



Estimation of Genetic Parameters for Milk Production Traits Using a Random Regression Test-day Model in Holstein Cows in Korea

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ABSTRACT : This study was conducted to compare three models: two random regression models with and without considering heterogeneity in the residual variances and a lactation model (LM) for evaluating the genetic ability of Holstein cows in Korea. Two datasets were prepared for this study. To apply the test-day random regression model, 94,390 test-day records were prepared from 15,263 cows. The second data set consisted of 14,704 lactation records covering milk production over 305 days. Raw milk yield and composition data were collected from 1998 to 2002 by the National Agricultural Cooperative Federation's dairy cattle improvement center by way of its milk testing program, which is nationally based. The pedigree information for this analysis was collected by the Korean Animal Improvement Association. The random regression models (RRMs) are single-trait animal models that consider each lactation record as an independent trait. Estimates of covariance were assumed to be different ones. In order to consider heterogeneity of residual variance in the analysis, test-days were classified into 29 classes. By considering heterogeneity of residual variance, variation for lactation performance in the early lactation classes was higher than during the middle classes and variance was lower in the late lactation classes than in the other two classes. This may be due to feeding management system and physiological properties of Holstein cows in Korea. Over classes e6 to e26 (covering 61 to 270 DIM), there was little change in residual variance, suggesting that a model with homogeneity of variance be used restricting the data to these days only. Estimates of heritability for milk yield ranged from 0.154 to 0.455, for which the estimates were variable depending on different lactation periods. Most of the heritabilities for milk yield using the RRM were higher than in the lactation model, and the estimate of genetic variance of milk yield was lower in the late lactation period than in the early or middle periods. (**Key Words** : Random Regression Model, Heritability, Test-day, Milk Production Traits, Heterogeneity)

INTRODUCTION

The genetic abilities of milk traits in Holstein cows in Korea have been evaluated single-trait lactation model using milk yield at 305 days and milk composition at first lactation (NLRI, 2003). Ptak and Schaeffer (1993) have proposed a test-day model which considers each test-day record. Ptak and Schaeffer (1993) argue that estimates based on pre-adjustment of their 305 days lactation might be biased and do not consider individual generic physiology and persistency. Jamrozik and Schaeffer (1997) have suggested using a random regression test-day model to fit the test day data to a regression curve treating the data as

random time series. A multiple trait test-day random regression model has been used in Canada since 1999 for a nationwide genetic evaluation of dairy cattle. Dairy cattle have been evaluated for milk yield, fat yield, protein yield and somatic cell score on the first to the third using Wilmlink's function (Wilmlink, 1987). The model uses 72 equations per cow and allows over 21 million equations when 1.3 million cows are included. Jamrozik and Schaeffer (2000) have described new technique for dealing with so many equations. Also, Jamrozik et al. (1997) have reported some comparison of efficiency for several covariates using several random regression models. However, Regardless of their disadvantages, many researchers have continued to work on these covariate functions with respect to their advantages. In contrast to traditional genetic techniques, the Gibbs sampler is an alternative algorithm based on iterative Monte Carlo methods which are useful for drawing marginal inference when a high dimensional integration is required (Gelfand

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Table 1. Number of records, sires, cows, herd-test-day classes and general statistics for milk production at the first parity using the random regression model

Random regression model	No	Means	SD	Min	Max
Records	94,390				
Sires	189				
Cows/sire		77.80	140.64	10	1,059
Cows	15,263				
Records/cows		6.18	2.68	3	11
HTD ¹ classes	10,824				
Records/HTD		8.72	5.55	3	78
Milk yields (kg)		28.25	6.24	4.00	68.50
Fat yields (kg)		1.07	0.27	0.11	2.78
Protein yields (kg)		0.90	0.19	0.10	2.19
SNF ² yields (kg)		2.50	0.55	0.29	6.34
Fat (%)		3.82	0.71	1.59	6.08
Protein (%)		3.21	0.30	2.21	4.23
SNF (%)		8.84	0.47	7.10	10.52

¹ HTD = Herd-test-day, ² SNF = Solid-not-fat.

and Smith, 1990). It provides realized values of marginal posterior distributions by sampling from full conditional posterior distributions.

