

26 Unexpected estimates of variance components with a true model containing genetic competition effects. L. D. Van Vleck*¹ and J. P. Cassady², ¹USDA-ARS, Roman L. Hruska U.S. Meat Animal Research Center, ²North Carolina State University.

Simulation of the model of Muir and Schinckel containing genetic competition effects was initiated to determine how well REML could untangle variances due to direct and competition genetic effects and pen effects. A two-generation data set was generated with 6 unrelated males, each mated to 5 unrelated females to produce 300 progeny from which 30 females (one per mating in previous generation) were mated to 6 unrelated males to produce 300 more progeny. Progeny were randomly assigned 6 per pen to 50 pens per generation. Parameters were V_g , V_c , C_{gc} , V_p and V_e representing direct and competition genetic variance with covariance, and pen and residual variance. Eight statistical models were used to analyze each of 400 replicates of 16 sets of parameters. Both V_g and V_e were fixed at 16. Values of C_{gc} were -2, -1, 0.1, 1 and 2. Values of V_c were 1 and 4 and of V_p were 0.1, 1, and 10. With the full model, average estimates resembled true parameters except that V_p was consistently overestimated when small (0.1 and 1) which, in turn, slightly changed other estimates. The most unexpected result was overestimation of V_p when V_c and C_{gc} were ignored in the analysis. The overestimation depended on V_c and number of competitors in common between records in a pen. The upward bias was greater when C_{gc} was positive than when negative. For example, with $C_{gc} = 2$, $V_c = 4$ and $V_p = 0.1$, mean estimate of V_p was 20.4 when C_{gc} and V_c were dropped from the model and 15.3 when $C_{gc} = -2$. When V_p was ignored, estimates of both C_{gc} and V_c increased proportional to V_p . Also V_g increased more with greater V_p . Another unexpected result was that when pen was considered fixed for the analysis, sampling standard errors of estimates of C_{gc} and V_c were reduced generally by factors of 2 to 30. These results suggest that a high estimate of pen variance may indicate genetic competition effects are important and that ignoring pen effects will bias estimates of other components.

Key Words: Genetic Parameters, Pen Effects, Simulation

27 An animal model with autoregressive covariance structures among residual and genetic effects for genetic evaluation of Holstein cows with test day records. R. M. Sawalha*¹, J. F. Keown², S. D. Kachman², and L. D. Van Vleck³, ¹University of Nebraska, Lincoln, ²Department of Statistics, University of Nebraska, Lincoln, ³USDA, ARS, Roman L. Hruska U.S. Meat Animal Research Center, Lincoln, NE.

This study was to evaluate an animal model with first order autoregressive covariance structures (AR1) among residual and genetic effects of test day (TD) records. This model was compared with a simple TD repeatability model and a 305-day lactation model. Data consisted of 106,472 test day records of 12,071 first lactation Holstein cows. Estimates of components of variance and autocorrelation coefficients were obtained for milk, fat, and protein yields and somatic cell scores (SCS) using ASReml. Likelihood ratio tests indicated that AR1 model was significantly more appropriate for the TD data than the simple repeatability model for all four traits. Estimates of heritability were slightly lower for yield traits (0.09) with AR1 model than with simple TD repeatability model (0.10-0.11). Estimates of heritability with 305-d yield traits were in the range of 0.14 to 0.36. For SCS, both TD models resulted in similar estimates of heritability of 0.06. Estimates of residual variance were probably underestimated with simple repeatability model compared with AR1 model. Average estimates of accuracy of PBV for all traits were always higher with simple repeatability model than with AR1 model for both sires and cows. The least change in rank of the top 100 elite sires and cows was between the two TD models (4-9% for sires). The greatest difference in ranking of elite animals was between simple repeatability model and 305-d model (26-36% for sires). Similar patterns were also observed for values of correlation among PBV of different models. The AR1 model resulted in similar or slightly lower correlations between actual lactation records of cows and the averages of PBV of their parents compared with the simple repeatability model. Average PBV tended to increase with advancement of lactation for yield traits and to decrease for SCS. Averages of PEV of PBV were highest at the beginning and at the end of lactation.

