

**M65 Test-day milk loss associated with elevated test-day somatic cell score.** R. H. Miller\*, H. D. Norman, G. R. Wiggins, and J. R. Wright, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

To determine usefulness of current and previous test-day somatic cell score (SCS) in predicting test-day milk yield, test-day records from Holstein first and second calvings between 1995 and 2002 were examined. Initial selection required that cows have at least the first four test days with recorded milk yield and SCS for both parities 1 and 2. Least-squares analyses were conducted for milk yield on test days 2 through 10 within herd and cow. The model included regressions on both current test-day SCS and mean SCS of all previous test days with separate estimates by parity; effects for parity and calving year also were included as well as a regression on days in milk on test day 1. Error degrees of freedom ranged from 143,748 to 214,526. Highest SCS was most often on test day 1 (20%) followed by test day 10 (14%). Ranges of regression

coefficients (kilograms of milk per unit of SCS) are in the table. Effect of current SCS on test-day milk yield was much greater for parity 2 than for parity 1 but only slightly greater than effect of mean of previous test-day SCS on milk yield for parity 1. Milk loss from elevated SCS likely results both from mammary status on test day and from direct and residual influences of elevated SCS earlier in lactation. Mastitis in early lactation appears to have a carryover effect on milk yield for the remainder of the lactation.

Parity	Previous test-day Maximum effect		SCS mean Minimum effect		Current test-day Maximum effect		SCS Minimum effect	
	Coeffi- cient	Test day	Coeffi- cient	Test day	Coeffi- cient	Test day	Coeffi- cient	Test day
1	-0.346	9	-0.142	2	-0.401	10	-0.216	3
2	-0.366	4	0.021	10	-1.209	10	-0.489	4

**Key Words:** Somatic cell score, Test-day milk, Mastitis

## Breeding & Genetics

**M66 Optimising genetic gain in a small population.** A. Karlsen\*, T. Steine, and E. Sehested, *GENO Breeding and A.I. Association.*

Small farms characterize dairy production in Norway. The average herd size in 2002 was 15.3 cows. Although the herd size is increasing, the number of cows has been slowly decreasing over the last years. The Norwegian Dairy Cattle (NRF) population is currently about 300,000 cows. Phenotypic data on health, fertility traits, production (yield and beef), calving information and management has been reported to the Norwegian Dairy Herd Recording System (NDHRS) since 1978, and recordings are compulsory for members. In 2002 96% of the cows were part of the NDHRS. These cows represent the breeding population of NRF. Dams are considered as sire mothers if their total merit index, milk production and pedigree meet the requirements. Every year about 400 bull calves are purchased based on their pedigree information at approximately 3-4 months of age. In the period between 5-12 months of age, they are evaluated for growth rate, conformation and semen quality. The 120 best young bulls are then selected for progeny testing. Several functional traits (fertility, mastitis resistance, other diseases, calving ease and stillbirths) are included in the total merit index. To perform progeny testing for these traits, breeding values are based on 250-300 daughters. After progeny testing the best 10-12 sires are selected as elite sires. Selection is based on total merit index and also on number of sire lines represented and number of close relatives in use. To prevent inbreeding, a restriction is put on the use of sires. The optimum distribution between use of young bulls for progeny testing and elite sires are 40:60 in the NRF population. A computer program is distributed to all farmers that optimise use of young bulls and elite sires in the herd, and suggest the optimum mating combinations. Farmers can download the program freely, or get a breeding plan from the dairy advisor that runs this program on routine basis for the farmers. It is assumed that approximately 90% of the farmers use the breeding plan. Through this breeding scheme a small population is turned into a large breeding population.

**Key Words:** Genetic gain, Small population, Norwegian dairy cattle

**M67 Identification of quantitative trait loci affecting birth and weaning weights in pigs.** J. W. Holl\*<sup>1</sup>, J. P. Cassady<sup>2</sup>, and R. K. Johnson<sup>1</sup>, <sup>1</sup>University of Nebraska, Lincoln, NE, <sup>2</sup>North Carolina State University, Raleigh, NC.