This study evaluates the genetic variation in test-day milk traits from a test-day random regression model, and compares the results to those obtained with the 305 day lactation model. The study is based on a sample data in order to determine model for evaluating the genetic basis of milk traits for Holstein cows in Korea to use their first lactation records.

MATERIALS AND METHODS

Data

Raw milk yield and composition data were collected from 1998 to 2002 by the National Agricultural Cooperative Federation's dairy cattle improvement center by way of its milk testing program, which is nationally basis. The pedigree information for this analysis was collected by the Korean Animal Improvement Association. The data for the

analyses were from animals in the first parity with full pedigree information and performance recorded more than three times in a lactation period. For the efficiency of data analysis, unusual records and animal records from the herd which was not connected in any blood relationships between herds were excluded. Two datasets were prepared for this study. To apply the test-day random regression model, 94,390 test-day records were prepared from 15,263 cows (Table 1). The second data set consisted of 14,704 lactation records day 305 covering milk production are 305 days (Table 2).

Milk traits considered were: test-day milk yield, fat yield, protein yield, solid-not-fat yield, fat percentage, protein percentage, SNF percentage.

Analytic statistical models

The test-day was treated as a covariate, age-season as fixed. In order to consider heterogeneity of residual variance in the analysis, test-days were classified into 29 classes covering the whole lactation period (Jamrozik and

Table 2. Number of records, sires, cows, Herd-year-season classes and general statistics for milk production at the first parity using the lactation model

Lactation model	No	Means	SD	Min	Max
Records	14,704				
Sires	189				
Cows/sire		77.80	140.64	10	1059
Cows	14,704				
HYS ¹ classes	3,280				
Records/HYS		4.49	3.79	1	52
Milk 305 d ² yields (kg)		8,320.40	1,504.15	2,094.00	15,536.00
Fat 305 d yields (kg)		310.80	63.68	82.00	676.00
Protein 305 d yields (kg)		265.34	46.43	69.00	492.00
SNF ³ 305 d yields (kg)		734.88	133.24	178.00	1,379.00
Fat 305 d (%)		3.76	0.53	1.35	5.76
Protein 305 d (%)		3.20	0.21	2.13	4.22
SNF 305 d (%)		8.84	0.40	5.56	13.66

¹ HYS = Herd-year-season, ² 305 d: 305 day corrected records, ³ SNF = Solid-not-fat.

Schaeffer, 1997). Restricted maximum likelihood algorithms were applied when heterogeneity of residual variance was not considered for the analysis.

Random regression model (RRM)

The coefficients of the L4 curve was calculated from the normalized Legendre polynomial (Kirkpatrick et al., 1990), P_j , as given by the following formula:

$$P_j(DIM_i^*) = \frac{1}{2^j} \sqrt{\frac{2j+1}{2}} \cdot \sum_{m=0}^{\lfloor j/2 \rfloor} (-1)^m \binom{j}{m} \binom{2j-2m}{j} (DIM_i^*)^{j-2m}$$

Where j is the order of the polynomial, and DIM is days in milk.

From the above equation, the first four polynomials are:

$$P_0 = \sqrt{1/2}$$

$$P_1 = \left[\sqrt{3/2} \left(-1 + \frac{2}{300} (DIM - 5) \right) \right]$$

$$P_2 = \left[\sqrt{45/8} \left(-1 + \frac{2}{300} (DIM - 5) \right)^2 - \sqrt{5/8} \right]$$

$$P_3 = \left[\sqrt{175/8} \left(-1 + \frac{2}{300} (DIM - 5) \right)^3 - \sqrt{63/8} \left(-1 + \frac{2}{300} (DIM - 5) \right) \right]$$

For changing scale of days in milk from 5 days to 305 day was standardized to the interval [-1, ..., 1], the following equation (Kirkpatrick et al., 1990) was used.

