Full Length Article

Estimates of Genetic Parameters for Lactation Shape Parameters with Multivariate Statistical Technique in Brown Swiss Cattle

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ABSTRACT

This study was conducted to estimate heritabilities of milk yield traits (305-d milk yield, persistency, peak time & lactation curve shape parameters as per Wood model) and two latent variables from Factor Analysis on the basis of 10 test day (TD) milk yield records. Data on pedigree and 504 production records of 272 Brown Swiss cattle were analyzed to estimate genetic parameters with univariate and bivariate animal models. Factor analysis was fitted to 10 TD milk yield records (assumed as independent measures) in order to define lactation curve shapes and two latent variables (FC1 & FC2) were derived from Factor analysis. Kaiser-Meyer Olkin (KMO) measure of sampling adequacy (0.93) and Bartlett's test of Spherity (P<0.001) were used to determine whether the available data were appropriate for factor analysis. Results suggested that application of factor analysis was an accurate decision to analyze the data. Of the 10 TD milk yield records, first five TD milk records reflected the first part of lactation, FC1, on ascending in milk yield until peak, whereas 6th to 10th TD milk records represented lactation persistency, the second part of lactation, FC2, on descending in milk yield after peak. Heritabilities of 305-d milk yield, a, b, c (lactation shape parameters on Wood model) persistency, peak yield, peak time, FC1 and FC2 were 0.25, 0.14, 0.18, 0.15, 0.29, 0.23, 0.42, 0.13 and 0.15, respectively. Genetic correlations of 305-d milk yield with FC1 and FC2 were 0.66 and unity, respectively. The genetic association of persistency of lactation with peak yield time (0.95) and FC2 (0.23) was observed. Medium to high genetic correlations of FC1 with b parameter (0.33) and peak yield (0.48) were observed in the present study. High genetic correlations among different traits under the study suggested that the scores of two latent (FC1 & FC2) variables, defining lactation curve shape, could be used reliably for genetic improvement in milk yield and peak yield through selection. © 2011 Friends Science Publishers

Key Words: Brown swiss; Factor analysis; Genetic correlation; Persistency; Lactation curve shape

INTRODUCTION

Lactation curve, which is influenced like other quantitative traits by a combined effect of genetic and environmental factors, allows researchers to obtain precious information about profitability of milk yield in dairy production operations. It has been of great interest in increasing the profitable effectiveness of income level per cow in dairy farms. Knowledge on biological parameters of the lactation curve enables animal breeders to realize efficient breeding program. Shape parameters of these curve models such as Wilmink, Wood model and Ali-Schaeffer models comprising two main parts are on increment rate to peak yield of lactation and decline rate of milk yield after peak yield in lactation of a cow. In selection programs, many researchers emphasize the major importance of lactation persistency, which is defined as the cow's capacity

to maintain milk production after peak point in a curve. Cow having more persistent lactation is more advantageous with respect to health and reduction of the feeding costs (Orhan & Kaygisiz, 2002; Guler & Yanar, 2009).

The sires and cows have been evaluated genetically on the basis of 305-day-milk yield, comprising monthly test day records during lactation to improve the selection strategies for genetic improvement in dairy animals (Cilek *et al.,* 2008; Rehman & Khan, 2009). In the context of test day records, mixed linear model has been used routinely in order to estimate variance components of lactation shape parameters. Nowadays, the random regression models have been used commonly for genetic evaluation. These regression models that have big computational difficulties (Macciotta *et al.,* 2006) describe general shape of lactation curve using fixed regression for all cows and the individual genetic deviation from the fixed regressions (Takma &

Akbas, 2009). However, some authors reported that two main factors or latent factors (which are increasing rate of milk yield until peak in early lactation & declining rate of milk yield after peak yield on lactation persistency) from factor and principle component analysis techniques could define lactation curve shape easily (Macciotta *et al.,* 2004 & 2006). Although there were some studies on using factor analysis for different species such as fish, goat and sheep (Keskin *et al.,* 2007a & b; Eyduran *et al.,* 2009; Eyduran *et al.,* 2010); however, published reports on using these analysis techniques for determining lactation shape are few especially for breeding purposes (Macciotta *et al.,* 2004 & 2006). To our knowledge, genetic correlations between Wood model parameters and latent variables from these techniques have not been estimated so far. On the other hand, these latent variables will present valuable information about describing lactation shape parameters.

The present investigation was designed to (a) estimate heritabilities of milk yield, lactation curve shape parameters on Wood model and all the latent variables; (b) describe lactation curve shape (as the increase until peak & persistency) using factor analysis; to estimate genetic correlation between latent variables (factor 1 & 2) and Y max values; between first latent variable and its parameter on increasing rate of Wood model and (c) estimate genetic correlation between second latent variable and its parameter on declining rate of Wood model.

