ghaleb Alhadrami, and Khalfan Abdulwahab, *United Arab Emirates University.*

The Local goat breed is the most common native breed of the United Arab Emirates and is adapted to its harsh environment. The data used in the present study was collected from the conservation flock at the Faculty of Agricultural Sciences Experimental Station. The traits recorded were body weights at birth (BWT), 30 days (WT30) and weaning (WWT), and average daily gains from birth to 30 days (ADG1), 30 to 90 days (ADG2) and birth to weaning (ADG3). Season of birth, type of birth or rearing, sex of kid and dam age at kidding were the environmental factors investigated. Genetic parameters and phenotypic and genetic correlations were estimated by REML procedures. By ignoring or including maternal genetic or environmental effects, four different models of analysis were fitted in order to determine the most effective model for each trait. Additive maternal effect was important ( $P < 0.05$ ) for BWT, when compared with a model containing only additive direct effects. Inclusion of maternal permanent environmental effect provided a better fit ( $P < 0.05$ ) for WT30, WWT and ADG1. Estimates of direct heritability from the most appropriate models were 0.18 for BWT, 0.16 for WT30, 0.32 for WWT, 0.11 for ADG1, 0.09 for ADG2 and 0.42 for ADG3. The estimates of genetic and phenotypic correlations were high and showed no genetic antagonisms among growth traits analyzed. It can be concluded that maternal effects have to be accounted for when estimating genetic parameters for BWT, WT30, WWT and ADG1.

**Key Words:** Local goats, Growth, Genetic parameters

**1699 Estimation of heritability and repeatability for superovulatory responses of Japanese Holstein population.** Y. Asada\*<sup>1</sup> and Y. Terawaki<sup>2</sup>, <sup>1</sup>The Graduate School of Dairy Science, Rakuno Gakuen University, <sup>2</sup>Rakuno Gakuen University Dairy Science Institute.

The subjects of this study were to estimate repeatability and heritability for the yield of embryos and transferable embryos in Holstein population in Hokkaido, Japan. Data consisted of 306 MOET treatments on 224 Holstein cows from 1997 to 2000. Data were analyzed to investigate the factors affecting superovulatory responses of Japanese Holstein cows using maximum likelihood method and generalized linear model. Variance components for the superovulatory responses were estimated using REML employing animal model. The mean number of embryos and transferable embryos yielded per flush were 6.7 and 4.4, respectively. A good fit exhibited for negative binomial distribution of number of embryos and transferable embryos yielded. A lack of fit exhibited for Poisson and Binomial distribution of the number of embryos and transferable embryos yielded. Factors identified as importance in affecting superovulatory response were the areas (branch offices) and the donors estrus condition after superovulation for the number of embryos. And for the number of transferable embryos the characteristics of each donor was an important factor in addition to affecting factors for the number of embryos. The estimated heritability and repeatability for the yield of embryos were 0.02 and 0.38, and for the yield of transferable embryos were 0.05 and 0.28, respectively. These results showed that prior to carrying out MOET schemes, the consideration of affecting the areas and the donor's estrus condition after superovulation is need to be taken into account when using a computer simulation to predict the genetic gain

and the rate of inbreeding. The results also showed that it is indispensable to use repeatability of donor's superovulatory responses including the characteristics of each donor, so that the computer simulation can produce the more realistic results.

**Key Words:** Holstein, heritability, transferable embryo

**1700 Genetic correlation between final scores over time in Holsteins.** S. Tsuruta<sup>\*1</sup>, I. Misztal<sup>1</sup>, L. Klei<sup>2</sup>, and T. J. Lawlor<sup>2</sup>, <sup>1</sup>University of Georgia, Athens, <sup>2</sup>Holstein Association USA, Inc., Brattleboro, VT.

