



Estimation of Genetic Parameters for First Lactation Monthly Test-day Milk Yields using Random Regression Test Day Model in Karan Fries Cattle

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ABSTRACT: A single trait linear mixed random regression test-day model was applied for the first time for analyzing the first lactation monthly test-day milk yield records in Karan Fries cattle. The test-day milk yield data was modeled using a random regression model (RRM) considering different order of Legendre polynomial for the additive genetic effect (4th order) and the permanent environmental effect (5th order). Data pertaining to 1,583 lactation records spread over a period of 30 years were recorded and analyzed in the study. The variance component, heritability and genetic correlations among test-day milk yields were estimated using RRM. RRM heritability estimates of test-day milk yield varied from 0.11 to 0.22 in different test-day records. The estimates of genetic correlations between different test-day milk yields ranged 0.01 (test-day 1 [TD-1] and TD-11) to 0.99 (TD-4 and TD-5). The magnitudes of genetic correlations between test-day milk yields decreased as the interval between test-days increased and adjacent test-day had higher correlations. Additive genetic and permanent environment variances were higher for test-day milk yields at both ends of lactation. The residual variance was observed to be lower than the permanent environment variance for all the test-day milk yields. (**Key Words:** Test-day Milk Yield, Random Regression Model, Heritability, Genetic Correlation, Karan Fries Cattle)

INTRODUCTION

Main objective of any breed improvement program is the selection of superior sires and dams at the earliest to bring about faster genetic improvement. The investigations conducted on genetic improvement of cattle around the world indicate that the proper genetic evaluation and selection of bulls brings about nearly 68 to 75 percent of realized genetic improvement. In India, the genetic evaluation of dairy animals is done mainly on the basis of 305 days or less first lactation milk yield. This leads to increased generation interval, decreased genetic gain per unit of time and fewer number of daughters per sire due to smaller herd size. In recent years, the interest in use of test-day milk yields (morning and evening measurement of milk of a test-day) for genetic evaluation of dairy animals instead of recording 305 days milk yield has gained considerable

importance (Jamrozik and Schaeffer, 1997; Schaeffer et al., 2000; Togashi and Lin, 2004; Kokate et al., 2013). A test-day model (TDM) is a statistical procedure which considers all genetic and environmental effects directly on a test-day basis (Swalve, 1995). Use of test-day (TD) records, reduces the cost of milk recording, early evaluation of dairy animals leading to higher genetic gain and increases accuracy and intensity of selection as more number of records per animal rather than the only single 305 days milk yield measurement are available. Now a days' random regression models (RRM) have been used for the genetic analysis of test-day milk yields as lactation curve varies from cattle to cattle. Use of RRM allows the shape of the lactation curve to differ for each animal by inclusion of random regression coefficients for each animal. RRM is used for the measurement of longitudinal data on individual over time measured on trajectory. These models provide a continuous treatment of observation over time and are able to incorporate heterogeneous variances and covariances along time (Schaeffer and Dekkers, 1994; Lidauer et al., 2003). Contribution of crossbred cattle to total cow milk produced in India is 54% (31.07 million tonnes) which is more than

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the milk produce from indigenous cattle viz. 26.69 million tonnes (46%) as per BAHS (2013). Karan Fries is a crossbred cattle developed at National Dairy Research Institute, Karnal in India using Tharparkar as a Zebu (*Bos indicus*) and Holstein Friesian as exotic (*Bos taurus*) cattle in the year 1980. The level of inheritance of Friesian cattle in Karan Fries is 50% to 75% (Gurnani et al., 1986). For maintaining high level of milk production/productivity of Karan Fries cattle and their further improvement, it is necessary to execute proper program of genetic evaluation of males and females for selection of animals of high genetic merit. So, there is a need to estimate the genetic parameters of test-day milk yields using RRM for genetic evaluation of dairy cattle. Genetic parameters like heritability and genetic correlations among test-day milk yields have been estimated in different *Bos taurus* breeds (Swalve, 1995; Rekaya et al., 1999; Kettunen et al., 2000; Faro et al., 2008; Elahi Torshizi et al., 2012). However, no literature is available regarding estimation of genetic parameters for monthly test-day milk yields (MTDMY) using RRM in Karan Fries cattle. The objective of this investigation was to estimate the genetic parameters for first lactation monthly test-day milk yields using RRM in Karan Fries cattle.

