

National Genetic Evaluation for Test-Day Milk Yield of First Parity Using Random Regression Test-Day Animal Model in Korean Holstein Cattle

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Summary

Single trait of random regression animal model was used to estimate genetic parameters of test day milk yield for Korean Holstein cattles. The model used for the analysis included the fixed effect of herd test day effect with regression coefficients to well describe the lactation curve nested within age and season classes and random effects of additive genetic and permanent environmental effects. He estimated heritabilities over the several intervals of first lactation yield ranged from 0.5 to 0.26. the maximum heritability was found in the beginning of the lactation and the minimum was found between days-in-milk(DIM) of 205 DIM and 255DIM. Relatively higher estimates were found compared with several previous studies.

Keyword: test-day milk yield, genetic parameter, random regression, Korean Holstein cattle

Introduction

Test-day (TD) model with random regression approach has been widely accepted to account for the accurate genetic merit of cow evaluations. The main advantage of TD random regression animal model has been numerously reported (Jamrozik *et al.*, 1997; Strabel & Misztel, 1999) compared with tradition animal model using 305 day records. In the traditional genetic evaluation using animal model did not account for the variations of individual cow's lactation curve. However, in the random regression animal model using TD records well accounts for the many factors affecting each TD record. The main objective of this study was to find the feasibility of implementation of random regression animal

model for the national genetic evaluation of dairy cattles in Korea. And also, the genetic parameter of milk yield was estimated using random regression animal model.

Material and Methods

Data comprised 30340 test day records for milk yields from 4616 cows collected in the 57 largest herds belonged to one of 142 testing stations in Korea from 1996 to 2001. Furthermore, 9213 animals with information on all sires and dams of cows with records were evaluated. Total 492 herd-TD was classified. Overall mean (SD) for TD milk yields was 27.8kg(7.0) and average for each TD yield was shown in Table 1.

Table 1. Number of records, means and standard deviations of TD yields in Korean Holstein cattle.

DIM	No Rec.	Mean	SD
5~20	1373	24.6	6.5
21~30	917	28.2	6.7
31~40	1026	29.8	7.0
41~50	965	29.9	6.9
51~60	1016	30.6	6.7
61~70	1027	30.4	6.7
71~80	1028	30.1	6.8
81~90	1051	30.5	6.5
91~100	1056	30.0	6.9
101~110	1024	29.7	6.9
111~120	1064	29.6	6.8
121~130	1072	29.5	6.9
131~140	1014	29.1	6.9
141~150	1092	28.8	6.8
151~160	1061	28.7	7.0
161~170	1048	28.5	6.8
171~180	1067	27.8	6.9
181~190	1049	28.1	6.8
191~200	1055	27.2	6.7
201~210	1080	27.2	6.9
211~220	1046	27.2	6.6
221~230	1034	26.7	6.6
231~240	1090	25.9	6.6
241~250	1016	26.0	6.6
251~260	1039	25.5	6.5
261~270	971	24.9	6.3
271~280	968	24.7	6.6
281~290	867	24.4	6.5
291~305	1224	24.0	6.4
Means	1046	27.8	6.7

Random regression model for TD yields at first parity was used as follow described by Jamrozik and Schaeffer (1997).

$$y_{ijlm} = HTD_i + \sum_{k=0}^4 b_{jk} z_{lmk} + \sum_{k=0}^4 a_{lk} z_{lmk} + \sum_{k=0}^4 p_{lk} z_{lmk} + e_{ijlm}$$

where y_{ijlm} is TD record m for milk yield of cow l belong to subclass j of calving age by calving season.; HTD_i is i^{th} herd TD effect; b is fixed regression coefficient; a and p are random regression coefficients; and z is a vector described by Jamrozik and Schaeffer (1997) as follow;

$$z' = \begin{bmatrix} 1 & c & c^2 & \ln(1/c) & [\ln(1/c)]^2 \end{bmatrix}$$

where $c = DIM/305$.

Fixed regressions were estimated within subclasses of age by season of calving. Age groups were 18 to 24 mo, 25 to 27 mo, and 28 to 40 mo. Seasons were March to May, June to August, September to November, and December or January to February. The following (co)variances were assumed;

$$Var \begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} G \otimes A & 0 & 0 \\ 0 & P \otimes I & 0 \\ 0 & 0 & E \otimes I \end{bmatrix}$$

where G is genetic covariance matrix among random regression coefficients; A is additive numerator relationship matrix; P is permanent environmental covariance matrix among random regression coefficients; and E is $diag\{\sigma_e^2\}$.