The goal of this study was to determine how the definition of final score changes in time. The first conformation final scores for cows born between 1951 and 1997 were obtained from Holstein Association USA Inc.; the number of cows born before 1970 was small. The model contained management group, age group, stage of lactation, and regressions on the year of birth as fixed effects; additive genetic random effects with random regressions on the year of birth using third order Legendre polynomials; and residual effects. Ten datasets, each having about 15,000 records, were randomly sampled from the original complete file (4,595,237 records). Estimates of additive genetic and residual variances were constant over the years (about 4.0 and 9.8, respectively). Genetic correlations between years of birth decreased from 1.0 to 0.7 as the distance between the years increased. These correlations between years 1997 and 1981 were .80 and between years 1951 and 1981 were 0.79; however, due to a small number of records in early years and/or low order polynomials, these correlations may have been under (or over)-estimated. The national genetic evaluation for final score may be more accurate if old scores are discarded or treated as separate traits.

**Key Words:** Holstein, Conformation final score, Random regression

**1701 The genetic relationships among milk yield, herd life and productive life in Holstein cows in Hokkaido, Japan.** T. Obayasi<sup>\*1</sup> and Y. Terawaki<sup>2</sup>, <sup>1</sup>The Graduate School of Dairy Science, Rakuno Gakuen University, <sup>2</sup>Rakuno Gakuen University Dairy Science Institute.

The objectives of this study were to estimate heritability for milk yield at first calving, lifetime milk yield, herd life and productive life of Holstein cows in Hokkaido, Japan. A total of 1,070,646 herds records of Holstein cows in Hokkaido, Japan, for animals born between 1963 and 1997 were classified into life span groups using three different criteria: less than 36 months; more than 36 months less than 72 months; and more than 72 months. These three groups were termed Group 1, Group 2 and Group 3, respectively. Milk yield at first calving, lifetime milk yield, herd life and productive life were all calculated for each animal. Analysis gave a mean for each trait for each group as follows: Group 1: 5531.3 kg, 2895.3 kg, 163.8 days, and 39.4 days; Group 2: 5506.7 kg, 13832.9 kg, 588.9 days, and 584.3 days; and Group 3: 5265.9 kg, 39149.6 kg, 1535.4 days, and 754.3 days, respectively. In Group 3, animals with a high milk yield at first calving showed a high lifetime milk yield, but herd life and productive life trend to be low. Next, we estimated heritability for each trait (milk yield at first calving, lifetime milk yield, herd life and productive life) in each group using REML F90. Heritability of each trait was estimated for a total number of 2,500 animals. In Group 1 heritability for each trait was found to be 0.32, 0.34, 0.08 and 0.22, respectively. In Group 2, heritability for each trait was found to be 0.34, 0.02, 0.20 and 0.19, respectively. And in Group 3, heritability for each trait was found to be 0.35, 0.01, 0.29 and 0.14, respectively. Animals with a high life span tend to show low heritabilities for lifetime milk yield and productive life. Heritability for herd life, however, was low. Animals with a low life span showed low heritability for herd life. Heritability for milk yield at first calving were similar in each group.

**Key Words:** Heritability, Longevity, Holstein

**1702 Suitability of physiological traits of young cattle for the evaluation of their performance stability.** L. Panicke<sup>\*1</sup>, R. Staufenbiel<sup>2</sup>, and E. Fischer<sup>3</sup>, <sup>1</sup>Research Institute for the Biology of Farm Animals, Dummerstorf, Germany, <sup>2</sup>Free University Berlin, Institute of Veterinary Physiology, Germany, <sup>3</sup>University Rostock, Faculty of Agricultural and Environmental Sciences, Germany.

