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Calving Ease (Co)Variance Components for a Sire-Maternal Grandsire Threshold Model

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ABSTRACT

Variance components for a sire-maternal grandsire (MGS) threshold model were estimated from subsets of the US calving ease (CE) database, which includes over 10 million calving records with CE scored 1 (no problem) to 5 (extreme difficulty). Selected records included sire and MGS among the 2601 most frequently appearing bulls. The data were further restricted by requiring at least 20 records in each herd year. Five mutually exclusive sample datasets of approximately 200,000 records each were created based on herd code. The model included random herd-year, sire, MGS, and residual effects and fixed year-season, parity-sex, and birth year of sire and MGS effects. Fewer than 50 iterations were required to reach convergence. The (co)variance component estimates from the five replicates were quite similar. The set of estimates (0.438, herd-year; 0.022, sire; 0.016, MGS; 0.009, sire-MGS) that yielded among the highest heritabilities (0.086, direct; 0.048, maternal) and a correlation of direct and maternal effects near the mean (–0.12) was selected for use in the implementation of a sire-MGS model for CE.

(**Key words:** calving ease, dystocia, threshold model)

Abbreviation key: CE = calving ease, **MGS** = maternal grandsire.

INTRODUCTION

A sire-maternal grandsire (**MGS**) model (Van Tassell et al., 2003) was implemented in 2002 for the calving ease (**CE**) evaluation in the United States and replaced a sire model. An animal model was not adopted because calf identification is incomplete and convergence with a threshold animal model was expected to be slow. The new model required (co)variance component estimates for the random sire and MGS effects. Preliminary model development used values from the preceding sire model and literature values (Wiggans et al., 2002). For implementation, variance components estimated from the current data were desired.

Calving ease is scored on a 1 to 5 scale, where each unit increase in score does not represent the same increase in difficulty; therefore, a threshold model based on these ordered categorical data was used. A threshold model (Djemali et al., 1987) was introduced for the US genetic evaluation of direct CE effects in 1988 (Berger, 1994). The National Association of Animal Breeders supported development of a sire-MGS model. The value of maternal effects was shown by Dekkers (1994), who found that the optimal breeding strategy for CE considers both the direct and maternal effects.

The CBLUP2F90 program developed as part of the BLUPF90 family of computer programs (Misztal et al., 2002) uses quasi-REML (Harville and Mee, 1984) for variance component estimation for threshold models. A related program, CBLUP90IOD (Tsuruta et al., 2001; Misztal et al., 2002), is used for breeding value estimation through iteration on the data.

The purpose of this research was to estimate genetic parameters for a sire-MGS model for use in the US national genetic evaluation system based on current US data.

MATERIALS AND METHODS

Data

The US national CE dataset includes over 10 million calving records of Holstein cows calving since 1980. About 73% of them have MGS identified (Van Tassell and Wiggans, 2002). For variance component estimation, datasets small enough to be computationally practical with large contemporary groups were desired. Calvings with unknown MGS were eliminated, and records were restricted to those with sire and MGS among the 2601 most commonly occurring bulls in the dataset. This number was derived by investigating frequency of appearance in the data as either a sire or MGS and included 2.1% of the bulls. Limiting records this way

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Table 1. Numbers of records and distribution of calving ease scores in sample data files.

	Sample 1	Sample 2	Sample 3	Sample 4	Sample 5
Number of records	216,319	229,974	229,020	181,326	205,652
Calving ease score			(%)		
1 – No problem	75	75	67	75	71
2 – Slight problem	13	11	11	12	13
3 – Needed assistance	8	9	16	9	10
4 – Considerable force	3	3	4	3	4
5 – Extreme difficulty	2	1	2	2	2

effectively limited bulls in the sample data to those returned to service after progeny testing. The potential for causing bias in variance component estimation by the selection of popular bulls is limited because little trend in evaluations is evident over time, indicating that little selection pressure has been placed on CE. Herd-years with <20 calvings were then eliminated. From the remaining 3.5 million records, five sample files of approximately 200,000 calvings were created based on the last two digits of herd codes, with different herds represented in each file. Distributions of CE scores (Table 1) were similar across sample files; however, Sample 3 included two herds with nearly 25,000 calvings that had a very high proportion of births (19,000) coded with a CE score of 3 (needed assistance). This anomaly caused code 3 to be more frequent than code 2 in this sample. It is not unusual for large herds to have nearly every birth attended and for assistance to be provided in a majority of cases. It is also possible that the people scoring calvings in those herds were attempting to make the data appear normally distributed rather than scoring according to category descriptions.

Model

The threshold model used for parameter estimation and the national genetic evaluation was:

$$y = HY + YS + PS + Y_s + Y_m + s + m + e,$$

where y = CE score on a 1 to 5 scale; HY = random herd-year effect; YS = fixed year-season effect; PS = fixed parity-sex of calf effect for parities 1, 2, and 3 or greater; Y_s = fixed birth year of sire effect; Y_m = fixed birth year of MGS effect; s = random sire effect; m = random MGS effect; and e = random residual effect. The residual variance (σ_e^2) was assigned a value of 1. The year-seasons started in May and October of consecutive years. Birth year groups were ≤1980, 1981 to 1982, 1983 to 1985, 1986, 1987,..., 1997. Relationships among bulls were ignored for both sire and MGS effects. For widely used sires, relationships would add little to accuracy of the evaluations; however, ignoring paternal half-sib relationships could result in underestimation of genetic variances.

The HY effect was random because convergence problems can occur in threshold model analysis when all records in a fixed environment group belong to an extreme category (Harville and Mee, 1984; Misztal et al., 1989). Across all sample data sets, 72% of the records included a CE score of 1 (no problem). In 1596 herd-years (8%) all records had a CE score of 1.

