GENETIC CORRELATIONS BETWEEN FIRST AND LATER PARITY CALVING EASE IN A SIRE-MATERNAL GRANDSIRE MODEL

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INTRODUCTION

Calving ease (CE) affects fertility and calf survival. Jamrozik et al. (2005) found that difficult calving (dystocia) was associated with a higher incidence of stillbirth and reduced fertility across all parities. Johanson and Berger (2003) found that first parity cows have 4.7 times greater incidence of dystocia and Dekkers (1994) found that hard pulls and surgical intervention occur at much lower rates for multiparous than for first parity animals. Calving ease for Holstein cattle has been evaluated in the United States since 1980 and for Brown Swiss since February 2005 (Cole et al., 2005). A sire-maternal grandsire threshold model in which calvings for all parities were considered the same trait was introduced in 2003 (Van Tassell et al., 2003; Wiggans et al., 2003). The higher frequency of dystocia in first parity cows than later parity cows suggests there may be genetic differences for this trait. High genetic correlations between first and later parities have been found in many studies (Carnier et al., 2000; Cue and Hayes, 1984; Hansen et al., 2004). Genetic correlations for sire effect are generally close to one, but for daughter CE or maternal grandsire (MGS) effect, the correlation estimates are lower in the range 0.74 to 0.91 (Carnier et al., 2000; Hansen et al., 2004). Most studies have found that while genetic correlations are high, direct and maternal CE genetic variances are different between first and later parities (Carnier et al., 2000; Dekkers, 1994; Johanson and Berger, 2003). Sex of calf significantly affects calving difficulty, but less so for multiparous cows (Cue and Hayes, 1984; Groen et al., 1999).

Because CE scores are reported on a categorical scale, modeling of evaluations may be difficult. Gibbs sampling or linear modeling may be used to estimate genetic correlations (Hansen *et al.*, 2004). Gianola and Foulley (1983) offered a method for linear transformation of CE data in order to allow for more traditional evaluation methods. Their transformation made the CE scores fit on a semi-normal scale and allowed for modeling in a multi-trait evaluation. A transformation of CE data using a Snell scoring allows for comparison of the repeatability of the evaluations and stabilizes the variances across subclasses (Klassen *et al.*, 1990). However, transformation may introduce bias into the evaluation and additional care must be used to handle this bias. The purpose of this study was to determine the genetic correlation between CE in first and later lactations for sire and MGS effects in US data.

MATERIAL AND METHODS

Data. To create datasets of manageable size, five samples of approximately 250,000 were selected from over 13 million calvings since 1980 in the national CE database. The samples contained records from the 2600 bulls most frequently occurring as a sire or MGS. Scores were on a 1 to 5 scale from easy or unobserved to extreme difficulty. Herd-years were required to have at least 20 calvings. The number of herds ranged from 721 to 860. Scores were transformed to a linear scale where each transformed value was the standard normal deviate at the midpoint of the probability for the category. Probabilities were calculated separately by sex of calf and for first and later parity.

Model. The model included fixed year-season of calving (two seasons per year starting in April and October), sex of calf within parity, and birth year for sire and MGS effects and random herd-year, sire, MGS, and error effects. Several birth years were combined for years

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before 1985. Third and greater parities were grouped together. Calving ease in first and later parities was analyzed as two correlated traits.

Variance Component Estimation. Both Average Information REML (AIREML) on the transformed data and Bayesian estimation through Gibbs Sampling on the original scores were used to estimate (co)variance components. The Gibbs sampler was continued until the values of the thresholds stopped increasing, then every tenth sample from the last 10,000 was included in the summary.

RESULTS AND DISCUSSION

The AIREML estimation converged quickly. The Gibbs sampling required over 20,000 samples for the thresholds to stabilize. Table 1 shows fairly close correspondence between Bayesian and AIREML analyses for genetic correlations between first and later parity effects for both sire and MGS. There was considerable between-sample variation for the sire correlations. The MGS estimates were lower and more stable. The average correlation for MGS of approximately 0.8 indicates substantial genetic difference by parity. Table 2 shows correlations from the Bayesian analysis of approximately 0.5 between sire and MGS effects for all parity combinations.