A whole-genome scan was used to identify chromosomal regions and estimate quantitative trait loci (QTL) that affect individual pig birth weight (BWT) and weaning weight (WWT). A three-generation resource population was developed by crossing a randomly selected control line with high-indexing pigs from a line selected for an increased index of ovulation rate and embryonic survival. Phenotypic data were collected on F<sub>2</sub> females, born in three replicates, for BWT (n = 428) and WWT (n = 405). Grandparent, F<sub>1</sub>, and F<sub>2</sub> animals were genotyped for 151 microsatellite markers. Calculations of logarithms of odds (LOD) scores were by least squares. The full model included fixed effects of replicate, sire-dam combination as a polygenic effect, and coefficients for additive and dominance effects as fixed regression coefficients. The reduced model included fixed effects of replicate and sire-dam combination. Genome-wide critical  $\alpha = 0.01$ ,  $\alpha = 0.05$ , and  $\alpha = 0.10$  levels

were established using a permutation approach. There was evidence (P < 0.10) for QTL affecting BWT on SSC8 between markers OPN and SO178 and on SSC12 between markers SO143 and SX957, with additive effects of the allele inherited from the control line of  $-0.020 \pm 0.017$  kg and  $-0.059 \pm 0.019$  kg and dominance effects of  $0.085 \pm 0.031$  kg and  $-0.073 \pm 0.037$  kg, respectively. No QTL were detected for WWT. Knowledge of QTL for BWT should be considered to maintain neonatal survival in selection programs that may indirectly have an adverse affect on BWT.

**Key Words:** Pigs, Quantitative trait loci, Weight

**M68 Detecting quantitative trait loci for twinning and production traits in Holstein dairy cattle.** J. Cruickshank\*<sup>1</sup>, M. R. Dentine<sup>1</sup>, P. J. Berger<sup>2</sup>, and B. W. Kirkpatrick<sup>1</sup>, <sup>1</sup>University of Wisconsin-Madison, Madison, Wisconsin, <sup>2</sup>Iowa State University, Ames, Iowa.

Twinning in dairy cattle has been associated with many negative health and reproductive events that cause economic loss to the producer. Reports have suggested that twinning rates are increasing and that there may be a positive relationship between milk production and twinning frequency. Quantitative trait loci (QTL) for twinning rate on bovine chromosomes 5, 7, 19, and 23 have been previously identified in other populations. The objectives of this study were to detect and confirm the existence and effects of these QTL and to look for QTL for milk yield, fat and protein yield and percent, somatic cell score (SCS), and productive life in those same chromosomal regions. Half-sib families of 25 North American Holstein sires with high twinning rate PTA comprised the population under investigation. This project utilized sire predicted transmitting ability (PTA) values for the production traits from USDA. Twinning rate PTA values were estimated from calving data. DNA extracted from semen samples was analyzed using 45 microsatellite markers across the four chromosomes. Marker heterozygosity of the patriarchs averaged 56%. Evidence of twinning QTL was found in multiple families on chromosomes 5 and 23 at a chromosome-wise p < 0.05. Similarly, evidence of QTL was found on chromosome 7 for milk; chromosomes 5, 7, and 19 for fat yield and fat percent; chromosome 7 for protein yield; chromosome 5 for protein percent; and chromosomes 5, 19, and 23 for SCS. Most of these families are related within three generations and will be combined into larger, multi-generation families for further analysis. For twinning QTL replicated in Holsteins, chromosomal positions will be more narrowly defined by haplotype analysis. Frequencies of haplotypes associated with twinning will be estimated in elite Holstein cow populations.

**Key Words:** QTL, Twinning, Cattle

**M69 Development of three repeat microsatellite loci in Korean cattle.** S. Chen, H. Chung\*, D. Yoon, I. Cheong, and S. Lee, *National Livestock Research Institute, Suwon, Korea.*

Microsatellite, which contained tri repeats, have been isolated in Korean cattle (Hanwoo). The pooled Korean cattle genomic DNA, which was digested with Sau3AI and separated onto agarose gels, was recovered

for 3 sections (200 to 500 bp, 500 to 1000, 1000 to 2000). For the construction of the bovine genomic libraries, a PCR-enrichment procedure was employed resulting in 14 libraries. Selection process for the tri and tetra repeat sequences were performed using PCR with biotined oligo primers. After blue/white colony selection, the positive colonies were sequenced with an ABI 3730 automatic sequencer to identify the repeat sequence. A total of 14 genomic libraries were constructed for Korean cattle using 4 unrelated individuals. Clones, which were 8,198 from 14 Hanwoo genomic libraries for 3 repeat sequences, were identified and sequenced. The association test was conducted for weight traits using the isolated microsatellite.

