

## Breeding And Genetics

**11 Development of EST sequence data and map locations for genes expressed in major female reproductive tissues.** C.K. Tuggle\*<sup>1</sup>, J.A. Green<sup>2</sup>, C. Fitzsimmons<sup>1</sup>, R. Woods<sup>2</sup>, R.S. Prather<sup>2</sup>, S. Malchenko<sup>3</sup>, M.B. Soares<sup>3</sup>, C.A. Roberts<sup>3</sup>, K. Pedretti<sup>3</sup>, T. Casavant<sup>3</sup>, D. Pomp<sup>4</sup>, A. R. Caetano<sup>4</sup>, J. B. Edeal<sup>4</sup>, S. Oberging<sup>4</sup>, Y. D. Zhang<sup>1</sup>, M. F. Rothschild<sup>1</sup>, K. Garwood<sup>5</sup>, and W. Beavis<sup>5</sup>, <sup>1</sup>*Iowa State University, Ames*, <sup>2</sup>*University of Missouri, Columbia*, <sup>3</sup>*University of Iowa, Iowa City*, <sup>4</sup>*University of Nebraska, Lincoln*, and <sup>5</sup>*National Center for Genomic Resources, Santa Fe, NM.*

A consortium of five institutions is developing extensive expressed sequence and mapping data for cDNAs expressed in major female reproductive tissues. We have produced 20 libraries from different stages of estrus or gestation for whole embryo, anterior pituitary, hypothalamus, ovary, uterus, and term placenta. The anterior pituitary, placenta and uterine libraries have been normalized. A total of 15,002 sequences from random clones has been produced and submitted to Genbank. The average read length across this dataset is ~400 base pairs. As assessed by clustering analysis, these data represent 9,042 different genes. A BLAST analysis indicates that 4,405 of these clusters are unique relative to existing porcine Genbank genes and ESTs (BLAST score <50). To facilitate selection of genes for comparative mapping, we have developed software to predict the cytogenetic location of pig ESTs. We identified human loci with a BLAST score >200 to our EST dataset, and then predicted the pig location of high-scoring ESTs based on human cytogenetic and RH mapping data, along with human:pig chromosome painting information. Pig EST matches to human loci with consistent cytogenetic and RH mapping locations total 1,486. Within the human genome, there is an average distance of  $9.4 \pm 5.8$  cR between loci with a pig EST match. On average, there is  $20.9 \pm 3.8$  RH-mapped genes between each human locus matched to a pig EST. To date, 50 loci have been mapped using both the SCHP and the RH panel. A WWW site has been established for access to these sequences and the analysis data (<http://pigest.genome.iastate.edu>).

**Key Words:** Pig EST Sequencing, Gene Mapping, Comparative Genomics

**12 Construction of a High Density Comparative Map of Bovine Chromosome 5 to Search for Genes Controlling Birth Weight.** Z. Liu\* and E. Antoniou, *University of Missouri-Columbia*.

The beef industry suffers an estimated \$226 million loss per year caused by dystocia. Dystocia is mainly due to calves with high birth weights. At the same time low birth weight in humans is associated with an increased risk of diabetes later in life. It might be the same genes in human and cattle that control birth weight. Bovine chromosome 5 (BTA5) was previously identified as containing genes controlling some of the genetic variance for birth weight (quantitative trait loci or QTL). We want to find these genes by applying the comparative candidate gene approach. However, the current comparative map of BTA5 with the human genome is too sparse to use this approach. Thus, we have created a high-density comparative map of BTA5. We used a radiation hybrid (RH) 12,000 rads DNA panel with 180 cell lines, which is by far the highest resolution bovine panel available. We mapped all known microsatellites (24) in the region as well as 40 genes selected from the human genome sequence. Our RH map for this region spans 26.45 cR and corresponds to a region spanning 71 cm on BTA5 genetic linkage map. Thus, the current resolution for this region of bTA5 is approximately one marker per cm.

**Key Words:** Comparative Map

**13 Evaluation of insulin-like growth factor binding proteins (IGFBP) in Angus cattle divergently selected for serum insulin-like growth factor-I (IGF-I) concentration.** M. Pagan\*<sup>1</sup>, M.E. Davis<sup>2</sup>, K. Kizilkaya<sup>1</sup>, R.J. Tempelman<sup>1</sup>, and C.W. Ernst<sup>1</sup>, <sup>1</sup>*Michigan State University, East Lansing*, <sup>2</sup>*The Ohio State University, Columbus*.

Angus cattle divergently selected for serum IGF-I concentration were genotyped for a *Hind* III restriction fragment length polymorphism at the IGFBP-2 locus identified in our laboratory. Genotyping of high and low IGF-I line individuals (born in spring 1995, fall 1995, fall 1997, fall

1998 and spring 1999; n = 366) indicated no difference in allelic frequencies between the high (0.32 A/0.68 B) and low (0.31 A/0.69 B) IGF-I lines or between bull (0.32 A/0.68 B) and heifer (0.33 A/0.67 B) calves. Analysis of variance (ASREML) using genotypes and phenotypic data (weight and gain data and serum IGF-I concentrations) indicated that animals of BB genotype had higher birth weights than AA and AB animals (P < 0.05). Phenotypic analysis of circulating IGFBP was also performed by <sup>125</sup>I-IGF-I western ligand blotting using serum samples obtained at d 56 of the postweaning test period from IGF-I selection line calves born in fall 1999 (n = 81). Four IGFBP species of 42-38, 34, 30 and 24 kDa were identified. The 34 kDa IGFBP species was determined to be IGFBP-2 by immunoblotting using a bovine specific anti-IGFBP-2 antibody. The effects of line, sex and the line x sex interaction were determined by analysis of variance of data obtained by densitometric analysis of autoradiographs. No significant line effects or line x sex interactions were observed. A significant effect of sex was found for IGFBP-2 such that levels of this protein were higher in heifer than in bull calves (P < 0.05). Serum levels of all IGFBP were positively correlated with each other and negatively correlated with growth traits and serum IGF-I concentrations (P < 0.0001). Results of this study indicate that an association may exist between economically important traits in beef cattle and alleles of the IGFBP-2 gene as well as between these traits and serum IGFBP concentrations. This work further supports IGFBP-2 as an important candidate gene for beef cattle growth.

**Key Words:** Beef Cattle, IGFBP, Immunoblotting

**14 Control of hypothalamic gene expression in mice selected for heat loss.** S.R. Wesolowski\*, M.F. Allan, M.K. Nielsen, and D. Pomp, *University of Nebraska, Lincoln*.

Understanding the genetic complexity of energy balance in livestock species is essential to improve production efficiency. In the mouse, many physiological genes controlling energy regulating pathways are known, while several predisposition genes (QTL) are being identified for energy balance traits. The genetic map locations for these two subsets of genes are not well correlated, creating a possible complex genetic paradigm whereby predisposition and physiological genes represent different loci. To test this theory, we plan to identify predisposition genes for expression levels of physiological genes regulating energy balance. Mouse lines divergently selected for heat loss using direct calorimetry were created as model populations to dissect the genetic complexity of energy balance. Inbred lines were generated from these populations. The inbred high (IH) heat loss mice have 50% greater heat loss, 35% less body fat, 20% greater feed intake, two-fold greater activity levels, and one degree higher core body temperature compared to the inbred low (IL) heat loss mice. Yet, both lines are similar in body weight. We evaluated differences in hypothalamic gene expression between the IH and IL lines using replicated cDNA microarrays, differential display PCR, and selected candidate genes. Northern blot analysis was used to confirm relative mRNA abundance for individual genes. Of primary interest, hypothalamic gene expression of oxytocin was higher in the IH line. Sensitive real-time PCR assays are being developed to facilitate high-throughput screening in a large F2 population originating from a cross between IH and IL, for which genome-wide markers have already been scored and hypothalami stored. Identification of QTL for regulation of relevant gene expression changes will facilitate direct correlation between predisposition and physiology, and contribute towards a greater understanding of the complex genetic architecture of polygenic traits.

**Key Words:** Energy Balance, Microarrays, Oxytocin

**15 Comparison of statistical methods to study microarray data.** S. Rodriguez-Zas\*, *University of Illinois at Urbana-Champaign*.

Reliable methods to study the abundant and complex gene expression data resulting from livestock functional genomic research need to be developed and tested. The objective of this study was to develop a model to characterize the expression of thousands of DNA sequences across several instances (e.g., treatments, time points). The adequacy of the proposed approach was evaluated using data from a model organism that has an advanced functional genomic status, hence reflecting the livestock genomic situation in the immediate future. Data from a

study with replicates on the level of expression of 17,871 genes from *Caenorhabditis elegans* along six developmental stages were examined. The logarithm of the Cy3 (common reference cDNA) and Cy5 (developmental phase cDNA) intensities were normalized for the effects of dye and background effects. The difference between the adjusted developmental and reference sample intensities was described with a mixed effects model that accounted for the replicate effect. Two complementary ways to study the differential expression across stages were considered. The developmental stage was fitted as a classification variable or as a covariate expressed as hours in the life cycle. The correlation between the proposed model-based adjusted and conventionally normalized (equal total Cy5 and Cy3 signal) intensities ranged between 84% and 94% suggesting that the conventional normalization fails to account for critical dye and background effects. Results from the stage-dependent model indicated that multiple known and putative (unknown function) collagen-related genes were over expressed in the intermediate developmental stages. Many known and putative sperm-specific protein genes were under expressed during the egg stage and were over expressed in the late stages. The adjustment and instance-modeling approaches proposed provided a statistically and biologically meaningful answer to the analysis and interpretation of functional genomic studies that can be readily applied to livestock species.

**Key Words:** Gene Expression, Functional Genomics, Mixed Effects Model

**16 Measurement error in detecting quantitative trait loci with genetic markers.** G. J. M. Rosa<sup>\*1</sup>, B. S. Yandell<sup>2</sup>, and D. Gianola<sup>2</sup>, <sup>1</sup>Michigan State University, East Lansing, <sup>2</sup>University of Wisconsin, Madison.