High milk performance connected with sound health regarding metabolism and sufficient fertility in dairy cows depends on a well balanced distribution of energy in the body. The concentration of glucose

in the blood is relatively constant. Enzymes, hormones, controlling proteins and transporters contribute to the enormous synthesis production of 3 to 4 kg glucose. These are capable of influencing the efficiency of glucose production and distribution. Glucose and growth hormone as "early predictors" are superior to other possible parameters such as free fat acids, urea, thyroxin, prolactin, somatropin and IGF-1 in comparing the relationship between physiological metabolic parameters and the performance of cows and sires. Insulin plays an outstanding role based on its central position in energy 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<sup>0.75</sup> because of the probable genetic determination of the reactive ability. The coefficient of heritability was estimated as  $h^2=0.28\pm 0.16$ . The metabolic reaction for young cattle was the same for females and males as the GTT-parameters basic concentration of glucose was 4.0, 4.2 and 4.1 nmol/l plasma and the glucose half-life was 51.0, 49.2 and 50.3 minutes for heifers (n=22) and young sires (n=20, n=87), respectively. The differences of insulin and glucose show a contrary course and depend on the age under standardized feeding. The correlation between GTT and offspring breeding value (EBV) is also influenced by the age (in half-life years). The best correlation is read at the 3rd half-year. Three independent groups of 24 and 28 young sires and 12 heifers were involved in the investigation. The correlation coefficients between the glucose half-life (GHWZ) and the offspring breeding value (EBV) of about -0.4 to -0.5 are higher compared to the pedigree breeding value (PBV). If the so far achieved results are confirmed, an additional recommendation for the evaluation of breeding bulls before the start of the progeny test could be given. The test capacity could be extended or costs for testing bulls could be lowered.

**Key Words:** Cattle, Breeding Value, Physiology

**1703 Influence of the quality of reproductive event data on heritability of gestation length in DHI herds.** W. Zhang<sup>\*</sup> and G. E. Shook, University of Wisconsin, Madison.

Genetic evaluations for reproductive traits in dairy cattle are economically important. Accurate genetic evaluations for these traits depend on accurate recording of reproductive events; recording which is notoriously poor or inconsistent in many herds. In order to measure the quality of reproductive event data, gestation length (GL) was investigated in this study because of its biological consistency, having a standard deviation of 5.8 d and coefficient of variation of only 2% in these data. Although GL is not a trait of economic interest, it can be useful for measuring the accuracy of recording reproductive events in general. Data from Wisconsin Holstein herds during 1992 to 2000 were provided by AgSource Cooperative. Gestation length was calculated as days from last breeding to calving. Normal GL (NGL) was defined as 280 d  $\pm$  21 d. Herds with 60 d non-return rate greater than 90% were excluded. Records that ended in abortion or had calculated GL outside the range 259 to 301 d were omitted. A basic data set with 3,906 herds including 244,222 parities was generated after the above editing. Several herd selection criteria based on within-herd percentage of NGL and/or within-herd standard deviation of GL (SDGL) were used to filter the basic data and eight data sets were created. REML estimation of the heritability ( $h^2$ ) was performed through sire model for each data set. Heritabilities are in the table below. Compared with the basic data, estimates of  $h^2$  based on selected data sets can be increased by at least 2%. The more stringent selection criteria resulted in higher  $h^2$ . The effect of these data selection criteria on heritabilities for economically important reproductive measures are yet to be determined.

Data	Herd Selection Criteria	Records Retained(%)	Herds Retained(%)	$h^2$ (%)
1	Basic data set	100	100	13.9
2	SDGL<8 d	99	96	15.6
3	NGL>40%	96	92	16.3
4	SDGL<8 d and NGL>40%	95	88	15.9
5	SDGL<6 d	77	69	16.4
6	NGL>50%	73	64	16.6
7	SDGL<6 d and NGL>50%	59	47	17.3
8	SDGL<5 d and NGL>60%	9	10	20.8

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

**1704 Heritabilities and genetic correlations between height, length, weight and body condition score of Holstein heifers in high producing Wisconsin dairy herds.** C. D. Dechow\*<sup>1</sup>, N. C. Dorshorst<sup>2</sup>, P. C. Hoffman<sup>2</sup>, K. A. Weigel<sup>2</sup>, J. Jensen<sup>3</sup>, and G. W. Rogers<sup>1</sup>, <sup>1</sup>*Pennsylvania State University*, <sup>2</sup>*University of Wisconsin-Madison*, <sup>3</sup>*Danish Institute of Agricultural Research*.

