

production. Heritabilities of functional longevity, estimated on a subset of data including approximately 150,000 animals, were .18, .20, and .18 for Braunvieh, Simmental, and Holstein, respectively. Breeding values were estimated for all sires having at least 6 daughters or 3 granddaughters in the data. Breeding values of sires can be expressed in genetic standard deviations or in days of functional productive life and published in sire catalogs along with breeding values for production traits.

Key Words: survival analysis, functional longevity, sire evaluation

260 Approximate ETA for lifetime production based on genetic evaluations for lactational production and herd life. P.J. Boettcher¹ and F. Miglior², ¹University of Guelph, Canada, ²Canadian Dairy Network, Guelph, Canada.

Dairy cattle breeders in Canada have expressed an interest in a genetic evaluation of sires for lifetime production of their daughters. Lifetime production is a function of production per lactation and the number of lactations expressed. In Canada, genetic evaluations are currently available for lactational production and herd life (HL). The objective of this study was to use the existing genetic evaluations to develop approximate ETA for lifetime production. The approach taken was to multiply ETA for production in each lactation by their respective probabilities of expression and then sum across lactations. Direct application of this proposed approach was limited by three factors: 1) EBV for production are calculated for only the first three lactations, 2) ETA for HL are for functional HL rather than true HL, being adjusted for effects of production, and 3) ETA for HL are expressed as the expected total number of lactations survived. Selection index theory was used to develop EBV for lactations >3 based on EBV for lactations 1 to 3. Regression was used to convert ETA for functional HL to true HL. Survival analysis theory was used to convert ETA for HL into probabilities of expression for each lactation. The probability of culling was assumed to follow a Weibull distribution. The Weibull survivor function (probability of survival to lactation $t = \exp[-(\lambda t)^r]$) was fit to average survival rates in Canada to establish a base-line. The best fit occurred when $\lambda=0.262$ and $r=2.0$. The ETA for true HL of sires (expressed as a difference from the average of 3.0 lactations) were then fit as covariables with $\beta = -0.617$. Based on these parameters for the survivor function, the proportion of daughters from a given sire that survived to express lactation t was $= \exp[-(0.262t)^2.0]^{exp[-0.617(ETA-3.0)]}$. Production ETA and survival proportions were calculated within each lactation and their products were summed across lactations to yield the final ETA for lifetime production.

Key Words: Lifetime Production, Approximation

261 Genetic parameters for three experimental feet and leg traits for Canadian Holsteins. P.J. Boettcher¹, L.R. Schaeffer¹, J. Fatehi¹, and J.J. Shannon², ¹University of Guelph, Canada, ²Canadian Holstein Association, Brantford, Canada.

In March 1998 the Canadian Holstein Association started to record three new feet and leg traits as part of their routine type classification. Traits were rear legs from the rear view, depth of heel, and claw uniformity. All traits were recorded on a nine-point scale, which is the standard for descriptive conformation traits evaluated by Holstein Canada. For rear legs-rear view, cows received lower scores if they hocked-in more severely. Cows with more depth of heel received greater scores. Cows with symmetric claws (right rear foot) received high scores and scores decreased as uniformity in shape and size of the claws decreased. More than 200,000 cows were scored over 15 months of classification. Due to expected increases in experience and precision of the classifiers, genetic parameters were estimated using 57,492 records from first lactation cows scored during the final 15 months of classification. Genetic parameters were estimated using a Bayesian procedure that employed Gibbs Sampling. Genetic relationships among the three traits and eight other conformation traits were estimated in a series of four 5-trait (3 experimental and 2 other) animal models. Factors in the model were herd*round*classifier, age and stage of lactation during classification, and animal. For each five-trait combination, six chains of 30,000 cycles were generated, discarding the first 5000 cycles in each chain. Means across chains were used as the point estimates of the parameters of interest. Heritabilities were 0.110, 0.096, and 0.045, for rear legs-rear view, depth of heel, and claw uniformity, respectively. Genetic correlations with rear legs-rear view were 0.34 and 0.55 for heel depth and claw uniformity. Genetic correlation between heel depth and claw uniformity

was 0.66. Foot angle and overall feet and legs had high correlations (>0.65) with claw uniformity.