MATERIALS AND METHODS

Data structure

In this investigation, data were collected from the history-cum-pedigree sheets and daily milk yield record registers of Karan Fries cattle maintained at Dairy Cattle Breeding Division of ICAR-National Dairy Research Institute, Karnal. Cows were milked by machine milking, three times a day and all animals are stall-fed and nutritional requirements are met through a balanced ration of green and dry fodder along with suitable roughages and concentrate. All animals of this breed are bred artificially and weaned at calving. Total 16,184 MTDMY records were analyzed from 1,583 Karan Fries cattle sired by 130 bulls during 1983 to 2012. Test-day milk yield records were taken at monthly intervals starting from day 6th of lactation (TD1) to 305th day (TD11). Bulls with 5 or more progenies were considered for the present study. Lactation yields shorter than 100 days and less than 800 kg were excluded from the study. Abnormal records like culling in the mid lactation, still birth, abortion, dystocia or any other pathological problems which affected the lactation yield were considered as abnormalities and were not taken for the present investigation. Each year was classified into 4 calving seasons—winter (December to March); summer (April to June); Rainy (July to September); and autumn (October to November). The data spread over 30 years duration (1983 through 2012) were classified into total 5

periods of calving of 6 year each. Age at first calving was classified into 11 groups at an interval of 60 days (≤ 800 , 801 to 860, 861 to 920, ..., ≥ 1341).

Model

A single trait linear mixed random regression test-day model (RR-TDM) was applied to MTDMY records of Karan Fries cattle for first lactation. The test-day milk yield data was modeled using a RRM considering different order of Legendre polynomial (LP) for the additive genetic effect (4th order) and the permanent environmental effect (5th order). The RRM used in the analysis was represented as:

$$y = Xb + Za + Wp + e$$

where, y = vector of test-day milk yields of cattle; b = vector of fixed effects (season, period, and age groups); X = incidence matrix relating test-day milk yields to fixed effects; p = vector of permanent environmental random regression coefficients; a = vector of additive genetic random regression coefficients; e = vector of random residual effects associated with Y ; Z and W are covariate matrices for 'a' and 'p' respectively with the assumption,

$$\begin{bmatrix} a \\ p \\ e \end{bmatrix} \sim N(0, V) \text{ and } V = \begin{bmatrix} G * A & 0 & 0 \\ 0 & I * P & 0 \\ 0 & 0 & R \end{bmatrix}$$

where, G and P are variance—covariance matrix of additive genetic and permanent environment random regression coefficients; A is additive genetic relationship matrix among the animals; $*$ is Kronecker product function; I is identity matrix and R is diagonal matrix of homogenous residual variances.

The mixed model equation for this model would be:

$$\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + G^{-1} * A^{-1} & Z'W \\ W'X & W'Z & W'W + I * P^{-1} \end{bmatrix} \begin{bmatrix} b \\ a \\ p \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}$$

Function used in random regression model

A common choice for the basic function is orthogonal polynomials, as advocated by Kirkpatrick and Heckman (1989). In particular, the LP have been used extensively in random regression analysis. Kirkpatrick et al. (1990) proposed the use of covariance function (CF) for longitudinal data of this kind. A CF is a way to model the variances and covariances of a longitudinal trait. Orthogonal polynomials were used in this model and the best order of fit was chosen.

