

# Breeding and Genetics: Feed Intake and Utilization

**66 Genetic correlations of gross feed efficiency with yield, body weight, body condition score, and energy balance in dairy cattle.** C. D. Dechow\*<sup>1</sup>, J. Vallimont<sup>1</sup>, M. D. Dekleva<sup>1</sup>, J. M. Daubert<sup>1</sup>, and J. W. Blüm<sup>2,1</sup>, <sup>1</sup>*Pennsylvania State University, University Park*, <sup>2</sup>*University of Bern, Switzerland*.

The objective of this study was to estimate genetic correlations of gross feed efficiency with 305 d fat corrected milk yield (FCM), 305 d protein yield, body weight (BW), body condition score (BCS), BCS change (BCSCH) from 5 to 30 d in milk (DIM), and cumulative energy balance (CEB) from 5 to 30 DIM. Intake, BW and BCS were recorded once per month for 6 consecutive months on 11 Pennsylvania tie-stall dairy farms. Feed samples were taken at each visit to determine net energy of lactation intake (NEI) and crude protein intake (CPI). Random regression models were used to analyze 35,390, 3999, 2195 and 4998 test day records of yield, intake, BW and BCS, respectively. Daily phenotypic FCM, protein yield, BW, BCS, NELI and CPI were derived from the random regression model solutions. Daily records were used to obtain 305 d totals (FCM, protein yield, NELI, and CPI), 305 d averages (BW and BCS), and BCSCH. Daily energy balance was derived from daily FCM, BW and BCS observations and summed from 5 to 30 DIM to obtain CEB. Net energy efficiency (NEE) was defined as FCM/NEI, whereas protein efficiency (PE) was defined as protein yield/CPI. The traits were analyzed with multiple-trait animal models that included fixed effects of lactation and herd-year-season of calving; random effects included animal, permanent environment, and error. NEE was genetically (0.92) and phenotypically (0.81) correlated with higher FCM. Likewise, genetic and phenotypic correlation estimates between PE and protein yield were strong at 0.96 and 0.80, respectively. BCS and BW were negatively correlated with NEE and PE (genetic correlation range = -0.42 to -0.54). Genetic correlation estimates of CEB with NEE and PE (-0.51 and -0.52, respectively) and of BCSCH with NEE and PE (0.64 and 0.73, respectively) were unfavorable. Genetic variation exists for feed efficiency, but measures of efficiency not unfavorably correlated with energy balance should be considered.

**Key Words:** feed efficiency, energy balance, genetic correlation

**67 Genetic characterization of feed intake and utilization in performance tested beef bulls.** D. H. Crews Jr.\*<sup>1</sup>, C. T. Pendley<sup>1</sup>, G. E. Carstens<sup>2</sup>, and E. D. M. Mendes<sup>2</sup>, <sup>1</sup>*Colorado State University, Fort Collins*, <sup>2</sup>*Texas A&M University, College Station*.

Feed intake, growth, and pedigree data from the Midland Bull Test database were used to estimate parameters required for genetic evaluation of feed utilization traits. Length of the feeding period was 70 d, and test ADG was estimated as the slope of the regression of BW on test d. Records on DMI, ADG, and estimated mid-test BW raised to the power of 0.75 (MBW) from bulls (n = 2,346) and heifers (n = 221) representing 11 breeds (1,819 Angus) were included in a multiple trait animal model to estimate variance components using average information REML. The model for all traits included the fixed effects of contemporary group (n = 99) and a linear covariate for age at the start of test, and random animal genetic effects (n = 10,327). Heritability estimates for DMI, ADG, and MBW were 0.45 ± 0.09, 0.35 ± 0.07, and 0.54 ± 0.09, respectively, and genetic correlation estimates (SE < 0.13) among the traits were positive, ranging from 0.38 to 0.60. Phenotypic residual feed intake (RFI) was defined as the difference between DMI and expected DMI from regression on ADG and MBW. A 4 trait model including phenotypic RFI failed to converge because of the linear dependence with DMI, ADG,

and MBW. Breeding values for genetic RFI were then estimated as the difference between EBV for DMI and expected DMI derived using genetic regression. Genetic RFI has the property of independence from EBV for ADG and MBW whereas traditional EBV for phenotypic RFI could have genetic correlations with ADG and MBW. Genetic RFI EBV ranged from -0.54 to 0.56 kg/d (SD = 0.08). Phenotypic or genetic RFI contain no more information than DMI, ADG, and MBW phenotypes or EBV, respectively. Therefore, genetic evaluation of RFI is equivalent to evaluation of a function of the component traits.