Key Words: Conformation, Feet and Legs, Genetic Parameters

262 Estimation of variance components for cow and parity effects from test-day yields. J. Bormann¹, G.R. Wiggans², J.C. Philpot², T. Druet^{1,3}, and N. Gengler^{1,3}, ¹Animal Science Unit, Gembloux Agricultural University, Gembloux, Belgium, ²Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, ³National Fund for Scientific Research, Brussels, Belgium.

The initial step in implementation of a US test-day model includes estimation of cow and parity test-day variances needed to calculate lactation stage, age, and pregnancy effects. Single-trait repeatability models were fitted, and variance components were estimated for milk, fat, and protein test-day yields using Method R and a preconditioned conjugate gradient (PCG) equation solver because of large data sets (0.7 to 7.7 million records). Data were obtained for calvings since 1990 for Brown Swiss and Jerseys and for Holsteins from California, Pennsylvania, Texas, and Wisconsin. A minimum of three observations were required per subclass for herd test date and milking frequency. Three parity groups were defined: first, second, and later. Test-day data were adjusted for environmental effects of age, calving season, and milking frequency. Estimated breeding values (EBV) were expressed on a daily basis. To assess effect of adjustments, data also were analyzed without correction. For adjusted data, variance ratios (residual divided by variance of effect) within parity were similar across breeds, subpopulations, and samples: 1.5 to 1.8 for milk, 3.0 to 4.3 for fat, and 1.8 to 2.3 for protein. Variance ratios across parities ranged from 3.5 to 6.8 for milk, 8.7 to 17.6 for fat, and 5.5 to 9.4 for protein. Adjustment for EBV reduced both cow genetic and nongenetic variances. Variance ratios for permanent environment within parity from unadjusted data were nearly identical to those from adjusted data. For unadjusted data, heritabilities ranged from 0.19 to 0.30 for milk, 0.13 to 0.15 for fat, and 0.17 to 0.23 for protein. Although computations took several weeks, use of Method R and a PCG solver enabled estimation of the variance components that will be used for US evaluations based on a test-day model.

Key Words: Test-day model, Genetic evaluation, Variance estimation

263 Optimizing single-generation selection on QTL in crossbreeding programs. J. C. M. Dekkers¹ and R. Chakraborty¹, ¹Iowa State University, Ames.

Molecular genetics has enabled detection of quantitative trait loci (QTL) in livestock. The use of QTL in selection requires a balance between the QTL and other genes (polygenes). For non-additive QTL, standard QTL selection, in which selection is on the sum of the standard EBV for the QTL and an EBV for polygenes, does not maximize progeny performance, as illustrated by Dekkers (1999, Genet. Sel. Evol. 31:421) for purebred selection. Often, however, the aim is to maximize crossbred performance. Therefore, the objective here was to develop methods to optimize single-generation purebred QTL selection for a 2-breed terminal cross. A deterministic model for within-line selection on an index of the known breeding value for a QTL and a purebred EBV for polygenes was developed. For simplicity, crossbred progeny were produced by random mating of unselected male and female progeny from the sire and dam lines. Lagrange multiplier methods were used to develop iterative algorithms that maximized crossbred performance. Optimal QTL selection was compared to standard purebred QTL selection for a biallelic QTL with 30 and 40% frequencies in the male and female line and 10 and 25% selection of sires and dams within each line. Optimal QTL selection resulted in greater crossbred performance for dominant QTL. Extra responses were 1, 5, and 12% greater for QTL with partial, complete, and over-dominance for a QTL with an additive effect (a) of 1 polygenic EBV standard deviation, and 3, 11, and 37% greater for a QTL with an equal to 3 polygenic EBV standard deviations. Optimal selection strategies differed by line and resulted in opposite trends in QTL frequencies for over-dominant QTL. Pure-line responses under optimal selection were similar to standard QTL selection for the male line but substantially less for the female line. In conclusion, QTL information