**Key Words:** Microsatellite, Bovine, Weight

**M70 Graphical approach to evaluate genetic estimates of calf survival.** H. Schlessler\*<sup>1</sup>, R. Shanks<sup>1</sup>, J. Berger<sup>2</sup>, and M. Healey<sup>2</sup>, <sup>1</sup>University of Illinois Urbana-Champaign, <sup>2</sup>Iowa State University.

Identification of bulls with bimodal pattern of inheritance could allow for more selective and efficient genotyping. A bimodal pattern of inheritance for calf survival was identified in sons of Holstein bulls. This pattern of inheritance is indicative of an allele effect or a sire of mates effect. Large allelic effects could lead to bimodal pattern of inheritance for bulls heterozygous for quantitative trait loci affecting calf survival. However, caution is needed because unequal distribution of sire of mates may indicate nonrandom matings. Data on predicted transmitting ability (PTA) for the first and second parity of 12034 sons were collected from 1984 through 1997 from seven Midwestern states. Fifty-four bulls had at least 50 sons and were included in the analysis. The data set was further restricted to fifty-two bulls having at least 25 sons with first parity PTA for calf survival. Seventeen bulls were identified with a potential bimodal pattern of inheritance, through a graphical method. In order to graphically determine a bimodal pattern of inheritance, PTAs for first parity were multiplied by one thousand and truncated to form an integer score for each son. This created several sons with the same score as other sons. These scores were then plotted against number of sons with each score. The bimodal patterns were quantified by equating coefficients of variation between the two groups. The seventeen bulls were analyzed to determine the distribution of the sires of mates between groups. Sires of mates were nonrandomly distributed between groups for fifteen of the seventeen bull families.

**Key Words:** Mating distribution, Calf survival

**M71 Analysis of health and fertility traits for proven and young sires in herds participating in a progeny test program using data from on-farm herd management software.** N. R. Zwald\*<sup>1</sup>, K. A. Weigel<sup>1</sup>, and B. Welper<sup>2</sup>, <sup>1</sup>UW-Madison, <sup>2</sup>Alta Genetics.

The objective of this study is to analyze health and fertility traits within a selected group of 126 Holstein herds using DC305, PCDART, or DHIPLUS and enrolled in the same progeny test program. Herds range in size from 200 #3300 cows and are located in the Northeast (VA, MA, NY, PA, OH), Midwest (WI, MN, IA, IL, MI), the West (CA, OR, WA, ID), and Texas. Herds have been tested to have accurate DNA results, and perform regular pregnancy exams. Service sires were analyzed for male fertility on a conception rate basis, with all AI services being considered. 301,777 services were analyzed on 95,321 animals for 3646 service sires from 1/1/01-2/1/03. The model was response=HYS + cow + herd\*service sire + service sire + type of sire (young sire vs. proven) + type of animal (heifer vs. cow) + dim. Overall conception rate was 26.2%, and conception rate on young sires was 22.9%, and was 29.2% on proven bulls. Conception rate on virgin heifers was 50.8% and was 23.3% on milking cows. The proportion of the total variance attributed to the service sire was 1.36%. The correlation between the results of this analysis and the ERCR ranking was 31%. This research shows that if pregnancy exam data was stored and could be used for fertility evaluations, the accuracy and heritability of both female and male measures of fertility would be increased. Disease incidence was also studied to determine possibilities for genetic evaluations for health traits. 60 of the 126 herds were recording some type of early metabolic disorder, 47 were recording clinical mastitis, and 44 were recording lameness or foot trimming events. Disease incidences on herds recording data were: 14.8% for mastitis and 11.0% for early metabolic disorders, which included

ketosis (5.2%), Metritis (1.8%), displaced abomasums (1.8%), and retained placentas (2.3%). This suggests that efforts need to be made to improve the recording of health traits on all farms before any national genetic evaluation for these traits is warranted, however groups of herds using similar sires with accurate identification and proper recording of health information could be used to test for genetic differences to disease resistance within progeny test situations.