The advent of molecular marker information has created opportunities for a better understanding of quantitative inheritance and for developing new strategies for genetic improvement in agriculture. Information on genetic markers is often used for two purposes: genetic marker map construction and quantitative trait loci (QTL) analysis. The map construction procedures use information from marker genotypes to make inferences regarding linkage, order and distances of marker loci. The QTL analysis puts together information on phenotypes and on marker genotypes to infer the number of QTL and their positions and effects on phenotypic variation. Most statistical methods ignore that molecular (marker) data may be read with error. Often, however, there is ambiguity about genotypes, which may lead to erroneous inferences. Moreover, QTL models for continuous traits rely almost invariably on Gaussian assumptions, which are known to be non-robust to discrepant (outlier) observations. Here, measurement error models are discussed for map construction and QTL search. Robust alternative methods consider the possibility of error-in-variables for both marker genotypes and trait phenotypes. For marker data, additional parameters are introduced to model the probability of genotyping error and, therefore, to correct miscoded genotypes. For measurement error in the phenotypes, thick-tailed (symmetric and skewed) distributions are used to accommodate outliers. A Bayesian framework is adopted throughout and Markov chain Monte Carlo methods are used to carry out the posterior analysis. Simulated and real data examples are discussed to illustrate the methodologies.

**Key Words:** QTL Analysis, Measurement Error, Robust Inference

**17 Power of least squares interval mapping compared to single marker analyses to detect QTL with selective DNA pooling.** J. Wang<sup>\*</sup> and J. Dekkers, Iowa State University, Ames.

Selective DNA pooling is an efficient method to identify chromosomal regions that harbor quantitative trait loci (QTL) by comparing marker allele frequencies in pooled DNA from phenotypically extreme individuals. Currently, single marker methods are used for analysis. These methods can detect linkage of markers to a QTL but do not provide separate estimates of QTL position and effect, nor do they utilize information on multiple linked markers. We recently developed a least squares regression interval mapping (LSIM) method to overcome these limitations. The objective of this research was to compare the power of this method to that of single marker analyses. Methods were applied to simulated DNA pooling data from the top and bottom 10% of 10 half-sib families with 500 or 2,000 progeny on 6 equi-distant markers on a 100 cM chromosome with one QTL with effect 0.25 phenotypic SD. Two models were used for LSIM: LSIM-2 fitted two QTL frequencies per family, one for each tail, whereas LSIM-1 fitted only a single QTL frequency by

setting upper tail frequency = (1 - lower tail frequency). A Chi-square test was used for single marker analyses. Power was estimated from 3,000 replicates using empirical 5% chromosome-wise significance levels. Power was highest for LSIM-1, followed by the single marker analyses and lowest for LSIM-2. For 500 progeny and a QTL at 11 or 46 cM, power was 56 and 69% for LS-1, 51 and 55% for single marker analyses, and 35 and 55% for LSIM-2. Trends were the same with 2,000 progeny but all powers were >90%. LSIM-1 also resulted in more accurate and precise estimates of QTL location and effect than LSIM-2, but estimates of position were biased toward the center of the chromosome for both. Bias was greater when power was low and with the QTL at 11 cM. Similar bias was observed for the single-marker method. Results show that LSIM-1 is the preferred method to analyze selective DNA pooling data.

**Key Words:** Selective DNA Pooling, QTL Mapping

**18 Extended analysis of a Berkshire x Yorkshire cross to detect QTL for growth and meat quality traits.** H. Thomsen<sup>\*</sup>, M. Malek, J. C. M. Dekkers, and M. F. Rothschild, Iowa State University, Ames.

An experiment was initiated to identify QTL affecting growth, body composition, meat and muscle composition in a cross between Berkshire and Yorkshire breeds. A three-generation resource family was created by using two Berkshire grand sires and nine Yorkshire grand dams to produce nine litters of F1 individuals. Eight boars and 26 gilts were chosen to produce 65 litters with 527 F2 offspring. In total, 28 traits for meat quality and 12 traits for growth and body composition were measured in the F2 animals. All animals were initially genotyped for 125 markers across the genome, which resulted in over 100 QTL identified at a 5% chromosome-wise level. The objective of this study was to extend this scan by genotyping for another 33 markers in special regions of interest. New marker linkage maps were derived for all autosomes and the X chromosome and used in QTL analysis based on line cross least squares regression interval mapping. Sex and year-season were included as fixed effects. Litter size was used as a covariable for some traits. Significance thresholds were derived at a chromosome-wise and genome-wise level on a single-trait basis by using a permutation test with 10,000 shuffles of the original data. A total of 49 QTL were discovered for growth and composition traits, of which 10 were significant at a 1% genome-wise level and another 5 were significant at the 5% genome-wise level. QTL for growth and composition traits were located on chromosomes 1, 2, 4, 5, 7, and 9. For meat quality traits, 73 QTL were detected, of which 5 were significant at a 1% genome-wise level and 14 were significant at the 5% genome-wise level. QTL for meat quality were detected on chromosomes 1, 2, 6, 7, 10, 14, 15, and 18. Results from this study were in good agreement with findings from the initial analyses. However, the increase of markers in regions of interest revealed approximately 20 new QTL at the 5% chromosome-wise level, of which at least one QTL was significant at a genome-wise level of 5%. Twelve of the original QTL were no longer significant at the 5% chromosome-wise level. These findings confirm the segregation of important QTL for growth and meat quality traits between the Berkshire and Yorkshire breeds. This work was supported by CSREES IFAFS # 00-52100-9610

**Key Words:** QTL, Growth, Meat Quality

**19 Tests of candidate genes in QTL mapping populations.** H. H. Zhao<sup>\*</sup>, J. C. M. Dekkers, and M. F. Rothschild, Iowa State University, Ames.

In recent years, several F<sub>2</sub> breed cross populations have been developed to identify quantitative trait locus (QTL) regions. These populations are phenotyped for many traits and genotyped for many genetic markers and, therefore, provide a valuable resource for further genetic analysis, including analysis of candidate genes. Although an association study is a robust method to test candidate genes within a closed population, their analysis in an F<sub>2</sub> population is problematic, because of the extensive between-breed linkage disequilibrium (LD). The objective of this study was to develop statistical tests for candidate gene analysis in F<sub>2</sub> populations. An F<sub>2</sub> of 600 progeny was simulated. In order to generate LD within parental breeds between the QTL and candidate genes, two generations were added to produce F<sub>0</sub> parents. A 100 cM chromosome was simulated with 6 equi-distant markers, a QTL with an effect of 0.25 phenotypic SD, and 9 candidate genes with distances from the QTL ranging from 0-30 cM. Gene frequencies in parental breeds were chosen to produce various combinations of within- and between-breed LD. QTL

were detected by least squares interval mapping. Three candidate gene tests were evaluated: (1) An association test based on the fixed effect of the candidate gene, (2) An association test based on a model that included between-breed QTL effects, and (3) Comparison of F-statistics for a QTL at the candidate gene position with and without the candidate gene as fixed effect. Comparison of tests (1) and (2) showed that incorporating QTL effects in the model removed the confounding effect of between-breed LD. Although test (3) showed a drop in the F-statistic at the candidate gene position, the result was not very informative. Test (2) was found to be most suitable because it was closely related to within-breed LD between the candidate gene and QTL. Further studies are in progress to determine the power of test (2) to detect candidate genes that are tightly linked to the QTL. This work was supported by CSREES IFAFS # 00-52100-9610.

**Key Words:** QTL Mapping, Candidate Gene, Linkage Disequilibrium

## 20 Effect of using approximate gametic variance covariance matrices on marker assisted selection by BLUP. L.R. Totir\*, R.L. Fernando, and J.C.M. Dekkers, *Iowa State University.*

Henderson's mixed model equations (HMME) can be used for genetic evaluation by BLUP with marker and trait data. In order to accommodate large pedigrees it is convenient to include in the model, as a random effect, the gametic effect of the QTL linked to the markers (MQTL), in addition to the random additive genetic effect of the remaining QTL (RQTL). The inverses of the variance covariance matrices for the gametic effects at the MQTL and the genetic effects at the RQTL are required to construct HMME. Algorithms have been developed to obtain these inverses efficiently. When a single marker locus is used, the algorithm for inverting the gametic variance covariance matrix at the MQTL yields exact results when marker genotypes are observed for all parents. When flanking markers are used, the marker genotypes as well as the linkage phase between the flanking markers must be known to obtain exact results. In large pedigrees, however, incomplete marker information is the rule rather than the exception. Further, the linkage phase is very likely to be unknown for some parents. When genotype and phase information is missing, approximations must be used. When phase is missing, a common practice is to ignore the marker information completely. An alternative to this approach is to use only the information at one marker when phase is missing. The objective of this study is to examine the consequences of these approximations on accuracy of genetic evaluations. For small simulated data sets, response to selection by marker assisted BLUP using the two approximations was calculated for flanking markers with 2,4 and 12 alleles. Greater response to selection was obtained with the second approximation in all situations considered so far. In subsequent research, the exact variance covariance matrix for the gametic effect will be obtained by Markov Chain Monte Carlo techniques, and response to selection on BLUP based on the exact matrix will be compared to response obtained from approximate matrices.

