Estimation of Genetic Parameters for Calving Ease by Heifers and Cows Using Multi-trait Threshold Animal Models with Bayesian Approach

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ABSTRACT: Genetic parameters for birth weights (BWT), calving ease scores observed from calves born by heifers (CEH), and calving ease scores observed from calves born by cows (CEC) were estimated using Bayesian methodology with Gibbs sampling in different threshold animal models. Data consisted of 77,458 records for calving ease scores and birth weights in Gelbvieh cattle. Gibbs samplers were used to obtain the parameters of interest for the categorical traits in two univariate threshold animal models, a bivariate threshold animal model, and a three-trait linear-threshold animal model. Samples of heritabilities and genetic correlations were calculated from the posterior means of dispersion parameters. In a univariate threshold animal model with CEH (model 1), the posterior means of heritabilities for calving ease was 0.35 for direct genetic effects and 0.18 for maternal genetic effects. In the other univariate threshold model with CEC (model 2), the posterior means of heritabilities of CEC was 0.28 for direct genetic effects and 0.18 for maternal genetic effects. In a bivariate threshold model with CEH and CEC (model 3), heritability estimates were similar to those in unvariate threshold models. In this model, genetic correlation between heifer calving ease and cow calving ease was 0.89 and 0.87 for direct genetic effect and maternal genetic effects, respectively. In a three-trait animal model, which contained two categorical traits (CEH and CEC) and one continuous trait (BWT) (model 4), heritability estimates of CEH and CEC for direct (maternal) genetic effects were 0.40 (0.23) and 0.23 (0.13), respectively. In this model, genetic correlation estimates between CEH and CEC were 0.89 and 0.66 for direct genetic effects and maternal effects, respectively. These estimates were greater than estimates between BWT and CEH (0.82 and 0.34) or BWT and CEC (0.85 and 0.26). This result indicates that CEH and CEC should be high correlated rather than estimates between calving ease and birth weight. Genetic correlation estimates between direct genetic effects and maternal effects were -0.29, -0.31 and 0.15 for BWT, CEH and CEC, respectively. Correlation for permanent environmental effects between BWT and CEC was -0.83 in model 4. This study can provide genetic evaluation for calving ease with other continuous traits jointly with assuming that calving ease from first calving was a same trait to calving ease from later parities calving. Further researches for reliability of dispersion parameters would be needed even if the more correlated traits would be concerned in the model, the higher reliability could be obtained, especially on threshold model with property that categorical traits have little information. (Asian-Aust. J. Anim. Sci. 2002. Vol 15, No. 8:1085-1090)

Key Words: Calving Ease, Genetic Parameter, Multivariate Threshold Model, Bayesian Method

INTRODUCTION

Calving difficulty (CD) is an important trait affecting calf mortality and profitability of cows. This trait is recorded in discrete categories as calving ease scores according to the amount of assistance rendered during calving. Ritchie and Anderson (2001) mentioned some factors affecting calving difficulties on the guideline of Beef Improvement Federation. Genetic evaluation for noncontinuous traits, as in case of CD, can be implemented using threshold models. Several studies (Gianola, 1982; Gianola and Foulley, 1983; Misztal et al., 1989) have suggested that threshold models, in which assumed the existence of an underlying normal variable, are theoretically appropriate for genetic analysis for categorical traits. Several studies (Renand et al., 1990; McGuirk et al., 1998; Varona et al., 1999) showed that heritability estimates for calving ease were two to five times higher using threshold models, compared to linear models. With respect to

theoretical aspects. Janss and Foulley (1993) described a bivariate analysis for joint analysis of birth weight and calving difficulty. Hoeschele et al. (1995) described multitrait genetic evaluation for one polychotomous trait and several continuous traits with missing data and unequal models. Bayesian inference, in particular Gibbs sampling (Geman and Geman, 1984), would be an alternative to estimating variance components and/or breeding values for categorical traits. Sorensen et al. (1995) described Bayesian analysis of univariate thresholds via Gibbs sampling in an animal breeding context. Wang et al. (1997) extended the work of Sorensen et al. (1995) to one multiple ordered categorical trait (calving ease) and one continuous trait (birth weight). Luo et al. (2001) applied different threshold models to one continuous trait and one categorical trait and compared the estimates between models. Varona et al. (1999) compared variance component estimates using a bivariate threshold-linear model for calving ease and birth weight with components estimated using a bivariate linear model. They suggested that the bivariate threshold-linear model was more suitable for analysis of calving ease. Carnier et al. (2000) presented estimates of heritability and