**M72 Post-weaning relative growth in body weight of black bengal and its half bred kids.** L. B. Singh\*<sup>1</sup>, D. K. Singh<sup>1</sup>, N. Kumar<sup>1</sup>, N. S. Singh<sup>1</sup>, A. K. Pal<sup>1,2</sup>, and S. B. Jadhao<sup>2</sup>, <sup>1</sup>Ranchi Veterinary College, Ranchi 834007, <sup>2</sup>Agricultural Research Service, Central Instt. Fisheries Education, Mumbai 400061, India.

The present study was conducted on 614 (145, Black Bengal; 310, 1/2 Jamunapari + 1/2 Black Bengal and 159, 1/2 Beetal + 1/2 Black Bengal) kids of 51 sires born during 1981-86 under All India Coordinated Research Project on Goats at this institute. Relative growth rate (RGR) in body weight was studied during 12-24, 24-36, 36-48, 12-36, 12-48 and 24-48 weeks of age. The variation in RGR during 12-24 weeks of age due to year of birth ( $P \leq 0.01$ ) was significant. While RGR during 24-36 weeks of age varied significantly due to season of birth and birth weight ( $P \leq 0.01$ ). During 36-48 weeks of age, the effects of year of birth and sex ( $P \leq 0.01$ ) on RGR was significant. However, during 12-36 weeks, it varied significantly due to season of birth ( $P \leq 0.05$ ) and birth weight ( $P \leq 0.01$ ). During 12-48 weeks of age, the effect of type of birth and parity of dams on RGR was significant ( $P \leq 0.05$ ). In general, the random effect of sire on RGR was not significant except during 24-36 weeks of age. Heritability estimate of RGR in post-weaning body weight ( $0.023 + 0.225$  to  $0.216 + 0.153$ ) was low to medium. The RGR during 12-24 weeks had positive and significantly ( $P \leq 0.01$ ) phenotypic (0.293) association with RGR during 12-48 weeks of age.

**Key Words:** Kids, Relative growth rate, Half bred

**M73 Genetic correlations among body condition score, dairy form and disease from the US.** C. D. Dechow\*<sup>1</sup>, G. W. Rogers<sup>1</sup>, T. J. Lawlor<sup>2</sup>, L. Klei<sup>2</sup>, A. E. Freeman<sup>3</sup>, and G. Azim<sup>3</sup>, <sup>1</sup>University of Tennessee, <sup>2</sup>Holstein Association USA, Inc., <sup>3</sup>Iowa State University.

The objectives of this study were to estimate genetic correlations among body condition score (BCS), dairy form (DF) and measures of cow health. Observations for BCS and DF were obtained from Holstein Association USA Inc. Body condition score and DF records were edited to include those cows with valid BCS and that were classified between 24 and 60 months of age and between 0 and 335 days in milk. A minimum of 10 cows per herd-classification visit (HV) and 20 daughters per sire were required. Only one record per cow was used in the analyses. Records were available for 183,044 cows after edits. Health data were obtained from several herds that participated in a Genex/CRI pilot health recording study and recorded all veterinary treatments. The diseases included in the analyses included displaced abomasums (DA), metabolic disease, foot diseases, uterine diseases and mastitis. Herd mates that calved during the same year and season of cows with one or more observations for disease, but that did not have a disease observation were assumed to be disease free. A minimum of 5 cows per herd-year-season (HYS) was required. The edited data set included 6247 cows, 221 of which had BCS and DF observations available. Genetic correlations among disease, BCS and DF were estimated with multiple trait sire models in ASREML. Models included age at calving nested within lactation group, 5th order polynomials of DIM nested within lactation group, fixed HV effects and random sire and error for BCS and DF. Models for disease traits included a fixed HYS effect, age at calving nested within lactation group, and random sire and error. Body condition score was significantly correlated with lower incidence of DA (-0.84) and metabolic disease (-0.95), whereas DF was significantly correlated with higher incidences of DA (0.86) and metabolic disease (0.96). Cows that are genetically inclined to have high dairy form or low BCS may be more susceptible to DA and metabolic disease.

