

**1000 Impacts of livestock forage and pasture use on carbon sequestration and greenhouse gas emissions.** D.E. Johnson\*, H.W. Phetteplace, A.F. Seidl, and R. Conant, *Colorado State University, Ft Collins, CO.*

Representative models of U.S. dairy (WI, CA) and beef (AL, TX, UT, VA, WI) production systems were constructed to sum the land use requirements, greenhouse gas (GHG) emissions and product outputs. Total GHG emissions expressed, as CO<sub>2</sub> equivalents per unit of milk were 1.4 and 1.5 kg/kg, while the production of beef as live weight at the farm gate resulted in from 13.8 to 18.2 kg/kg. The 2 dairy systems utilized 0.6 (CA) and 1.1(WI) ha of land per mature cow unit. Beef systems', including stocker and feedlot, land use was projected to range from 1 to 3.7 ha per mature cow unit. Best management practices applied to all land used in these operations is expected to store .12 and .22 Mg/cow unit for dairy systems and from .2 to .7 Mg of carbon/beef cow unit, anywhere from 4 to 50% of total system GHGs. Twenty-yr

simulations of soil C were run using the Century model for 7 to 10 soil types in 3 locations assuming normal tillage operations. Changing from pasture to either hay or various grain cropping regimens generally decreased soil-C (av. -0.25 Mg/ha/yr), however, the changes were quite variable by soil type. The reverse simulation, change from grains or hay to pasture, at the third location showed wide variations also but averaged +0.28 Mg/ha/yr. Thus changing to increased pasture usage could yield additive C sequestrations above those realized from BMP's. Potential grazing land C-sequestration in the U.S. has been estimated at 4 fold the total agricultural grazing land GHG emissions. Caution must be exercised since tradeoffs, as will be discussed, can occur e.g., if reduced rate of production increases CH<sub>4</sub>/product or excess forage N enhances N<sub>2</sub>O emissions. Also, long term measurements of soil C in intensively managed pastures can show C losses as noted for a location in NZ.

**Key Words:** Pasture and forage, Carbon sequestration, Greenhouse gases

**ASAS/ADSA Breeding and Genetics: Genetic Parameters of Beef Cattle**

**1001 Development and use of genetic markers to predict marbling and tenderness in beef cattle.** F. L. Fluharty\* and D. J. Jackwood, *The Ohio State University, Wooster, OH.*

Detecting animals with the genetic potential for superior performance or meat characteristics requires identifying those genes controlling the desired traits. Since identifying the genes controlling performance and meat characteristics is not practical at this time, genetic markers are used. These markers are used to identify a specific location, or loci, on an animal's chromosome. The key to developing a useful genetic marker is to find one that identifies the specific loci of genes responsible for the trait of interest. We have used the random amplified polymorphic DNA (RAPD) assay to identify two markers that correlate highly with marbling and four markers that correlate highly with tenderness in crossbred beef cattle. Diagnostic tests for these markers that are ultimately developed for commercial use must be relatively low cost, extremely reliable, and logistically appropriate to allow for large numbers of samples to be analyzed in a short period of time. Once an animal's genetic potential is known, management and nutritional strategies must be developed to target the animal toward a known outcome or consumer group. From the standpoint of the seedstock sector, knowing the genetic result of a planned mating shortly after the calf's birth could enhance genetic selection. Feeder calves could be sold in genetically similar groups that are targeted toward a specific consumer group and managed in the feedlot to achieve their potential. The widespread use of genetic technology could lead to a formalized market system in the cattle industry.

**Key Words:** genetics, markers, beef

**1002 Evidence for an association between a *Hind III* PCR-RFLP of the bovine insulin-like growth factor binding protein-2 (IGFBP-2) locus and growth and carcass traits in beef cattle.** M. Pagan\*, J. Cowley, N.E. Raney, and C.W. Ernst, *Michigan State University, East Lansing.*