**Key Words:** Marker Assisted Selection, BLUP, Gametic Covariance Matrix

## 21 Trends in heritability of serially measured ultrasound ribeye area measures in Angus cattle. A. Hassen\*, D. E. Wilson, and G. H. Rouse, *Iowa State University, Ames.*

Serially measured ultrasound ribeye area (REA) measures from 675 purebred Angus bulls and heifers were used to evaluate general trend in heritability values. Cattle were born during the spring of 1998, 1999, and 2000 at the Rhodes beef research farm. Each year bulls and heifers were scanned four to six times for REA starting at a mean age of 36 weeks, with 4 to 6 weeks interval between scans. The objective of this study was to evaluate the general trend in variance component estimates and heritabilities of serially obtained REA measurements. REA observations across the three years were analyzed by scan session using a single-trait animal model. In further analysis, serial data pooled over the three year period were analyzed using random regression models (RRM) that included fixed effects of contemporary group and fixed linear regression on Legendre polynomials of age at measurement. Random effects considered were Legendre polynomials of age at measurement for animal direct genetic and animal permanent environmental effects. Heritabilities of REA for the first five scan sessions across years were 0.30 0.10, 0.35 0.10, 0.28 0.09, 0.41 0.10, and 0.31 0.18, respectively. These scans represented mean ages of 36, 41, 47, 52, and 54 weeks, respectively. Results from RRM analysis showed a general increase in heritability values

from a minimum of 0.26 at mean ages of 28 to 29 weeks to a maximum of 0.44 at mean ages of 61 to 63 weeks. A heritability value of 0.40 at 52 weeks of age was the same as the corresponding estimate from single trait analysis for scan session four (age = 52 weeks). The permanent environmental variance contributed up to 52% of the total phenotypic variance at earlier ages, followed by a constant decline until it reached a minimum of 38% at 63 weeks of age. The results suggest that individual selection for REA at earlier ages may not be effective due to a large contribution of non-genetic effects.

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

## 22 Genetic parameters for sex-specific traits in beef cattle: mature weight of cows and carcass traits of steers. K. A. Nephawe\*<sup>1</sup>, L. V. Cundiff<sup>2</sup>, and L. D. Van Vleck<sup>3</sup>, <sup>1</sup>*University of Nebraska, Lincoln*, <sup>2,3</sup>*USDA, ARS, USMARC*, <sup>2</sup>*Clay Center, NE*, <sup>3</sup>*Lincoln, NE.*

Data from the first four cycles of the Germplasm Evaluation Program (USMARC) were used to estimate genetic parameters of and among female mature weights (n=37,710) and carcass traits of their steer paternal half-sibs (n=4,031). Female mature weights were available from four through eight years of age. Cows (n=1,801) were measured in four different seasons each year. Data were analyzed by REML. Estimates of heritability for mature weight (MW) and mature weight adjusted for body condition score (AMW) using repeatability models were 0.52 and 0.57, respectively. Estimates of heritability for hot carcass weight (HCWT), retail product percentage (RP%), fat percent (FAT%), bone percent (BONE%), rib eye area (REA), adjusted fat thickness (AFAT), estimated kidney, pelvic and heart percent (EKPH%), marbling score (MARB), Warner-Bratzler shear force (WBSF), taste panel flavor (TPF), taste panel juiciness (TPJ) and taste panel tenderness (TPT) measured on steers were 0.52, 0.59, 0.53, 0.52, 0.57, 0.46, 0.65, 0.46, 0.29, 0.05, 0.01 and 0.26, respectively. Estimates of genetic correlations between MW and HCWT, RP%, FAT%, BONE%, REA, AFAT, EKPH%, MARB, WBSF, TPF, TPJ and TPT were 0.81, -0.13, -0.07, 0.25, 0.34, -0.03, 0.00, -0.15, 0.15, 0.29, -0.32 and -0.20, respectively. Similar estimates were obtained between AMW and carcass traits. Genetic correlations between mature weight of cows and carcass traits also were estimated for mature weights analyzed separately by season of measurement and by age (in years). Estimates were consistent with overall data. Estimates of genetic correlations between mature weight and carcass composition or meat quality traits were relatively low. To change percentage retail product (or marbling or tenderness), direct selection for carcass and meat traits would be needed. Direct selection for most carcass and meat traits could be effective and would lead to only minor changes in mature weight.

**Key Words:** Genetic Correlations, Heritabilities, Body Condition Score

## 23 Effect of sire misidentification on estimates of genetic parameters for weaning weight. S. Senneke\*<sup>1</sup>, M. D. MacNeil<sup>2</sup>, and L. D. Van Vleck<sup>3</sup>, <sup>1</sup>*University of Nebraska, Lincoln*, <sup>2</sup>*USDA, ARS, LARRL, Miles City, MT*, <sup>3</sup>*USDA, ARS, USMARC, Lincoln, NE.*

This study was based on records of Line I Herefords collected at the Fort Keogh Livestock and Range Research Laboratory in Miles City, Montana. A total of 4,170 records between the years of 1935-1989 were available. Sires of progeny within year were randomly misidentified based on the number of progeny the sires contributed that year. Sire misidentification levels ranged from 5 to 50% with increments of 5%. For each level of sire misidentification 100 replicates were obtained. The misidentified data were then analyzed using single trait analyses with a REML algorithm. Two different models were used to analyze the data (Model 1 and Model 2). Both models contained year by sex and age of dam as fixed effects, julian birth date as a covariate, and animal and maternal genetic effects and maternal permanent environment as random effects. Model 2 also included sire by year as a random effect. Direct and maternal heritability decreased (0.20 to 0.03 and 0.16 to 0.05, respectively) as the level of misidentification increased using Model 1. However, the direct-maternal correlation increased from -0.38 to 0.38 as the fraction of misidentification increased. With Model 2, similar to Model 1, direct and maternal heritability decreased (0.17 to 0.03 and 0.15 to 0.05, respectively) as the level of misidentification increased. The direct-maternal correlation increased from -0.31 to 0.50

as the level of misidentification increased. Use of Model 2 caused estimates of the correlation to be more positive than with Model 1. As the level of misidentification increased, fraction of sire by year variance decreased, by a small amount, from 0.015 to 0.004. Results from this study indicate that sire misidentification may severely bias estimates of genetic parameters.

**Key Words:** Heritability, Direct-Maternal Correlation, Beef Cattle

**24 Genetic estimates of parameters for hip height at different ages for four lines of Hereford cows.** 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>2,3</sup>USDA, ARS, USMARC, <sup>2</sup>Clay Center, NE, <sup>3</sup>Lincoln, NE.

Measurements of hip height were recorded a maximum of three times per year for a control and three selection lines of spring calving Hereford heifers and cows: before calving (BC, n = 2,210), before breeding (BB, n = 3,231), and during weaning of calves and pregnancy checking via rectal palpation (PA, n = 3,435). The lines were selected for increased weaning weight, yearling weight, and an index of yearling weight and muscling score. Measurements were for yearling heifers through 10-year old cows. Based on the likelihood ratio test, a simple model that included only additive genetic and environment as random effects was determined to be sufficient. Fixed effects included were year x age x line and age of dam x line. When all ages were included in a repeatability model, heritability (standard error) was estimated to be 0.65 (0.02), 0.66 (0.02), and 0.70 (0.01) for BC, BB, and PA heights. With measurements from all three seasons together in a univariate analysis that included season x line as an additional fixed effect, the estimate of heritability was 0.60 (0.01). With ages analyzed separately, most estimates of heritability were greater than 0.50, but the small number of observations at older ages (> 7 yr) caused both the heritability estimates to be small and standard errors to be high relative to estimates for other ages. In bivariate analyses to estimate the correlation between heights at two ages within a season, most of the heritability estimates were greater than 0.50. Most estimates of genetic correlations were greater than 0.80. Hip height is a highly heritable trait that would respond to selection to alter mature size of the cow herd.

**Key Words:** Correlation, Heritability, Mature Size

**25 Genetic trends for mature weight for four lines of Hereford cows.** 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>2,3</sup>USDA, ARS, USMARC, <sup>2</sup>Clay Center, NE, <sup>3</sup>Lincoln, NE.

Mature weights (MW) were obtained a maximum of three times from a control (CTL) and three selection lines born over an 11-year period for 5-year-old spring calving Hereford cows. The seasons of measurement were before calving (BC), before breeding (BB), and during weaning of calves and pregnancy checking via rectal palpation (PA). The selection lines were selected for increased weaning weight (WWL), yearling weight (YWL), and an index of yearling weight and muscling score (IXL). Mature weights for each season were analyzed separately in bivariate analyses with birth weight (BW) or weaning weight (WW). The model for MW included fixed effects of year x age x line, age of dam x line, pregnancy status x line, and birth and method of rearing of calf x line. Random effects were direct genetic, maternal genetic, direct permanent environmental, maternal permanent environmental, and temporary environmental (residual). Based on the mean EBV by year of birth from analyses with birth weight for BC, direct EBV changed by 1.79, 1.45, 2.14, and -0.65 kg/yr for WWL, YWL, IXL, and CTL, respectively. For BC, maternal EBV changed by 0.21, 0.16, 0.18, and -0.06 kg/yr. For BB, direct EBV changed by 1.68, 1.62, 1.98, and -0.60 kg/yr and maternal EBV changed by 0.21, 0.16, 0.18, and -0.06 kg/yr. For PA, direct EBV changed by 2.13, 1.54, 2.38, and -0.67 kg/yr and maternal EBV changed by 0.21, 0.16, 0.18, and -0.06 kg/yr. Based on the mean EBV from analyses with weaning weight, BC for direct EBV changed by 1.50, 1.57, 1.63, and -0.23 kg/yr for WWL, YWL, IXL, and CTL, respectively and maternal EBV changed by 0.53, 0.53, 0.46, and -0.10 kg/yr. For BB, direct EBV changed by 1.37, 1.69, 1.35, and -0.17 kg/yr and maternal EBV changed by 0.57, 0.56, 0.48, and -0.10 kg/yr. For PA, direct EBV changed by 1.76, 1.72, 1.66, and -0.19 kg/yr and maternal EBV changed

by 0.55, 0.53, 0.48, and -0.09 kg/yr. Selection for increased weaning or yearling weights also increased breeding values for mature weight.