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genetic correlations for calving ease in different parities on an Italian Piemontese population using an animal model. In their study, estimation of genetic parameters was done via REML which assumed calving ease to be a continuous variable. Carnier et al. (2000) claimed that variance components and heritabilities were heterogeneous over parities. The purpose of this study was 1) to estimate heritabilities and genetic correlations for BWT, CEH, and CEC using multivariate threshold animal models with Bayesian inference, 2) to investigate whether calving ease scores for calves out of heifer should be treated as a different trait than calving ease scores for calves out of cows, and 3) to determine the genetic relationship between birth weight and calving ease.

MATERIALS AND METHODS

Data preparation

Sampled data with 77,458 records were prepared for this study from the original data with 512,176 records for birth weight and calving ease scores observed calves born from 1991 to 2000 at American Gelbvieh Association (AGA). These data were selected by herd in which records were greater than 999 (eventually 52 herds selected), and by herd-year-season (HYS) in which records were greater than three records after preparing data steps. As preparing data for analysis. HYS was defined by percentage Gelbvieh of calf, work order group, herd, year, and season. Percentages of Gelbvieh were categorized into three (44<PCT<50, 50<PCT≤88, 88<PCT≤100) after discarding records on which breed of calves were less than 45% of Gelbvieh. Seasons were categorized into four with spring, summer, fall, and winter. The CE scores observed were modified as 1. 2. and 3 for no assistance, minor assistance, major assistance or caesarian, respectively. Sex of calf was grouped into male and female. Age of dam for CEH was grouped into 4 categories (AOD<675 d. 675 d to 750 d. 750 d to 825 d. and 826 d to 930 d) and AOD for CEC was grouped into 5 categories (AOD=3 yrs, 4 yrs, 5-6 yrs, 7-8 yrs, and ≥ 9 yrs).

Data sampled by herds after data preparation steps were divided into two subsets, that one subset (DSH) contained 17.333 records for CE scores observed on calves born by heifers (CEH) (assumed age of dam≤930 d) and the other data set (DSC) contained 60.125 records for CE scores observed on calves born by cows (CEC) (assumed age of dam>930 d). Connectedness of sires by herds was checked and records on groups of sires were discarded. Total HYS on data from heifers and cows were 728 and 843, respectively. Overall and subclass means and proportions of each category for CEH and CEC are shown in table 1 and table 2. Numbers of animals by pedigree information were 42279, 84364 and 101891 in DSH, DSC, and DST.

Table 1. Simple statistics for number of records per sire and birth weight on dataset observed from calves born by heifers (DSH) and dataset observed from calves born by cows (DSC) in Gelbyieh

	DSH			DSC		
	No. Obs	Mean	SD	No. Obs	Mean	SD
No. records/sire	853	20.3		1,554		
BWT (kg)	17,333	36.4	4.8	60.125	39.8	4.8

respectively.

Models

Let y_W, y_H, y_C be $n \times 1$ vectors of observations for BWT. CEH and CEC and u_H, u_C be $n \times 1$ vectors of underlying liabilities for CEH and CEC. We also denote $y_W = u_W$ for the notation convenience. In the present study, three different threshold models were considered as follows.

Model 1: A single trait threshold animal model for CEH with no missing observations was:

$$\mathbf{u}_{H} = X\beta + Z_{h}h + Z_{o}a + Z_{m}m + e \tag{1}$$

where u_H was a vector of observations or underlying liabilities for CEH: β was a vector of fixed effects associated with sex and age of dam; h was a vector of herd-year-season random effects; a and m were vectors of direct and maternal genetic random effects; e was a vector of residual effects. X, Z_h, Z_a and Z_m were incidence matrices that linked data with respective effects. This model assumed that maternal effects were correlated with direct genetic effects.

Model 2: Calving ease for calves born from cows (CEC) with no missing observations were considered in this model which was similar to model 1 except permanent maternal environmental effects (PE) were included

$$\mathbf{u}_{C} = X\beta + Z_{b}h + Z_{o}p + Z_{a}a + Z_{m}m + e \tag{2}$$

where p was a vector of permanent maternal environmental effects for CEC and Z_p was a incidence matrix with respect to p. The other notations were same as in model 1.