Insulin-like growth factor binding protein-2 (IGFBP-2) was selected as a candidate gene for growth and carcass merit in beef cattle. Simmental (n = 21), Shorthorn (n = 13), Tarantaise (n = 7), Angus (n = 17), Hereford (n = 17), Salers (n = 5), Red Angus (n = 1), MARC II (n = 8), and Maine Anjou (n = 11) sired cattle were genotyped for an IGFBP-2 *Hind III* RFLP that was previously identified in our laboratory. Two alleles were found to be segregating in all breeds with frequencies of 0.14 A/0.86 B for Simmental, 0.59 A/0.41 B for Hereford, 0.15 A/0.85 B for Angus, 0.3 A/0.7 B for Salers, 0.31 A/0.69 B for Shorthorn, 0.5 A/0.5 B for MARC II, 0.54 A/0.46 B for Maine Anjou, 0.5 A/0.5 B for Red Angus and 0.07 A/0.93 B for Tarantaise sired cattle. Data from the Hereford, Shorthorn and Maine Anjou breeds (AA, AB, BB genotypes represented) was analyzed for possible associations between IGFBP-2 genotypes and growth and carcass traits. A statistically significant effect of genotype (P < 0.05) was found for days on feed, hot carcass weight, dressing percentage, trimmed hot carcass weight, cold carcass weight, ribeye area and USDA yield grade. Animals with the BB genotype had fewer days on feed, higher hot carcass weight and higher dressing percentage than those with the AB genotype (P < 0.05). No significant differences were observed between AA and BB individuals or

between AA and AB individuals for these traits (P > 0.05). For trimmed hot carcass weight and cold carcass weight, the AA and BB genotypes represented the animals with higher weights in relation to the heterozygous (AB) animals (P < 0.05). The BB individuals had higher ribeye areas and better USDA yield grades than the AA and AB animals (P < 0.05). Therefore, animals with the BB genotype appear to have more desirable growth and carcass characteristics. Results of this study indicate that an association may exist between alleles of the IGFBP-2 gene and growth and carcass traits in beef cattle. Validation of these results in additional populations is warranted.

**Key Words:** PCR-RFLP, IGFBP-2, Growth

**1003 Effects of selection for yearling ultrasound intramuscular fat percentage in Angus bulls on carcass traits of progeny.** R. L. Sapp\*, J. K. Bertrand, and T. D. Pringle, *University of Georgia, Athens.*

Twenty-one Angus bulls from three purebred farms were used to determine the effects of selection for phenotypic yearling ultrasound intramuscular fat percentage (USIMF) on the carcass traits of steer progeny managed for commercial slaughter. Bulls were selected based on their high or low phenotypic USIMF within a contemporary group. Average USIMF was 4.01% (SD = 1.07, n = 10) and 1.59% (SD = 0.53, n = 11) for high USIMF (HU) and low USIMF (LU) line bulls, respectively. Each bull was randomly mated to a group of 14 to 30 purebred Angus females for 1 to 5 years. One bull from the HU and one bull from the LU were used throughout the project. Birth weight, weaning weight, yearling and carcass weight, fat thickness at the 12th rib (FAT), longissimus muscle area at the 12th rib (REA), and marbling score (MB) measurements were taken on 196 steer progeny. Carcass data were linearly adjusted to 480 d of age at slaughter. Fixed effects for all traits were birth year of calf, phenotypic USIMF line of sire, and interaction between year and line. Sire, nested within year and line, was included as a random effect. Progeny data were analyzed using the MIXED procedure of SAS. Least squares means of progeny sired by HU (LU) bulls for MB and quality grade (QG) were 447.16 ± 10.13 (408.19 ± 10.09) and 606.23 ± 5.30 (585.09 ± 5.29), respectively, where MB of 400 = small and QG of 500 - 599 = Select, 600 - 699 = Choice. Birth weight (P < 0.05), MB (P < 0.02), and QG (P < 0.02) were found to be larger in steers sired by HU bulls. Longissimus muscle area was larger (P < 0.02) for steers sired by LU bulls. Sire selection based on USIMF was effective in increasing MB and QG in steer progeny. These results suggest that yearling bull ultrasound measurements can be used as selection criteria for genetic improvement of steer carcass traits, and selection for higher levels of marbling can be obtained without increasing fat thickness.