**Key Words:** beef cattle, feed intake, genetic evaluation

**68 Analysis of published genetic parameter estimates for feed utilization traits in beef cattle.** C. T. Pendley\*, R. M. Enns, and D. H. Crews Jr., *Colorado State University, Fort Collins*.

Increasing profitability of beef production through the reduction of inputs has been documented by an increasing number of published genetic parameter estimates for feed intake and utilization traits. The inclusion of input traits in genetic improvement programs requires knowledge of parameters for those traits, but an understanding of these parameters, especially for feed intake, is limited due to the cost of recording individual feed intake on cattle and reports are scarce. Fourteen sets of estimates involving more than 34,000 cattle and published between 1995 and 2010 were included in a meta-analysis of genetic parameters for feed intake and related traits. Papers were required to include individual feed intake, and computed SE for heritability and genetic correlation estimates. A generalized least squares approach was used to compute weighted mean heritability and genetic correlation estimates, as well as their weighted SE, where weights were a function of inverse SE. Weighted heritability estimates for feed conversion ratio (FCR), residual feed intake (RFI), ADG, metabolic body weight (MBW) and DMI were 0.28 ± 0.08, 0.38 ± 0.08, 0.32 ± 0.08, 0.39 ± 0.08, and 0.41 ± 0.07, respectively. Weighted genetic correlations of FCR with RFI, ADG, MBW, and DMI were 0.60 ± 0.11, -0.31 ± 0.14, 0.03 ± 0.15, and 0.35 ± 0.12, respectively. Weighted genetic correlations of RFI with ADG, MBW were near zero, but were 0.38 ± 0.09 with DMI. The phenotypic correlation of RFI with ADG and MBW are forced to zero by definition. The weighted genetic correlation of ADG with MBW was 0.45 ± 0.13. These weighted heritability and genetic correlation estimates may be more useful in the design of genetic improvement programs than relying on estimates from individual studies with low numbers of feed intake observations.

**Key Words:** feed intake, genetic parameters, meta-analysis

**69 Heritability and genetic correlations of residual feed intake between Angus and Simmental bulls and resulting steer relatives.** W. C. Rutherford\*, L. A. Kriese-Anderson, and G. S. Hecht, *Auburn University, Auburn, AL*.

Objectives of this research are to observe breed differences for feed intake (FI) and trait differences of low, medium and high residual feed intake (RFI) bulls and steers, estimate h<sup>2</sup> in central tested bulls and steers and compare RFI in bulls and steers. Individual FI was measured on 1433 Angus, Simmental and composite Simmental-Angus bulls at the Auburn University Beef Evaluation Center (AUBEC) from 1977 to 2007. Bulls were consigned by producers and housed at the AUBEC a minimum of 70 d. Bulls were measured for weight and height biweekly or monthly depending on year. SC and ultrasound measurements for carcass traits

were taken at yearling age (330 to 400 d). FI and carcass trait data from 760 Angus and Simmental-composite steers were acquired courtesy of the American Simmental Association Carcass Merit Project. RFI was determined by regressing metabolic mid-weight and ADG on intake by year of test for bulls and by contemporary group (cg) for steers. High percentage Angus bulls consumed more DM per day, had higher FCR and RFI than purebred Angus, 50% Angus: 50% Simmental (50:50), high percentage Simmental and Simmental bulls. Angus steers consumed more DM per day had higher FCR and RFI than high percentage Angus and 50:50 steers. Heritability was estimated for RFI using a bivariate model and MTDFREML in bulls ( $0.42 \pm 0.05$ ) and in steers ( $0.20 \pm 0.05$ ). Fixed effects for bulls included year and breed percentage. Fixed effects for steers included cg and breed percentage. Covariates of final age, final wt or final frame score were used. Genetic correlations between steer and bull RFI ranged from  $-0.18$  to  $0.33$  depending on covariate. Bulls and steers classified as low RFI consumed less DM per day and had more favorable FCR than medium and high RFI animals. Results indicate RFI is a moderately heritable trait and improvements for FI and FCR should be achievable when selection is made using RFI. However, selection of bulls based on their RFI in an attempt to sire more efficient steers may not be practical as the genetic relationships between steer RFI and bull RFI were variable and moderate.

**Key Words:** residual feed intake, heritability, genetic correlations

**70 A region on BTA6 is associated with feed intake and gain in beef cattle.** A. K. Sexten<sup>\*1,2</sup>, L. A. Kuehn<sup>1</sup>, T. P. L. Smith<sup>1</sup>, H. C. Freely<sup>1</sup>, W. M. Snelling<sup>1</sup>, and A. K. Lindholm-Perry<sup>1</sup>, <sup>1</sup>USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, <sup>2</sup>Oklahoma State University, Stillwater.

