PERFORMANCE OF A LINEAR-THRESHOLD MODEL TO EVALUATE CALVING EASE AND BIRTH WEIGHT IN A MULTIBREED BEEF POPULATION

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INTRODUCTION

Calving ease (CE) is an economically important reproductive trait, especially for the beef industry. In Canada, herds in the breeding program of Beef Improvement Ontario (BIO) are using rotational and terminal crossbreeding systems. They record both birth weight (BW) and CE. Genetic evaluation of CE is currently performed by transforming the categorical data to Snell scores, adjusting it by heterosis, and applying a linear bivariate model. BIO would like to improve this system by estimating heterosis dynamically and using a bivariate model, assuming a threshold model for CE and a linear model for BW, to improve the accuracy of genetic evaluation of CE. This study used simulation based on parameters from the current evaluation to 1) evaluate the performance of a linear-threshold model in a multibreed population using a Bayesian approach and 2) determine if this linear-threshold model is suitable for estimating direct and maternal heterosis.

MATERIAL AND METHODS

Simulation and data. The simulation was designed using a general crossbred population structure and genetic parameters from genetic evaluations performed by BIO. A three breed random crossbreeding scheme was implemented, including Angus (AN), Charolais (CH) and Hereford (HE). Animals were culled randomly up to age 7 and generations overlapped. Herds were connected via bulls from an AI center, which consisted of purebred sires. Random mating between sire and dams was assumed and dams had an equal chance to mate with an AI sire or with a within-herd sire. Sire-to-dam ratios were 1:10 and 1:100 for within-herd and AI sires, respectively. An animal model was assumed while simulating data. Observations of BW and underlying liability for CE of each animal were simulated using model (1a) and adjusted for direct and maternal heterosis using equation (1b).

$$\begin{bmatrix} y^0_{1ijk} \\ U^0_{2ijk} \end{bmatrix} = \begin{bmatrix} \mu_1 \\ \mu_2 \end{bmatrix} + \begin{bmatrix} \sum_{q=1}^{3} \left(b_{1dq} * cd_{kq} \right) \\ \sum_{q=1}^{3} \left(b_{2dq} * cd_{kq} \right) \end{bmatrix} + \begin{bmatrix} \sum_{p=1}^{3} \left(b_{1mq} * cm_{kq} \right) \\ \sum_{p=1}^{3} \left(b_{2mq} * cm_{kq} \right) \end{bmatrix} + \begin{bmatrix} s\_a_{1i} \\ s\_a_{2i} \end{bmatrix} + \begin{bmatrix} mg_{1j} \\ mg_{2j} \end{bmatrix} + \begin{bmatrix} d_{1k} \\ d_{2k} \end{bmatrix} + \begin{bmatrix} m_{1kd} \\ m_{2kd} \end{bmatrix} + \begin{bmatrix} mpe_{1kd} \\ mpe_{2kd} \end{bmatrix} + \mathbf{L_r w} \qquad (1a)$$

$$\begin{bmatrix} y^1_{1ijk} \\ U^1_{2ijk} \end{bmatrix} = \begin{bmatrix} y^0_{1ijk} \\ U^0_{2ijk} \end{bmatrix} * \left(\begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} HV_{1d} * hd_k \\ HV_{2d} * hd_k \end{bmatrix} + \begin{bmatrix} HV_{1m} hm_k \\ HV_{2m} hm_k \end{bmatrix} \right) \qquad (1b)$$

Where: $\mathbf{L_r L_r'} = \mathbf{R^0}$ and $\mathbf{R^0}$ is the residual (co)variance matrix, $\mathbf{w}$ is a 2×1 vector of random numbers from N~(0,1). y^0_{1ijkl} and U^0_{2ijkl} are BW and underlying liability of CE of individual k, respectively, within age-of-dam by sex- of-calf group i and management group j. Subscripts 1

and 2 refer to BW and CE, respectively. y^1_{1ijkl} and U^1_{2ijkl} are BW and underlying liability of CE of individual k, respectively, after adjusting for direct and maternal heterosis. μ is the population mean. cd_{kq} and cm_{kq} are the direct and maternal breed compositions of individual k, respectively, for breed q. b_{dq} and b_{mq} are the direct and maternal regression coefficients, respectively. s_a_i is the age-of-dam by sex-of-calf group i. mg_j is the management group j. d_k is the direct additive genetic effect of individual k and m_{kd} is the maternal genetic effect of dam d. mpe_{kd} is the maternal permanent environmental effect of dam d. hd_k and hm_k are the direct and maternal heterozygosities of individual k and HV_d and HV_m are the direct and maternal heterosis, respectively. The liability of CE was transformed to categorical data (1, 2, 3 or 4) based on the thresholds: 0 σ, 1 σ and 2.4 σ, where σ is the standard deviation of the liability. Thirty replicates were simulated.