Model 3: This model was a bivariate threshold model with two underlying variables (CEH and CEC). Calving ease scores of calves from heifer and cows were assumed to be different traits and direct and maternal genetic effects were assumed to be mutually correlated. Residual effects

between traits were assumed to be mutually independent. This model can be denoted as:

$$\mathbf{u}_{H} = X\beta + Z_{h}h + Z_{a}a + Z_{m}m + e$$

$$\mathbf{u}_{C} = X\beta + Z_{h}h + Z_{p}p + Z_{a}a + Z_{m}m + e$$
(3)

Model 4: This model (A three-trait linear-threshold animal model) included two underlying variables (CEH and CEC) and one continuous variable (BWT). This model assumed to have all effects for the categorical traits considered in model 3. It was also assumed that permanent maternal environmental effects (PE) were included in BWT. This model can be denoted as follow:

$$\mathbf{u} = X\boldsymbol{\beta} + Z_h h + Z_a \boldsymbol{\alpha} + Z_m \boldsymbol{m} + \mathbf{I}\boldsymbol{e} \text{, for CEH}$$

$$\mathbf{u}_i = X\boldsymbol{\beta}_i + Z_h h_i + Z_p \boldsymbol{p}_i + Z_a \boldsymbol{a}_i + Z_m \boldsymbol{m}_i + \mathbf{I}\boldsymbol{e}_i \text{, } i = BWT \text{ and CEC}$$

where each notation is same with as in model 1 and model 2.

Analysis

Bayesian analyses were carried out with Gibbs sampling algorithm presented by VanTassell et al. (1998) as a hierarchical Bayesian approach (Geman and Geman, 1984).

For the model 1, the conditional distributions of underlying liabilities for CEH given θ and R were assumed a normal distributions with density as:

$$p(u_H \mid \theta, R) \sim N(W\theta, R)$$

where $\theta = (\beta', h', a', m')^{\prime}$ is the vector of unknown location parameters for each effects. The prior distributions of all parameters in this model were assumed noninformative. For guarantee identifiability, first and second thresholds were fixed to zero and one described by Sorensen et al. (1995).

In model 2, the notations about the prior distributions for each unknown parameter were the same to those in Model 1 except replacing CEH with CEC.

In a bivariate model (model 3), we assumed to same prior distributions for parameters of interest with in model 1 and model 2. The conditional distributions for liabilities for calving ease were assumed as:

$$\begin{pmatrix} \mathbf{u}_H \\ \mathbf{u}_C \end{pmatrix} \boldsymbol{\theta}, \boldsymbol{R} \end{pmatrix} \sim N \begin{pmatrix} \boldsymbol{W} \boldsymbol{\theta}_H \\ \boldsymbol{W} \boldsymbol{\theta}_C \end{pmatrix}, \boldsymbol{R}_{2,2} \otimes \boldsymbol{I}_n \end{pmatrix}$$

In model 4 considered three traits, the conditional distributions of BWT and underlying variables on CEH and CEC were the multivariate normal distribution with density

$$\begin{pmatrix} \mathbf{u}_{w} \\ \mathbf{u}_{H} \\ \mathbf{u}_{c} \end{pmatrix} \boldsymbol{\theta}, \boldsymbol{R} \sim N \begin{pmatrix} W \boldsymbol{\theta}_{w} \\ W \boldsymbol{\theta}_{H} \\ W \boldsymbol{\theta}_{c} \end{pmatrix}, \boldsymbol{R}_{3/3} \otimes \boldsymbol{I}_{n}$$

where u_C was a vector of underlying liabilities for CEC and θ_c is a vector of location parameters for CEC.

The Gibbs sampler consisted of a set of fully conditional posterior distributions of unknown parameters, which followed the work by VanTassell et al. (1998) in these models. Since the posterior distributions can be obtained from joint posterior distribution of parameters with Bayes theorem, the Gibbs sampler can be drawn from the certain marginal posterior densities of all the unknown parameters (VanTassell et al., 1998). Gibbs sampling algorithms for location parameters were implemented with assuming prior distributions for each parameter described above. The posterior distributions of (co)variance matrices were belong to the inverted chi-square distributions in univariate models and the inverted Wishart distributions in multivariate models according to noninformative priors. The underlying variables for CEH and CEC in model 1 and 2 were drawn from truncated normal distribution presented by Wang et al. (1997). In model 3 and model 4 with assuming missing traits, because these traits cannot be observed simultaneously due to the nature of the traits, the underlying variables of CEH (u_{Hi}) given θ . R. t, u_{Ci} ,