**Key Words:** Breeding Values, Mature Size, Selection

**26 Genetic parameters for lifetime production of Hereford cows.** G. E. Martinez<sup>\*1</sup>, R. M. Koch<sup>1</sup>, L. V. Cundiff<sup>2</sup>, K. E. Gregory<sup>2</sup>, and L. D. Van Vleck<sup>2,3</sup>, <sup>1</sup>University of Nebraska, Lincoln, NE, <sup>2,3</sup>USDA, ARS, USMARC, <sup>2</sup>Clay Center, NE, <sup>3</sup>Lincoln, NE.

Genetic parameters for number of calves born (NB), weaned (NW) and cumulative weaning weight (CW, kg) were estimated from 2,454 records of Hereford cows with opportunity to live to 3 to 7 yr of age, from a control line (CTL) and lines selected for weaning weight (WWL), yearling weight (YWL), and an index of yearling weight and muscle score (IXL) collected from 1964 through 1982. Weaning weights were adjusted for sex and age of dam. Estimates were obtained from bivariate animal models within trait (NB, NW and CW) for all pairs of opportunity groups (3 to 7 yr of age). Data were analyzed using REML with year of birth of the cow as a fixed effect and direct genetic and residual as random effects. Genetic trends were estimated by regressing means of estimated breeding values (EBV) by year of birth and line on birth year. Estimates of heritability (SE) for opportunity groups of 3 to 7 yr respectively were: 0.11 (0.03), 0.13 (0.04), 0.13 (0.04), 0.14 (0.03) and 0.13 (0.03) for NB; 0.15 (0.03), 0.15 (0.04), 0.11 (0.03), 0.15 (0.03) and 0.13 (0.03) for NW; and 0.11 (0.03), 0.14 (0.04), 0.13 (0.03), 0.13 (0.03) and 0.14 (0.03) for CW. Genetic correlations between opportunity groups ranged between 0.91 (0.01) and 1.00 (0.01). Estimates of genetic trend for cows with opportunity for 6 yr were: 0.00, 0.00, and 0.00 for NB/year; 0.00, 0.01, and 0.01 for NW/year; and 0.19, 0.90, and 0.48 kg for CW/year, for WWL, YWL, and IXL, respectively. Mean EBV for cows born in 1982 were: -0.03, -0.00, and 0.02 for NB; -0.00, 0.01, and 0.01 for NW; and 0.23, 1.38, and 1.11 kg for CW. Results suggest that selection for lifetime production measured by NB, NW or CW during a cow's lifetime could be effective but relatively slow due to low estimates of heritability and possibly prolonged generation interval. The high genetic correlations among opportunity groups indicate that cumulative records through 3 years of age predict subsequent cumulative records through 7 years of age.

**Key Words:** Genetic Correlation, Heritability, Selection

**27 Genetic parameters for longevity and lifetime production of Hereford cows.** G. E. Martinez<sup>\*1</sup>, R. M. Koch<sup>1</sup>, L. V. Cundiff<sup>2</sup>, K. E. Gregory<sup>2</sup>, and L. D. Van Vleck<sup>2,3</sup>, <sup>1</sup>University of Nebraska, Lincoln, NE, <sup>2,3</sup>USDA, ARS, USMARC, <sup>2</sup>Clay Center, NE, <sup>3</sup>Lincoln, NE.

Genetic parameters for longevity (LO, days between first calving and disposal date) and lifetime production (LT, weaning weight in kg of all calves weaned by disposal date) were estimated using records collected from 1964 to 1982 of 2,242 Hereford cows from a selection experiment with three lines selected for weaning weight (WWL), yearling weight (YWL), and an index of yearling weight and muscle score (IXL), and a control line (CTL). Weaning weights were adjusted for sex and age of dam. Heritabilities were estimated by REML using a bivariate animal model with year of birth of the cow (Y) as a fixed effect and direct genetic and residual effects as random. The genetic trends were estimated by regressing means of estimated breeding values (EBV) by year of birth and line on birth year. Estimates of heritability (SE) were: 0.14 (0.03) and 0.14 (0.03) for LO and LT, respectively. Estimated genetic correlation was 0.99 (0.05) and environmental correlation was 0.51 (0.02). Genetic trends were for LO 7.2, 8.7, and 7.5 days/year and for LT 3.4, 3.9, and 3.5 kg/year for WWL, YWL and IXL, respectively. The average EBV for cows born in 1982 were: 135.5, 145.1, and 132.4 days for LO and 63.0, 65.2, and 62.5 kg for LT, for WWL, YWL and IXL, respectively. These results suggest that selection for LO or LW could be successful in a breeding program, but relatively slow due to the low magnitude of heritability and possible extended generation interval. However, the favorable genetic trends for LO and LT indicate that selection for weights at relatively young weaning or yearling ages had a favorable effect on longevity and lifetime production without increasing the generation interval nearly as much as would be expected with selection for LO and LT directly.

**Key Words:** Genetic Correlation, Heritability, Selection

**28 Estimation of genetic parameters of lamb mortality using discrete survival analysis.** B. R. Southey\*<sup>1</sup>, S. L. Rodriguez-Zas<sup>1</sup>, and K. A. Leymaster<sup>2</sup>, <sup>1</sup>University of Illinois, Urbana, <sup>2</sup>USDA-ARS, U. S. Meat Animal Research Center, Clay Center, NE.

Lamb mortality from a composite population at the US Meat Animal Research Center was studied using discrete time survival analysis since the actual time of mortality may be unavailable, but information about a particular interval is available. Mortality records from 8,642 lambs were separated according to age into three stages, birth to weaning (BW), weaning to 365 d of age (WY) and birth to 365 d of age (BY). Within each stage, animal-period records were constructed with period defined as weekly or fortnightly. In addition, a daily animal-period was studied for BW and a monthly animal-period was studied for WY and BY. The logistic and complementary log-log link functions were used in sire, animal, and animal and maternal effects models and compared to continuous time survival Weibull model. The estimates of the sire variance were very similar between link functions and length of animal-period in all stages and to estimates obtained using the Weibull sire model. The complementary log-log link function heritabilities (standard errors) were 0.18 (0.06), 0.20 (0.20) and 0.13 (0.04) for BW, WY and BY stages, respectively, and were very similar to those obtained using a Weibull sire model. However, these estimates were approximately twice the magnitude of the estimates obtained with a logistic link function. These differences are probably due to the different variances of the link functions. Estimates of additive genetic variance and the associated heritability obtained with animal or animal and maternal effects models were lower than the sire model for the same scenario. These results illustrate that the use of discrete time approaches constitutes a feasible alternative to continuous time approaches in survival analysis.

**Key Words:** Sheep, Frailty, Proportional Hazards

**29 Comparison of models for traits of Rambouillet sheep.** L. D. Van Vleck\*<sup>1</sup>, K. J. Hanford<sup>2</sup>, and G. S. Snowder<sup>3</sup>, <sup>1</sup>USDA, ARS, USMARC, Lincoln, NE, <sup>2</sup>University of Nebraska, Lincoln, <sup>3</sup>USDA, ARS, USSES, Dubois, ID.

Several analytical models for birth weight (BWT, 17, n = 35,604), weaning weight (WWT, 11, n = 34,114), fleece weight (FWT, 8, n = 38,113) and number born (NB, 8, n = 39,029) were compared for Rambouillet sheep born at the USSES (1950-1998). For BWT, direct and maternal heritability were 0.26 and 0.19 (correlation of about zero) for all models. Likelihoods for models that also included dam by year, dam by number born, and sire by dam effects were significantly better than the basic maternal effects model, accounting for 0.06, 0.04, and 0.03 of phenotypic variance, respectively. Effects of cytoplasmic line and sire by cytoplasmic line were not significant. For WWT, direct and maternal heritability were 0.18 and 0.10 with correlation of 0.31 between direct and maternal genetic values. Of the other effects, only maternal permanent environmental effects (0.05 of variance) was not zero. For FWT, direct heritability was 0.55 for all models, but estimates of relative variance due to dam by year (0.02), sire by dam (0.05), and sire by cytoplasmic line (0.02) were jointly significant compared to a model with permanent environmental effects. For NB, for all models only direct heritability (0.08) and relative permanent environmental variance (0.04) were not zero. None of the traits showed evidence of variation due to cytoplasmic effects. Adding seldom considered effects to the model did not change estimates of variance due to direct and maternal genetic effects for any trait. Variance due to dominance effects inferred from estimate of the sire by dam component of variance may be important for BWT and FWT. The basic direct-maternal effects model seems sufficient for genetic evaluations for WWT and FWT but models for BWT and NB may need to include other effects. Variation due to these effects seems to be partitioned primarily from variation due to animal permanent environment effects for FWT but for BWT about 0.10 more of total variance is accounted for by the model with dam by year, dam by number born, and sire by dam interaction effects.

**Key Words:** Birth Weight, Weaning Weight, Fleece Weight

**30 Genetic parameters for subjective milk score and litter weight for Targhee, Columbia, Rambouillet, and Polypay Sheep.** R. Sawalha\*<sup>1</sup>, J. F. Keown<sup>1</sup>, G. D. Snowder<sup>2</sup>, and L. D. Van Vleck<sup>3</sup>, <sup>1</sup>University of Nebraska, Lincoln, <sup>2</sup>USDA, ARS, U.S. Sheep Experiment Station, Dubois, ID, <sup>3</sup>USDA, ARS, U.S. Meat Animal Research Center, Lincoln, NE.