**Key Words:** Body condition score, Dairy form, Health

**M74 Estimation of genetic parameters in Japanese Holsteins using random regression test-day models with Legendre polynomials.** C. Fujii\* and M. Suzuki, *Obihiro University of A & VM, Obihiro-shi Japan.*

Legendre polynomials were adopted for drawing lactation curves. The objective of this study was to test statistically which order of polynomial can fit the lactation curve most effectively. Data were provided by Livestock Improvement Association of Japan and consisted of 19,397,399 test-day records and 4,087,621 pedigree records. The test-day records included 6 to 365 DIM. To determine the order of the polynomial, a sample data set with about 30,000 test-day records for 3000 cows in the first lactation was extracted from the entire data set. Pedigree records included up to three generations per animal. Using the sample data set, additive genetic variance-covariance components were estimated by REML for four models with second to fifth order Legendre polynomials. All effects in the models, except the order of the polynomial, were the same. The models included herd-test-day, season and age group effects as fixed, and additive genetic and permanent environmental effects as random. Setting the estimate from the fifth order polynomial to the criterion, the F test was used to find out the goodness of fit among the models. The difference between random regression models with the second and the third order polynomials was significant, and no difference was found between those with the third and the fourth order polynomials. The model with the third order polynomial better explained the lactation curve with fewest parameters. All data were divided into 400 datasets because of lack of computation memory, and ten sub datasets were sampled randomly. Genetic parameters were estimated using the random regression test-day model with the third order polynomial for the ten sub datasets. For each dataset, heritability was estimated at twelve points from DIM 30 to 360. The heritability estimates were 0.23 and 0.34 at DIM 30 and 360, respectively, increasing with DIM. The range of the heritability estimates (0.11) was smaller and more stable than that of other studies.

**Key Words:** Random regression, Test-day record, Holstein

**M75 Comparisons of purebreds and multi-breed crosses for preweaning performance, in swine.** A. Barreras-Serrano\*, J.G. Soto-Avila, and M. Montaño-Hodgers, *Universidad Autónoma de Baja California, Mexicali, B.C. México.*

A total of 214 litters sired by Landrace, Yorkshire or Duroc-Hampshire boars out of Landrace, Yorkshire, or multi-breed crosses sows were evaluated for preweaning performance. Traits of the dam (litter) that were studied included litter size, number born alive, litter birth weight, number alive at weaning, litter weight at weaning, and percentage of piglets born alive surviving at weaning. Other traits studied were piglet birth weight, weaning weight, and preweaning average daily gain. Six-subclass year-season were defined as result of combining three years (1999 to 2001) and two seasons (hot=from May to October, and cold=from November to April). The records were collected from 1999 to 2001. Data was analyzed using Henderson methods 1,2 and 3 and maximum likelihood using computer program PC-2, and using GLM and Mixed procedures from SAS software. Sire breeding values were estimated using progeny records. Landrace- or Duroc-Hampshire-sired litters were larger in number ( $P<.01$ ) and heavier at birth ( $P<.01$ ) than Yorkshire-sired litters. However, pigs sired by Yorkshire boars had higher birth weight ( $P<.01$ ) than pigs sired by Landrace boars. Landrace-sired litters were larger in number alive ( $P<.05$ ) at weaning than Yorkshire-sired litters. No significant differences among the sow breeds were noted in number at birth and alive at weaning or birth weight. Pigs out of Landrace and Yorkshire sows had higher weaning weight ( $P<.01$ ) and higher ( $P<.05$ ) preweaning average daily gain than pigs out of multi-breed crossed sows. Litters sired by Yorkshire boars showed higher percentage of pigs born alive surviving at weaning than litters sired by Landrace or Duroc-Hampshire boars. Heritability values estimated were moderates for growth performance indicating presence of genetic variability. In general, Duroc-Hampshire sires were the best ranked by breeding values for preweaning traits.

