ESTIMATION OF GENETIC PARAMETERS FOR FIRST LACTATION MILK YIELD OF HOLSTEIN COWS USING RANDOM REGRESSION MODEL

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ABSTRACT

Data used in this study were collected from the Assiout private Farm in Assiout Governorate in the South of Egypt. In total, a data set of 3875 test-day milk yield (TDMY) records for the first lactation of 414 cows daughters of at least 66 sires and 197 dams were available from 1998 till 2004. Data were classified according to the month of calving into four seasons, winter, spring, summer and autumn. The statistical model included year-season, the linear and quadratic order of age, fixed regression, a random additive genetic effect for each animal, a random permanent environmental effect for each cow, and a random residual effect. The incomplete Gamma function (IGF) was chosen to describe the shape of the lactation curve. This function was fitted for each lactation for each cow. DFREML software was used to estimate the components of (co)variance of TDMY in a Random Regression model (RRM). Estimates of the phenotypic, additive genetic and permanent environmental correlations between daily milk yields ranged form 0.07 to 0.68, 0.18 to 0.98 and -0.6 to 0.99, respectively. Estimates of heritability varied from 0.03 for DIM 65 and 275 to 0.14 for DIM 185.

Key words: Random regression model, Genetic parameters, Test-day milk yield, Lactation curve Incomplete Gamma Function

INTRODUCTION

Many factors affect milk production of the cow from one test-day (TD) to the next. It is difficult to model for whole 305-day yields taking into account all such factor (Jamrozik et al 1996). These factors such as, day of the year , management groups, number of records, interval between records and, for each cow, day in milk (DIM), pregnancy status and number of times milking daily. Many models have been described for the analysis of test-day yields by several studies (Wood, 1967 and Wilmink, 1987). Random regression model (RRM) has become a popular choice for the analysis of longitudinal data or repeated records. This analysis is challenging because it requires to the (co)variance structure of the test-day yields (Liu et al 2000).

The goal of the present study was to estimate genetic parameters for first lactation in single trait model with a small data set from a private Holstein dairy farm using random regression with the covariance function technique.

MATERIAL AND METHODS

Data used in this study were collected from the Assiout private farm in Assiout Governorate in the south of Egypt. Most of records used in the analyses were taken on 210 Holstein cows imported from Germany as heifers-in-calf in 1998 and their daughters. In total, a data set of 3875 test-day milk yield (TDMY) records for first lactation of 414 cows daughters of at least[1] 66 sires and 197 dams were available from 1998 till 2004. TD records

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[1] some of the animals had unknown sires

were taken from day 5 until day 305. Data were classified according to the month of calving into four seasons, winter, spring, summer and autumn. The average of TDMY was 10.41 kg with standard deviation of 5.1 kg.

Animals were kept in open yards. Each twenty five cows were joined with a bull for mating. Cows were fed corn silage in summer and alfalfa in winter. Concentrates were provided at a daily rate of 5.5 kg/dry cow, 7.5 kg for freshening non-milked cows and 4 kg for maintenance requirement and 1 kg for each 2 kg milk produced for milking cows. Cows were machine-milked twice a day and the amount of milk was automatically recorded.

The RRM in matrix notation was assumed as follows:

$$\mathbf{Y = Xb + Za + Wp + e,}$$

where, **Y** is the TDMY vector, **b** the fixed effect of year-season, the fixed regression coefficients of TDMY on age at calving and the fixed regression coefficients of TDMY on DIM vector, **a** the random regression coefficients vector, **p** the random permanent environmental effects vector of cows, **X, Z, and W** are the covariables and incidence matrices, and **e** the random residual effects vector. Random effects (a, p and e) are assumed to be normally distributed with mean 0 and variance V where,

$$\mathbf{V} = \mathbf{Var}\begin{bmatrix} \mathbf{a} \\ \mathbf{p} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{G\,\text{Ä}\,A} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{I\,P} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{R} \end{bmatrix},$$

where,

G = Var (α_{j0} α_{j1} α_{j2}), according to Jamrozik *et al.* (1997) i.e. the matrix of additive genetic covariance between RR coefficients, assumed to be homogenous for all animals, while the a_{jm} is the random regression coefficients (m) of TDMY on DIM, **P** the covariance matrix of the permanent environmental effect, **I** is the identity matrix, **A** the matrix of additive genetic numerator relationship between the animals, Ä the Kronecker product function, **and R** a diagonal matrix with elements that depend on DIM where, **R** is estimated for each group of DIM, where each lactation is divided into ten periods within each of them the residual variance matrix is constant for all DIM, so that R has 10 different values on the diagonal. Residual variance was assumed to be constant for each subclass (k) within lactation. The covariance between residuals in TD records on different DIM records was assumed zero in the single trait models for both within and between cows.