$$DIM_i^* = -1 + \frac{1 - (-1)}{305 - 5} (DIM - 5)$$

L4 curve: A 3rd order normalized Legendre polynomial can be written as:

$$\lambda = \alpha_0 * P_0 + \alpha_1 * P_1 + \alpha_2 * P_2 + \alpha_3 * P_3$$

The variance-covariance matrix is as follows:
It is assumed that

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

Where G is genetic (co-)variances of the covariate on the analyzed trait, A is a numerator relationship matrix, P is a permanent environment (co-)variances of the covariate on the analyzed trait, I is the identity matrix, and E is heterogeneous residual variance classified into 29 classes

with respect to DIM.

For genetic analysis of test-day milk traits, random regression animal models were fitted using a 3rd order Legendre polynomial function. The equations of the model are shown below:

$$Y_{ijkl} = HTD_i + \sum_{m=0}^3 b_{jm} z_{klm} + \sum_{m=0}^3 a_{lm} z_{klm} + \sum_{m=0}^3 p_{km} z_{klm} + e_{ijkl}$$

Where:

Y_{ijkl} : i^{th} HTD, j^{th} age-season at birth and l^{th} cow and k^{th} record for analytic trait,

HTD_i : i^{th} HTD fixed effect ($i = 1, 2, \dots, 10,824$),

b : fixed covariate effect on the l^{th} cow,

a : random covariate animal effect for additive genetic value on the l^{th} nested cow,

p : random covariate permanent effect on the l^{th} nested cow,

Z_{0-3} : 3rd order Legendre polynomial covariate provided by Kirkpatrick et al. (1990),

e_{ijkl} : random residual effect.

The applied random regression model was a single trait animal model in which each lactation record was considered as an independent trait. Estimates of covariance were assumed to be different. The RRGibbs program (Meyer, 2002) was utilized and the 3rd Legendre polynomial covariate function was applied for the analysis. In the function, the test-day was set up as a covariate and the effect of age-season was considered as a fixed effect. In order to study the heterogeneity of residual variance in the analysis using the RRGibbs program (Meyer, 2002), test-days were classified in 29 classes in a lactation period. Gibbs sampler was operated 100,000 rounds in order to estimate the variance of random effects with the above statistical model, and the software provided by Meyer (2002) was used to calculate fully conditional posterior means after the first 10,000 samples were discarded during a burn-in period. We used RRGibbs program to reduce computing time for RRM considering heterogeneous residual variances.

To estimate genetic variations in the considered traits, an REMLF90 (restricted maximum likelihood) implemented in FORTRAN90 by Misztal (2002) was used in both the test-day random regression without considering heterogeneous residual variances and lactation model. REMLF90 that uses an accelerated EM algorithm, was applied to compute variance components with restriction of convergence criteria (less than $<10^{-10}$).

Lactation model (LM)

Using 305 day lactation records, a single trait animal model was set up for estimating genetic parameters as below:

Table 3. Variance and covariance components for regression coefficients of each trait in random regression model considering heterogeneous residual variances using RRGibbs