MATERIALS AND METHODS

The data on pedigree and lactation performance records (504) from 1-5 + parities of 272 Brown Swiss cows progeny of 85 bulls maintained at Ulaş State Farm, Sivas, Turkey during the years 1992-2001 were utilized for the present study. The year was divided into four seasons spring (March, April, May), summer (June, July, August), autumn (September, October, November) and winter (December, January, February).

As a routine practice two recordings on milk production one in the morning and one in the evening, were recorded monthly in control milking day. Monthly test-day data were used to model lactation curves for individual lactations, using Wood's equation as given in Lopez-Ordaz *et al.* (2009):

$$Y_n = an^b e^{-cn}$$

Where:

Y_n = Milk production at n^{th} day; a, b and c = are the equations' parameters;

a = is a position factor representing production at the beginning of lactation;

b = is the increasing rate until peak production is reached;

c = is an index of gradual decline from peak production;

e = is the base of the natural logarithms (Ln).

These parameters were estimated via the linear form of equation $Y_n = an^b e^{-cn}$ and the equation can be written as:

$$LN\ Y = ln(a) + b\ ln(n) - cn$$

The 305-d milk yield (MP305) for each lactation was obtained by adding the daily milk yield predicted from the model from day 1 to day 305, with the following equation:

$$PL305 = \sum an^b e^{-cn}$$

Peak milk yield (PMAX) was calculated from $PMAX = a\ (b/c)^b\ e^{(-b)}$. Day at peak production (DPMAX): b/c days after calving. Wood's persistency (PERSW) was:

$$PERSW = -(b+1)\ ln\ (c)$$

In addition, the natural logarithm of PERSW (LNPERSW) was obtained to analyze a variable with a distribution closer to normal.

The lactation persistency was also obtained (PERS), as the percentage of the production at day 305 (Y305) with respect to peak milk production as:

$$(Y305/PMAX) \times 100$$

Variance components were estimated using the following animal model:

$$Y = Xb + Za + e$$

Where;

Y = a vector of the observations, b = a vector of fixed effects (year = (1992-2001); season (spring, summer, autumn, winter); parity (1-5+), a = a vector of animal direct genetic effects, e = a vector of random error.

The variance-covariance structure of the model can be defined as follows:

a_1		$A\sigma^2_{a1}$	$\sigma a_1 a_2$	0	0
a_2	=	$\sigma a_2 a_1$	$A\sigma^2_{a2}$	0	0
e_1		0	0	$I_{n1}\sigma^2 e_1$	$\sigma^2 e_1 e_2$
e_2		0	0	$\sigma^2 e_2 e_1$	$I_{n2}\sigma^2 e_2$

Where

A = the numerator relationship matrix.

$\sigma^2_{a1}, \sigma^2_{a2}$ = direct genetic variance for a trait (milk yield or lactation curve traits).

$\sigma^2_{e1}, \sigma^2_{e2}$ = residual variance effects,

$\sigma a_i a_j$ = direct genetic covariance items between any pair of the traits.

$\sigma e_i e_j$ = all the residual covariance items between any pair of the traits.

The following equation was used to estimate heritability (h^2) for each trait studied:

$$h^2 = [(\sigma^2_A)/(\sigma^2_A + \sigma^2_E)]$$

Where,

σ^2_A is additive direct genetic variance,

σ^2_E is the residual variance.

The mixed model equations (MME) for the best linear

unbiased estimator (BLUE) of estimable functions of b and for the best linear unbiased Prediction (BLUP) of a in matrix notation can be written as follows:

$$\begin{vmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1} \propto^1 \end{vmatrix} \begin{vmatrix} \hat{b} \\ \hat{a} \end{vmatrix} = \begin{vmatrix} X'y \\ Z'y \end{vmatrix}$$

Where, $\alpha_1 = \sigma^2 e / \sigma^2 a$.

Genetic parameters, (co) variance components and genetic parameters of milk yield and lactation curve traits were estimated using MTDFREML software (Boldman *et al.,* 1995). Convergence for the REML solutions was thought to be reached when the variance of function values (-2 log L) in the simplex was less than 10^{-6}. To guarantee that a global maximum was given, analyses were restarted for some other rounds of iterations by results from the earlier round as starting values. When estimates did not change, convergence was verified.

The goal of factor analysis is to reduce a large number of observed variables to a smaller number of factors and to provide an effective definition (regression equation) for an underlying process by observed variables. Factor scores are known to be nearly uncorrelated.