The objectives of this study were to estimate genetic and phenotypic parameters for heifer growth in selected high producing Holstein herds. Height, length, heart girth circumference and body condition score (BCS) of heifers were recorded in 19 Wisconsin dairy herds with rolling herd averages greater than 13,500 kg. Each herd was visited one time. Therefore, measurements were recorded only once per heifer. Body weight was estimated from heart girth measurements. Sire information was available for 1163 heifers from 75 to 800 days old. Heifers were sired by 295 bulls. Heritabilities and correlations were estimated assuming a multiple-trait sire model using Average Information REML. All models included a fixed herd effect, linear and quadratic age covariables, and a random sire effect. Heritability estimates were 0.31, 0.26, 0.32 and 0.14 for height, length, weight and BCS respectively. Genetic correlations were 0.58 between height and length, 0.27 between height and weight, and 0.3 between length and weight. Residual correlations among height, length and weight ranged from 0.23 to 0.39. Genetic correlations between BCS and height, length and weight were -0.39, -0.23 and 0.1 respectively. Residual correlations between BCS and the growth measurements ranged from 0.22 to 0.41. Standard errors for all genetic correlations ranged from 0.22 to 0.4, while residual correlations ranged from 0.08 to 0.1. Heifers that were genetically inclined to grow more rapidly tended to have lower BCS. However, management and environmental conditions that increased growth rate also increased BCS.

**Key Words:** heifers, growth, heritability

**1705 Accuracy of reported birth and calving dates of dairy cattle in the United States.** H.D. Norman\*, J.L. Edwards, and J.R. Wright, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*.

Frequencies of births that were reported for specific days of the month were documented for US dairy cattle born since 1987 by birth year, herd size, and registry status and compared with calving frequencies for those dates. Because birth dates are expected to be random and uniformly distributed throughout each month, percentages of births on individual dates were expected to be equal (3.3% for d 1 through d 28, 3.2% for d 29, 3.0% for d 30, and 1.9% for d 31). However, percentages of reported birth dates for d 1, 2, 10, 15, and 20 were higher than expected. Percentage of reported births for d 1 was highest (5.3%) of all days of the month regardless of herd size or registry status. The nonuniform distribution of birth dates within month indicated that a substantial number of birth dates were unknown and that estimated birth dates had been reported. About 1.5% of birth dates overall appeared to have been estimated. The highest frequencies for birth dates on d 1 (5.9 to 7.4%) were found for registered cows during months that initiated age groupings for dairy shows (March, June, September, and December). Alteration of birth dates to gain an advantage in cattle shows is likely to have occurred. Birth dates for some registered cows were intentionally misrepresented as confirmed by comparison of birth dates of individual cows with calving dates of their dams. Reported calving dates appeared to be more accurate than reported births; the inflated frequency of recorded calvings on d 1 was only about 30% as large as the inflated frequency of recorded births. Because cow age is determined by birth date, proper reporting of birth dates is important to ensure the accuracy of standardized yield and fitness records and the genetic evaluations that are based on those records. When animals' recorded birth dates and their dams' calving dates differ, more credence should be given to the latter to improve accuracy.

**Key Words:** Birth date, Calving date, Accuracy

**1706 Expected correlated responses for conformation traits, 48 month stayability and milk yield of Mexican Holstein cattle.** M Valencia-Posadas<sup>1</sup>, F Ruiz-Lopez\*<sup>2</sup>, J Moro-Mendez<sup>3</sup>, and H Montaldo-Valdenegro<sup>1</sup>, <sup>1</sup>*Instituto de Ciencias Agrícolas. Universidad de Guanajuato. Guanajuato, Mexico.*, <sup>2</sup>*Cent. Nal. de Invest. en Fisiología y Mejoramiento Animal. INIFAP-SAGARPA*, <sup>3</sup>*Holstein de Mexico A.C.*