Key Words: Milk Yield, Test Day, Autoregression

28 Detection of different shapes of lactation curve in cattle by standard mathematical models. N. P. P. Macciotta*¹, D. Vicario², C. Di Mauro¹, and A. Cappio Borlino¹, ¹Dipartimento di Scienze Zootecniche Via De Nicola 9, 07100 Sassari, Italia, ²ANAPRI Via Nieve 19, 33100 Udine, Italia.

Four mathematical models of lactation curve (Wood WD, Wilmik WIL, Ali and Schaeffer AS parametric models and Legendre fifth order polynomials LEG) were fitted to individual milk yield patterns of 27,837 Italian Simmental cows, each having at least 7 records. Aims of the work were: i) to assess goodness of fits; ii) to check sensitivity of models in discriminating different shapes of lactation curve; iii) to analyse relationships among curve shapes and parameter values and (co)variances. About 70% of individual regressions showed an adjusted $R^2 > 0.75$ for all models. Among these best fits, three-parameter models (WD and WIL) detected two main families of curve shape, the typical curve (with a first increasing phase till a peak followed by a declining phase), and the so-called atypical curve, characterised only by the declining phase. AS and LEG models assigned most of lactation patterns to the two main families but, due to their greater flexibility, around 15% of curves were allocated in about 10 other not well defined forms. Each family of curve shape had a specific combination of signs of parameters. Range of absolute values of parameters and correlations among them were similar in the two families highlighted by WD and WIL models, whereas differences among some families were detected by AS and LEG functions. The great heterogeneity of lactation curve shape could explain some problems encountered in the analyses that require comparison between parameter values and estimation of their (co)variances, as the anomalous variance of estimated yields at the first phase of lactation. The drastic solution to discard atypical lactations could not be applied when the occurrence of these patterns is relevant, as in the present study (about 30%). An alternative solution suggested by results of this study could be to perform separate analysis within each of the main family of lactation curve shape.

Key Words: Mathematical Models, Lactation Curve Shape, Parameter Values

29 Impact on calving ease evaluations of excluding herds with abnormal distribution of scores. C. P. Van Tassell, G. R. Wiggins, and L. L. M. Thornton*, Animal Improvement Programs Laboratory, Agricultural Research Service, USDA Beltsville, MD.

Threshold model sire and maternal grandsire (MGS) calving ease evaluations for the United States were calculated after excluding two sets of 10% of the data. Herds were excluded based on χ^2 goodness of fit test. To determine the first set of herds to be excluded, frequencies of observed (O) records were determined by parity (1 vs. 2+) and difficulty score (1-5). Expected (E) numbers of records were calculated as the total number of calvings by parity multiplied by the fraction of difficulty scores across all herds in each parity. Goodness of fit values were calculated as the sum of $(O-E)^2/E$ across parity and difficulty score. The 299 herds failing this test tended to be large. The second set of 8605, mostly small herds, was identified using frequencies in place of counts. Evaluations were calculated using data from all years or only calvings before 1999. Pedigree indexes ($0.5 \times \text{sire} + 0.25 \times \text{MGS}$) were calculated from two earlier data sets (abnormal distribution herds included or excluded). Correlations were calculated between pedigree index and solutions from evaluations for bulls with at least 30 calvings in the complete data. Correlations were higher between solutions from sets with abnormal distribution herds excluded. For the first set of excluded herds, for sire solutions, the increase was from .579 to .599 for 25,067 bulls, and for MGS, from .598 to .617 for 21,221 bulls. For the second set, the increases were .004 greater. Differences between evaluations from early and complete data were also examined. Variances of these differences and mean and maximums of the absolute values of differences tended to be larger when the first set of abnormal distribution herds were excluded. These differences are likely due in part to the reduction in total data represented in the predicted breeding values. The differences tended to be smaller when the second set was excluded. These improvements indicate that the evaluations should better predict

future performance when data from herds with abnormal distributions is excluded.