The factor analysis equation can be written in matrix form:

$$Z = \lambda F + \varepsilon$$

Where Z is a px1 vector of variables, λ is a pxm matrix of factor loadings, F is an mx1 vector of factors and ε is a px1 vector of error or residual factors (Sharma, 1996). Due to differences in the units of variables used in factor analysis, the variables were standardized and a correlation matrix of variables was used to obtain eigen values. VARIMAX rotation was used to facilitate interpretation of factor loadings (L_{ik}). Factor coefficients (C_{ik}) were used to acquire factor scores for selected factors (Keskin *et al.,* 2007a & b).

The appropriateness of factor analysis was decided with two criteria; namely, Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy as a measure of homogeneity of variables (Sharma, 1996). A KMO measure of above 0.90 is marvelous level for factor analysis. Additionally, Bartlett's test of sphericity tests whether the correlation matrix is an identity matrix (Keskin *et al.,* 2007a & b).

RESULTS AND DISCUSSION

Descriptive statistics of monthly TD milk yield records on Brown Swiss cattle are depicted as mean ± SE in Table I. TD milk yields from the first TD to the 10th TD ranged from 18.308 to 10.752 kg (Table I).

Table II presents heritabilities and genetic correlations among lactation traits such as lactation curve parameters, peak yield (Ymax), peak yield day (Tmax), 305-d milk yield, latent variables (FC1 & FC2) derived from factor analysis. Variance components computed through REML

method were used to estimate heritabilities of these traits. Heritability estimated for 305-d milk yield in Brown Swiss was 0.25. This estimate was lower than those reported by many workers [Meinert *et al.,*1989 (0.28); Santus *et al.,* 1993 (0.28); Bakir *et al.,* 2004 (0.37); Zulkadir & Aytekin, 2009 (0.28)] by REML method in Brown Swiss cattle and Tuna, (2004) (0.27); Atashi *et al.* (2006) (0.3177); Guler *et al.,* (2010) (0.36) by REML method in Holstein Friesian Cattle, However, it was higher than those reported by Ferris *et al.* (1985) in Holstein cattle (0.16) and Javed *et al.* (2001a & a) in Sahiwal (0.013) and (0.157) in Cholistani cattle, Ahmad *et al.* (2001) in dairy crossbred cattle (0.18) in Pakistan.

Heritability for yield at the beginning of lactation, a parameter of Brown Swiss cattle was 0.14. This estimate was higher than the estimate (0.06) reported by Ferris *et al.* (1985) for the first lactation in Holstein Friesian cattle.

In the present investigation, a heritability estimate for b (ascent to peak) parameter was 0.18, which was higher than the estimate reported (0.07) by Guler *et al.* (2010) in Holstein Friesian cattle. Heritability estimate for c (descent after peak) parameter (0.15) in Brown Swiss cattle was similar to the findings of Ferris *et al.* (1985) for Holstein Friesian cattle in the first lactation. Heritability of persistency of lactation through REML analysis was 0.29 in Brown Swiss cattle, which is higher than the estimates (0.15 & 0.04) reported by Guler *et al.* (2010) and Ferris *et al.* (1985), respectively in Holstein cattle.

In the present study, heritability estimate (0.42) was found for peak time, which was much higher than those reported by Ferris *et al.* (1985) with 0.07 for the first lactation of Holstein cattle and Muir *et al.* (2004) with 0.09 for the first lactation Canadian Holsteins. Heritability of peak time for Brown Swiss cattle was much higher than heritabilities of other lactation traits (Table II). Peak time trait as well as 305-d milk yield, persistency and peak yield time would be considered as an indicator trait for achieving genetic improvement in lactation curve shape. The heritability (0.23) of peak yield in Brown Swiss was similar to the finding of Guler *et al.* (2010), who found heritability of 0.22 for the trait under the study. Heritabilities of FC1 (increase rate) and FC2 (persistency) latent variables, defining lactation curves, from Factor Analysis were 0.13 and 0.15, respectively in Brown Swiss cattle. These results were in agreement with those of Macciotta *et al.* (2006), who found heritability as 0.13 for both latent variables. Differences among previous estimates with heritability estimates obtained in the present study for lactation shape parameters may be due to genetic and environmental factors.

Genetic correlations between 305-d milk yield and persistency, peak time, FC1, FC2 in Brown Swiss were 0.37; - 0.16; 0.66 and 1 respectively. Genetic correlation between persistency and peak yield time was 0.95, whereas it was estimated as 0.48 between peak yield and FC1.