Genetic selection for animals that require less feed while still achieving acceptable levels of production could result in substantial cost savings for cattle producers. The purpose of this study was to identify DNA markers with predictive merit for differences among cattle in feed intake and BW gain. Crossbred steers ( $n = 1,195$ ) were fed a high-corn diet for 140 d and ADFI, residual feed intake (RFI), and ADG were measured. Steers were genotyped with the Illumina Bovine SNP50 BeadChip. An association analysis of these SNP on each trait was performed using MTDFREML, from which 14 SNP clustered in a 1.7Mb region at BTA6: 37.4 to 39.1 were identified as having significant association ( $P \leq 0.009$ ) with one or more of the 3 traits. All statistical models included fixed effects of year and location; covariates of age, heterosis, and breed percentage; and a random polygenic effect. To develop markers with the maximum ability to discriminate favorable alleles and potentially identify the functional variation, 44 additional SNP, not present on the BeadChip, were identified in and around potential candidate genes in this chromosomal region. These new SNP were genotyped on the same animals and the statistical analysis program Mendel was used to test for association with feed intake and gain. Four markers located in a 90Kb region on BTA6 were significant for both ADFI and ADG. After correction for multiple testing, all markers remained significant for ADG ( $P \leq 0.02$ ) and 2 markers were significant for ADFI ( $P \leq 0.01$ ). These markers are located in a bovine gene that is homologous to a human gene that has been associated with skeletal frame size, thus providing a potential link between the observed bovine variation and growth-related traits of ADFI and ADG. Genetic markers predictive for feed intake and growth in this population of cattle may be useful for the identification and selection of animals that are more efficient, although potential impact of marker-assisted selection on all production traits will need to be assessed.

**Key Words:** beef cattle, genomics, feed efficiency

**71 A neural network approach for association between a low-density whole genome SNP marker panel and residual feed intake and dry matter intake.** H. Wang<sup>\*1</sup>, X. Liu<sup>1</sup>, B. Woodward<sup>2</sup>, S. Bauck<sup>2</sup>, and R. Rekaya<sup>1</sup>, <sup>1</sup>University of Georgia, Athens, <sup>2</sup>Merial Limited, Duluth, GA.

The predictive ability of a low-density SNP panel derived from the Illumina Bovine SNP50 and developed for marbling, backfat thickness, hot carcass weight, ribeye area, yearling weight, and heifer pregnancy rate was evaluated for residual feed intake (RFI) and dry matter intake (DMI). Data consisted of the genotypes of 1,032 Angus animals and their corresponding EPDs computed from actual individual weight and intake data. Missing genotypes were replaced with the most likely genotype. Linear regression (LR) and neural network (NN) approaches were implemented and compared. For LR, a cross validation procedure was adopted where the data was randomly divided into 5 groups with equal size. In each one of the 5 replicates, 80% of the data was used for training and the remaining 20% for validation. For the NN approach, randomly 2/3 and 1/3 of the data were used for training and validation, respectively. The process was replicated 5 times. A NN is an artificial system of massively interconnected neurons. The network architectures and the learning algorithm define the manner in which the neurons are related and structured. In this study, a feed-forward NN with one hidden layer was used. The parameters of the NN such as the number of neurons in the hidden layer, and learning rate were set heuristically. For RFI, the correlation between the observed and predicted breeding values for the validation data was 0.22 and 0.28 for the LR and NN, respectively. The correlation was 0.23 and 0.36 for DMI using LR and NN, respectively. These results indicate that, although the low-density SNP panel was developed for other traits, it still has some ability to predict RFI and DMI. The lower correlations observed for RFI could be due in part to the uncertainty on the trait of RFI compared with DMI that tends to be more accurately measured. The superiority of the NN approach could be due to its ability to intrinsically accommodate the non-linear relationship between variables.

**Key Words:** SNP, whole genome, feed efficiency

**72 Effects of divergent selection for serum insulin-like growth factor-I concentration on mature weight and growth curves in Angus cattle.** Q. Qin<sup>\*</sup> and M. E. Davis, *The Ohio State University, Columbus.*