Model. Preliminary results showed that an animal model including maternal genetic and maternal permanent environmental effects yielded very biased estimates of parameters. Therefore, the following linear-threshold bivariate sire maternal-grandsire model (SMM) was chosen as the model for genetic evaluation,

$$\begin{bmatrix} y_{1fghijk} \\ U_{2fghijk} \end{bmatrix} = \begin{bmatrix} \mu_1 \\ \mu_2 \end{bmatrix} + \begin{bmatrix} \sum_{q=1}^{3}\left(b_{1dq} * cd_{kq}\right) \\ \sum_{q=1}^{3}\left(b_{2dq} * cd_{kq}\right) \end{bmatrix} + \begin{bmatrix} \sum_{q=1}^{3}\left(b_{1mq} * cm_{kq}\right) \\ \sum_{q=1}^{3}\left(b_{2mq} * cm_{kq}\right) \end{bmatrix} + \begin{bmatrix} b_{1dHV} * hd_k \\ b_{2dHV} * hd_k \end{bmatrix} + \begin{bmatrix} b_{1mHV} * hm_k \\ b_{2mHV} * hm_k \end{bmatrix}$$
$$+ \begin{bmatrix} s\_a_{1i} \\ s\_a_{2i} \end{bmatrix} + \begin{bmatrix} mg_{1j} \\ mg_{2j} \end{bmatrix} + \begin{bmatrix} s_{1f} \\ s_{2f} \end{bmatrix} + \begin{bmatrix} mgs_{1g} \\ mgs_{2g} \end{bmatrix} + \begin{bmatrix} mpe_{1h} \\ mpe_{2h} \end{bmatrix} + \begin{bmatrix} e_{1fghijk} \\ e_{2fghijk} \end{bmatrix} \qquad (2)$$

where symbols are the same as the model used for simulation (1a and 1b), except b_{dHV} and b_{mHV} are the direct and maternal linear regression coefficients of response on direct and maternal heterozygosities, respectively. s_k is the sire of individual k. mgs_k is the maternal grandsire of individual k and e_{ijk} is the residual.

Methods of analysis. A Bayesian approach was chosen to estimate all location and dispersion parameters of the linear-threshold SMM. The joint conditional distribution of observations of BW and the underlying liabilities of CE was assumed to be bivariate normal. Flat priors were used for fixed effects, multivariate normal priors for random effects, and Inverted Wishart (IW) distributions were assumed for (co)variances. A Gibbs Sampling (GS) algorithm (Luo, 2001 and Wang *et al*., 1997) was used to continuously sample underlying liabilities, fixed effects, random effects, and variance components from their fully conditional distributions until convergence criteria were met (Raftery and Lewis, 1992). A single chain of 100,000 cycles was generated and saved for each replicate. The first 10,000 cycles were discarded as a burn-in period. Averages and standard errors (SE) of posterior means for all parameters, accuracy and rank correlation (correlation of true and estimated genetic values), mean square error and mean bias were calculated.

RESULTS AND DISCUSSION

On average, there were 9212.5 BW and CE records, 448.8 sires and maternal grandsires in each replicate. True and estimated values of genetic parameters are in Table 1. For all dispersion parameters, the average estimated value ± 1.1 SE (from 30 replicates) included the true value. Heritabilities were slightly underestimated, because other components of total phenotypic variances were generally overestimated (Table 2). Parameters for the continuous and categorical traits were estimated with similar levels of precision. The SE of maternal genetic variances were generally greater than those for direct genetic variances. Variances were estimated more precisely than were covariances and estimated genetic correlations were not as close to the true value as were heritabilities.