and u_{nv} were obtained given by:

$$f(u_{H_j} \mid u_{H_j}, u_{C_j}, \theta, R, t) = \phi \left(\frac{u_{H_j} - \xi_{H_j}}{\sigma_{H_j}} \right)$$

if y_{H_l} was not observed

$$f(u_{H_{j}} \mid u_{\mathcal{B}_{j}^{*}}, \theta, R, t) = \frac{\phi\left(\frac{u_{H_{j}} - \xi_{H_{j}}}{\sigma_{H}}\right)}{\Phi\left(\frac{t_{H\lambda} - \xi_{H_{j}}}{\sigma_{H}}\right) - \Phi\left(\frac{t_{H\lambda-1} - \xi_{H_{j}}}{\sigma_{H}}\right)} I\left(u_{H_{j}} \in \left[t_{H\lambda-1}, t_{H\lambda}\right]\right)$$

if u_{Hi} was observed.

where $I(\cdot)$ was an indicator function: $\phi(\cdot)$ and $\Phi(\cdot)$ is the density and distribution function of a normal distribution with $\xi_{H_j} = w'_{J}\theta_{H} + r_{HW}r_{WW}^{-1}e_{W}$ and $\sigma_{H_j}^2 = r_{HH} - r_{HW}r_{WW}^{-1}r_{WH}$ with w'_{i} being the j^{th} row of W.

The underlying variables of CEC (u_C) given θ , R, t. u_{Hi} , and u_{Hj} were obtained given by similar manner as above

Gibbs sampling analysis was carried out on each of the assumed models using DSH, DSC and DST. This analysis 1088 D. H. LEE

for each sample consisted of 100,100 iterations, with the 1st 30100 samples discarded as "burn-in" period. Posterior means and Monte Carlo errors for (co)variance components from Gibbs sampler were calculated. These algorithms for threshold model with Gibbs sampling were implemented by modification of GIBBS2F90 (Misztal, 2001).

RESULTS AND DISCUSSION

General means and frequency analysis for calving ease

In DSH, the total number of sires was 853 with average number of progeny per sire of 20.3. On the data set from cows, the total number of sires was 1554 with the average number of progeny per sire of 38.7 (table 1).

Means and standard deviation for birth weights were 36.4±4.8 kg on 17,333 observations from heifers and 39.8±4.8 kg on 60,125 observations from cows. The proportions of calving ease for calves from heifers were 77.9% for score 1 (unassisted), 15.0% for score 2 (easy calving), 7.1% for score 3 or 4 (difficult calving or Caesarean) (table 2). Those from cows were 97.9, 1.6 and 0.5% for score 1, 2, and 3 or 4, respectively (table 2). As shown the table 2, most births were unassisted especially for cows that calved females rather than males. These proportions were in good agreement with several literatures (Varona et al., 1999; Ramirez-Valverde et al., 2001). The proportions of CE in this study would imply very little information for calving difficulty, especially CE of calves born by cows. The effects for Age of dam on CEH were classified to four because this effect predictably much affect to calving eases due to maturity. The same effects on CEC were classified to five. The calving ease scores for heifer and cow by herd-year-season contained a large number of calving ease scores that was all the same. For example,

Table 2. Percentages of frequencies by calving ease scores on each effect on dataset observed from calves born by heifers (DSH) and dataset observed from calves born by cows (DSC) in Gelbvieh

Calving ease		D\$H			DSC	
score	1	2	3	l	2	3
Overall %	77.9	15.0	7.1	97.9	1.6	0.5
Sex						
Female	86.3	10.0	3.7	99.0	0.7	0.3
Male	69.7	19.8	10.5	96.8	2.4	0.8
Age of dam(1)						
550-674 (3)	68.9	21.3	9.8	96.4	2.6	1.0
675-749 (4)	76.7	15.8	7.5	98.3	1.3	0.4
750-824 (5-6)	85.2	10.0	4.8	98.7	1.0	0.3
825-930 (7-8)	87.9	7.5	4.6	98.6	1.1	0.3
(Over 8)				98.6	1.2	0.2

⁽¹⁾ Unit of age of dam on data from heifer (cow) is days (vrs).

49.9% of HYS classes on CEH and 69.9% of HYS class on CEC contained only easy calving observations.