The purpose of this study was to investigate the effect of divergent selection for serum insulin-like growth factor-I (IGF-I) concentration on mature weight estimated using growth curve functions in Angus cattle. Multiple serum IGF-I measurements (d 28, d 42, d 56 of the 140-d postweaning period) from a total of 2,514 animals and weight records from birth to at least 3 yr of age from a total of 172 animals were collected from an ongoing divergent selection experiment involving IGF-I that was initiated in 1989. Four growth curve functions (Brody, Logistic, Gompertz, Von Bertalanffy) were used to estimate the parameters for mature weight (A) and maturing rate (k) using the NLIN procedure in SAS (SAS Inst. Inc., Cary, NC). The heritability estimates for serum IGF-I at different ages and growth curve parameters from each function were estimated using a multiple-trait, derivative-free, REML program. Genetic, environmental, and phenotypic correlations between IGF-I and growth curve parameters were also obtained. The direct heritability ( $h_d^2$ ) estimates for serum IGF-I at d 28, 42, and 56 were 0.42, 0.42, and 0.33, respectively. The  $h_d^2$  estimates for A from the 4 growth functions ranged from 0.72 to 1.00, whereas  $h_d^2$  estimates for k ranged from 0.01 to 0.21. The genetic correlations between A and k within each growth curve function ranged from  $-0.57$  to  $-0.49$ . The genetic correlations

between IGF-I (d 28, 42, and 56) and A within each growth curve function ranged from  $-0.46$  to  $-0.01$ . Although serum IGF-I was negatively correlated with mature weight genetically, the phenotypic correlation between these 2 traits was moderate (0.47 to 0.59) due to a highly positive environmental correlation (1.00). The shapes of growth curves from the 4 functions were almost identical, as were the growth curves for the high and low IGF-I selection lines.

**Key Words:** Angus cattle, growth curve, insulin-like growth factor

**73 Bayesian estimation of a genetic covariance matrix with different degrees of belief via a Generalized Inverted Wishart distribution.** R. J. C. Cantet\*, *Facultad de Agronomía, Universidad de Buenos Aires - CONICET, Buenos Aires, CABA, Argentina.*

When taking a Bayesian approach for estimating a genetic covariance matrix, animal breeders use an Inverted Wishart (IW) prior density. The advantage of this formulation is that the posterior distribution is in conjugate form, so that the sampling is from an updated IW. Also, the degrees of belief are the same for all genetic parameters, i.e., any (co)variance component is assumed to have the same amount of prior information. However, there are situations where this assumption does not hold. Take for example a model with grand-maternal effects. There is more prior information and information on the data for the additive direct variance than for the additive maternal variance and this, in turn, has more information than the additive grand-maternal variance. The objective of this research was to develop an algorithm for estimating a genetic covariance matrix with different degrees of belief for the (co) variance components. The method employs the Bartlett decomposition of a matrix to produce a conditional covariance matrix from the generalized inverted Wishart distribution (GIW). As a result, the algorithm consists of successive samplings from inverted chi-squared (or IW) densities for the additive variances, and from normals (or multivariate normals) for the additive covariances. It should be mentioned that the genetic parameters have to be ordered within the covariance matrix so that their degrees of belief decrease when going from the first row (or column) to the last. The algorithm was employed on a beef cattle data set, and the model fitted included additive direct, maternal and grand-

maternal effects. The classic algorithm using the IW to sample from the conditional posterior of the additive covariance matrix was also fitted to the data. Convergence was faster for the GIW methods than for the IW, as samples of the (co)variance components were less dependent. In conclusion, the GIW algorithm allowed the use of different degrees of belief for the dispersion parameters and converged faster to the stationary distribution.

**Key Words:** generalized inverted Wishart, Bayesian estimation, additive covariance matrix

**74 A simulation approach for analyzing genomic data using a package of specific FORTRAN 90 functions.** P. Faux\*<sup>1,2</sup> and N. Gengler<sup>1,3</sup>, <sup>1</sup>*University of Liège - Gembloux Agro-Bio Tech, Gembloux, Belgium,* <sup>2</sup>*National Research Fund, Luxembourg, Luxembourg,* <sup>3</sup>*National Fund for Scientific Research, Brussels, Belgium.*

A panel of FORTRAN 90 functions was developed to simulate the distribution of bi-allelic (e.g., SNP) genetic markers along a defined genome and the distribution of their alleles in a given population. The simulation program used 3 parameters, those related to the species studied (number of autosomes, average length of autosomes, average number of crossovers by chromosome), the number of markers and those related to the studied population (pedigree). The simulation proceeds in 3 steps: a) random choice of marker positions and allelic frequencies for the minor allele of each marker (range: 0.05 to 0.475), b) simulation of genotypes of the ancestors in the pedigree based on randomly chosen allelic frequencies and c) planned mating of the ancestors according to the pedigree and according to the average crossover rate as a genetic recombination parameter. The simulation returns a fully-genotyped population. This method is flexible because it can be applied to a wide range of cases (not restricted to a single species) and the FORTRAN functions can be extended and used to simulate phenotypes. It is also realistic, because it performs mating plans and selection of animals based on real pedigrees. Development of this simulation panel was the first step in research around advanced methods to compute and invert genomic relationship matrices.

**Key Words:** genomic prediction, SNP simulation