The covariance matrix for residuals was assumed to be an identity matrix with covariances across lactations equal to zero. Heritabilities were calculated according to the formula given by Jamrozik and Schaeffer (1997).

REMLF90 (Miszta, 2001), which used an accelerated EM algorithm, was used to compute variance components with restriction of convergence criteria with less than $<10^{-10}$.

Results and Discussion

Milk yield heritabilities as a function of DIM for single trait model at first lactation are shown in Figure 1. The estimated heritability for TD5 was

0.5 and thereafter steadily decreased to 0.33 at TD 72. The lowest heritability of 0.26 was estimated around between TD 210 to TD 250. The estimated heritability at complete lactation of TD 305 was 0.3. The estimated heritabilities for different TDs in this study were slightly lower than the findings of Jamrozik and Schaeffer (1997). For the genetic correlations among different TDs, the genetic correlation between TD 30 and the rest of following TDs were constantly decreased to 0 at around TD 250 and afterwards showed negative correlations. For those between TD 150 and the rest of TDs were approximately symmetric on both side of following TDs. Those between TD 305 and the rest of TDs were constantly decreased. After estimation of genetic parameters, the estimated breeding values were computed for the annual genetic trend. The estimated yearly trend was found 13.452 kg. However, this estimate was quite biased downward due to lack of pedigree information in the analytical model in this study.

Table 2. Genetic and permanent environmental (PE) (co)variance components of random regression coefficients for test-day milk yield in Korean Holstein cattle.

	Intercept	C	c^2	$\ln(1/c)$	$[\ln(1/c)]^2$
Genetic (co)variance					
Intercept	43.1280	-3.4714	-40.5065	-30.8878	5.3081
C	-3.4714	1.5840	4.2118	-0.1393	0.2436
c^2	-40.5065	4.2118	43.0560	30.4989	-5.5278
$\ln(1/c)$	-30.8878	-0.1393	30.4989	30.6180	-6.0473
$[\ln(1/c)]^2$	5.3081	0.2436	-5.5278	-6.0473	1.2960
PE (co)variance					
Intercept	4.7920	-0.3857	-4.5007	-3.4320	0.5898
C	-0.3857	0.1760	0.4680	-0.0155	0.0271
C^2	-4.5007	0.4680	4.7840	3.3888	-0.6142
$\ln(1/c)$	-3.4320	-0.0155	3.3888	3.4020	-0.6719
$[\ln(1/c)]^2$	0.5898	0.0271	-0.6142	-0.6719	0.1440

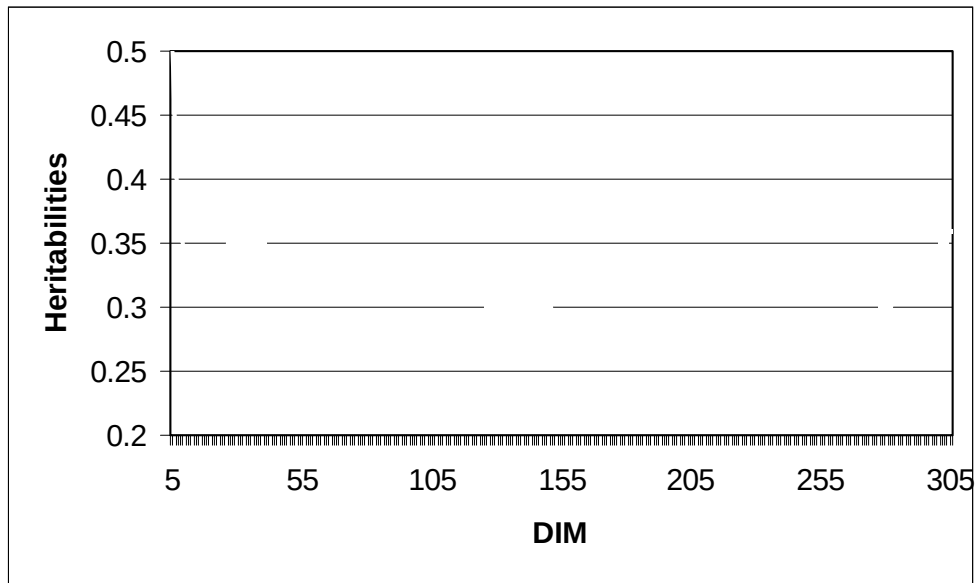


Figure 1. Heritability estimates for TD milk yields at first parity in Korean Holstein cattle.