Parameters	Days in milk	No. of records	Milk yield	Fat yield	Protein yield	SNF ² yield	Fat %	Protein %	SNF %
Genetic									
a0	a0		15.754	0.023	0.015	0.056	0.175	0.038	0.089
a0	a1		-0.700	0.001	0.001	0.017	0.015	0.005	0.003
a0	a2		-1.821	-0.001	-0.002	-0.012	-0.016	-0.003	-0.003
a0	a3		-0.275	0.002	0.000	-0.005	0.000	0.002	0.002
a1	a1		1.961	0.005	0.003	0.020	0.022	0.003	0.008
a1	a2		-0.395	0.000	0.000	-0.001	-0.003	0.000	-0.001
a1	a3		-0.644	0.000	0.000	-0.001	-0.002	0.000	0.000
a2	a2		1.093	0.002	0.001	0.007	0.010	0.002	0.003
a2	a3		-0.050	0.000	0.000	0.000	-0.002	0.000	0.000
a3	a3		0.559	0.001	0.001	0.004	0.005	0.001	0.002
PE¹									
p0	p0		13.872	0.017	0.010	0.155	0.132	0.021	0.051
p0	p1		2.030	0.001	0.001	-0.003	0.028	0.004	0.003
p0	p2		-0.296	-0.002	0.000	-0.004	-0.019	0.000	-0.002
p0	p3		1.267	-0.001	0.001	0.011	0.010	-0.001	0.000
p1	p1		2.469	0.002	0.002	0.015	0.020	0.006	0.005
p1	p2		0.092	0.000	0.000	-0.002	-0.002	0.000	0.000
p1	p3		0.444	0.000	0.000	0.000	-0.003	-0.001	0.000
p2	p2		0.748	0.002	0.001	0.008	0.014	0.001	0.003
p2	p3		-0.127	0.000	0.000	-0.001	-0.003	0.000	0.000
p3	p3		0.423	0.001	0.000	0.004	0.009	0.001	0.001
Residual									
e1	5-20	3,891	20.403	0.030	0.012	0.136	0.492	0.135	0.084
e2	21-30	2,778	9.081	0.024	0.009	0.070	0.207	0.020	0.036
e3	31-40	3,054	10.418	0.025	0.009	0.080	0.216	0.020	0.038
e4	41-50	3,004	8.813	0.023	0.009	0.069	0.195	0.018	0.035
e5	51-60	3,111	7.279	0.022	0.008	0.058	0.176	0.015	0.028
e6	61-70	3,319	6.362	0.021	0.007	0.051	0.160	0.013	0.027
e7	71-80	3,322	6.808	0.020	0.008	0.055	0.152	0.015	0.027
e8	81-90	3,231	6.492	0.018	0.008	0.054	0.143	0.014	0.027
e9	91-100	3,449	6.832	0.021	0.008	0.054	0.149	0.013	0.025
e10	101-110	3,445	5.842	0.017	0.007	0.049	0.135	0.011	0.025
e11	111-120	3,354	5.852	0.019	0.007	0.048	0.142	0.012	0.025
e12	121-130	3,503	5.969	0.019	0.007	0.049	0.128	0.012	0.027
e13	131-140	3,452	5.948	0.019	0.007	0.050	0.135	0.012	0.028
e14	141-150	3,399	5.855	0.018	0.006	0.048	0.131	0.012	0.024
e15	151-160	3,521	5.949	0.018	0.007	0.049	0.125	0.012	0.027
e16	161-170	3,533	6.059	0.018	0.007	0.050	0.130	0.012	0.026
e17	171-180	3,372	6.004	0.017	0.007	0.050	0.128	0.011	0.024
e18	181-190	3,459	5.430	0.016	0.006	0.044	0.122	0.011	0.024
e19	191-200	3,521	5.579	0.017	0.007	0.046	0.118	0.012	0.027
e20	201-210	3,328	6.428	0.017	0.007	0.052	0.120	0.012	0.024
e21	211-220	3,491	4.966	0.016	0.006	0.041	0.114	0.012	0.025
e22	221-230	3,312	5.329	0.015	0.006	0.044	0.112	0.012	0.023
e23	231-240	3,193	5.631	0.015	0.006	0.046	0.117	0.012	0.026
e24	241-250	3,235	6.418	0.018	0.008	0.053	0.120	0.012	0.025
e25	251-260	3,101	6.176	0.016	0.007	0.050	0.114	0.014	0.029
e26	261-270	2,812	6.547	0.017	0.008	0.055	0.122	0.012	0.026
e27	271-280	2,687	5.073	0.013	0.006	0.041	0.118	0.013	0.027
e28	281-290	2,418	4.951	0.015	0.006	0.041	0.116	0.013	0.025
e29	291-305	3,095	4.028	0.011	0.005	0.032	0.107	0.013	0.023

¹ PE = Permanent environment. ² SNF = Solid-not-fat.