**Key Words:** Swine, Growth performance, Genetic evaluation

**M76 Genetic parameters for longevity in a colony of German Shepherd dog guides.** J. B. Cole\*<sup>1</sup>, D. E. Franke<sup>1</sup>, and E. A. Leighton<sup>2</sup>, <sup>1</sup>*Louisiana State University, Baton Rouge, LA,* <sup>2</sup>*The Seeing Eye, Inc., Morristown, NJ.*

Data on longevity for 1,304 German Shepherd dogs (GS) was used to estimate genetic parameters for working life. A Cox proportional hazards model on unadjusted working life was used to test the assumption that the baseline hazard function for the population is a Weibull hazard. The rejection of that assumption led to the definition of two measures of working life: estimated for working life to 18 months post-graduation (EWL) and working life beyond 18 months post-graduation (LWL). For EWL, 92.45% of the records were censored after 540 days, while for LWL 47.89% of the records were censored after 4,361 days. The Survival Kit v3.12 was used for variance components and breeding value estimation. Estimates of additive sire genetic value for Cox and unstratified Weibull models were 0.87 and 0.36 for EWL and 0.05 and 0.03 for LWL, respectively. Heritability estimates on a log scale (assuming no censoring) were 0.19 and 0.61 for EWL and 0.09 and 0.04 for LWL, respectively. For both traits, the standard deviations and skewness of the posterior densities of the sire variance were fairly large. Due to the small size of the dataset and the large number of censored records, it was not possible to obtain more precise estimates of the sire variance. The large heritabilities observed for EWL under the Cox and Weibull models should be interpreted with caution because virtually all EWL records were censored. Pearson's product-moment correlation coefficients for sire breeding values estimated under the Cox and Weibull models were 0.99 for EWL and 0.88 for LWL, respectively. The low correlation between the models for LWL may be due to large prediction error variances and the skewness of the posterior distribution of sire effects, although these problems were noted for EWL as well.

**Key Words:** Variance components, Working life, Dog guides

**M77 Genetic parameters for net feed efficiency of beef cattle measured during postweaning growing versus finishing periods.** D. H. Crews, Jr.\*, N. H. Shannon, B. M. A. Genswein, R. E. Crews, C. M. Johnson, and B. A. Kendrick, *Agriculture and Agri-Food Canada Research Centre, Lethbridge, Alberta, Canada.*

Individual feed intake was recorded during 84-d growing and 112-d finishing periods on Charolais-sired crossbred steers ( $n = 410$ ). Steers consumed a barley silage-based diet during the growing period, and a barley grain-based diet during the finishing period. Following finishing, steers were harvested at a commercial packing facility where carcass data were collected 24 h postmortem. Net feed efficiency was estimated for the growing (NFG) and finishing (NFF) periods using linear regression procedures such that within-period phenotypic correlations of efficiency measures with average daily gain and average metabolic body weight were zero. Net feed efficiency during the growing (finishing) period varied from an efficient -4.10 (-4.77) kg per d to an inefficient 4.65 (3.30) kg per d. Using an animal model and restricted maximum likelihood, genetic parameters were estimated among NFG, NFF, and age-adjusted (463 d) carcass traits, including hot carcass weight (HCW), fat thickness (FAT), longissimus muscle area (REA), and marbling score (MAR). The relationship matrix among 975 animals included a minimum of a three generation pedigree for the 34 Charolais bulls that sired steers with records. Heritability estimates were moderate for NFG ( $0.30 \pm 0.06$ ) and NFF ( $0.26 \pm 0.07$ ), whereas carcass trait heritabilities were constrained to literature averages to avoid convergence failure. Phenotypic and genetic variance estimates for NFG were higher than those for NFF. The genetic correlation between NFG and NFF was 0.55. Genetic correlations of NFG and NFF with HCW and REA were weak to moderate and positive, but were negative and generally weak with FAT. The genetic correlation of MAR with NFG was near zero (0.08) but was strongly negative (-0.44) with NFF. These results suggest that a high and positive genetic association exists between net feed efficiency measured when cattle were consuming roughage- versus grain-based diets, although these traits may not be biologically equivalent.