**Key Words:** Ultrasound, Intramuscular Fat, Selection Response

**1004 Estimation of heritability for serially measured ultrasound fat thickness and percentage of intramuscular fat in Angus cattle using random regression models.** A. Hassen\*, D. E. Wilson, and G. H. Rouse, *Iowa State University, Ames, IA, USA.*

The present study included serially measured ultrasound fat thickness (FTK) and percentage of intramuscular fat (PIMF) measures from 423 purebred Angus bulls and heifers. Cattle were born during the spring of 1998 and 1999 at Rhodes beef research farm. Each year, bulls and heifers were scanned four to six times for FTK and PIMF starting at an age of 180 to 269 days, with 30 to 40 days interval between scans. The objective of this study was to evaluate the general trend in heritability and variance component estimates for FTK and PIMF measures spanning ages at measurements. Initially, FTK and PIMF observations from each scan session were analyzed using single-trait animal model. In further evaluation, data were subjected to random regression (RR) models that included fixed effects of contemporary group as well as a linear and quadratic regression on orthogonal polynomials of age. Random effects considered were RR coefficients on orthogonal polynomials of age for each of animal direct genetic and permanent environmental effects. For both traits measurement error variances were assumed independent and homogeneous across ages. Heritability of FTK increased from 0.16 at 196 days age to 0.45 at ages 413 to 441 days. Similarly, heritability of PIMF increased from a minimum of 0.39 at 217 to 266 days of age to a maximum of .58 at 441 days of age. Heritability and repeatability of FTK at one year of age were 0.41 and 0.79, respectively. The corresponding values for PIMF were 0.49 and 0.70, respectively. Heritability estimates from single trait analysis were similar when compared at measurement ages of the respective sessions. Permanent environmental variance contributed to a relatively large proportion of the phenotypic variance for FTK measures ranging from 22.1% to 47.3%, as compared to 21% to 27.7% for PIMF measures. The results suggest that individual selection based on FTK at earlier ages may not be effective due to a large contribution of non-genetic effects to the total phenotypic variance.

**Key Words:** Composition, Ultrasound, Heritability

**1005 Use of repeatedly measured ultrasound percentage of intramuscular fat data to evaluate individual animal rankings.** A. Hassen\*, D. E. Wilson, and G. H. Rouse, *Iowa State University, Ames, Iowa, USA.*

This study used serially measured percentage of intramuscular fat (PIMF) measures of 82 purebred Angus bulls born in the spring of 1999 at Rhodes beef research farm. Bulls were serially scanned six times for PIMF by a certified technician starting at an age of 180 to 254 days. Intervals between scans ranged from 27 to 40 days and at each session all cattle were scanned twice at two consecutive days (day-I and II). The objective of the study was to compare overall and individual animal ranking for PIMF based on day I and II measurements at each session. The overall mean PIMF values for scans one to six were 3.01, 3.65, 4.10, 4.25, 4.47, and 4.96%, respectively. The absolute difference between day I and II for scan sessions one to six were 0.47, 0.67, 0.62, 0.66, 0.62, and 0.63%, respectively. Repeatability of PIMF values increased with scan session ranging from 0.41 at the second scan to 0.72 at the sixth. A similar analysis of pooled data using random regression model showed a general increase in repeatability values with age ranging from 0.63 at ages 252 to 287 days to a maximum of 0.79 at ages 427 to 441 days. Individual animal curves based on mean values of day I and II of each session often provided a clear view of changes in PIMF than separate plots from the respective days. When PIMF values were compared to carcass intramuscular values, day II measures showed less bias (0.55% vs. 0.58%), absolute difference (0.90% vs 1.00%), and a better rank correlation (0.75 vs. 0.66) and root mean square error (0.96% vs. 1.09%) than measurements taken on day I. In trials involving evaluation of individual animal body composition in young cattle using relatively small sample size, taking PIMF measurements from each animal at two consecutive times (days) for each session may provide a better view of trends.