Heritabilities and correlations

In the univariate threshold model using DSH, the posterior mean of heritabilities (MCSD) for CEH was 0.35 (±0.06) for direct and 0.18 (±0.04) for maternal genetic effects (table 3). These heritability estimates were greater than the report (0.25 and 0.12) by Varona et al. (1999) under a threshold animal model. Genetic correlation between direct and maternal genetic effects was -0.26 (±0.13). They claimed that a bivariate model with highly correlated linear trait such as birth weight were much better to evaluate calving ease as a result of reliability based on the simulated data. Bennett and Gregory (2001) reported heritability estimates for 2-yr-old calving ease in 12 purebred and composite populations with average estimates of 0.43 for direct genetic effects and 0.23 for maternal genetic effects.

In the univariate threshold model using DSC, heritabilities (MCSD) for CEC were 0.28 (± 0.04) for direct genetic effects and 0.14 (± 0.03) for maternal genetic effects. These estimates were smaller than the results from CEH in model 1. Genetic correlations between direct and maternal genetic effects were -0.20 (± 0.13). The proportion of permanent environmental variation was 0.07 (± 0.02). There had been no reports for genetic parameters of CEC in a threshold animal model to enable to compare to these results in this model. However, the estimates in this model were expected with low reliabilities because of very little information for calving ease such that most of calves have easy calving (98%).

Using the bivariate threshold model (model 3) with CEH and CEC, heritability estimates (MCSD) for CEH were 0.35 (±0.04) and 0.18 (±0.03) for direct and maternal genetic effects, respectively (table 4). These estimates for CEC were 0.21 (±0.03) and 0.17 (±0.03). These estimates

Table 3. The posterior means (Monte-Carlo SD) of direct heritabilities (h_d^2) , maternal heritabilities (h_m^2) , genetic correlations between direct and maternal genetic effects $(r_{g(d-m)})$ and proportion of permanent environmental effects (p) for calving ease scores by heifers (CEH) and by cows (CEC) in single trait threshold animal models

	CEH	CEC
h_d^2	0.35(0.06)	0.28(0.04)
h_m^2	0.18(0.04)	0.14(0.03)
$r_{g(d-m)}$	-0.26 (0.13)	-0.20 (0.13)
p		0.07(0.02)

Table 4. The posterior means (Monte-Carlo SD) for heritabilities and genetic correlations for CEH and CEC in a bivariate threshold animal model (model 3)

	Direct genetic effects		Maternal genetic effects		
	CEH	CEC	CEH	CEC	
CEH	0.35 (0.04)	0.89 (0.02)	-0.24 (0.10)	-0.04 (0.09)	
CEC		0.21 (0.03)	-0.38 (0.10)	-0.10 (0.11)	
CEH			0.18 (0.03)	0.87 (0.03)	
CEC				0.17 (0.03)	

were similar or a little lower than estimates in univariate threshold models (model 1 and model 2). This phenomenon would be come from the correlated trait. Genetic correlations between CEH and CEC were 0.89 (±0.02) and 0.87 (±0.03) for direct and maternal genetic effects, respectively. Genetic correlations between direct and maternal genetic effects were moderately negative correlated as -0.24 (± 0.10) and -0.10 (± 0.11) for CEH and CEC, respectively. The high correlation between CEH and CEC would imply that these traits could be combined to single trait. With respect to algorithm on threshold model, restriction of two of thresholds to '0' and '1' could be circumvented the identifiable problems of parameters and good mixing rates were showed in multiple trait threshold model included several categorical traits. Furthermore, This model showed that threshold animal model for several categorical traits could feasible even Luo et al. (2001) claimed that sire model would be better than animal model.

The genetic parameters for calving ease and birth weight and their relationship were shown the results in the three-trait linear-threshold animal model using DST (model 4). This model provided heritability estimates for BWT of 0.50 (± 0.02) for direct genetic effects and 0.10 (± 0.01) for maternal genetic effects (table 5). These estimates were in good agreement with the results of other studies (Bennett and Gregory, 1996; Lee and Bertrand, 2002). The heritability estimates for CEH were 0.40 (± 0.03) for direct genetic effects and 0.23 (± 0.03) for maternal genetic effects. These estimates were greater than estimates from model 1.