**Key Words:** Beef cattle, Net feed efficiency, Genetic parameters

**M78 Preliminary study of daily gain in central station-tested Nelore bulls.** J.A.C. Pereira\*<sup>1</sup> and J. E. Chavez<sup>2</sup>,  
<sup>1</sup>Gabriel Rene Moreno University, <sup>2</sup>ASOCEBU.

The objectives of the study were 1) to investigate a method to base the selection of Nelore bulls on their growth performance in a grassing system under subtropical conditions, and 2) to determine the preferable trait to be used as a selection criterion in a central evaluation station. Each year approximately 1,500 weaned, young bulls were available to be tested. This number was restricted due to the physical limitations of the station. Therefore, each year, a pre - classification of the bulls was performed. Only young bulls with weaning weights above the herd average and acceptable conformation were selected. In this study data was collected on 130 young sires from different farms over four consecutive years. They were kept on pasture before and during the test (280 days). All the animals were managed under a rotational grazing system. The only *ad libitum* supplementation was mineral salt. During the test period the animals were weighted every 28 days. Six traits were measured; Birth Weight (BW), Beginning Weight at Test (BGT), Age in Days at the beginning of the Test (ADT), Daily Gain from birth to the beginning of the test (DG1), Daily Gain during the test (DG2) and the Final Weight at the test (FW). Harvey's least square program was used to analyze the data. The model used was the pre determined "model 1" of fixed effects. The results showed that BW, DG1 and FW were significantly different among farms and were not used as selection criteria. It is proposed to select bulls using their DG2 value, which is a preferable selection criterion because it was not affected by farm. The results also indicated that Nelore bulls might have great potential to be selected under grazing systems. The adjusted daily gain measured in the four consecutive years ranged between 0.658 and 0.726 grams per day. Further research should be performed including other effects such as dam's parity, in order to estimate the genetic performance more accurately. In addition, a new approach (testing on farms) should be investigated in order to include all the young bulls weaned each year.

**Key Words:** Grazing systems, Nelore, Daily gain

**M79 Setting up the Gelbvieh multiple breed evaluation.** A. Legarra\*<sup>1</sup>, T. Strabel<sup>2</sup>, J. K. Bertrand<sup>1</sup>, and I. Misztal<sup>1</sup>,  
<sup>1</sup>University of Georgia, Athens, GA, <sup>2</sup>Agricultural University of Poznan, Poznan, Poland.

The Multiple Breed Evaluation for the Gelbvieh breed was developed, generally following ideas applied first in the Simmental evaluation by Cornell University. The main challenges for genetic evaluation were related to assumptions of grouping breeds to form super-breeds and fixing the (arbitrary) accuracy of the priors for heterosis and breed of founder genetic group effects. The data set did not allow for a correct estimation of all these effects, so priors were taken from literature. Genetic difference between Gelbvieh and Angus breed of founder priors were 26.5 (var=7.48E-05) and -3.7 (var=0.11E-05) kg for weaning weight and yearling gain respectively. Some results of the evaluation were strongly

affected by the priors, although results for Gelbvieh as the main breed stayed basically the same. Gametic trends for Gelbvieh were: 0.34 and 0.33 kg/year for weaning weight and 0.43 and 0.44 kg/year for yearling gain with or without priors, respectively. For Angus, trends were non-linear and about 0.10 and 0.32 kg/year for weaning weight and 0.71 and 0.67 for yearling gain with or without priors, respectively. As the number of pure-bred Angus animals in data was very low (97 out of 666,513) it seems that gametic trends for Angus were a mixture of the evolution of Angus genes in the Gelbvieh population and the original Angus population. Differences between Gelbvieh and Angus gametic average breeding value for year 1995 were 0.87 and 9.91 kg for weaning weight and -3.64 and -4.04 kg for yearling gain with and without priors, respectively. The results from the study indicate that estimation of genetic differences between breeds in current pure-breed associations data banks is very dependent on the weight given to the prior literature values relative to the data. More understanding on how results are influenced by priors and data is needed.