The b (ascent to peak) parameter was positively

Table I: Descriptive statistics of monthly TD milk yield records (kg) for Brown Swiss cattle

	N	Mean ± SE (kg)
1st TD record	504	18.308 ± 0.183
2nd TD record	504	18.451 ± 0.201
3rd TD record	504	18.357 ± 0.201
4th TD record	504	17.773 ± 0.185
5th TD record	504	17.065 ± 0.180
6th TD record	504	15.980 ± 0.178
7th TD record	504	15.034 ± 0.186
8th TD record	504	13.449 ± 0.177
9th TD record	504	11.985 ± 0.164
10th TD record	504	10.752 ± 0.159

Table II: Heritability and genetic correlation estimates on lactation shape curves

	305-d yield	a	b	c	Persistency	Peak Milk Yield (Ymax)	Day at peak yield (Tmax)	FC1	FC2
305-d yield	**0.25**								
a		**0.14**							
b			**0.18**						
c				**0.15**					
Persisteny	0.37				**0.29**				
Ymax						**0.23**			
Tmax	-0.16				0.95		**0.42**		
FC1	0.66	0.33				0.48		**0.13**	
FC2	1		-0.31	0.23					**0.15**

*Heritability estimates (bold) are on diagonal, genetic correlations are below diagonal

Table III: Results of factor analysis for milk yield

Variables	Factor Score Coefficients (c_{ik})		Rotated Factor Loadings (l_{ik}) and Communalities		
	Factor 1	Factor 2	Factor 1	Factor 2	Communality
1st TD record	0.367	-0.217	**0.919**	0.174	0.875
2nd TD record	0.324	-0.162	**0.896**	0.274	0.878
3rd TD record	0.270	-0.104	**0.839**	0.356	0.830
4th TD record	0.205	-0.030	**0.778**	0.470	0.826
5th TD record	0.149	0.028	**0.707**	0.543	0.795
6th TD record	0.021	0.158	0.546	**0.705**	0.795
7th TD record	-0.016	0.194	0.492	**0.742**	0.793
8th TD record	-0.123	0.297	0.336	**0.851**	0.838
9th TD record	-0.168	0.338	0.265	**0.889**	0.860
10th TD record	-0.201	0.356	0.182	**0.871**	0.791
Variance			4.2126	4.0673	8.280
Variance explained (%)			0.421	0.407	0.828

correlated (0.33) with FC1 in Brown Swiss cattle, whereas a positive genetic correlation (0.23) between persistency and FC2 was observed. The high genetic correlations among different traits suggest that lactation shape traits can be improved through selection on the basis of two latent variables as expressed by Macciotta *et al.* (2006). Thus, the latent variables from factor analysis permit us to reach a desirable genetic improvement for milk yield.

Result of factor analysis for milk yield is expressed as factor scores coefficients, rotated factor loadings, and communalities in Table III. Suitability of the available data to factor analysis was determined through two criteria; Kaiser-Meyer Olkin (KMO) measure of sampling adequacy (a marvelous level of 0.93) and Bartlett's test of Spherity (P<0.001). These results showed clearly that the data were the most appropriate for factor analysis. VARIMAX rotation enabled all variables to assign into accurate factors. Thus, 10 TD milk yield records were exposed to Factor analysis in order to define lactation curve shapes in Brown

Swiss cattle. Two latent factors obtained from these 10 TD records were eigen value greater than 1. These two factors explained 82.8% of variance of the current data. The first and second factors accounted for 42.1 and 40.7% of this explained variance. In the present study, percent of the explained variance (82.8%) in Brown Swiss cattle was almost similar to that variance (80%) reported by Macciotta *et al.* (2006), working on Simmental cattle, but lower (86%) than the findings of Macciotta *et al.* (2004) on the explained variance for Simmental cattle. These differences may have resulted from various numbers of TD milk records, and environmental and genetic factors. As reported by Macciotta *et al.* (2006) in Simmental cattle, it could be suggested that these two factors characterized all lactations with the first latent factor on the amount of milk production in early lactation (ascending rate until peak yield) and in the second factor on persistency (descending rate after peak). The first latent factor was highly-positively correlated with 1 to 5 TD milk records ranging from 0.707 to 0.919, whereas the

second latent factor was highly-positive correlated with 6-10 TD milk records varying from 0.705 to 0.889. In other words, 1st to 5th TD milk records defined the first part of lactation, on increasing rate in milk yield until peak, while 6th to 10th TD milk records represented lactation persistency, the second part of lactation, on declining rate in milk yield after peak. Communality scores for each TD milk record were higher. For instance, communality score of the first TD milk record was 0.875, which was explained by the first and second factors (Table III).

CONCLUSION

Moderate to high heritability estimates for different lactation curve shape parameters suggest that these traits can be included in selection schemes. However, more studies are required on other breeds of exotic and indigenous cattle to generalize these results. Also high genetic correlations between FC1 and FC2 with other traits under study "(persistency and 305 d milk yield)" suggested that selection on the basis of these parameters will bring improvement in other traits as correlated response.

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