To calculate LP, first define; $P_{0(x)} = 1$, and $P_{1(x)} = x$. Then, in general, the $n+1$ polynomial is described by the following recursive equation:

$$p_{n+1}(x) = \frac{1}{n+1} [(2n+1)xp_n(x) - np_{n-1}(x)]$$

These quantities were normalized using:

$$\phi_n(x) = \left(\frac{2n+1}{2}\right)^{0.5} P_n(x)$$

where, n is the order of the polynomials. Test-day records in the interval 6 to 305 t_i days were standardized to the interval -1 to $+1$ with the following formula:

$$\alpha_i = -1 + 2 \left(\frac{t_i - t_{min}}{t_{max} - t_{min}} \right)$$

where, t_{min} and t_{max} were the earliest and latest age represented in data (Schaeffer, 2004). Legendre Polynomial was defined within the range of values from -1 to $+1$.

Estimation of genetic parameters and (co) variances

The genetic parameters such as heritability of test-day milk yields and genetic correlations between test-day records were estimated using the genetic (co)variances, permanent environmental (co)variances and homogeneous residual variances of test-day milk yields as per the procedures given by Jamrozik and Schaeffer (1997). The genetic variances of test-day milk yields at different test-days (6, 35...275, and 305) was estimated using the covariates of LP function as $\sigma_{a(i)}^2 = z_i'Gz_i$. The estimate of genetic covariance between test-day milk yields on day i and j is $\sigma_{a(ij)}^2 = z_i'Gz_j$ where G is additive genetic variance covariance matrix. The permanent environmental variance of test-day milk yields was estimated as $\sigma_{pe(i)}^2 = z_i'Pz_i$ and permanent environmental covariance is calculated as $\sigma_{pe(ij)}^2 = z_i'Pz_j$ where, P is permanent environmental variance covariance matrix. A mixed model analysis was carried out to obtain restricted maximum likelihood estimate of covariance components using WOMBAT software (University Of New England, Armidale, NSW, Australia) (Meyer, 2010).

The heritability and genetic correlations among different test-day milk yield records in first lactation were estimated as described by Jamrozik and Schaeffer (1997) as follows:

$$h_{(i)}^2 = \frac{\sigma_{a(i)}^2}{\sigma_{a(i)}^2 + \sigma_{pe(i)}^2 + \sigma_{e(i)}^2}$$

where $h_{(i)}^2$ is the heritability of; $\sigma_{a(i)}^2$ is the additive

genetic variance on i^{th} TD milk yield; $\sigma_{pe(i)}^2$ is the permanent environmental variance and $\sigma_{e(i)}^2$ is the homogeneous residual variance on i^{th} TD milk yield. The genetic correlations among different MTDMY were calculated from the analysis of variance and covariance among test-day milk yields. The Variance components for different test day milk yields were also estimated using Harvey's LSMLMW software (Ohio State University, Columbus, OH, USA) (Harvey, 1990) designed for complete mixed model analysis. In analysis the fixed effect of year and season of calving, age at calving and random effect of sires on phenotypes of test-day milk yield in cows in first lactation were considered. Heritability was estimated using paternal half sib method.

Genetic correlation (r_g):

$$r_{gij} = \frac{\sigma_{aij}}{\sqrt{\sigma_{ai}^2 \sigma_{aj}^2}}$$

where r_{gij} is the genetic correlation between milk yields on TD i and j ; σ_{aij} is the genetic covariance between milk yields on TD i and j ; σ_{ai}^2 is the additive genetic variance on i^{th} TD yield and σ_{aj}^2 is the additive genetic variance in j^{th} TD yield.

RESULTS AND DISCUSSION

Random regression coefficients

Different RRM were fitted and on the basis of Akaike information criterion, Bayesian information criterion, and mean square error values best model were identified (Table 1). The RRM with fourth order LP for additive genetic effect and fifth order LP for modeling permanent environment effect had lower Bayesian information criterion values and lower mean square error compared to other models. Therefore, on fitting best RR-TDM to MTDMY records by using LP, fifteen regression coefficients were estimated for each cattle viz. six fixed regression coefficients which were same for all cattle within a season-period-age groups, four additive genetic random regression coefficients ($A_0, A_1, A_2,$ and A_3) and five permanent environmental random regression coefficients ($P_0, P_1, P_2, P_3,$ and P_4). The estimated variances (a_i, a_i) and

Table 1. Description of different random regression model fitted

Model	K_a	K_p	$-2 \log L$	BIC	MSE
LP 33	3	3	44,068	44,193.97	6.718
LP 44	4	4	42,735.40	42,938.61	5.31036
LP 45	4	5	42,213.22	42,464.81	4.6714
LP55	5	5	42,193.00	42,493.00	4.6706

LP, Legendre polynomial; K_a , order of fit for additive genetic effect; K_p , order of fit for permanent environmental effect; BIC, Bayesian information criterion; MSE, mean square error.