**Key Words:** Ultrasound, Intramuscular fat, Beef Cattle

**1006 Heritability estimates of visceral fat weight.** L. S. Gould\*<sup>1</sup>, J. A. Marchello<sup>2</sup>, and S. K. DeNise<sup>2</sup>, <sup>1</sup>*Red Angus Association of America, Denton, Texas,* <sup>2</sup>*University of Arizona, Tucson, Arizona.*

Heritabilities were evaluated for body composition traits on calves sired by two different groups of bulls. One group of bulls (AHA) were registered with the American Hereford Association and were representative of the Hereford breed in the U.S. The other group of bulls (SCA) came from a closed herd on the San Carlos Apache Reservation in central Arizona that has been selected for 34 years to perform in a nutritionally stressful environment with no supplemental feed. Over a period of three breeding/calving seasons, 127 calves were produced from artificial matings with these sires and raised in adequate nutritional environments. Calves were fed, post weaning, to maximize gain and were slaughtered at constant weight: 520 kg for bulls, 450 kg for heifers. Bull calves remained intact the first season, but were castrated subsequently. Traits analyzed included rib eye area (RE), 12th rib back fat (BF) and visceral fat weight (VF). Differences in VF have been hypothesized to indicate differences in energy requirements for maintenance and/or growth. Because of limited data, genetic correlations and maternal effects were not estimated. All traits were analyzed using the derivative free restricted maximum likelihood procedure. Models to evaluate heritability of RE and BF included sex, and season as fixed effects. Random components included additive genetic and residual effects. Age at slaughter (SLA) for these traits was used as a covariate due to common industry practice. Heritabilities for RE and BF were .39 and .29 respectively. Because BF and RE heritability estimates are similar to estimates from other sources, the data structure of this study, although small, may be appropriate for estimating heritability of VF. Three models, differing only by which covariate was included, were used to evaluate VF. Covariates included SLA, 12th rib back fat and none. Using SLA or no covariate produced similar results with  $h^2 = .10$ . Using a BF covariate,  $h^2 = .35$ . Heritability estimates indicate that differences in VF are likely to be heritable and could enhance future predictions of genetic merit for energy requirements in beef cattle.

**Key Words:** Heritability, Body composition, Energy utilization

**1007 Simulation of economic responses to simulated selection for increased conception rate in beef cattle.** Lowell Gould\*<sup>1</sup> and Dale VanVleck<sup>2</sup>, <sup>1</sup>*Red Angus Association of America, Denton, Texas,* <sup>2</sup>*USDA, ARS, MARC, Lincoln, NE.*

A stochastic simulation program was developed to quantify differences in herds of commercial beef cattle using bulls from sire lines with different genetic trends for conception rate. Breeding values were simulated for 15 traits. Conception rate (CR) and calving difficulty were modeled as threshold traits. All genetic change in commercial herds came through selection of male seed stock from sire lines with either positive conception rate (genetic) trends or no trend (NT). Income was derived from sales of weaned steer calves and cull animals. All heifer calves were retained through winter. Herds that utilized bulls from positive CR trend, had breakeven prices that were smaller by \$0.30/kg ( $P < .01$ ). Selection for increased conception rate increased pregnancy rate by 8.0% ( $P < .01$ ) after 25 years of selection. Increased pregnancy rate directly affected subsequent weaning rates by 9.3% ( $P < .01$ ) between the two herds, making that herd more biologically efficient on the basis of calves weaned per cow exposed basis. However, cows were culled before calving only if they were not pregnant. Therefore, the higher pregnancy rate caused more mature cows to be retained over winter. Total body weight of all cows wintered was 161,529 kg for 350 cows in the high fertility herd and 150,558 kg in the commercial herd with no increase in conception rate ( $P < .01$ ). Because feed consumption was based on weight of each animal, more feed was required in the high conception rate herd causing increased feed costs. Although pounds per calf weaned did not differ between the herds, the additional calves gained from increased conception rates were significant enough to overcome increased feed costs by \$12 per cow ( $P < .01$ ). Birth weight per calf was not significantly different between the two herds, but number of assisted calvings was greater by 1.6% ( $P < .01$ ) in the NT herd due to the different age distributions. The simulation model successfully predicted differences between selection strategies which may allow improved management decisions.