The numbers of levels for effects in the five datasets are in Table 2. To allow for estimation of the correlation between sire and MGS effects, a bull was included as both even if it had no observations for one of the effects (i.e., even if a bull was present only as sire or only as MGS). Because the most recently born sires were not yet MGS, more sire birth year effects were present than MGS birth year effects.

Solutions for sire variance (σ_s^2), MGS variance (σ_m^2), and sire-MGS covariance (σ_{sm}) were converted to direct (D) and maternal (M) effects:

$$\begin{bmatrix} \sigma_D^2 \\ \sigma_{DM} \\ \sigma_M^2 \end{bmatrix} = \begin{bmatrix} 4 & 0 & 0 \\ -2 & 4 & 0 \\ 1 & -4 & 4 \end{bmatrix} \begin{bmatrix} \sigma_s^2 \\ \sigma_{sm} \\ \sigma_m^2 \end{bmatrix}$$

Table 2. Frequencies of model effects in sample data files.

	Sample				
Effect[1]	1	2	3	4	5
HY	4117	4004	3785	3587	3681
YS	44	44	44	44	44
PS	6	6	6	6	6
Y_s	15	15	15	15	15
Y_m	13	13	13	13	13
S	2594	2594	2598	2601	2601
MGS	2594	2594	2598	2601	2601

[1] HY = random herd-year; YS = fixed year-season; PS = fixed parity-sex (three parities, two genders); Y_s = fixed sire birth year; Y_m = fixed maternal grandsire birth year; S = random sire; MGS = random maternal grandsire.

Table 3. Calving ease score thresholds and numbers of iterations to converge from sample data files.

Sample	Threshold 1	2	3	4[1]	Iterations to converge
1	–1.90	–1.35	–0.61	0.00	47
2	–1.90	–1.35	–0.61	0.00	45
3	–2.27	–1.76	–0.66	0.00	46
4	–1.80	–1.25	–0.54	0.00	47
5	–1.95	–1.34	–0.58	0.00	46

[1] This threshold is set to 0 as part of the model definition to ensure parameter identifiability.

to facilitate comparison with previous variance component estimates. Phenotypic variance (σ_p^2) on the underlying scale was calculated as

$$\sigma_p^2 = \sigma_s^2 + \sigma_m^2 + \sigma_e^2.$$

The covariance σ_{sm} was not included in the formula because matings of sire to daughter are rare; therefore, the sire and MGS were assumed to be different bulls. The formulation also ignores relationships between sire and MGS.

RESULTS

Iteration was continued until convergence was achieved. Table 3 gives the threshold estimates from the last iteration. Those thresholds along with the variance components define the underlying scale applied to CE. The samples required similar numbers of iterations to reach convergence and had similar threshold estimates. The slightly different values for Sample 3 may reflect the different frequency of code 3 described previously. The variance components calculated for each sample were also similar (Table 4). That similarity may be because nearly the same sires were included in each sample.

The variance components from Table 4 were used to calculate heritability for, and correlation between, direct and maternal effects. For the calculation of heritabilities, only the genetic and residual (co)variances were used. Herd-year variance was not included in the total variance to make the results more comparable with those from traditional mixed models where contemporary group effects are treated as fixed. Estimated genetic correlations between direct and maternal effects in Table 5 are negative even though the estimated covariance between sire and MGS effects is positive. The positive estimate of the covariance results from a portion of the direct effect being included in both the sire effect (1/4) and the MGS effect (1/16).

Table 4. Variance components for sample data files.

Sample	Herd-Year variance	Sire variance	MGS[1] variance	Sire-MGS covariance
1	0.375	0.021	0.014	0.0080
2	0.452	0.019	0.014	0.0084
3	0.497	0.022	0.014	0.0071
4	0.410	0.019	0.013	0.0075
5	0.434	0.022	0.016	0.0091

[1] MGS = maternal grandsire.

Table 5. Heritabilities of direct and maternal calving ease effects and genetic correlations from sample data files.

	Heritability (%) Direct	Maternal	Correlation
Minimum	7.2	3.9	–0.25
Maximum	8.6	4.8	–0.08
Mean	8.0	4.4	–0.15
Used in Evaluations	8.6	4.8	–0.12

Variance components from Sample 5 were selected as the values used for the routine evaluation. They gave among the highest heritabilities and a correlation near the mean.

DISCUSSION

Pasman et al. (2003) reported the development of a multitrait, across-country evaluation for CE. Among the 10 countries included, only France and the United States employed a threshold model. The heritability estimates currently used in the French model (0.054 for direct and 0.031 for maternal effects) are slightly lower than the values that were estimated in this project. Luo et al. (1999) found values similar to those used by France based on a Bayesian analysis of Canadian data. The genetic correlation between direct and maternal effects found in that study was –0.16, which is within the range of values found in this study. Sample estimates including the highest heritabilities were selected for model implementation to minimize the difference from parameters in the previous sire model. In addition, heritability is less likely to be overestimated than underestimated because sire relationships were ignored.

Including sire and MGS birth years as fixed effects in the model accounted for change over time and differences between records with and without MGS. As a future enhancement, differences in CE between first and later parities could be accounted for by defining first and later parities as separate traits in a multitrait model.

CONCLUSIONS

(Co)Variance estimates obtained from this study were used in the implementation of a sire-MGS model for CE for the United States (Van Tassell et al., 2003). The sire-MGS model provides evaluations that include both direct (sire) and maternal CE effects and better adjusts the sire effects for differences in the maternal CE of their mates. The values estimated were similar to those found in other studies. Heritability for the direct effect is lower than the 0.15 reported for a threshold model by Djemali et al. (1987) and used in previous sire model evaluations. This results in lower reliability of evaluations based on the same number of records.

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