(Co)Variance components were estimated for mature equivalent first lactation milk yield (MY1), 48 month stayability (48ST) and 11 conformation traits: stature (ST), body depth (BD), rump angle (RA), thurl with (TW), foot angle (FA), rear legs side view (RS), bone quality (BQ), fore udder attachment (FU), front teat placement (FT), udder cleft (UC), udder depth (UD) and final score (FS). Mexican Holstein Association's pedigree information and classification system results were used on 3,409 cows. Derivative free REML was used to estimate (co)variance components under an animal model. Heritabilities for MY1 and 48ST were 0.25 and 0.01, respectively. Heritabilities for conformation traits ranged from 0.04 (UD) to 0.34 (ST). Genetic correlations among MY1 and the conformation traits ranged from -0.27 (UD) to 0.48 (UC) while those among 48ST and the conformation traits ranged from -0.30 (BD) to 0.69 (RS). Due to the high genetic correlations found specially between FT (0.40), FS (0.51), UD (0.52), and RS (0.69) with 48ST it could be recommended that these traits are used in selection programs to improve 48ST. Selecting for MY1 alone will improve UC, TW and to a lesser degree RA, since the genetic correlations were 0.48, 0.26, 0.10, respectively. When MY1, 48ST and FS were combined in an index, the optimum genetic advancement was obtained using a 3:1:1 ratio, which resulted in improvements of 739 kg, 0.40 % and 0.87 points per generation, respectively.

**Key Words:** Correlated responses, stayability, milk yield

**1707 The relationship between the estrous situation of donor cows and genetic gain in Japanese Holstein MOET populations.** Yoshinori Terawaki\*<sup>1</sup> and Yohei Asada<sup>2</sup>, <sup>1</sup>*Rakuno Gakuen University Dairy Science Institute*, <sup>2</sup>*Rakuno Gakuen University*.

The relationship between the estrous situation of donor cows and genetic gain in Japanese Holstein MOET (multiple ovulation and embryo transfer) populations was examined using Monte Carlo simulation. The observed data (n = 306) used in this study were from an MOET program that has been carried out in Hokkaido, Japan. The data were divided into three parts, according to the degree of estrus (strong, normal or delicate) of donor cows. For each of those parts, the distribution of the number of transferable embryos collected per flush (NTECPF) was researched. Determination methods, using the Poisson and gamma (alpha = 1.0) distributions, were developed in order to generate the numbers fitting the distribution of NTECPF. The genetic gains and inbreeding coefficients in MOET populations with several different estrous situations were estimated using these determination methods. Four estrous situations, referred to as A, B, C and D, were assumed. Strong, normal and delicate estrus were assumed to occur in the ratio 7:2:1, 5:4:1, 3:6:1 and 1:8:1 in A, B, C and D, respectively. The base population was assumed to be 200 cattle. Ten males and 30 females were selected in each generation. The rates of strong, normal and delicate estrus in the observed data were 33, 58 and 9 %. The generated numbers were best fitted to the distributions on the observed data when beta of the gamma distribution was set at 7.6, 4.4 and 2.6 for strong, normal and delicate estrus, respectively. The mean NTECPF was highest (6.3) in A and lowest (4.6) in D. The frequencies of flushes that collected no transferable embryos were lowest (14.7%) in A and highest (18.7%) in D. For juvenile schemes, the largest genetic gain (5.4 genetic standard deviation unit) in the 10th generation was predicted to occur in C. The genetic gains in A and D were about 5.2 in the 10th generation, and these were the smallest. For adult schemes, the largest genetic gain (8.4) was predicted in A. The mean genetic gains increased as the ratio of strong estrus increased.