**Key Words:** Economics, Fertility, Management

**1008 Genetic correlations between mature and birth or weaning weights of Hereford cattle.** J. M. Rumph\*<sup>1</sup>, R. M. Koch<sup>1</sup>, K. E. Gregory<sup>2</sup>, L. V. Cundiff<sup>2</sup>, and L. D. Van Vleck<sup>2,3</sup>, <sup>1</sup>University of Nebraska, Lincoln, NE, <sup>2</sup>USDA, ARS, USMARC, <sup>3</sup>Clay Center, NE, <sup>3</sup>Lincoln, NE.

The genetic correlations between mature weight (MW) measured at three different times per year and birth (BW) or weaning weight (WW) were estimated. The data were from a control and three selection lines, selected for weaning weight, yearling weight, and an index of yearling weight and muscle score. Weights available were taken at brand clipping (generally before calving, 1123), at breeding (1537), and when calves were weaned and when cows were pregnancy checked (573). Bivariate analyses of data from all lines were performed that paired a single seasonal MW with one of the immature weights. The one MW was taken when the cow was 6-, 7-, 5-, or 8-years-old. For MW, the model included fixed effects of year by age by line, age of dam by line (DAXL), pregnancy status by line, and birth and method of rearing of calf by line. A covariate for the interval between when the weight was measured and when the cow calved was also fit to the data. For BW (11,313 records) and WW (10,011 records), the model included fixed effects of DAXL, birth and method of rearing by age of dam by year of birth, and sex by age of dam by year of birth. A covariate for Julian birth date was also used. Random direct genetic, maternal genetic, and maternal permanent environmental effects were included in the model. Estimates of correlations between MW and BW ranged from .56 to .69 for direct and -.05 to .84 for maternal genetic effects. Estimated correlations between MW and WW ranged from .64 to .73 for direct and .50 to .91 for maternal genetic effects. Estimated correlations between maternal permanent environmental effects were from .00 to .53 between MW and BW and from .78 to .99 for MW and WW. Selection to reduce BW would be expected to decrease MW and selection to increase WW would be expected to increase MW. An index including BW, WW, and MW would be needed to optimize total productivity.

**Key Words:** Growth, Weight, Beef Cattle

**1009 Effect of separating contemporary group by age of dam in Simmental genetic evaluation.** Z. Zhang\*, E.J. Pollak, and R.L. Quaas, Cornell University.

Young cows are frequently managed differently than older cows. If progeny records of heifers and cows are improperly assigned to the same contemporary group (CG) this can create a CG by age of dam interaction that is not modeled. To ensure that this does not happen, age of dam is made part of the CG definition. This will eliminate potential bias but at the expense of increased variance due to many more contemporary effects and fewer data (loosing connection). A comparison study was done with 3,337,268 records extracted from American Simmental Association (ASA) database on calves born between 1968 and 1999. The CG in 'combined' CG model was defined as in current genetic evaluation of ASA. For 'split' CG model these were separated by age of dam: greater (less) than 990 days. There were 20.3% of the calves out of young cows. Separating CG by age of dam increased number of CG (22.3%, 26.3% and 18.7 for BWT, WWT, and YWT respectively), and decreased numbers of records accepted (4.0%, 4.4% and 5.2% for BWT, WWT, and YWT, respectively). Numbers of sires, dams and nonparents decreased 4.1%, 2.9% and 2.7%, respectively. The EPD differences (combined minus split) were investigated for 10027 bulls with at least ten calves. The correlation between EPD differences and the percentage of calves out of two year old dam were negative for BWT, WWT and YWT (-0.08, -0.11 and -0.11), and positive for milk (0.05).

P	N	Mean difference ± Se (Kg)			
		BWT	WWT	YWT	Milk
0.0-0.2	3041	-0.01±0.00	+0.01±0.02	+0.07±0.03	0.15±0.02
0.2-0.4	3501	-0.01±0.00	-0.04±0.02	+0.00±0.03	0.23±0.02
0.4-0.6	1451	-0.04±0.01	-0.15±0.05	-0.19±0.07	0.21±0.02
0.6-0.8	800	-0.05±0.02	-0.33±0.08	-0.50±0.11	0.23±0.03
0.8-1.0	1234	-0.08±0.02	-0.56±0.08	-0.75±0.11	0.32±0.03
Total	10027	-0.02±0.01	-0.13±0.02	-0.14±0.03	0.21±0.01

P is percentage of calves out of two year old dams; N is number of bulls in each category.

