

GENETIC PARAMETERS OF DAYS OPEN AND CALVING DIFFICULTY FOR FIRST PARITY KOREAN HOLSTEIN CATTLE USING A THRESHOLD ANIMAL MODEL WITH GIBBS SAMPLING

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INTRODUCTION

The genetic evaluation of some economic traits by nature is applied for the categorical data following the discrete distribution such as calving difficulty. Janss and Foulley (1993) used a Bayesian method for bivariate genetic evaluation of both continuous and discrete natures. Wang *et al.* (1997) implemented a fully Bayesian analysis via Gibbs sampling to infer the genetic merit and the genetic parameters in a joint analysis of calving ease and birth weight. Abdallah and McDaniel (2000) reported that the heritability estimate of days open was 0.03. In this study, the genetic parameters of heritabilities, genetic and phenotypic correlations were estimated using the bivariate threshold animal model via Gibbs sampling for both discrete and continuous natures of calving difficulty and days open.

MATERIAL AND METHODS

Data. Edited data consisted of 14 790 days open (DO) and calving ease records (CE) from cow's parturition from 1996 to 2001. The herd-year-season (HYS) for DO and CE were defined by herds, years and seasons when cow gave birth to calf. All records in which HYS were less than 2 were eliminated. The CE scores were categorized with 1, 2, 3, 4, and 5 for no assistance, minor assistance, major assistance, mechanical assistance and caesarian, respectively. Days open was measured as the interval between first calving and the following conception. Data information and overall means for the observations of traits are shown in Table 1. The total number of animals for genetic evaluation used was 20 075. Among these animals, 14 790 cows had no missing records for the two traits included for the analysis. Total number of sires and the average number of progeny per sire in the data set were 256 and 15.1, respectively.

Model. Let y_D and y_C be two vectors of order n of phenotypic observations for DO and CE, respectively, and u_C be a $n \times 1$ vector of underlying liabilities for CE. For notation convenience, $y_D = u_D$ are denoted. On the liability scale, the following mixed linear model was used:

$$u_i = Z_h h_i + Z_a a_i + I e_i, \quad i = \text{DO and CE}$$

where u_i was a vector of observations/liabilities for i^{th} trait; h_i was a vector of the herd-year-season effects; a_i was vectors of additive genetic effects; and e_i was a vector of the residual effects. Z_h, Z_a and I were known incidence matrices that link data with corresponding effects.

Conditionally on the model parameters, the joint distribution of observations and liabilities was assumed normal with density as:

$$p(\mathbf{u} | \boldsymbol{\theta}, R_0) \sim N(W\boldsymbol{\theta}, R), \text{ where } R = R_0 \otimes I, R_0 \text{ was residual variance-covariance matrix;}$$

$$\mathbf{u} = (u'_D \ u'_C)', \boldsymbol{\theta} = (\boldsymbol{\theta}'_D \ \boldsymbol{\theta}'_C)', \boldsymbol{\theta}_i = (h'_i, a'_i)' \text{ for } i = D \text{ for DO, and } C \text{ for CE, respectively,}$$

$$W = [Z'_h, Z'_a]', \text{ and } \otimes \text{ was direct product.}$$

Prior distributions. In order to avoid possible impropriety of the joint posterior distribution, proper priors were used to all model parameters. For herd effects, additive genetic effects and permanent effects, normal distributions were assumed:

$$p(h | Q_h) \sim MVN(0, Q_h \otimes I)$$

$$p(a | G) \sim MVN(0, G \otimes A)$$

where *MVN* was multivariate normal distribution, Q_h was the 2 x 2 variance-covariance matrix for HYS effects, G was the 2 x 2 variance-covariance matrix for a random effect and A is a known numerator relationship matrix. For all precision parameters, flat bounded priors were used.

Implementation. After augmentation of the model parameter vector with the liabilities, the Bayesian implementation via Gibbs sampler is straightforward. The derivation of the needed conditional posterior distributions are well described by Sorensen *et al.* (1995) being normal for the position parameter (herd and additive genetic effects) and scaled inverted Wishart for the precision parameters (herd variance, additive genetic variance, and residual variance). Efficient sampling algorithms from those distributions are widely available and easy to use.

The conditional posterior distribution of the underlying variables has a closed form as it was shown by Sorensen *et al.* (1995) and Van Tassell *et al.* (1998). With no missing calving ease records, this conditional distribution is a truncated normal:

$$u_{ij} | y_{ij} = \ell, u_{-ij}, \boldsymbol{\theta}, R, t \sim TN_{t_{i\ell-1}, t_{i\ell}}(\xi_{ij}, \sigma_{i\cdot}^2)$$

where *TN* was a truncated normal distribution between truncation points $t_{i\ell-1}, t_{i\ell}$ and $\xi_{ij} = w'_{ij}\boldsymbol{\theta}_i + R_{i(-i)}R_{(-i)(-i)}^{-1}e_{-ij}$; $\sigma_{i\cdot}^2 = r_{ii} - R_{i(-i)}R_{(-i)(-i)}^{-1}R_{(-i)i}$ where $R_{i(-i)}$ and $R_{(-i)(-i)}$ are sub-matrices of residual (co)variance matrix.

With Gibbs sampling algorithms, a unique chain of 100,100 iterations was implemented. The first 20,100 samples were discarded as "burn-in" period. For the remaining samples, every 10th cycle was retained. Thus, 8,000 samples were saved and used to compute means and standard deviations of the posterior distributions of parameters of interest. A modified version of GIBBSF90 (Misztal, 2001) based on formulas provided by VanTassell *et al.* (1998) was used for the post-Gibbs analysis.

RESULTS AND DISCUSSION

Data information. Means and standard deviations (SD) for DO were 147 ± 75 days (Table 1). On the categorical trait (CE), the proportions of each categorical observation were 73% for 1 (no assistance), 24% for 2 (minor assistance), 2% for 3 (major assistance), and less than 1% for 4 (mechanical assistance) or 5 (caesarean). Furthermore, 62% of CG's had CE of 1 (easy calving). These proportions were in good agreement with several studies (Varona *et al.*, 1999; Ramirez-Valverde *et al.*, 2001). The posterior means (SD) for the third and fourth threshold

were 1.483 and 1.637, respectively (Table 3). In all cases, the distribution of this parameter was sharp and almost symmetric, suggesting that a full convergence was reached. Table 4 presents the posterior means of genetic parameter in the present study.

Table 1. General information for days open (DO) and calving ease score (CE) in Korean Holstein cattle

Item	Results
No. animals	20075
No. records	14790
No. sires	256
Ave. no progenies/sire	15.1
No. Herd-Year-Season	3881
Means \pm SD	
DO (days)	146.6 \pm 74.8
CE (score)	1.29 \pm 0.52

Table 2. Proportions of categories for calving ease in Korean Holstein cattle

Score	1	2	3	4	5
Proportion	73.35%	24.29%	2.15%	0.15%	0.07%

Table 3. The marginal posterior means (Monte-Carlo standard deviations) of thresholds for calving ease score in Korean Holstein cattle

Threshold ⁽¹⁾	3 rd	4 th
Posterior means(MCSD)	1.482(0.032)	1.635(0.054)

⁽¹⁾First and second thresholds were restricted as zero and one0

Table 4. The marginal posterior means (Monte-Carlo standard deviations) of genetic parameters for days open (DO) and calving ease score (CE) in Korean Holstein cattle

	DO	CE
DO	0.090(0.014)	-0.478(0.253)
CE	-0.484 (0.012)-	0.132(0.020)

Diagonal: heritability, upper diagonal : genetic correlation, below diagonal : phenotypic correlation

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