Genetic parameters for subjective milk score (MS) and litter weight at 70 days (LW) were estimated independently by breed. Data collected from 1990 to 2000 at the U. S. Sheep Experiment Station were analyzed with an animal model using REML. Number of records was 13,900 for 5,807 ewes. Records were grouped according to parity as: first, second, third and greater, and all records. Single and two trait analyses resulted in similar genetic parameter estimates within a trait. Estimates of heritability for MS by parity ranged from 0.05 to 0.18 for first, 0.01 to 0.27 for second, 0.05 for Targhee and 0.10 for the other breeds for mature MS and from 0.08 to 0.13 for all records. Milk score at first and second parities was highly correlated genetically; estimates ranged from 0.74 to 1.00. Similarly, MS at first and second parities were highly genetically correlated with mature MS. Consequently, additive genetic milking ability at maturity could be evaluated as early as first parity. Heritability estimates for LW ranged from 0.00 to 0.18 for all breeds and parity groupings. Genetic correlation estimates at first parity between MS and LW were high (1.00) for Rambouillet and Polypay; moderate for Targhee (0.27) but near zero for Columbia (-0.02). At second parity, estimates were more variable and ranged from -1.00 to 1.00. For mature records, estimates ranged from -0.28 to 0.84. For all records, estimates were positive and moderate for all breeds (0.15 to 0.68). Estimates of genetic correlation between LW at first or second parity with mature LW were mostly high and positive except for Targhee (-0.10) and Polypay (0.14) at first parity. Litter weight for mature ewes could be improved by selection at first or second parity. Although estimates are variable, the average genetic correlation suggests that LW can be improved by selecting ewes for favorable milk scores.

**Key Words:** Heritability, Genetic Correlations, Breeds

**31 Genetic parameters for growth, feed intake, and feeding behavior in a composite population of sheep.** K. M. Cammack\*<sup>1</sup>, M. K. Nielsen<sup>1</sup>, K. A. Leymaster<sup>2</sup>, and T. G. Jenkins<sup>2</sup>, <sup>1</sup>University of Nebraska, Lincoln, <sup>2</sup>U.S. Meat Animal Research Center, Clay Center, NE.

The objective of this study was to estimate genetic parameters for growth, feed intake, and feeding behavior in composite rams (\*Columbia, \* Hampshire, \* Suffolk). Data were collected from 1986 to 1997 in Pinpointer units on 1,241 rams from 10 to 17 wk of age. Each Pinpointer unit was an elevated pen with an entrance chute that permitted feeder access for only one ram at a time with disappearance of feed measured electronically. Rams were grouped 11 per pen in 1986 through 1989, and 9 per pen in 1990 through 1997. Data were edited to exclude invalid feeding events. Approximately 80% of the feeding records remained after edits were applied. Estimated direct and maternal heritabilities for initial weight (weight0) were 0.34 and 0.30, respectively. The correlation between direct and maternal genetic effects was -0.88. Average daily gain (ADG) was estimated using three separate sets of data and heritability estimates ranged from 0.27 to 0.29. Results indicated that recording body weight at only the initiation and conclusion of a testing period is sufficient to accurately measure ADG and estimate genetic parameters. Estimated heritability of daily feed intake (DFI) was 0.23. Heritability estimates for number of feeding events per day (NE) and daily feeding time (DT) were 0.33 and 0.24, respectively. Feed efficiency had an estimated heritability of 0.15. Genetic correlations were positive between growth, feed intake, and feeding behavior traits. Phenotypic correlations were generally similar to genetic correlations. Direct genetic correlations were high (0.80) between ADG and DFI; intermediate (0.27 to 0.55) between DFI and DT, DFI and NE, ADG and NE, and NE and DT; and low (0.10 to 0.19) between ADG and weight0, DFI and weight0, and ADG and DT. Results suggest that selection for indices of ADG and DFI will likely change feeding behavior.

**Key Words:** Feeding Behavior, Feed Intake, Genetic Parameters

**32 Genetic parameters and responses to nine generations of selection to increase litter size in swine.** J. W. Holl\* and O. W. Robison, *North Carolina State University, Raleigh.*

Nine generations of direct selection for increased litter size were practiced. The select line consisted of approximately 15 sires and 75 dams per generation. Selection was based on estimated breeding values for number of live pigs. A control line of approximately 10 sires and 25 dams was maintained with stabilizing selection. Heritabilities estimated from REML procedures, daughter-dam regression within sires, and half-sib analysis were 0.01, 0.04, and 0.00 for number of pigs born alive (NBA); 0.02, 0.16, and 0.00 for total born per litter (TB); 0.17, 0.09, and 0.27 for backfat thickness adjusted to 104 kg (BF); and 0.50, 0.35, and 0.56 for days to 104 kg (DAYS), respectively, for the select line. Corresponding estimates for the control line were 0.01, 0.06, and 0.23; 0.02, 0.07, and 0.09; 0.27, 0.10, and 0.40; and 0.43, 0.28, and 0.43, respectively. Using weighted multiple regression, heritability estimates for NBA were  $0.09 \pm 0.075$  for select and  $0.11 \pm 0.156$  for control lines. Regression of difference of response between lines on cumulative selection differentials yielded a heritability estimate of  $0.13 \pm 0.07$ . At Generation nine, the select line exceeded the control line by 0.86 pigs ( $P > 0.05$ ). Estimated breeding values differed between the lines by 0.63 for NBA ( $P < 0.01$ ) and cumulative selection differential for NBA differed by 9.05 ( $P < 0.01$ ). Differences between the lines for TB, BF, and DAYS were not significant. Genetic trends in the select line were  $0.053 \pm 0.002$  pigs/yr for NBA,  $0.054 \pm 0.013$  mm/yr for BF, and  $0.398 \pm 0.113$  days/yr for DAYS. Corresponding phenotypic trends were  $0.144 \pm 0.053$  pigs/yr,  $-0.012 \pm 0.087$  mm/yr, and  $0.307 \pm 0.278$  days/yr, respectively. Genetic trends in the control line were  $-0.026 \pm 0.004$  pigs/yr for NBA,  $0.026 \pm 0.023$  mm/yr for BF, and  $-0.532 \pm 0.166$  days/yr for DAYS. Corresponding phenotypic trends were  $0.001 \pm 0.079$  pigs/yr,  $-0.043 \pm 0.153$  mm/yr, and  $-0.519 \pm 0.463$  days/yr, respectively.

**Key Words:** Pigs, Selection, Litter Size

**33 Genetic parameters for primal cut weights in pigs.** D. W. Newcom\*<sup>1</sup>, T. J. Baas<sup>1</sup>, and R. N. Goodwin<sup>2</sup>, <sup>1</sup>*Iowa State University, Ames*, <sup>2</sup>*National Pork Board, Des Moines, IA.*

The objective of this study was to estimate genetic parameters for primal cut weights in pigs. Carcass and dissection data from 456 Halothane negative, purebred Yorkshire, Duroc and Other breed pigs with three generation pedigrees were analyzed to estimate heritabilities and genetic correlations. The traits of interest were the primal cuts of Ham 401 (HAM), Loin 410 (LOIN), Boston Butt 406 (BB), Picnic 405 (PIC), and Belly 409 (BELLY) cut to Institutional Meat Purchase Specifications (IMPS). With a lack of previous literature estimates for these traits, 10<sup>th</sup> rib backfat (BF10) and loin muscle area (LMA) were included as reference traits. A multiple trait animal model was performed using MTDFREML to estimate additive genetic (animal) and residual variances and covariances. The model included the fixed effects of breed, sex and group with off-test weight as a covariate. Heritability estimates for HAM, LOIN, and BELLY weights were higher than expected, however BF10 and LMA were well within the range of previous literature estimates ( $h^2 = 0.58$  and  $0.69$ ). BB and PIC were both found to be lowly heritable traits. Genetic correlations were generally high with BF10 and BELLY showing a positive correlation with one another and a negative association with LMA and the four lean cuts. The four lean cuts were all positively correlated with each other and with LMA. Results from the seven trait primal analysis are shown below.

	HAM	LOIN	BB	PIC	BELLY	BF10	LMA
HAM	0.61	0.60	0.37	0.74	-0.62	-0.64	0.57
LOIN		0.63	0.76	0.88	-0.59	-0.64	0.80
BB			0.09	0.79	-0.66	-0.14	0.54
PIC				0.20	-0.76	-0.62	0.81
BELLY					0.67	0.61	-0.40
BF10						0.58	-0.57
LMA							0.69

Heritabilities on diagonal, Genetic correlations above diagonal

**Key Words:** Pigs, Genetic Parameters, Primal Cuts

**34 Two Pit-1 RFLPs and their association with growth traits in beef cattle.** Q. Zhao\*, M.E. Davis, and H.C. Hines, *The Ohio State University, Columbus.*

Pit-1 is a pituitary specific transcription factor that has been shown to positively regulate the expression of growth hormone, prolactin, and thyrotrophin b subunit (TSH-b). Therefore, it may be a good candidate gene for genetic markers for growth traits. Growth traits have been shown to be under control of multiple genes, and genetic marker information on these genes can be used to facilitate selection and breeding through marker assisted selection (MAS) in domestic animals. Two highly linked polymorphisms were found in introns 3 and 4 of the Pit-1 gene. The intron 3 polymorphism was examined in 121 and the intron 4 polymorphism in 86 Angus beef cattle, which were divergently selected for high or low blood serum IGF-I concentration. The genotypic frequencies were 0.09 for CC, 0.49 for CD, and 0.42 for DD for the intron 3 polymorphism. Frequencies for the EE, EF and FF genotypes of the intron 4 polymorphism were 0.08, 0.56, and 0.36, respectively. The intron 3 polymorphism was shown to have an AAT deletion in allele C, which can be recognized by digestion with restriction enzyme Hinf-1. The intron 4 polymorphism has a G to T transition in allele F, which can be recognized by digestion with restriction enzyme BstNI. The associations of the polymorphisms with growth traits and IGF-I concentration were also analyzed using the GLM procedure in SAS. A linear model was fitted for birth weight, weaning weight, preweaning gain, on-test weight, weight at d 28 and 56 of the 140-d postweaning test, off-test weight, postweaning gain, serum IGF-I concentration on d 28, 42, and 56 of the postweaning test, and mean serum IGF-I concentration. No significant associations were found between the Hinf-1 genotypes and growth or IGF-I traits. A moderate association with on-test weight ( $P = .09$ ) was observed. Calves with genotype CD tended to have higher on-test weights than CC and DD calves. No significant relationships of the BstNI genotypes with growth traits or IGF-I concentrations were observed.