Table 4. Variance and Covariance components for regression coefficients of each trait in random regression model without considering heterogeneous residual variances using REMLF90

Parameters		Milk yield	Fat yield	Protein yield	SNF ² yield	Fat %	Protein %	SNF %
Genetic								
a0	a0	18.1200	0.0134	0.0046	0.0830	0.1858	0.0344	0.0968
a0	a1	-1.1230	0.0017	0.0009	0.0092	0.0232	0.0071	0.0053
a0	a2	-1.6360	-0.0013	-0.0006	-0.0084	-0.0276	-0.0024	-0.0058
a0	a3	3.3970	0.0003	0.0003	-0.0018	0.0103	0.0008	0.0017
a1	a1	0.3540	0.0018	0.0008	0.0050	0.0155	0.0040	0.0050
a1	a2	0.1596	-0.0004	-0.0002	-0.0013	-0.0080	-0.0008	-0.0007
a1	a3	-0.2855	0.0001	0.0002	0.0010	0.0039	0.0006	0.0006
a2	a2	0.1685	0.0010	0.0004	0.0019	0.0273	0.0016	0.0040
a2	a3	-0.3279	-0.0002	-0.0001	-0.0005	-0.0159	-0.0006	-0.0011
a3	a3	0.9026	0.0007	0.0003	0.0018	0.0151	0.0012	0.0018
PE ¹⁾								
p0	p0	16.2800	0.0292	0.0213	0.1462	0.1569	0.0288	0.0569
p0	p1	1.2590	0.0001	0.0014	0.0042	0.0154	0.0020	0.0006
p0	p2	-0.2489	-0.0013	-0.0009	-0.0074	-0.0074	-0.0010	0.0005
p0	p3	-1.5700	0.0005	0.0002	0.0069	-0.0008	-0.0002	0.0003
p1	p1	4.9670	0.0056	0.0039	0.0324	0.0369	0.0070	0.0107
p1	p2	0.0254	-0.0008	-0.0004	-0.0052	-0.0102	-0.0015	-0.0017
p1	p3	0.4317	-0.0005	-0.0001	-0.0001	0.0021	0.0014	0.0007
p2	p2	0.0118	0.0029	0.0015	0.0140	0.0066	0.0033	0.0034
p2	p3	0.0802	-0.0011	-0.0003	-0.0043	-0.0041	-0.0021	-0.0017
p3	p3	0.6496	0.0015	0.0009	0.0079	0.0107	0.0033	0.0029
Residual								
r1	r1	7.0330	0.0183	0.0071	0.0518	0.1399	0.0145	0.0273

¹ PE = Permanent environment. ² SNF = Solid-not-fat.

$$Y_{ij} = \mu + HYS_i + a_j + e_{ij}$$

Where Y_{ij} = observation on j^{th} cow and i^{th} HYS.

μ = overall mean,

HYS_i = i^{th} fixed herd-year-season effect.

a_j = j^{th} random animal genetic effect,

e_{ij} = random residual effect.

RESULTS AND DISCUSSIONS

Variance estimates in test-day random regression model

By considering heterogeneity of residual variance (Table 3), variation for lactation performance in the early lactation classes was higher than during the middle classes and variance was lower in the late lactation classes than in the other two classes. This may be due to feeding management system and physiological property of Holstein cows in Korea. Over classes e6 to e26 (covering 61 to 270 DIM), there was little change in residual variance, suggesting that a model with homogeneity of variance be used restricting the data to these days only.

However, further research should be performed in order to understand the properties of the data in the early lactation period before the test-day model can be applied to evaluating genetic performance of dairy cattle in Korea.

Jamrozik and Schaefer (1997) have reported that

residual variances at early lactation stages were high, in a random regression model considering heterogeneous residual effects classified into 29 classes. Our study showed similar trends in all the considered traits, although low residual variances were shown at later lactation stages. These results are probably due to long lactation periods.