Table 1. True and estimated direct and maternal genetic (co)variances, heritabilities and genetic correlations for BW and CE using SMM

	True value				Estimated value ($\overline{X}$ ± SE, n=30)			
	BW_d[B]	CE_d[C]	BW_m[B]	CE_m[C]	BW_d	CE_d	BW_m	CE_m
Genetic (co)variances								
BW_d	34.06				37.95±3.65			
CE_d	-3.41	34.07			-3.68±3.18	36.09±6.51		
BW_m	-2.27	0.00	15.14		-3.39±2.68	-0.68±2.95	14.66±2.38	
CE_m	0.00	-2.78	-3.71	22.71	0.94±3.77	-5.25±2.16	-3.63±2.54	23.24±4.73
Heritabilities and genetic correlations[A]								
BW_d	0.45				0.47±0.04			
CE_d	-0.10	0.15			-0.10±0.08	0.15±0.02		
BW_m	-0.10	0.00	0.20		-0.14±0.12	-0.03±0.12	0.18±0.03	
CE_m	0.00	-0.10	-0.20	0.10	0.03±0.13	-0.17±0.16	-0.20±0.13	0.09±0.02

[A]Heritabilities on the diagonal, genetic correlations below the diagonal. [B]Birth weight direct and maternal genetic effect. [C]Calving ease direct and maternal genetic effect.

Table 2 represents true and estimated maternal permanent environmental, residual and phenotypic variances. All parameters were at least slightly overestimated, especially residual (and phenotypic) variances. A possible reason for the over-estimation may be the use of SMM rather than the animal model. Residual variance of SMM included part of the genetic (co)variances.

Table 2. True and estimated maternal permanent environmental (σ^2_{mpe}), residual (σ^2_e) and phenotypic variance (σ^2_p) and some variance ratios for BW and CE using SMM

	True value				Estimated value ($\overline{X}$ ± SE, n=30)			
	σ^2_{mpe}	$\sigma^2_{mpe}/\sigma^2_p$	σ^2_e	σ^2_p	$\hat{\sigma}^2_{mpe}$[A]	$\hat{\sigma}^2_{mpe}/\hat{\sigma}^2_p$	$\hat{\sigma}^2_e$	$\hat{\sigma}^2_p$
BW	7.6	0.11	18.9	73.43	8.15±3.32	0.10±0.04	23.31±1.83	80.68±1.49
CE	22.7	0.10	147.6	224.30	27.56±6.92	0.11±0.03	166.04±6.55	247.67±9.71

[A] ^ refers to estimated parameters.

Parameters associated with heterosis were estimated accurately, except for BW direct heterosis (Table 3). The SE of heterosis for CE were greater than for BW. Breed differences were reported instead of breed effects. All true breed differences fell within one SE of mean estimates, except for maternal breed difference for BW between AN and CH. For some parameters, however, ranks of the estimated breed effects were not consistent with true effects.

Table 3. True and estimated heterosis and breed differences for BW and CE

	True value				Estimated value ($\bar{X}$ ± SE, n=30)			
	BW_d	BW_m	CE_d	CE_m	BW_d	BW_m	CE_d	CE_m
Heterosis (%)								
	5.00	3.00	1.00	5.00	4.31±0.34	2.59±0.44	1.06±0.59	4.79±0.64
Breed difference								
AN vs CH	-13.81	-0.10	1.90	1.02	-14.38±1.84	0.79±1.36	3.03±1.08	0.54±1.57
AN vs HE	-7.37	-1.00	2.70	1.30	-7.23±1.86	-1.19±1.33	2.93±1.15	1.08±1.36
CH vs HE	6.43	-0.90	0.80	0.28	7.16±0.91	-1.97±1.49	-0.11±1.01	0.54±1.58

Table 4 shows statistics associated with accuracy of EBV. Accuracy and rank correlation of true and estimated breeding values showed similar patterns. Estimated BW direct genetic effects were closer to true values than maternal genetic effects for both BW and CE. Mean square error clearly showed that breeding values of BW were more precisely estimated than CE. Maternal genetic effects for CE were estimated with the greatest bias.

Table 4. Mean and standard error of accuracy, rank correlation, mean square error, bias of estimated breeding value for direct (D) and maternal (M) BW and CE

	Accuracy		Rank correlation		Mean square error		Bias	
	D	M	D	M	D	M	D	M
BW	0.71±0.18	0.31±0.09	0.72±0.15	0.30±0.09	20.20±5.23	12.88±1.33	0.15±0.28	-0.02±0.15
CE	0.51±0.15	0.31±0.09	0.49±0.13	0.30±0.08	25.04±3.16	20.14±1.78	-0.06±0.30	0.36±0.24

CONCLUSION

Under linear-threshold SMM, true dispersion parameters were well recovered. Regression of CE liability on heterozygosities and breed compositions can be fitted in the threshold model to account for heterosis in the genetic evaluation of a multibreed population.

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