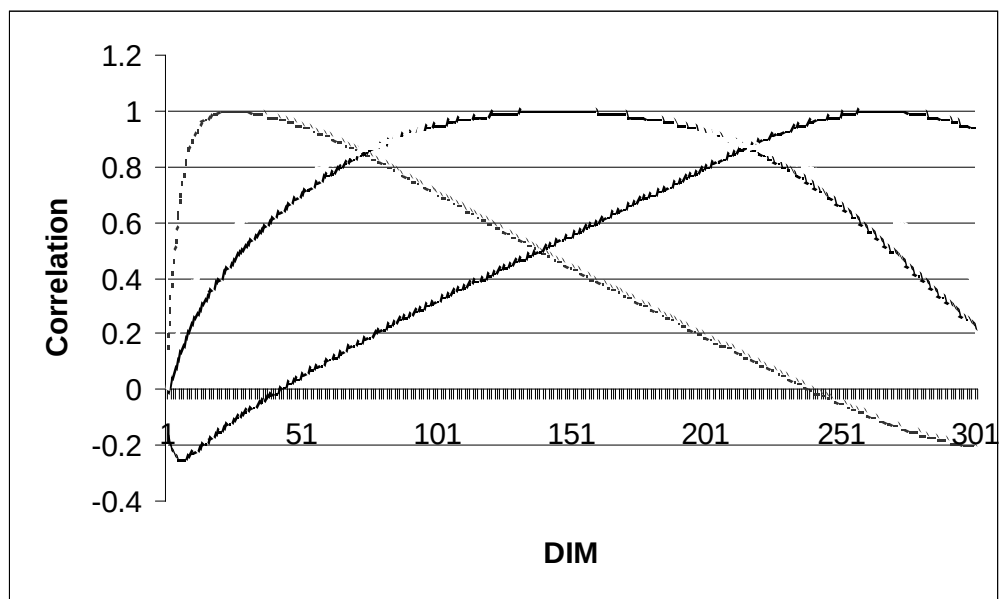


Figure 2. Genetic correlation estimates between test-day milk yield at 30, 150, 270 DIM, 305 total milk yields and the remaining part of first lactation in Korean Holstein cattle.

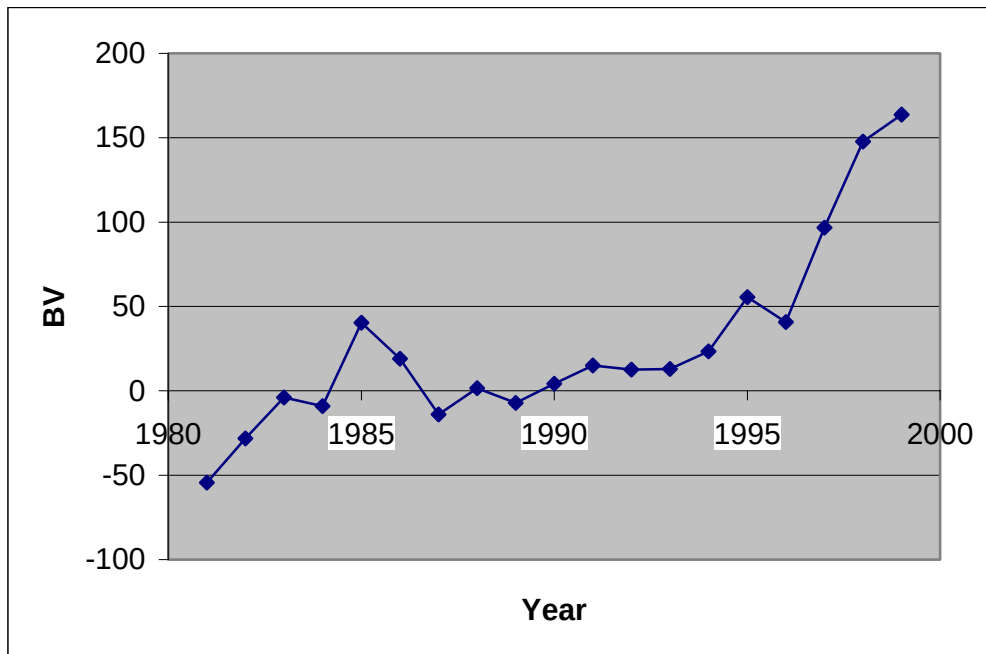


Figure 3. Annual genetic trend of milk yield for Korean Holstein cattle.

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