**Key Words:** Genetic gain, Estrous situation, Holstein MOET

**1708 Economic weight and selection index with variance of milk yield, herd life, and depreciation cost .** Y. Matsuoka\*<sup>1</sup> and Y. Terawaki<sup>2</sup>, <sup>1</sup>*The Graduate School of Dairy Science, Rakuno Gakuen Univ.*, <sup>2</sup>*Rakuno Gakuen Univ. Dairy Science Institute.*

The goals of this study were to estimate the economic weight of the aggregate breeding value and to create a selection index from the point of view of milk yield and longevity. Aggregate breeding value was defined as  $H = aMY \text{ GMY} + aHL \text{ GHL}$ . Economic weights were  $aMY$  and  $aHL$  for milk yields and herd life, respectively. These values were estimated based on the partial derivatives of milk yield and herd life to the derived function which was calculated as the revenue minus cost per year per cow in Hokkaido, Japan. The relative economic weight of milk to herd life was calculated as  $aMY/aHL$ . Selection index traits were actual milk yield and four body traits—mammary system, angularity, rear udder height and udder support—for herd life at 48, 60, and 72 months. Therefore, the selection index was  $I = bMY \text{ pMY} + bMS \text{ pMS} + bAG \text{ pAG} + bUH \text{ pUH} + bUS \text{ pUS}$ . In these analyses, milk yield, herd life, and depreciation cost were changed from -60 to 60 percent. With change in the milk yields,  $aMY$  decreased,  $aHL$  increased to 6,400kg of milk, after which it showed a decrease. Both  $aMY$  and  $aHL$  decreased with the change in herd life, whereas they increased with the change in depreciation cost. The two curves of the relative economic weight of milk to adjusted herd life with the change in milk yield and the depreciation cost change were similar; the relative economic weight decreased within the range of approximately from 3 to 12 as the percentage increased. With the change in herd life, the tendency of the relative economic weight differed from the change in milk yields and depreciation cost change, while the relative economic weight increased within the range of approximately from 1 to 12. Each tendency of the weighting factors of the selection index regarding the changes in milk yield and herd life were similar in fluctuation:  $bMY$  and  $bMS$  increased, whereas  $bAG$ ,  $bUH$ , and  $bUS$  decreased.

**Key Words:** Economic weight, Selection index

**1709 Determining Weights in a Multiple Objective Programming Dairy Breeding Problem.** Peter Tozer\* and Jeffrey Stokes, *The Pennsylvania State University.*

A survey of animal breeding scientists and representatives from breeding companies provided two sets of information regarding the rankings and relative importance of three objectives in the breeding decision: maximizing net merit; minimizing inbreeding; and minimizing semen cost. Each group ranked the objectives in a slightly different order; net merit was the top objective for both groups, while each group ranked the other two objectives in opposite order. The scores were analyzed through an application of the analytic hierarchy process to determine the set of weights from each group for use in multi-criteria decision making (MCDM) models. The models were used to examine the impact the different rankings and weights had on the sire portfolio selected. Another aspect of the MCDM model tested was the sensitivity of the results to the degree of non-linearity of the function chosen. Linear programming models of the three single objectives were estimated to provide the ideal and anti-ideal values for use in the MCDM models. The single objective models were based on selecting sires for a representative group of 60 cows to be bred. Constraints were placed on the total number of semen units to be purchased in total and on the number of units from any one sire. The portfolios of sires selected by the MCDM models for each set of weights are similar, in that sires with high net merit were selected. This is not surprising given that the net merit weights were approximately 4 times greater than the next objective for each group. Minor differences in the portfolio selected occurred when the model was changed from a linear formulation to the quadratic form. However, a major difference in the portfolios selected occurred when the degree of non-linearity increased from the quadratic to the MINIMAX formulation. In the MINIMAX portfolios the levels of the second objective, either inbreeding or semen cost, were reduced by 27% and 23% when compared to the linear specification portfolios, however, these reductions came at a reduction in average net merit of the portfolios, 9% and 12%, respectively.