**Key Words:** Age of dam, Contemporary group, Simmental

**1010 Experimental selection for reduced calving difficulty: estimated breeding value trends.** G. L. Bennett\*, USDA, ARS, US Meat Animal Research Center.

Heifer calving difficulty is heritable but unfavorably correlated with growth. The objective of this experiment was to evaluate multiple-trait genetic evaluation as a tool for simultaneously reducing calving difficulty and maintaining growth. Select and control lines were established in four purebred (Angus, Charolais, Gelbvieh, and Hereford) and three composite (MARC I, MARC II, and MARC III) populations. The select line goals were reduced heifer calving difficulty and average yearling weights. Control line goals were average birth and yearling weights. Average weights for purebreds were defined as industry average EPD. Selection was based on EPD for heifer calving difficulty score and yearling weight EPD in select lines, and birth and yearling weight EPD in control lines. Four phenotypes (heifer calving difficulty score, birth weight, weaning weight, and yearling weight) were used to compute the multiple-trait EPD. During seven years of selection, 6,888 calves were born to 353 select sires and 2,033 calves were born to 237 control sires. Calving difficulty scores were recorded on 1,807 select and 560 control calves born to 2-yr-old dams. Estimated breeding values (EBV) in the table below show strong trends for improved direct calving difficulty score and lower direct genetic birth weight and no trend in yearling weight. For calves born in 1998 and 1999, more control calves (36%) than select calves (15%) born to heifers required assistance ( $P \leq .01$ ). Results show that substantial genetic change in heifer calving difficulty can be made while maintaining growth to yearling age.

EBV	1993	1994	1995	1996	1997	1998	1999
Calving Difficulty Score							
Direct	-0.33	-0.65	-0.74	-0.83	-0.99	-1.06	-1.03
Maternal	0.04	0.08	-0.02	0.09	0.00	-0.08	0.01
Birth Weight, kg							
Direct	-1.10	-2.11	-2.49	-2.76	-3.37	-3.48	-3.55
Maternal	0.17	-0.20	0.05	-0.11	-0.32	0.00	-0.24
Yearling Weight, kg							
Direct	3.0	-2.9	0.2	-0.4	-2.9	2.1	-1.8

**Key Words:** Calving difficulty, Selection, Breeding value

**1011 Nonlinear relationship between birth weight and calving ease determined with ecological analysis in a multi-breed commercial beef herd.** Y. Wang\*, S.P. Miller, J.W. Wilton, P. Sullivan, and L.R. Banks, University of Guelph, Guelph, Ontario, Canada.

Ecological analysis were applied to a multi-breed commercial beef herd to examine the non-linear relationship between birth weight (BW) and calving ease (CE). Data included 133,280 records on both BW and CE for calves born between 1986 and 2000. Based on the assumption of normality and homogenous residual variances, Snell Scores were calculated by combining individual CE, age of the dam, sex of calf and mating liability (ML) of parents. ML of parents involved five categories with thresholds -1.0, -0.2, 0.2 and 1.0 based on the standardized difference between standardized sire BW ABC (Across Breed Comparison) and standardized dam yearling weight ABC. Ecological correlations, as a correlation of averages, between BW and percent of un-assisted calving and between BW and Snell Score were -0.7399 and -0.7611, respectively. A quadratic regression model described the relationship between BW (independent) and percent of un-assisted calving (dependent) explaining 87% of the variation in CE. It was evident that BW is a major indicator of CE. Snell Scores retained the nature of CE while converting the categorical record to a continuous variable. At a given BW, age of the dam was a larger source of variation for CE than sex of calf and ML of parents. For a 2-year-old dam, 90% or more calving would be expected to be un-assisted in calf weighing 22-35 kg. With age of the dam increased to 3 years and more, the same level of CE can be achieved with a broader range of BW (20-45 kg). However, Pearson correlation of -0.1930 between BW and Snell Score indicated ecological correlations cannot be extrapolated to individuals due to variation in CE with a BW category. Regression coefficients calculated enable more accurate prediction of calving difficulty with changing BW across age of dam and sex categories.