**Key Words:** Pit-1, Growth, Beef Cattle

**35 Comparison of the glycolytic potential and DNA-based test for predicting Rendement Napole genotype.** D. N. Hamilton\*<sup>1</sup>, M. Ellis<sup>1</sup>, K. D. Miller<sup>2</sup>, F. K. McKeith<sup>1</sup>, A. D. Higgerson<sup>1</sup>, and J. E. Beever<sup>1</sup>, <sup>1</sup>*University of Illinois at Urbana-Champaign*, <sup>2</sup>*Elanco Animal Health, Greenfield, Indiana.*

This study was carried out to evaluate the relationship between the phenotypic method (glycolytic potential) and the DNA-based test to determine Rendement Napole (RN) genotype. Glycolytic potential (GP) was determined on live-animal biopsy (n=161) or postmortem longissimus samples (n=90) to predict the RN genotype and a PCR-RFLP based test was used to determine the RN genotype. Prediction of RN genotype was on the basis of the breakpoint between the two parts of the bimodal frequency distribution for GP. The breakpoints in the distributions for the population in which GP was measured on live-animal and postmortem samples were 190 or 158  $\mu\text{mole/g}$ , respectively; animals with GP's below these values were classified as homozygous normal ( $rn^+rn^+$ ) and those with GP's above these values were classified as carriers ( $RN^-rn^+$ ). Longissimus GP was higher for carrier compared to homozygous recessive animals ( $242.6 \pm 52.11$  vs  $168.2 \pm 30.97$   $\mu\text{mole/g}$  and  $185.7 \pm 47.36$  vs  $118.6 \pm 18.36$   $\mu\text{mole/g}$  for the live-animal and postmortem samples, respectively;  $P < 0.05$ ). Only carrier and homozygous recessive animals were identified using the DNA test. Predicting genotype on the basis of GP resulted in 12.5 % of animals being mis-classified compared to the DNA test. There was a trend ( $P = 0.07$ ) for greater agreement between the two tests when genotype prediction was based on postmortem compared to live-animal samples (8.9 vs 18.3 % mis-classified, respectively). The percentage mis-classified was similar ( $P > 0.05$ ) for carrier and homozygous recessive animals (14.4 vs 11.1 %, respectively). Eight (29.6 %) of the 27 mis-classified samples were within 5  $\mu\text{mole/g}$  of the breakpoint value used to predict genotype; the remainder of the mis-classified samples were distributed across the range of GP values. Results from this research suggest that predicting RN genotype on the basis of muscle GP will result in a relatively limited number of mis-classifications.

**Key Words:** Rendement Napole, Glycolytic Potential, Pigs

**36 Study of factors influencing sow longevity in swine breeding herds.** S. L. Rodriguez-Zas<sup>\*1</sup>, B. R. Southey<sup>1</sup>, R. V. Knox<sup>1</sup>, and J. F. Connor<sup>2</sup>, <sup>1</sup>University of Illinois at Urbana-Champaign, <sup>2</sup>Carthage Veterinary Service, Ltd.

Early removal of sows from the herd due to mortality, health problems and poor performance is a major bottleneck in the swine industry. This situation amounts to animal welfare and economic concerns due to lower productivity, replacement and veterinary treatment costs. The goal of this study was to study sow longevity and production determinants and their interplay. Over 17,000 sow-parity longevity and production records obtained between 1993 and 2001 were studied. Complementary indicators of longevity including the parity and age, total number and weight of piglets (born alive, weaned) at removal or death were evaluated. Survival analysis, in the form of a linear proportional hazards model, was applied to the different measures of sow longevity. Sow productivity indicators across parities were analyzed using a repeated measurement model. The explanatory variables included parity, age, year, genetic line and sow specific removal reasons. A sow had an 81% probability to remain in the herd until the end of the first parity and this probability dropped to 50% after the fourth parity. Reproductive failure was the major removal cause in the first two parities. The probability of a sow remaining in the herd until the first parity was 88% when only reproduction failure was considered. Health, death, and locomotor problems were critical limiting factors of sow longevity in the later parities. Genetic line was a significant factor contributing to sow longevity. Assuming 2.35 parities per year and four parities to cover the replacement cost, the difference in the probability of survival to 620 d between the two most extreme genetic lines was 45%. Year and month of farrowing, parity and genetic line have significant effects on litter size. The ranking of the genetic lines in terms of longevity probability did not entirely correspond to that based on productivity. Results from this study suggest that culling policies together with genetic line must be considered in sow longevity and productivity improvement programs.

**Key Words:** Survival Analysis, Lifetime Production, Proportional Hazards

**37 Introgression of multiple QTL with limited population size in livestock.** N. Chaiwong<sup>\*</sup> and J. Dekkers, Iowa State University, Ames.

Genetic markers can be used to introgress favorable alleles at one or more quantitative trait loci (QTL) from a donor to a recipient breed through marker-assisted introgression (MAI). Current MAI programs require selected backcross individuals to be heterozygous for all QTL. This requires large numbers of backcross progeny to be produced, which is not feasible in livestock, in particular when QTL positions are not well known and several sizeable QTL regions must be introgressed. Furthermore, heterozygosity at all QTL is not required if the objective is to introduce favorable QTL alleles in the recipient breed for further genetic improvement. The objective of this study was to evaluate the potential for MAI of multiple QTL in a population of limited size. Backcross generations of 500 individuals were simulated and 100 individuals were selected per generation for backcrossing to the recipient breed. Selection was on the expected number of recipient QTL alleles carried by the individual at three unlinked QTL. Two cases were considered: known QTL and QTL regions marked by six informative markers in a 21 cM region centered around the QTL. For known QTL, selection was on observed QTL genotypes. For marked QTL regions, selection was on the number of intact marker intervals inherited from the donor breed, weighted by the probability of presence of a QTL in each interval. Weights were 0.1 for the external marker intervals, 0.2 for internal intervals, and 0.4 for the central interval. Effectiveness of MAI was evaluated based on the average frequency of favorable QTL alleles after five generations of backcrossing. Results for the known QTL case, which are based on a single replicate, showed a gradual decrease in average frequencies of donor QTL alleles from 0.5 in the F1 to 0.35 in the 5<sup>th</sup> backcross generation. Similar results were obtained for the marked QTL case, but further replication is needed to verify these results. Nevertheless, these preliminary results show that MAI of multiple QTL within a population of limited size can result in the introduction of donor QTL alleles into the recipient breed at reasonable frequencies that would allow subsequent within-breed improvement. This work was supported by CSREES IFAFS # 00-52100-9610.

**Key Words:** QTL, Marker-Assisted Introgression, Backcross

**38 Confirmation of quantitative trait loci (QTL) affecting body weight and fatness in a congenic line of mice.** N. Jerez-Timaure<sup>\*1</sup>, D. Pomp<sup>1</sup>, and E. J. Eisen<sup>2</sup>, <sup>1</sup>University of Nebraska-Lincoln, Lincoln, <sup>2</sup>North Carolina State University, Raleigh.

Understanding the genetics and physiology of growth and obesity is important in both animal production and human medicine. Fine-scale mapping of QTL using congenic lines provides a significant shortcut to the ultimate goal of gene positional cloning and identification. To isolate and examine a QTL with large effect on murine growth and fatness on distal chromosome 2 (MMU2), a congenic line was produced. The congenic line (MC) was created using the polygenically obese M16i selection line as the recipient for a 24 cM region (encompassing the broad QTL peak) from the inbred line C57BL6/J. Following 8 generations of marker-assisted introgression, the region was fixed by inter-se mating. We have compared M16i and MC for a variety of relevant phenotypes at three ages (6, 15, 24 wk) and on two diets (normal, high fat). M16i mice gained more weight than MC (significantly different up to 12 week of age), with no differences in feed intake at any stage. As a result of an improved feed efficiency, M16i mice fed with either diet were heavier than MC mice. The greatest differences in body composition between MC and M16i were detected at 15 weeks of age; M16i mice had more (P<0.05) epididymal fat (2.79% vs. 1.17%) and total lipids (23.3% vs. 16.1%) than MC. Reduction in plasma leptin, insulin and glucose levels were observed (P<0.05) in MC compared to M16i. Obesity of M16i was not diet-dependent. The differences detected between M16i and MC confirm the large effects of QTL in this region of MMU2 and support the use of MC for fine mapping. A large F<sub>2</sub> population using MC and M16i was developed to increase QTL map resolution. Synergistic strategies such as recombinant progeny testing and candidate gene expression are in progress to pinpoint the location of the QTL. The combination of these strategies will facilitate positional cloning of genes affecting fatness and growth.

**Key Words:** QTL, Congenic, Fatness

**39 Birth weight, calving ease, and other factors affecting perinatal mortality in Holstein cattle.** J. M. Johanson<sup>\*</sup> and P. J. Berger, Iowa State University, Ames.

Birth weights of Holstein cattle are rarely recorded, so the effect of birth weight on perinatal mortality has been difficult to determine. This research explores the effect of birth weight and other factors on perinatal mortality. The Iowa State University dairy research farm in Ankeny, IA collected 5,166 records of births between 1968 and 1999. The frequency of perinatal mortality was 9.8%. Due to the binary nature of the observations, the logistic regression model was used to predict perinatal mortality. The model included effects of year of birth, sex of calf, calving ease (unassisted or assisted), age within parity, birth weight, and gestation length. All factors were significant except sex of calf and age within parity. Odds ratio estimates were 1.014 for year, 1.156 for male versus female calves, and 3.897 for assisted versus unassisted births. The age within parity odds ratio estimates were 0.9878, 0.9779, 0.9855, and 0.9889 for parities 1 through 4 and greater, respectively. Birth weight and gestation length were fit as quadratic factors. Probabilities of perinatal mortality for birth weights 27, 33, 40, 46, and 52 kg were 3.2, 1.8, 1.5, 2.1, and 4.5%, respectively, when other factors were set at the average value. Similarly, gestation length of 267, 272, 278, 284, and 290 d yield probabilities of mortality of 3.2, 2.0, 1.6, 1.5, and 1.6%, respectively.