**Key Words:** analytic hierarchy process, breeding, multiple objective programming

**1710 Relationships and inbreeding among young dairy bulls entering AI progeny test programs.** K. A. Weigel\*, *University of Wisconsin, Madison.*

Inbreeding is an expected but undesirable consequence of rapid genetic progress in modern breeding programs. Reproductive technologies allow rapid propagation of a few elite individuals and families, and this can increase inbreeding levels quickly. In a two-stage selection scheme, inbreeding is primarily a function of relationships between young bulls entering artificial insemination (AI) progeny test programs. Our objective was to examine the genetic diversity present within the young AI sire populations of the five major US dairy breeds. Assuming an inbreeding base year of 1960, young sires born in 1998-1999 were, on average, related to their respective breeds by 13.1% for Ayrshires, 11.6% for Brown Swiss, 11.8% for Guernseys, 10.1% for Holsteins, and 14.6% for Jerseys. Individual sires of sons were extremely influential. The percentages of these young bulls that were sired by the five most popular sires of sons were 100% for Ayrshires, 68% for Brown Swiss, 71% for Guernseys, 42% for Holsteins, and 76% for Jerseys. Genetic diversity is also limited on the maternal side of the pedigree. Among the current elite cows (top 5%) in the US, the percentages of cows that were offspring of the five most popular sires were 45% for Ayrshires, 46% for Brown Swiss, 51% for Guernseys, 17% for Holsteins, and 57% for Jerseys. Dairy cattle breeding is a global business, and it appears that the major dairy countries are all drawing from the same gene pool. Data from countries that currently participate in the Interbull dairy sire evaluations were also examined. Individual sires of sons were used very heavily internationally. The percentages of bulls born in 1995 that were sired by the ten most popular sires of sons were 54% for Ayrshires, 59% for Brown Swiss, 100% for Guernseys, 43% for Holsteins, and 66% for Guernseys. Strategies such as computerized mating programs can help reduce inbreeding in the next generation of replacement heifers, but long term maintenance of genetic diversity will require constraining the relationships between young AI bulls.

**Key Words:** inbreeding, dairy sires, progeny testing

**1711 The use of fuzzy set to reduce inbreeding in MOET breeding schemes.** Atsushi Nakamura\*<sup>1</sup>, Kenji Togashi<sup>2</sup>, Naoyuki Yamamoto<sup>2</sup>, and Akiko Nishiura<sup>2</sup>, <sup>1</sup>*Japan Science and Technology Corporation*, <sup>2</sup>*Hokkaido National Agricultural Experiment Station.*

Increased rates of inbreeding in multiple ovulation and embryo transfer (MOET) breeding schemes may have an important effect on genetic response to selection and reproductive ability through inbreeding depression and loss of genetic variability. The assumption of constant family size per donor has been assumed in earlier studies of mate selection to control inbreeding. However, the number of mates per donor will vary because the family size changes, depending on the number of embryos per donor. Therefore, the objective of this study was to examine mate selection using fuzzy set to control inbreeding on the assumption of a variable family size. Mate selection was carried out based on a selective mating criterion (FMC), which is an aggregated value of two fuzzy sets by algebraic product and trade-off parameters. These fuzzy sets were described as 'higher average breeding value of mate pair' and 'lower coancestry', respectively. The fuzzy membership functions were defined as logistic function. The value of the trade-off parameter between these two fuzzy sets was set to from 0 to 1. Stochastic simulation was used to study the effect of mate selection on rates of genetic response and inbreeding with a closed adult MOET nucleus breeding program. Milk production the the selected trait and heritability was 0.30. The number of embryos collected from a donor in one flush was sampled from a Poisson distribution. Hierarchical and factorial mating designs were examined. When the trade-off parameter changed from 0.25 to 0.75, the genetic response and inbreeding rates in the hierarchical mating design ranged respectively from 100 to 98% and from 64 to 47% of those in a hierarchical random mating design. The responses in the factorial mating design ranged from 102 to 95% and 57 to 40%, respectively. In conclusion, mate selection based on FMC does not guarantee optimum mate decision as does mate selection with a mathematical programming method. However, this mate selection criterion avoided mating of close relatives and reduced inbreeding on assumption of a variable family size.

**Key Words:** Fuzzy set, Inbreeding, Mate selection