In RR model many functions can be used to describe the lactation curve. The only function that met the conditions of the present data and gave full results was the incomplete Gamma function (IGF) which was fitted for each lactation for each cow. According to Wood (1967) this function is:

$$\mathbf{Y_t = a_0 .\, t^{a1} .\, exp^{a2t}}$$

where, $\mathbf{Y_t}$ is TDMY at time t, **exp** refers to the natural exponential function, $\mathbf{a_0}$ the initial MY, $\mathbf{a_1}$ the ascent to peak, $\mathbf{a_2}$ the descent from peak, and a_0, a_1 and a_2 are constants for a given lactation. So, the linear function of the three covariates that describe TDMY at t time is:

$$\mathbf{Ln\ Y_t = ln\ a_0 + a_1\ ln\ t + a_2\ t}$$

DFREML software package (Meyer, 1998) was used to estimate the components of variance and covariance of TDMY in RRM.

In RRM every TDMY is a single trait. So there are many variables to analyze. Multivariate analysis can be used to derive a smaller number of unobservable abstract variables that retain as much of the information in the original variables as possible. The number of the resulting eigenvalues (D) and eigenvectors (E) equals to the number of the observed variables and the sum of these eigenvalues is equal to the total variance. Eigenvalue pattern for genetic and permanent effect may help in determining strategies to alter the shape of the lactation curve.

RESULTS AND DISCUSSION

The three eigenvalues for the additive genetic and permanent environmental covariances for TDMY in the first parity are presented in Table (1) and Figure 1. The first eigenvalues for the additive and permanent environmental effects accounted for 80.99% and 69.58%, respectively. Genetic eigenvalues estimated in this study are smaller as compared to the environmental, thus indicating that changing the shape of lactation curve is more likely to be through environment than genetics. For the genetic part, the first three eigenvalues explained 100% of the variation. Similarly, three eigenvalues were needed to explain the variation for permanent environmental. It seems that three eigenvalues are sufficient to account for the genetic and permanent environmental variations. These results are similar to those of Pool et al (2000).

Table 1. Estimates of eigenvalues for the additive genetic and permanent environmental covariances for TDMYs.

	Eigenvalues		Proportion of total variance (%)		Cumulative proportion of total variance (%)	
	Additive	Permanent	Additive	Permanent	Additive	Permanent
F1[1]	0.046953	0.234380	80.99	69.58	80.99	69.58
F2[1]	0.010678	0.084122	18.42	24.97	99.41	94.55
F3[1]	0.000342	0.018342	0.590	5.45	100.00	100.00

[1] F1, F2 and F3: highest three roots of the additive matrix whose values > zero.

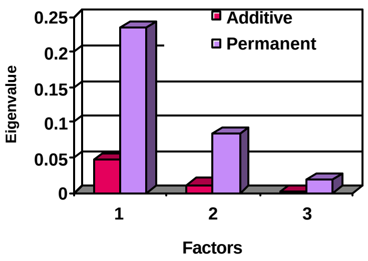

Fig. 1. Estimates of eigenvalues for the additive genetic and permanent environmental effect of TDMY.

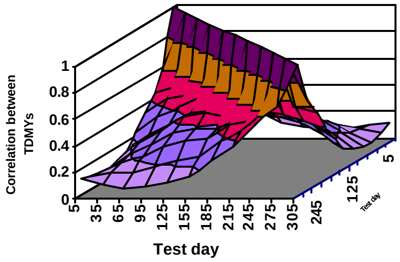

Fig. 2. Phenotypic correlations between TDMYs

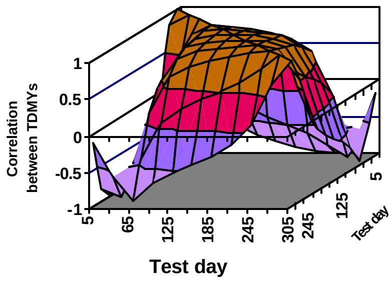

Fig. 3. Genetic correlations between TDMYs.

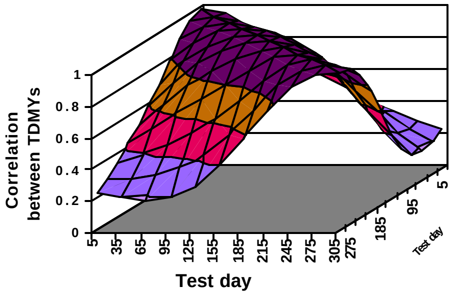

Fig. 4. Permanent environmental correlations between TDMYs.