Key Words: Calving Difficulty, Dystocia, Abnormal Distribution

30 Effects of heteroscedasticity on sires' predicted transmitting ability in grazing and confinement herds. A. G. Fahey*, M. M. Schutz, D. L. Lofgren, A. P. Schinckel, and T. S. Stewart, *Purdue University, Lafayette, IN.*

The number of grazing (G) herds in the USA is increasing. Heteroscedasticity (HV) of data may affect the ability of sires' predicted transmitting ability (PTA) to predict actual performance of daughters. The objective of this study was to investigate the effect of HV on the predictability of PTA for mature equivalent (ME) milk (MEM), ME protein (MEP), and ME fat (MEF) for daughters in G and confinement (C) herds. Data consisted of 366 G herds from 11 states with 72,489 records and 373 C herds from 12 geographically similar states with 117,629 records. Herds were divided into mean quartiles (Q_{M1} - Q_{M4} , from low to high) and variance quartiles (Q_{V1} - Q_{V4}) based on MEM, and a transformation was applied to reduce HV. The method of transformation was to standardize the within herd variance to the average variance of a base year for each parity, and was similar to that used in the USDA-DHIA genetic evaluations. Coefficients of regression (RC) of daughter yield on PTA in G herds indicated that PTA overestimated daughters' production for all traits in Q_{M1} - Q_{M3} ($P < 0.01$) and for MEF in Q_{M4} ($P < 0.05$). In C herds, RC in Q_{M1} and Q_{M4} for MEP and in Q_{M1} , Q_{M2} , and Q_{M4} for MEF were less than unity ($P < 0.05$). After transformation, changes in RC for G herds were negligible. For C herds, only the RC for MEP in Q_{M4} was different from unity ($P < 0.05$). Analysis within variance quartiles also showed that PTA overestimated production of all traits in Q_{V1} - Q_{V3} ($P < 0.01$) and MEM in Q_{V4} ($P < 0.05$) in G herds. For C herds, yields of MEM in Q_{V1} and Q_{V2} ($P < 0.05$), and of MEP ($P < 0.01$) and MEF ($P < 0.01$) in Q_{V1} were overestimated; MEP was underestimated in Q_{V4} ($P < 0.05$). Reducing HV had little effect on G herds; but for C herds, RC was no longer different from unity for MEM and MEP in Q_{V1} and Q_{V2} . Production was more accurately predicted by PTA in C herds than G herds. Accounting for HV had little effect on the predictability of PTA, indicating that observed scaling effects do not arise solely from effects of HV.

Key Words: Heteroscedasticity, Predicted Transmitting Ability, Grazing

31 Effects of heteroscedasticity on the heritability and genetic correlations of production traits in grazing and confinement herds. A. G. Fahey*, M. M. Schutz, D. L. Lofgren, T. S. Stewart, and A. P. Schinckel, *Purdue University, West Lafayette, IN.*

Grazing (G) herds in the USA are increasing in number. Heteroscedasticity (HV) of data may bias estimates of genetic correlation (r_G) for yield traits between environments, an indicator of genotype-by-environment interaction (GxE). The objective of this study was to investigate the effect of HV on estimates of heritability (h^2) and r_G for mature equivalent (ME) milk (MEM), ME protein (MEP), and ME fat (MEF) yield of daughters in G and confinement (C) herds. Data consisted of 366 G herds from 11 states with 72,489 records and 373 C herds from 12 geographically similar states with 117,629 records. Herds were divided into mean quartiles and variance quartiles based on MEM. A transformation was used to reduce HV. The method of transformation was to standardize the within herd variance to the average variance of a base year for each parity, and was similar to that used in the USDA-DHIA genetic evaluations. In G herds, estimates of h^2 were near 0.19, 0.19, and 0.20 for MEM, MEP, and MEF. For C herds, h^2 from lowest to highest quartile. Estimates of r_G between G and C were greater than 0.89 in all mean quartiles, implying little GxE. Reducing HV by transforming yield records had little effect on h^2 or r_G . For variance quartiles, h^2 fluctuated as variance quartiles increased. For MEM, MEP, and MEF, h^2 were approximately 0.17, 0.17, and 0.19, respectively. The r_G for yield traits between C and G environments within each variance quartile suggested a GxE only for the lowest quartile for MEM. Transforming the records had negligible effects on the h^2 and r_G for variance quartiles. For G and C herds, h^2 were similar for all traits. The r_G near unity for the highest variance quartiles suggests that traits in both environments are controlled largely by the same genes. Reducing HV did not affect

estimates of h^2 or r_G , indicating that modest evidence for existence of GxE, especially in the lowest quartile, did not arise solely from HV.