**Key Words:** birth weight, calving ease, beef cattle

**1012 Genotype by country interactions for growth traits in Charolais populations across four countries.** K. A. Donoghue\* and J. K. Bertrand, *University of Georgia, Athens GA.*

The importance of genotype by country interactions was evaluated for data from Charolais associations in Australia (AUS), Canada (CAN), USA and New Zealand (NZ). Data were composed of edited birth and weaning weight and postweaning gain records from the four countries. Only herds with more than 500 trait records, with an average contemporary group size greater than 9 animals, and that had trait records from progeny of 66 international sires were used in this study. Pairwise country samples were created that ranged from 20000 to 30000 trait records and a multiple trait animal model that considered each trait as a different trait in each country was used to estimate parameters in each pairwise analysis. Direct and maternal (in parentheses) estimated genetic correlations for birth weight for AUS vs. CAN, AUS vs. USA, USA vs. CAN, NZ vs. CAN and NZ vs. USA were 0.88 (0.86), 0.85 (0.82), 0.88 (0.82), 0.85 (0.83), and 0.84 (0.80), respectively. Direct and maternal (in parentheses) estimated genetic correlations for weaning weight for AUS vs. CAN, AUS vs. USA, USA vs. CAN, NZ vs. CAN and NZ vs. USA were 0.96 (0.91), 0.95 (0.90), 0.95 (0.91), 0.95 (0.92), and 0.95 (0.92), respectively. Direct estimated genetic correlations for postweaning gain for AUS vs. CAN, AUS vs. USA, USA vs. CAN, NZ vs. CAN and NZ vs. USA were 0.89, 0.91, 0.94, 0.90, and 0.91, respectively. Direct and maternal heritabilities were similar across all countries for birth and weaning weight, while direct heritabilities for postweaning gain in AUS and NZ were slightly lower than those in CAN and USA. The absence of genotype by country interactions observed in this study strongly indicates that a joint genetic evaluation for growth traits for Charolais populations could be conducted. A model that treated information from AUS, CAN, USA and NZ as one population, while adjusting for possible heterogeneous variances, could be implemented for this purpose.

**Key Words:** Genotype by Country Interaction, International Evaluation, Beef Cattle

**1013 Evaluation of milk yield and udder characteristics in beef cows sired by high or low Milk EPD bulls.** K. J. Stutts\* and D. S. Buchanan, *Oklahoma Agricultural Experiment Station, Stillwater, OK.*

Maternal milk is an important influence on weaning weight that affects production efficiency in beef herds. The objective of this study was to evaluate High and Low Milk EPD sires for milk production and udder characteristics of their daughters. Cows used in this study were produced through the mating of Angus and Hereford bulls that differed in Milk EPD level to Hereford-Angus and Hereford-Angus-Brahman cows. They ranged in age from 7 to 11 yr old. All cows were bred by artificial insemination to South Devon bulls and calves were born in the spring from early February to early April. Milk production data were collected 7 times prior to weaning at 28 d intervals using the weigh-suckle-weigh method. The final milk production data corresponded to a 205-d weaning age for all calves. Udder measurements and scores were taken during periods 3 and 6 after complete removal of milk from the udder by suckling. Cows were restrained in a squeeze chute and visual conformation scores were given to each teat and the udder. Linear measurements were taken on the length of each teat, distance between the front teats, distance between the rear teats, and the diagonal distance from the left front to the right rear teat. Data were analyzed using least squares. Factors included in the model were breed, Milk EPD level, sex of calf, age of dam, and all two-way interactions. Age of calf was included as a covariate. High Milk EPD cows produced more milk than Low ( $P < .05$ ), but there was not a difference ( $P = .71$ ) in milk production between breeds. The interaction between breed and Milk EPD level was approaching significance ( $P = .15$ ). Hereford sired cows had longer teat length ( $P < .02$ ) and higher (more pendulous) udder scores ( $P < .05$ ) than Angus. Low Milk EPD cows had slightly lower udder scores than High ( $P < .10$ ). These results further confirm the utility of Milk EPD to predict milk production differences and provide only small evidence that there may be a negative effect on udder conformation for older High Milk EPD cows.