**Key Words:** Birth Weight, Perinatal Mortality, Holstein

**40 Differences in performance between growing pigs fed using electronic versus commercial feeders.** D.S. Casey<sup>\*</sup> and J.C.M. Dekkers, Iowa State University, Ames.

Single-space electronic feeders are increasingly used to measure feed intake on group-housed pigs in breeding herds, whereas multi-space feeders are used in commercial herds. The objective of this study was to evaluate the effect of electronic feeders on performance of Yorkshire boars and gilts during the growing period. Littermate Yorkshire boars and gilts (n=475) were randomly assigned to pens with single-space FIRE<sup>®</sup> feeders and pens with 5-hole Smidley<sup>®</sup> feeders. At the beginning and end of test, pigs were weighed (mean 39 and 116 kg) and loin muscle area and backfat thickness were measured using real-time ultrasound.

Amount of feed consumed by each pen (n=39) was measured and average daily feed intake (ADFI) per pig for each pen was calculated. The traits average daily gain (ADG), backfat thickness (BF) and loin muscle area (LMA) at the end of test, difference in backfat thickness (DBF) and loin muscle area (DLMA) between the beginning and end of test, ADFI, and feed conversion ratio (FCR) were analyzed with a model that included the fixed effects of feeder type, sex, feeder type by sex interaction, and group (based on beginning test date, n=7) and the covariates weight at the end of test and floor space per pig. Weight at the beginning of test was used as an additional covariate for all traits except for BF and LMA. Feeder type had no significant effect (P<.05) on any trait except on ADFI and FCR. Pigs on electronic feeders used less feed (-.086 kg/day) and converted feed more efficiently (-.085 kg feed/kg gain). Feeder type by sex interaction was significant only for ADG. Gilts grew slower on electronic feeders (-.024 kg/day), whereas no feeder differences were found for boars. Significant sex differences were found for all traits except for DBF and ADFI. For all traits, group was significant and floor space per pig was not significant. In conclusion, the use of electronic feeders has no effect on growth performance, but does result in slightly lower feed usage, which could be explained by decreased feed wastage in electronic feeders.

**Key Words:** Swine, Electronic Feeder, Performance

**41 Effects of Rendement Napole gene and HAL 1843 gene on fresh and cooked pork loin quality.** R. N. Goodwin\*<sup>1</sup>, T. J. Baas<sup>2</sup>, K. Prusa<sup>2</sup>, C. Fedler<sup>2</sup>, and D. Newcom<sup>2</sup>, <sup>1</sup>National Pork Board, Des Moines, IA, <sup>2</sup>Iowa State University, Ames.

The HAL 1843 gene (N,n) and the Rendement Napole gene (rn+,RN-) are known to be major genes influencing pork carcass composition and pork meat quality. There were 1,202 tested progeny pigs, 654 barrows and 548 gilts, representing eight pure breeds. The 1999, 2000 and 2001 National Barrow Show Sire Progeny Test pigs were classified by HAL 1843 (1,127 NN, 75 Nn) and Rendement Napole (1,135 rn+rn+, 67 RN-rn+) genotype. Each sire group of eight pigs represented at least three litters. The loin was scored for color (PC), marbling (PM) and firmness (PF) and ultimate pH (pH) was measured. Light reflectance (MINP) and Hunter L score (HUNTP) were measured with a Minolta 310 Chromameter using a 50 mm orifice. Forty-eight hours post mortem the loin was divided into three chops. Water holding capacity (WHC) was measured using the filter paper method. The tenth rib chop was used for total lipid analysis (IMF). The eleventh and twelfth rib chops were aged for seven days, not frozen. Chops were cooked to 70 C and evaluated for cooking loss (CLOSS), star probe pressure (INSTRON), sensory panel juiciness score (JUICY), and sensory panel tenderness score (TENDER). A mixed linear model was used for data analysis. Fixed effects were date of slaughter, breed of pig, sex of pig, HAL 1843 genotype of pig, and Napole genotype of pig. Random effect was sire within breed. Table 1. Least squares means and standard errors.

Trait	Units	Napole		Signif P<.05
		normal, rn+rn+	mono RN-rn+	
PH	pH	5.72 .015	5.48 .025	*
MINP	percent	25.8 .29	27.7 .49	*
HUNTP	L score	50.6 .29	52.6 .48	*
PC	1-6 score	3.1 .07	2.5 .11	*
PM	Est %	2.1 .08	1.7 .13	*
PF	1-5 score	2.2 .04	1.8 .08	*
IMF	percent	2.32 .084	2.10 .130	.08
WHC	mg loss	59 1.8	89 3.2	*
CLOSS	percent	22.5 .34	25.4 .60	*
INSTRON	kg	5.95 .091	5.57 .151	*
JUICY	1-10 score	5.3 .12	5.6 .22	NS
TENDER	1-10 score	6.0 .13	6.9 .23	*

**Key Words:** Pig, Genetics, Pork Quality

**42 Fertility of intra-uterine vs. intra-cervical insemination of semen in swine.** T Gall\*, *Pork Technologies, Danville, IA.*

New technology has been developed that permits intra-uterine insemination of swine semen (IUI) as opposed to the current technique of intra-cervical insemination (ICI). Three hundred multiparous sows were

used in a paired study to determine the fertility of a low dose intra-uterine insemination compared to an industry standard conventional AI. Following weaning, estrus detection was performed and confirmed in the presence of a mature boar. Sows detected in estrus were paired according to parity, lactation length, number of pigs weaned and wean-estrus interval, randomly assigned to treatment and moved to breeding stalls. Forty-five minutes after estrus detection, an individually sterilized, disposable spiral tipped catheter with an inner canula (Soft Quick) was passed through the vagina and locked into the cervix of each IUI sow (n = 150), and 30 ml of extender at 43°C were inseminated intra-cervically. Two minutes following extender insemination, the inner canula was passed through the cervix into the uterine body and an 18 ml dose of semen (6.2 x 10<sup>8</sup> viable sperm) was inseminated via the inner canula. Following mating of IUI sows, a boar was introduced and the ICI sows (n = 150) were inseminated intra-cervically with a 75 ml dose of semen (3 x 10<sup>9</sup> viable sperm) from the same pool of boars using a disposable spiral tipped catheter. Sows were mated once each day until estrus was no longer observed. Nine ICI and 5 IUI sows were excluded from data analysis (provided by W.L. Flowers, NCSU, Raleigh, NC) due to culling, abortion or death. ANOVA was determined using the GLM procedure in SAS (v8.0, SAS, Cary, NC). Farrowing rate, average total pigs born and born alive were similar between IUI and ICI treatments (86.2% vs. 85.1%, 10.8 ± .3 vs. 11.2 ± .3, and 9.9 ± .3 vs. 10.1 ± .3; respectively). Parity, breeding group and sire interactions with treatment were not detected. These results suggest that reproductive performance can be maintained with a reduced number of sperm using this IUI delivery system.

**Key Words:** Swine, Semen, Intra-Uterine Insemination

**43 Growth and puberty traits of topcross heifer progeny of Hereford, Angus, Red Angus, Simmental, Gelbvieh, Limousin, and Charolais sires.** L. V. Cundiff\*<sup>1,2</sup>, L. D. Van Vleck<sup>1,3</sup>, and R. M. Thallman<sup>1,2</sup>, <sup>1</sup>USDA, ARS, Roman L. Hruska U.S. Meat Animal Research Center, <sup>2</sup>Clay Center, NE, <sup>3</sup>Lincoln, NE.

Data were obtained on 698 heifers born in the spring of 1999 and 2000 resulting from artificial insemination matings of Hereford (H, 21 sires), Angus (A, 22), Red Angus (Ra, 21), Simmental (S, 20), Gelbvieh (G, 23), Limousin (L, 20), and Charolais (C, 22) bulls, to Hereford, Angus, and composite MARC III (1/4 each Angus, Hereford, Red Poll, and Pinzgauer) cows. Data on 550-d weight, (550WT) 550-d height (550HT), frame score (FS as defined by Beef Improvement Federation), weight at puberty (PUBWT), age at puberty (PUBAGE), and pregnancy rate at 18 months (PREG) were analyzed by least squares procedures using a model that included random effects for sire in sire breed and fixed effects for sire breed, dam breed, sex of calf, age of dam (4,5,..10 yr), birth year, and sire breed x dam breed. Effects of sire breed were not significant (P>0.05) for PREG, but were significant for 550WT, 550HT, FS, PUBWT, and PUBAGE. Least squares means for H, A, Ra, S, G, L, and C sired progeny were 431, 424, 432, 436, 418, 423, and 431 kg, respectively for 550WT with a mean least significant difference (LSD, P<0.05) of 15 kg. Corresponding sire breed means were 128.4, 127.2, 126.9, 130.2, 128.8, 129.9, and 129.5 cm for 550 HT (LSD, P<0.05, 1.6 cm); 5.5, 5.3, 5.3, 5.9, 5.6, 5.8 and 5.8 for FS (LSD, P<0.05 = 0.3 score units); 333, 340, 338, 344, 323, 356, and 344 kg for PUBWT (LSD, P<0.05 = 16 kg); 357, 343, 342, 342, 329, 377, and 358 d for PUBAGE (LSD, P<0.05 = 16 d), and 94, 88, 91, 90, 83, 87, and 91% for PREG (LSD, P<0.05, 13%). Means for 550HT and FS were significantly greater for heifers with S, C, L, and G sires than those with A and Ra sires. PUBAGE was greater in L sired heifers than those by any other sire breed.