Heritabilities

Heritabilities of milk traits as a function of DIM for single trait model with and without considering 29 residual classes are shown in Figure 1 and Figure 2. As shown in those figures, estimates of heritability were higher in RRM considering 29 residual classes than in RRM not considering them on most of DIM. Heritabilities of milk traits in the lactation model are shown in Table 5.

The heritability of milk yield by DIM was estimated to be between 0.154 and 0.455, and a sudden increase in heritability during the early lactation period (between the 20th and 25th DIM) was observed. Between the early and the middle lactation period, heritability changed only slightly. After the 215th DIM, heritability slowly decreased. The highest estimate of heritability was 0.455, at the 215th DIM, and the lowest one was at the 305th DIM. The analysis showed a broad variation in the heritability of milk yield by DIM. All the heritability estimated using the test-day model was higher than that ($h^2 = 0.146$) found using the lactation model. The low genetic variance of milk yield estimated in

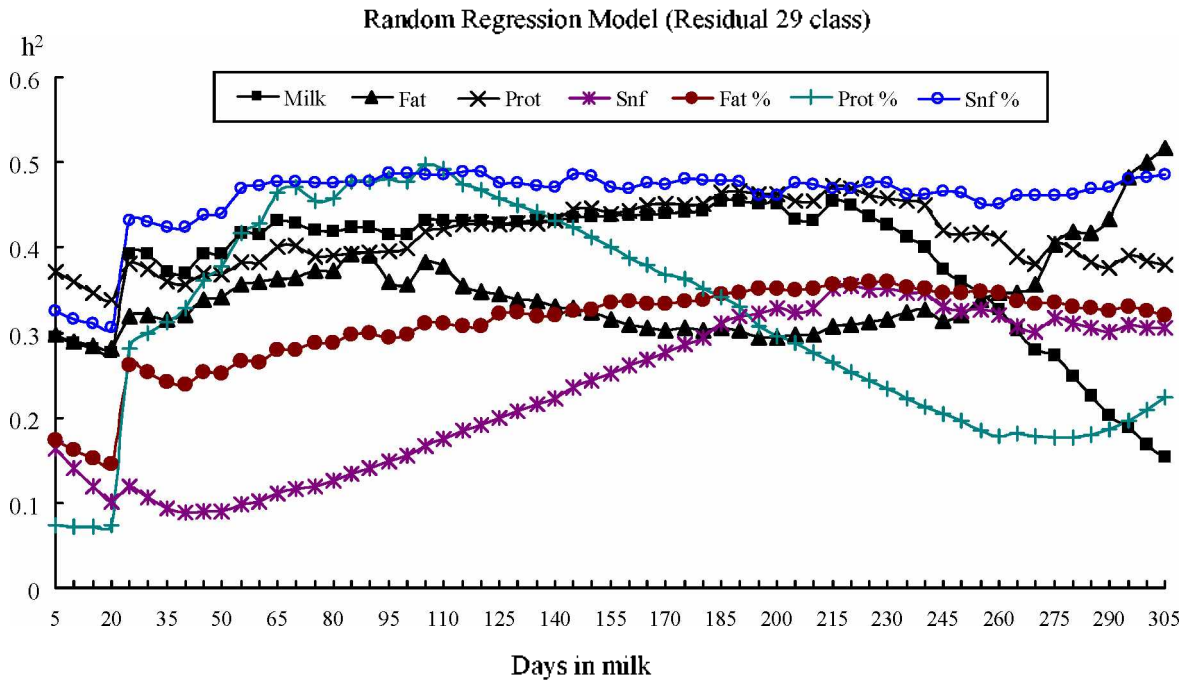


Figure 1. Estimates of heritability for milk production traits using the random regression model considering 29 residual classes.

the late lactation period indicates that individual variation in milk yield is higher in the late lactation period than in earlier periods.