Table (2) shows estimates of the phenotypic, genetic and permanent environmental correlations between TDMYs. Phenotypic correlations (Figure 2) ranged from 0.07 to 0.68. All estimates of phenotypic correlations were positive. As the interval between days increased, the estimates of phenotypic correlations decreased. White et al (1999) showed that

Table 2. Correlations between TDMYs.

Genetic(above diagonal) and Phenotypic(under diagonal)											
DIM	5	35	65	95	125	155	185	215	245	275	305
5		0.85	-0.1	-0.6	-0.7	-0.8	-0.9	-0.9	-1	-0.8	-0.1
35	0.59		0.46	-0.1	-0.3	-0.4	-0.5	-0.6	-0.8	-1	-0.6
65	0.44	0.49		0.86	0.73	0.64	0.54	0.41	0.2	-0.4	-0.9
95	0.34	0.45	0.48		0.98	0.94	0.9	0.82	0.6	0.1	-0.7
125	0.22	0.35	0.42	0.49		0.99	0.97	0.92	0.8	0.3	-0.5
155	0.14	0.26	0.34	0.42	0.43		0.99	0.96	0.9	0.4	-0.4
185	0.11	0.24	0.33	0.43	0.46	0.43		0.99	0.9	0.5	-0.3
215	0.09	0.19	0.27	0.36	0.39	0.39	0.47		1	0.6	-0.2
245	0.1	0.17	0.22	0.3	0.34	0.35	0.46	0.49		0.8	0.12
275	0.12	0.13	0.15	0.19	0.23	0.26	0.38	0.45	0.6		0.67
305	0.14	0.1	0.07	0.07	0.1	0.15	0.27	0.37	0.6	0.7	
Permanent environmental											
35	0.97										
65	0.9	0.97									
95	0.79	0.91	0.98								
125	0.68	0.83	0.93	0.98							
155	0.59	0.74	0.86	0.94	0.98						
185	0.5	0.64	0.76	0.85	0.92	0.98					
215	0.42	0.52	0.62	0.71	0.8	0.89	0.97				
245	0.35	0.4	0.46	0.53	0.62	0.74	0.86	0.96			
275	0.28	0.28	0.3	0.35	0.44	0.56	0.72	0.87	1		
305	0.24	0.2	0.18	0.2	0.27	0.4	0.58	0.76	0.9	1	

DIM : day in milk, TDMY: test-day milk yield.

Table 4. Estimates of heritability, permanent variances and additive variances for TDMYs.

Parameter	DIM										
	5	35	65	95	125	155	185	215	245	275	305
Heritabilty (h^2)	0.12	0.04	0.03	0.08	0.12	0.11	0.14	0.10	0.07	0.03	0.04
Permanent variances, kg^2	0.23	0.17	0.15	0.13	0.12	0.12	0.12	0.14	0.18	0.26	0.40
Additive variances, kg^2	0.05	0.01	0.01	0.02	0.04	0.05	0.05	0.04	0.02	0.01	0.02

phenotypic correlations declined from 0.76 between adjacent lactation stages to 0.40 between initial and day 255 for the first parity. The estimates of the present study are lower than these of Alnajjar (2001). Estimates of genetic correlations between TDMYs (Figure 3), ranged from -0.98 to 0.99. Liu et al (2000) reported that using the biological lactation curves resulted in negative genetic correlations between the beginning and the end of lactation. Table (4) shows estimates of heritability for TDMY in different DIM. These estimates varied between 0.03 for DIM 65 and DIM 275 to 0.14 for DIM 185. Heritability estimates were generally low for all DIM. Low hertability observed here could be due to the relatively low production as Strabel and Misztal (1999) noticed that lower production, as the case in the present study, usually leads to lower heritabilities. Veerkamp and Goodard (1998) reported heritability average around 0.13 for a herd with an average TDMY around 18 kg which was greater than in this present study. Low heritabilty in the present study could also be due to the small number of selected sires. The pattern of estimates of heritability agreed with those reported by Jamrozik et al (1998), high estimates at the beginning (0.12 at DIM 5) followed by a decrease in the next period, and rising estimates toward the end of lactation.

CONCLUSIONS

The IGF was suitable to describe the lactation curve in dairy cattle under the condition of this study. The lactation curve of the present farm animals could be improved by improving management rather than genetics. Genetic progress could be slow because of low estimates of heritability and of genetic correlations between early and late DIM.

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