**Key Words:** Beef Cattle, Breeds, Germplasm

**44 Economic analysis of selection response in the NE Index line estimated in pure line and crossbred litters.** D. Petry\*, B. McAllister, and R. Johnson, *University of Nebraska, Lincoln.*

Economic effects of 19 generations of selection for litter size in the NE Index line were estimated by simulating production for 1,250 sow herds based either on Line I (I) females or Control Line (C) females. During generations 17-19, pure line I and C pigs, F1 crosses of I and C with Danbred<sup>®</sup> USA LLC Landrace (L), and 3-way crosses of LxI and LxC females mated with Danbred<sup>®</sup> USA LLC DH terminal boars (T) were compared for reproductive, growth, and carcass traits. Those data

were used to simulate enterprises based on either I or C females. All replacement females and replacement boars for I and C were produced within the herd. AI was used to produce F1 and 3-way cross litters. The number of I or C sows was set at 50, and the distribution of F1 and 3-way cross litters was determined by farrowing rates, litter sizes, imposed selection rates and sow culling policies. Gross revenue was estimated assuming pigs were sold on the Sioux-Preme Packing Co. carcass grid. The numbers marketed for each group within the I enterprise were 909 Line I, 564 LxI, and 22,944 T(LxI) pigs. The numbers marketed for each group within the C enterprise were 733 Line C, 524 LxC, and 18,909 T(LxC) pigs. Variable and fixed costs per pig marketed were \$3.21 and \$2.98 less, respectively, for the enterprise based on I. Net revenue per pig

marketed averaged \$116.91 for the I enterprise, and \$115.76 for the C enterprise. Differences in net revenue per pig marketed between groups within the enterprises were \$3.05 for pure line I and C, -\$2.50 between F1 LxI and LxC, and \$2.89 between T(LxI) and T(LxC). The rate of return on investment was 6% greater for the I enterprise. Net return per pig marketed averaged -\$18.49 for pure line I and C, \$1.74 for F1 LxI and LxC, and \$22.14 for 3-way cross T(LxI) and T(LxC) pigs. The effect to a breeding enterprise of 18 generations of selection for increased litter size was estimated to be \$7.33 net return per pig marketed, which is \$0.41 per pig marketed per generation.

**Key Words:** Selection, Costs, Revenue

## Extension

**45 Evaluation of particle length reduction during silage removal using a bunker facer.** D. Sutter<sup>1</sup> and R. D. Shaver<sup>2</sup>, <sup>1</sup>*Brown County Extension, UW Extension*, <sup>2</sup>*Department of Dairy Science, UW Madison, UW Extension*.

Bunker-facer systems are being used on dairy farms in Wisconsin for silage removal. The objective of this study was to determine the effect of these systems on silage particle length. Silage was sampled three ways for particle length analysis: 1) hand removal from face, 2) after bucket removal from face, and 3) after facer-unit removal from face. Both corn silage and alfalfa silage bunkers were sampled. Hand removal was done using a trowel. Bucket removal was by working the bucket up the face to dislodge 10-15 cm of silage. Facer units were attached to either skid steers or sky lifts. The facer units were started at the top of the bunker and were worked down the face to remove 10-15 cm of corn silage or 5-10 cm of alfalfa silage. Composite samples were collected from the pile at the foot of the bunker. Particle length measurements were done using the Penn State-Nasco shaker box. Samples were taken on one day each week for three weeks on each farm. Bunker-facer systems evaluated were Valmetal (VM; Valmetal Co.), Bunker Buster (BB; Gehl, Co.), and Bunker Claw (BC; D&D Equipment). On Farm A, silage removal with VM was compared to hand removal for alfalfa silage. On Farm B, silage removal with VM was compared to hand removal for corn silage. On Farm C, silage removal with VM, BB, and BC were compared to hand removal for alfalfa silage. On Farm D, silage removal with BB was compared to hand and bucket removal for alfalfa silage and corn silage. Data were pooled across farms and analyzed using Proc GLM of SAS; the model included farm, forage type, sample day, bunker-facer system, forage by bunker-facer system, and farm by bunker-facer system effects. Corn silage was finer than alfalfa silage ( $P < 0.001$ ) and silage particle length varied by farm ( $P < 0.01$  and  $P < 0.001$  for coarse and fine screens, respectively). Silage particle length was unaffected by day of sampling, indicating that silages and sampling and sieving techniques were consistent across the study. Silage particle length was unaffected by bunker-facing system. Under the conditions of this study, we found no evidence that the bunker-facing systems evaluated reduce silage particle length during removal of silage from the bunker.

**Key Words:** Silage, Particle Length

**46 Influence of a rumen-fluid drench at calving on milk production and incidence of health disorders in early lactation dairy cows.** I. Possin<sup>1</sup>, J. Keuning<sup>2</sup>, and R. D. Shaver<sup>3</sup>, <sup>1</sup>*Fond du Lac County Extension, UW Extension*, <sup>2</sup>*Kewaunee County Extension, UW Extension*, <sup>3</sup>*Department of Dairy Science, UW Madison, UW Extension*.

We hypothesized that administering a rumen-fluid drench around the time of calving may reduce the incidence of health disorders and enhance milk production. Both no drench and warm-water drench were used as controls for the rumen-fluid drench treatment. The experiment was conducted on two commercial dairies. Cows were blocked by parity and expected calving date and assigned randomly to treatments. For Farm A, there were 300 cows assigned to the trial. Milk yields at the first (1-30 DIM) and second (31-60 DIM) tests averaged 27.7 kg/cow/day and 37.1 kg/cow/day, respectively, and were unaffected by treatment ( $P > 0.10$ ). Post-calving rectal temperatures were normal and unaffected by treatment across ten days of recording rectal temperatures ( $P > 0.10$ ). Incidence of retained placenta was higher ( $P < 0.001$ ) for fever (33.6%) than non-fever (14.3%) cows. Metritis incidence was higher ( $P < 0.01$ ) for fever (22.4%) than non-fever (10.3%) cows. Mastitis incidence was

higher ( $P < 0.05$ ) for fever (26.4%) than non-fever (15.4%) cows. The only significant ( $P < 0.01$ ) treatment observation for Farm A was for mastitis being higher for drenched cows (28.0% and 21.1% for water and rumen-fluid drenches, respectively) than control cows (11.4%). For Farm B, there were 189 cows assigned to the trial. Days in milk, milk yield, and 3.5% FCM yield at the first DHI test averaged 15.6 days, 34.1 kg/cow/day, and 37.5 kg/cow/day, respectively, and were unaffected by treatment ( $P > 0.10$ ). Days in milk, milk yield, and 3.5% FCM yield at the second DHI test averaged 45.9 days, 42.0 kg/cow/day, and 40.5 kg/cow/day, respectively, and were unaffected by treatment ( $P > 0.10$ ). Post-calving rectal temperatures were normal and unaffected by treatment across five days of recording rectal temperatures ( $P > 0.10$ ). Metritis incidence was higher ( $P < 0.001$ ) for fever (39.2%) than non-fever (5.2%) cows. The only significant ( $P < 0.05$ ) treatment observation for Farm B was for cow deaths, which totaled four of 64 for the control group and zero of 62 and 63 for the warm-water and rumen-fluid drench groups, respectively. Under the conditions of this experiment, a rumen-fluid drench around the time of calving did not improve early lactation milk production or reduce the incidence of health disorders.

**Key Words:** Rumen Fluid, Dairy Cows, Health

**47 The effect of antibiotic residues in raw milk on yogurt manufacture.** P.N. Dias<sup>1</sup>, D.W. Kellogg<sup>1</sup>, K.F.S.T. Silva<sup>2</sup>, and S. Dureiratnam<sup>3</sup>, <sup>1</sup>*University of Arkansas, Fayetteville*, <sup>2</sup>*University of Peradeniya, Sri Lanka*, <sup>3</sup>*Milk Industries of Lanka Co., Ltd., Sri Lanka*.

The experiment assessed inhibitory effects of antibiotics (penicillin, oxytetracycline, ampicillin, and cloxacillin) that are registered for dairy cattle management in Sri Lanka on yogurt culture that contained a ratio of 1:1 *Streptococcus thermophilus* and *Lactobacillus bulgaricus*. The raw milk samples that contained different levels of commonly used antibiotics were tested in three replicates. The minimum detectable concentration of penicillin in milk was 0.005 mg/kg by bromocresol dye reduction method and was 0.05 mg/kg by disc assay technique. The inhibitory levels of the other antibiotics tested were below their detectable limits using the bromocresol and disc assay methods. Penicillin was the most sensitive antibiotic on the yogurt starter culture. In the process of yogurt production under 44°C incubation temperature and 2 h of incubation, 0.01 mg/kg of penicillin totally inhibited ( $P < 0.05$ ) acid production by yogurt culture. The inhibitory concentrations of ampicillin, cloxacillin, and oxytetracycline were 0.05, 0.3, and 0.5 mg/kg, respectively. Above these concentrations there was no yogurt setting observed. Titratable acidity development was reduced ( $P < 0.05$ ) with increasing concentrations of all antibiotics tested in milk, and beyond the inhibitory concentrations there was only slight increase ( $P < 0.05$ ) in acidity with time. Antibiotics in milk also affected ( $P < 0.05$ ) the total bacterial count (mean = 120,000) and the ratio of cocci to rods in yogurt mixture. In conclusion, the presence of specific antibiotic residues in milk inhibited acid production by starter culture bacteria markedly and affected the yogurt making process, leading to longer manufacturing time and poor setting of curd.

**Key Words:** Antibiotic Residues, Milk, Yogurt