Table 1.	Genetic	correlations	between	first	and	later	parity	calving	ease	effects	for	sire
and mat	ernal gra	andsire (MGS	5)									

Sampling		Estimation Procedure			
Effect	Group	Bayesian	AIREML		
Sire	0	0.958	0.969		
	2	0.881	0.840		
	4	0.845	0.842		
	6	0.992	0.993		
	8	0.992	0.941		
	Mean	0.934	0.917		
MGS	0	0.807	0.822		
	2	0.793	0.815		
	4	0.767	0.788		
	6	0.835	0.828		
	8	0.773	0.778		
	Mean	0.795	0.806		

Table 2. Correlations betwee	n sire and maternal	grandsire (MGS)	parity effects
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		MGS		
Pa	rity	1	2+	
Sire 1	0	.551	0.518	
2 -	+ 0	.513	0.547	

Variance component estimates are presented in Table 3. They are expressed relative to the residual variance for first parity. This scaling makes them comparable to the (co)variance components currently used (Wiggans *et al.*, 2003), which were 0.438 for herd-year, slightly higher than those in Table 3, and 0.0223 for sire, which was slightly lower. The biggest difference was 0.0159 for MGS. The value in Table 3 for first parity is 0.033, which is twice as large, and larger than the value for sire. The variances for later parities were lower than for first for both sire and MGS. For MGS, the variance for later parities was about half that for

first. Table 4 shows that the thresholds were lower for later parity, which is consistent with their lower variance. These differences in variance by parity, along with the correlation of approximately 0.8, indicate the value of modeling the MGS CE effect separately by parity.

Animal	Parity	Variance	SD
Sire	1	0.026	0.004
	2 +	0.021	0.001
Maternal grandsire	1	0.033	0.003
	2 +	0.016	0.002
Residual	2 +	0.921	0.068
Herd-year	1	0.346	0.012
-	2 +	0.308	0.018

Table 3. Variances relative to parity 1 residual

Table 4. Mean thresholds across 5 samples

	Threshold			
Parity	3	4		
1	2.42 ± 0.10	3.71 ± 0.18		
2 +	2.27 ± 0.09	3.24 ± 0.12		

Thresholds 1 and 2 set to 0 and 1 respectively

CONCLUSION

Correlations between first and later parity were high for sire, but were below 0.8 for MGS. Variances for the later parity group were less than for first parity, particularly for MGS. Evaluations, particularly for MGS can be improved by treating first and later parities as correlated traits. A national implementation of a bivariate threshold model should be considered. A non-Markov Chain Monte Carlo (MCMC) implementation following the methodology of Gianola and Foulley (1983), where thresholds are estimated, would be complicated. With thresholds known, such implementation can be much simpler by generalization of formulas by Quaas (1996). An MCMC can be used with variances and thresholds fixed where sampling involves only liabilities and solutions (Lee et al., 2002). In that study, a trivariate analysis involving about 500,000 animals required about 10,000 samples for satisfactory convergence of breeding values. The number may be even smaller with the sire-MGS. The computer program THRGIBBS1F90 completed 600 samples/day when processing 6 million animals thus required about 2 weeks. Program optimization, a faster computer and possibly implementation of parallel processing could reduce the total computing time to a few days. A linear model on the transformed scores also is possible, but the impact of the approximation necessary to apply a linear model might be unacceptably high. Additional research is required to implement separate genetic effects for first and later parities.

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REFERENCES

Carnier, P., Albera, A., dal Zotto, R., Groen, A.F., Bona, M. and Bittante, G. (2000) J. Anim. Sci. 78 : 2532–2539.

Cole, J.B., Goodling, R.C., Wiggans, G.R. and VanRaden, P.M. (2005) J. Dairy Sci. 88 : 1529–1539.

Cue, R.I. and Hayes, J.F. (1984) Res. Reports McGill Univ., Dept. Anim. Sci. 1984: 13-14.

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Dekkers, J.C.M. (1994) J. Dairy Sci. 77: 3441-3453.

Gianola, D. and Foulley, J.L. (1983) Genet. Sel. Evol. 15: 201-224.

Groen, A.F., van Aubel, J.P.J.M. and Hulzebosch, A.A. (1999) Stocarstvo 53: 331-335.

- Hansen, M., Lund, M.S., Pedersen, J. and Christensen, L.G. (2004) *Proc EAAP 2004* G2.7 : 1–5.
- Jamrozik, J., Fatehi, J., Kistemaker, G.J. and Schaeffer, L.R. (2005) *J. Dairy Sci.* 88 : 2199-2208.
- Johanson, J.M. and Berger, P.J. (2003) J. Dairy Sci. 86: 3745-3755.
- Klassen, D. J., Cue, R.I. and Hayes, B.J. (1990) J. Dairy Sci. 73: 205-212.
- Lee, D., Misztal, I., Bertrand, J.K. and Rekaya, R. (2002). J. Appl. Genet. 43: 209-216
- Quass, R.L. (1996). Threshold model, In: *Guidelines for uniform beef improvement programs* **125** : 139, < http://www.beefimprovement.org/guidelines.html>
- Van Tassell, C. P., Wiggans G. R., and Misztal, I. (2003) J. Dairy Sci. 86: 3366-3373.
- Wiggans, G.R., Misztal, I. and Van Tassell, C.P. (2003) J. Dairy Sci. 86 : 1845-1848.