939 Use of a mathematical computer model to predict feed intake in Angus cattle: Genetic parameters between observed and predicted values, and relationships with other traits. D. P. Kirschten*, E. J. Pollak, and D. G. Fox, *Cornell University*, *Ithaca, NY*.

The objectives of this study were to investigate the suitability of using dry matter required (DMR) as predicted by the Cornell Value Discovery System (CVDS) in genetic evaluations and to determine relationships between model predicted and individual DMI and other traits. Group 1 (659 finishing steers) and group 2 (309 yearling bulls) had observed feed intake (FI) records. Group 3 (1586 yearling bulls and heifers) had pedigree ties to the other datasets, but did not have FI data. The data also contained records of ADG and body weight (BW). Two predictions of DMR were made with the CVDS model iterating on BW (DMR-W) and ADG (DMR-G). For purposes of parameter estimation, CVDS DMR predictions were considered surrogates for FI. Genetic parameters were estimated with MTDFREML, using an animal model with fixed effects of weaning weight contemporary group and pen. Phenotypic correlations between FI and DMR-W and DMR-G were 0.69 and 0.71. The phenotypic correlation between DMR-W and DMR-G was 0.98. Genotypic correlations between FI and DMR-W and DMR-G were 0.79 and 0.85. The genetic correlation between DMR-W and DMR-G was 0.97. Heritabilities for FI, DMR-W and DMR-G were 0.42, 0.31 and 0.33, respectively. Genetic correlations between ADG and FI, DMR-W and DMR-G were 0.45, 0.80, and 0.83, respectively. Genetic correlations between mean body weight (MW) and FI, DMR-W, and DMR-G were 0.50, 0.64 and 0.58, respectively. Residual feed intake (RFI) was calculated using FI, metabolic MW ($MW^{0.75}$) and ADG. The heritability of RFI was 0.36. The phenotypic correlation between RFI and FI was 0.57. Phenotypic correlations between RFI and MW and ADG were not estimated. Genetic correlations between RFI and FI, MW, and ADG were 0.77, 0.09, and 0.01, respectively. Heritabilities of ADG and MW were 0.27 and 0.48. Standard errors for all genetic correlations were less than 0.06. The genetic relationships between FI, DMR-W and DMR-G suggest that CVDS predictions of FI may be used as surrogates for actual FI in genetic evaluations.

Key Words: Feed Intake, Mathematical Models, Beef Cattle

940 Computing options for genetic evaluation with a large number of genetic markers. S. Tsuruta, I. Misztal*, and J. K. Bertrand, *University of Georgia*, *Athens*.

Test data set included records on about 110,000 animals for 11 growth, reproduction and other traits. Also available were marker genotypes or marker probabilities on 78 markers. The model included the effects usually fitted for these traits plus two covariables per marker; only selected markers were fit for each trait. Computing was by program blup90iod, which uses iteration on data using a preconditioned conjugate gradient algorithm with a diagonal preconditioner. Without the markers in the model, the evaluation finished in 421 rounds and 2.5 h. With the markers included, the evaluation took one week of computing and 797 rounds of iteration. Modifications included the algorithm by Strandén and M. Lidauer (SL) to reduce the number of operations for each record, a block preconditioner for traits (BT), and a block preconditioner for all markers (BM). With the markers included in the model, the number of rounds (computing time) were 797 (7.8 h.) for SL, 544 (6.2 h) for SL+BM, 459 (4.3 h) for SL+BT, and 431 (5.2 h) for SL+BT+BM. The memory requirements for all methods except BT were around 60 Mbytes; with BT, the memory requirements increased 10 times. The most important modification to decrease the computing time was the SL algorithm. Setting up BM was computationally demanding, and would be very expensive if the number of markers is increased. BT would show greater advantage with higher genetic correlations among traits. With careful programming, adding markers fitted as covariables to a genetic evaluation increases the computing time only a few times.

Key Words: Genetic Evaluation, Genetic Markers, Molecular Information

941 Sampling genotype configurations in large complex pedigree. M. Szydlowski*[1] and N. Gengler[1,2], [1]*Gembloux Agricultural University*, *Gembloux, Belgium*, [2]*National Fund for Scientific Research*, *Brussels, Belgium*.

Efficient genotype samplers are needed for Bayesian and maximum-likelihood analysis of complex genetic problems implemented via Markov Chain Monte Carlo (MCMC) algorithms. The examples of such analysis include polygene mapping in complex pedigrees and prediction of total genetic value using genome-wise dense marker maps. For large complex pedigree sampling from desired probability is impossible. We present a simple method to sample genotype configurations for large pedigree from approximate probability. The sampler uses combination of exact (simple peeling) and iterative methods (iterative peeling) to approximate target probability. Two techniques were applied to reduce computational burden: genotype elimination and set-recoding of alleles. The new sampler was evaluated on a large complex pedigree using simulated data sets for various experimental designs and degree of marker polymorphism. The pedigree used in simulation was real bovine pedigree of 907 903 animals born between 1960 and 2005 derived from Belgian dairy and dual-purpose cattle database. Four types of experimental designs were considered: (i) genotyping sires only, (ii) genotyping dams only, (iii) genotyping half of the dams but no sires, and (iv) genotyping half of the sires and half of the dams. For hypothetical single nucleotide polymorphism the new sampler reached 100%, 100%, 44% and 89% of maximum efficiency for the four experimental designs respectively. For microsatellite polymorphism the efficiency of the sampler reached 100%, 100%, 32% and 76%, respectively. To exemplify the use of the new sampler it was applied to estimate genes shared identical by descent (IBD). The calculation of genes shared IBD among relatives is an important component of gene mapping in complex diseases and quantitative traits. The convergence diagnostic methods gave indirect evidence of irreducibility of the new sampler and showed its good mixing performance.

Key Words: MCMC Sampler, Genotype Estimation, IBD

942 Comparisons of single and multiple trait random regression models for analyses of multi-parity test-days. S. Tsuruta* and I. Misztal, *University of Georgia*, *Athens*.

The objective of this study was to compare a single-trait (ST) test day model with combined covariance functions for DIM within lactation