The heritability of milk fat yield by DIM was estimated to be between 0.282 and 0.517 and a sudden increase in heritability was observed in the early lactation period (between the 20th and 25th DIM). From the early to the

middle lactation period, heritability changed only slightly. After the 250th DIM, heritability slowly increased. The highest estimate of heritability was 0.517, at the 305th DIM, and the lowest one was at the 20th DIM. The heritability estimated using the test-day model was higher than that ($h^2 = 0.130$) found using the lactation model.

The heritability of milk protein yield by DIM was

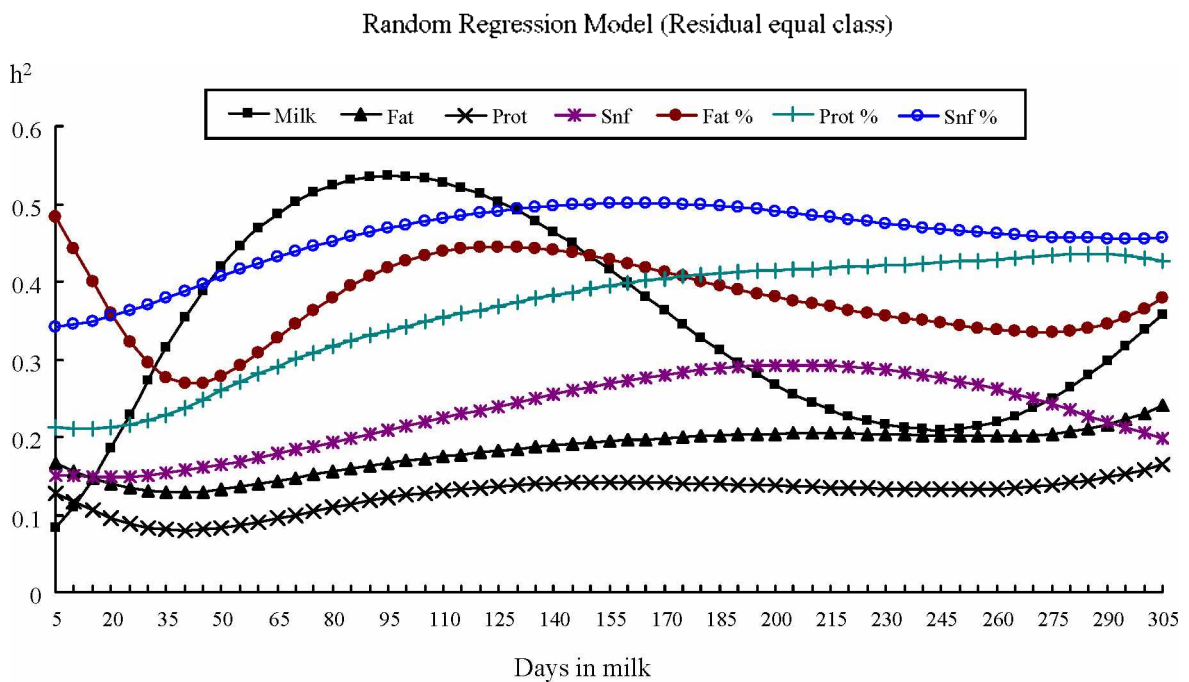


Figure 2. Estimates of heritability for milk production traits using the random regression model considering equal residual classes.

Table 5. Estimates of heritability for each trait with the lactation model

Milk 305 day	Fat 305 day	Protein 305 day	SNF ¹ 305 day	Fat % 305 day	Protein % 305 day	SNF % 305 day
0.146	0.130	0.115	0.113	0.411	0.426	0.414

¹ SNF = Solid-not-fat.

estimated to be between 0.263 and 0.338, and showed an increase in the early lactation period (between the 20th and 25th DIM). From the early to middle lactation periods, heritability changed only slightly. After the 240th DIM, heritability slowly decreased. The highest estimate of heritability was 0.338 at the 20th DIM, and the lowest was at the 215th DIM. The analysis showed little variation in the heritability of milk protein yield by test-day. Most of the heritability estimated using the test-day model was higher than that ($h^2 = 0.115$) seen using the lactation model.