**Key Words:** Gelbvieh, Multiple breed evaluation, Genetic evaluation

**M80 Differences in growth trajectories in seven beef breeds.** J. Bohmanova\*<sup>1</sup>, I. Misztal<sup>1</sup>, and J. Pribyl<sup>2</sup>, <sup>1</sup>University of Georgia, Athens, GA, <sup>2</sup>Research Institute of Animal Production, Prague, Czech Republic.

The objective of this study was to estimate average breed growth curves and assess differences in growth performance between breeds and sexes. A total of 140,503 weight records from birth to 360 days on 60,284 animals provided by Czech Beef Breeders Association were used to compare growth of Charolais (14,340), Simmental (10,382), Angus (9,622), Limousin (6, 046), Hereford (16,362), Blond D' Aquitaine (2,020) and Piedmontese (1,512). Effects included in the model of analysis were herd, year and dam age class and regression on orthogonal polynomials nested within sex. Adjusted mean weight from birth to 360 days was estimated for heifers and bulls. All computations were by breed. Charolais bulls and heifers had the highest birth weights with 41 kg and 39 kg, respectively. Hereford bulls and heifers had the lowest birth weights with 30 kg and 29 kg, respectively. Simmental and Charolais were the fastest growing breeds, with bulls from these breeds weighing 484 kg and 467 kg at 360 days of age, respectively. Herefords had the slowest growth of all breeds. Simmental, Charolais, Angus and Blonde D' Aquitaine bulls had similar growth trajectories. Sex differences in body weight at 240 days of age ranged from 33 kg in Blond D' Aquitaine to 18 kg in Hereford. Growth of heifers slowed down considerably after 240 days of age. Angus and Piedmontese heifers stopped growing at 330 days. Bulls grew linearly till 270 days of age, after which their growth accelerated considerably. This increased growth after 270 days of age can be explained by an increasing proportion of records coming from bulls raised in test stations.

**Key Words:** Beef cattle, Growth, Breed differences

**Swine: Impact of Weight and Sex on Meat Quality, Effect of Age Management on Biochemical Parameters, Disinfectant, Gilt Selection and Sow Longevity**

**M81 Economic evaluation of sow longevity using data from commercial herds.** S. L. Rodriguez-Zas\*<sup>1</sup>, B. R. Southey<sup>1</sup>, R. Knox<sup>1</sup>, J. F. Connor<sup>2</sup>, J. F. Lowe<sup>2</sup>, and B. Roskamp<sup>2</sup>,  
<sup>1</sup>University of Illinois Champaign-Urbana, Urbana, IL, <sup>2</sup>Carthage Veterinary Service, Ltd., Carthage, IL.

Sow longevity and lifetime production are critical determinants of the profitability of pork production systems. A study was conducted to assess the impact of genetic line on multiple indicators of sow longevity and production traits. Records from more than 100,000 sows in 32 US commercial herds across five years were analyzed using survival and mixed effect repeatability models. The variation among genetic lines was evaluated in biologic and economic units using the net present value per sow. Explanatory variables included herd, year of entry into the herd and genetic line. Significant differences in sow longevity and production traits were observed between genetic lines. Since the economic magnitude of the effect of sow longevity primarily depended on the discount rate and net income per litter per sow, all genetic lines were assumed to differ in the median longevity. Hence, the results from the economic analysis apply to the average sow from each genetic line. Assuming zero

discount rate per parity, the genetic line with longer herd life showed greater profit than genetic lines with the shorter herd life. Under these conditions and assuming a \$10 net income per litter, no genetic line was profitable. Assuming a \$50 net income per litter, the difference in net present value per sow between the highest and lowest lines for longevity was \$52.39 and the difference between the highest two lines for longevity was \$13.94. Assuming a \$10 net income per litter, the difference between the highest and lowest lines for longevity was \$10.48 per sow and the difference between the highest two lines for longevity was \$2.79 per sow. The difference in net present value between genetic lines was considerably reduced with increasing discount rates and was reversed with high discount rates and low net income per litter. The significant differences in sow longevity among genetic lines were not translated into substantial economic differences for the range of discount rates considered. Results from this economic analysis indicate that the manipulation of the genetic line composition of a herd is an important factor in the achievement of a profitable swine production.

**Key Words:** Economic, Survival, Swine