**Key Words:** Beef Cattle, Milk Production, Udder Characteristics

## ASAS/ADSA Breeding and Genetics: Genetic Parameters of Dairy Cattle

**1014 Possibilities for genetic improvement of fertility in US dairy cattle.** K. A. Weigel\*<sup>1</sup> and J. S. Clay<sup>2</sup>, <sup>1</sup>*University of Wisconsin, Madison*, <sup>2</sup>*Dairy Records Management Systems, Raleigh, North Carolina.*

Interest in improving conception rates has skyrocketed in recent years. Direct costs of poor fertility include increased semen costs, veterinary costs, days open, and involuntary culling. Indirect costs include reduced genetic progress due to a larger number of repeat inseminations and an increased proportion of pregnancies to genetically inferior natural service bulls. Selection for male (service bull) fertility is possible using Estimated Relative Conception Rate data from Dairy Records Management Systems. Service bulls are evaluated for 70-day non-return rate on first inseminations. Evaluations for all bulls with at least 300 inseminations in the past three years are published. Sire evaluations for female (daughter) fertility are not yet available, but a system is under development. Female fertility can also be measured as 70-day non-return rate; in this case male and female fertility can be analyzed jointly using a maternal effects model. Days to first insemination can also be evaluated, but measurements may be biased by the use of heat synchronization products. In a pilot study, male and female fertility were evaluated as 70-day non-return rate using 8.03 million insemination records from 1995 to present. The range in daughter fertility PTA for Holstein sires was roughly 10%, similar to the range in service bull fertility solutions. The correlation between male and female fertility solutions of Holstein sires was 0.02, and the correlation between female fertility and PTA milk was 0.09. Therefore, it will be possible to improve conception rates with little or no loss in genetic merit for milk yield by practicing secondary selection for male and female fertility. Fertility evaluations can be improved by increasing the quantity and quality of DHI insemination data, by utilizing repeat service data, and by considering models that account for the binary nature of the data.

**Key Words:** genetic selection, fertility, dairy cattle

**1015 Effect of heat stress on Non-Return rate in Holstein cattle.** O Ravagnolo and I Misztal\*, *The University of Georgia, Athens, GA.*

The objective of this study was to examine the relationship between reproductive traits and heat stress. Non-return rate at 45 days (NR45) was analyzed in a fixed effect model that included Temperature Humidity Index from a nearby weather station as a measurement of heat stress. Data consisted of 150,200 first inseminations at first and later parities of 110,860 Holstein cows from 550 herds in Georgia, Tennessee and Florida with weather information from 16 weather stations. THI on the day of the insemination, 2 days prior, 5 days prior, 10, 20 and 30 days after insemination were studied as independent variables. THI on the day of insemination showed the highest effect on NR45, followed by 2 days prior, 5 days prior and 5 days after insemination, but no relationship was found with THI at 10, 20 and 30 days after insemination. NR45 showed a decrease of 0.005 per unit increase in THI on the day of insemination for THI > 68. First and later parities presented similar thresholds but responded differently to increase in THI, with NR45 being significantly lower and more susceptible to increases of THI in cows in their first parity than in later parities (0.008 vs. 0.005 decrease per unit THI). Threshold for sensitivity to heat stress changed with the states, with FL, GA, TN having thresholds of 66, 70 and 70 respectively. The decrease in NR45 per unit increase of THI was 0.006, 0.005 and 0.007 for FL, GA and TN respectively (or a total of 0.07, 0.07 and 0.10). On the TN data only, the final fixed effect model used was  $NR45 = \text{Herd}(\text{Year}) + \text{Month}(\text{Year}) + \text{age}(\text{parity}) + \text{days in milk} + 100\text{d milk} + \text{THI} + \text{error}$ . Animals with more than 150 DIM had a 0.16 lower NR45 than animals with less than 60 days in milk at insemination. Lower milk producing animals showed 0.08 higher NR45 than higher producing animals. A difference of 0.10 in NR45 was observed between THI lower than 70 and THI 84. This variation in NR45 due to THI changes is sufficient to merit further studies to examine genetic components for heat tolerance for this trait.

**Key Words:** Heat Stress, Non-return rate, Holstein