The heritability of SNF yield by DIM was estimated to be between 0.088 and 0.354, and heritability decreased from the early lactation period, increased from 45 days after parturition, and decreased again after the 220th DIM. The highest estimate of heritability was 0.354 at the 220th DIM, and the lowest was at the 40th DIM. The analysis showed broad variation in the heritability of SNF yield by DIM. Most of the heritability estimated using the test-day model was higher than that ($h^2 = 0.113$) found using the lactation model.

The heritability of milk fat percentage by DIM was estimated to be between 0.145 and 0.359, and increased suddenly in the early lactation period (between the 20th and 25th DIM). From the 25th DIM to the middle lactation period (the 230th DIM), heritability slowly increased. After that period, heritability decreased a little. The highest estimate of heritability was 0.359 at the 230th DIM, and the lowest was 0.145 at the 20th DIM. The analysis showed little variation in the heritability of milk fat percentage by DIM. Most of the heritability estimated using the test-day model was lower than that ($h^2 = 0.411$) seen using the lactation model.

The heritability of milk protein percentage by DIM was estimated to be between 0.072 and 0.497, and suddenly increased in the early lactation period (between the 15th and 25th DIM). From the 15th DIM to middle lactation period (the 105th DIM), heritability increased. From the 275th DIM, heritability decreased, and then slightly increased. The highest estimated heritability was 0.497 at the 105th DIM, and the lowest was 0.072 at the 15th DIM. The analysis showed broad variation in the heritability of milk protein percentage by DIM. Most of the heritability estimated using the test-day model was lower than was seen ($h^2 = 0.426$) using the lactation model.

The heritability of SNF percentage by DIM was estimated to be between 0.305 and 0.489. It suddenly increased in the early lactation period (between the 20th and

25th DIM). From the 25th DIM to the middle lactation period (the 120th DIM), heritability slowly increased. After the 120th DIM, heritability showed almost no change. The highest estimated heritability was at the 120th DIM, and the lowest was at the 20th DIM, but showed little change over the rest of the lactation period. The heritability estimated using the test-day model was similar to that ($h^2 = 0.414$) observed when using the lactation model.

Using the lactation model, heritability estimates were 0.146 for milk yields, 0.130 for fat yields, 0.115 for protein yields, 0.113 for solid-not-fat yields, 0.411 for fat %, 0.426 for protein % and 0.414 for solid-not-fat % (Table 5). These results were lower than those have reported by Lee and Han (2001), Park and Lee (2006) and Han (1995).

However, heritability estimates were some different when residuals' heterogeneity was or was not considered. Estimate of heritability on milk yields was highest at 215 DIM and lower at early and later lactation stages in the test-day random regression model. In the lactation model, genetic parameters were moderate or low.

One aspect of Korean dairy farmers' management system was their tendency toward a high energy feeding system during the growing stage, because rearing within the barn and age at parturition were late. Therefore, milk yields at the early lactation are high influenced by environmental effects. Due to these management systems, estimates of heritability for 305 day milk traits at this stage would be low. Furthermore, milk yields at peak lactation stages were shown to be high, for that reason, the 3rd order Legendre polynomials would not be the best fitting of the lactation curve. Further study is needed to investigate other polynomial functions for fitting the lactation curve.

CONCLUSIONS

This study investigated the influence of heterogeneous residual effect by days in milk on estimating genetic variation. From the results considering heterogeneity of residual variance, variation for lactation performance in the early lactation classes was higher than during the middle classes and variance was lower in the late lactation classes than in the other two classes. The results show that residual effects would not be influenced by days in milk, except during the early and late lactation stage in test-day random regression models. This may be due to feeding management system and physiological property of Holstein cows in Korea. Over classes e6 to e26 (covering 61 to 270 DIM),

there was little change in residual variance, suggesting that a model with homogeneity of variance be used restricting the data to these days only. However, further research should be performed in order to understand properties of the data in the early lactation period before the test-day model can be applied to evaluating genetic performance of dairy cattle in Korea.

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