On the other hand, heritability estimates for CEC were

 $0.23~(\pm 0.03)$ for direct genetic effects and $0.13~(\pm 0.02)$ for maternal genetic effects, respectively. These estimates were much higher than estimates by REML in the linear model reported by Carnier et al. (2000). These differences for heritability estimates according to type of model were in a good agreement with report by Weller et al. (1988), in which heritability estimates would be two to five times greater in threshold model than in the linear model. Furthermore, the higher heritability estimates for in this model with comparing to model 1 and model 2 would be inferred by affecting from correlated trait.

Genetic correlations for direct genetic effects were 0.82 (± 0.05), 0.85 (± 0.03), and 0.89 (± 0.05) between BWT and CEH. BWT and CEC, and CEH and CEC, respectively. These correlation estimates indicated that CEH was higher correlated to CEC than BWT and were in a good agreement with other literatures (Varona et al., 1999; Carnier et al., 2000; Bennett and Gregory, 2001).

Correlation estimates for maternal genetic effects were 0.34 (± 0.06), 0.26 (± 0.06), and 0.66 (± 0.05) between BWT and CEH. BWT and CEC, and CEH and CEC, respectively. Similar to direct genetic effects, maternal genetic effects for CEH were higher correlated to maternal genetic effects for CEC than to maternal genetic effects for BWT. Genetic correlations between direct and maternal effects were -0.29 (± 0.04), -0.31 (± 0.06), and 0.15 (± 0.07) on BWT, CEH, and CEC, respectively.

Genetic correlations between CEH and CEC. as main interest in present study, were greater than correlation to BWT for direct and maternal genetic effects. These estimates were slightly lower than the result (0.99) for calving ease between on first parity and on second or third parities by Carnier et al. (2000). The correlation estimates between direct genetic effects and maternal genetic effects for BWT were slightly lower than the result (-0.36) with the threshold model by Varona et al. (1999). The proportions of permanent environmental variation (PE) on total variation were 0.02 (±0.01) for BWT and CEC in model 4 (table 6). The correlation estimates for PE between BWT and CEC were -0.83 (±0.06) in model 4.

As theoretical aspect, the more information are include

Table 5. The posterior means (Monte-Carlo SD) for heritabilities and genetic correlations in a three-trait threshold animal model (model 4)

	Direct genetic effects			Maternal genetic effects			
	BWT	CEH	CEC	BWT	CEH	CEC	
BWT	0.50 (0.02)	0.82 (0.05)	0.85 (0.03)	-0.29 (0.04)	-0.16 (0.06)	-0.11 (0.08)	
CEH		0.40(0.03)	0.89 (0.05)	-0.14 (0.07)	-0.31 (0.06)	0.06 (0.07)	
CEC			0.23 (0.03)	-0.10 (0.06)	-0.19 (0.09)	0.15 (0.07)	
BWT				0.10(0.01)	0.34 (0.06)	0.26 (0.06)	
CEH					0.23 (0.03)	0.66 (0.05)	
CEC						0.13 (0.02)	

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Table 6. The posterior means (Monte-Carlo SD) for proportion of permanent environment effects and correlations in model 4

	BWT	CEH	CEC
BWT	0.02 (0.00)	N/A	-0.83 (0.06)
CEH	0.52 (0.02)	N/A	N/A
CEC	0.42 (0.01)	0.44 (0.03)	0.02 (0.01)

Diagonal: proportion of PE, Upper diagonal: correlation for PE between traits, Below diagonal: phenotypic correlation between traits.

in the model, the higher reliability of the estimates can be obtained. However, further study for the reliability problem in a threshold model with several categorical traits with little information are needed especially in animal model approach even standard error of estimates can be easily gotten using Bayesian approach as Monte-Carlo stand deviation.

IMPLICATIONS

Variance and covariance components and genetic parameters for calving ease (CE) scores observed calves born by heifers (CEH) and CE scores observed calves born by cows (CEC) and birth weight were successfully estimated in the multivariate threshold animal models. CEC were assumed the different trait with CEH in a bivariate threshold model and a three-trait linear-threshold model. Genetic merit for calving ease of calves whichever was born from heifer or cow can be jointly evaluated with other traits correlated regardless of type of traits. This should be increased the precision of genetic merits. Heritability estimates for direct (maternal) genetic effects of calving ease from heifer and cow were 0.40 (0.23) and 0.23 (0.13), respectively, in three-trait threshold animal model with two categorical traits. Genetic correlation estimate for direct genetic effects between CEH and CEC was 0.89 and 0.66 for direct genetic effect and maternal genetic effects. respectively.

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