Key Words: Heteroscedasticity, Heritability, Genotype-By-Environment Interaction

32 Segregation analysis of milk flow in Swiss dairy cattle by Bayesian approach. H. Ilahi and H. N. Kadarmideen*, *Statistical Animal Genetics Group, Institute of Animal Science, Swiss Federal Institute of Technology (ETH) Zurich ETH Zentrum (UNS), CH-8092 Zurich, Switzerland.*

Segregation analyses via Gibbs sampling were applied to investigate the mode of inheritance and to estimate the genetic parameters of milk flow of 3 breeds of Swiss dairy cattle. Data consisted of 204,397, 655,989 and 40,242 lactation records of milk flow in Brown Swiss (BS), Simmental (SM) and Holstein (HO), respectively (collected in the last 4 to 22 years). Number of animals in pedigree ranged from 343,969 to over 1 million (1,013,610) animals. Separate segregation analyses of first and multiple lactations were carried out for each breed by an individual animal model, implemented by Gibbs sampling algorithm with blocked sampling of genotypes and a polygenic model for first lactation data sets of all breeds by Restricted Maximum Likelihood Method. Genetic parameters of milk flow were very similar under both mixed inheritance (polygenes and major gene) and polygenic models. Estimated marginal posterior means of additive and dominance effects of the major gene were 0.016, 0.010, 0.023 for first lactation data set of BS, SM and HO, respectively and 0.013 and 0.012 for multiple lactations data set of BS and SM, respectively. Segregation analyses yielded very low major gene variances which favor the polygenic determinism of this trait, in contrast to confirmed mixed inheritance of this trait in dairy goats. Heritabilities and repeatabilities of milk flow in both BS and SM were high (0.44 to 0.48 and 0.54 to 0.59, respectively), however the heritability of this trait (based on scores of milking ease) in HO was intermediate (0.25). Variance components and heritabilities in the first lactation were slightly larger than those estimates for multiple lactations especially for error variances. Our results suggest that milk flow (quantity of milk per minute of milking) is a relevant measurement to characterize cows milking ability which is a good candidate trait to be included in selection program in dairy cattle.

Key Words: Segregation Analysis, Milk Flow, Bayesian Method

33 Prediction of longevity breeding values for U.S. Holstein sires using survival analysis methodology. D. Z. Caravillo*, K. A. Weigel, and D. Gianola, *University of Wisconsin, Madison.*

Breeding values of Holstein sires for daughter longevity in each of nine geographical regions of the US were predicted using a Weibull proportional hazards model. Longevity was defined as days from first calving until culling or censoring after correction for within-herd-year 305-d mature equivalent production. Records from 2,322,389 Holstein cows with first calving from 1990 to 2000 were used. In addition to the sire's additive genetic merit, the failure time model included time-dependent effects of herd-year-season of calving, parity-stage of lactation, and within-herd-year quintiles for mature equivalent fat plus protein yield, as well as the time-independent effect of age at first calving. The relative risk of culling for daughters of each individual sire was expressed relative to that of a daughter of an average sire (within a specific region). Predicted breeding values for functional longevity, expressed as relative risk ratios, ranged from 0.7 to 1.3. Sizable differences in sire rankings were observed between geographical regions, suggesting that a single national ranking may not hold in every region. Substantial differences in estimates of the sire variance and the gamma parameter of the distribution of herd-year-season effects occurred between regions. Two random samples of herds were selected from the full national data set; these samples contained 375,086 records and 256,751 records, respectively. PTA of sires for daughter longevity were compared with predictions from a linear (animal) model, as currently used for routine national (US) genetic evaluation of length of productive life. Logistic regression of daughters' stayability to 36, 48, 60, 72 or 84 months of life, among animals that had opportunity to stay that long, on sires predicted transmitting ability indicated that the proportional hazards model yielded more accurate predictions of daughter longevity than the linear animal model, even though the latter relies on more dense pedigree information.

Key Words: Longevity, Survival Analysis, Holsteins