Table 2. Estimates of variances and covariances among additive genetic random regression coefficients of test day milk yields using Legendre polynomial of order 4

	A0	A1	A2	A3
A0	3.088			
A1	0.376	0.415		
A2	-0.498	-0.219	0.215	
A3	0.268	0.047	-0.065	0.027

covariances (a_i, a_j) among the additive genetic and permanent environment random regression coefficients using LP in first lactation of Karan Fries cattle have depicted in Table 2 and 3. Eigen values represent the amount of variation explained by the corresponding eigen function (Kirkpatrick et al., 1990). First three eigen values 3.26 (86.89%), 0.43 (11.57%), and 0.06 (1.54%) of the additive genetic CF accounted for at least 99% of the sum of all eigen values but the first four eigenvalues 8.77 (64.61%), 2.99 (22.04%), 1.31 (9.64%), and 0.42 (3.08%) for permanent environment effect accounted 99% of total variation. It showed that the three main eigen values and associated eigen function explained the most of the additive genetic and permanent environmental effect variance and little variation was associated to other eigen values for additive genetic effects and permanent environment effects. The size of the first eigen values indicated that selection based on this would result in quick change in average milk yield. Similar result was reported by Elahi Torshizi et al. (2012) who reported the first three eigen values 14.11 (93.44%), 0.62 (4.10%), and 0.37 (2.45%) for additive genetic effect and first three eigen values 16.17 (93.43%), 0.65 (3.74%), and 0.36 (2.05%) for permanent environment effects using 3rd order of LP.

Variances of test-day milk yields

The variances (additive genetic, permanent environment and residual) of different test-day milk yields were

Table 3. Estimates of variances and covariances among permanent environment random regression coefficients of test day milk yields using Legendre polynomial of order 5

	P0	P1	P2	P3	P4
P0	8.682				
P1	-0.475	2.639			
P2	-0.425	0.326	1.310		
P3	0.252	-0.896	-0.090	0.675	
P4	-0.272	0.082	-0.239	-0.211	0.264

estimated using variance-covariances structure among random regression coefficients and covariate of the functions used in RR-TDM. The residual variance was assumed constant for all MTDMY in the lactation. The additive genetic (V_A), permanent environment (VE_p) phenotypic variance and residual variances estimated for first lactation of Karan Fries cattle using LP are presented in Table 4. Perusal of the table showed that the highest V_A was observed for the TD-6 (2.24 kg²) and the lowest was observed for TD-2 (1.30 kg²). In general, V_A increased up to TD-6; thereafter a gradual decline was noticed till the end of lactation and became higher for TD-11. The residual variance (2.34 kg²) was observed higher than additive genetic variance (2.23 kg²). The VE_p was observed higher for TD-1 (8.32 kg²) and lower (5.6 kg²) for TD-7. It was revealed from the results that the magnitude of VE_p was higher in initial test-days (TD-1 to TD-3) and decreased thereafter with a slight increase at the end of lactation. The magnitude of VE_p and V_A seemed to have inverse relationship across the trajectory of lactation curve estimated by RR-TDM. The magnitude of VE_p was higher in the beginning and end of lactation and relatively lower in the mid-lactation. Contrarily, the magnitude of V_A was lower in the beginning and end of lactation and relatively higher in the mid-lactation. The residual variance was observed to be lower than the permanent environment variance for all the test-day milk yields. Geetha et al. (2007)

Table 4. Additive genetic, permanent environment and phenotypic variance (kg²) and temporary environment of monthly test day milk yields using random regression method

Test-day	Additive genetic variance		Permanent Environ. variance		Phenotypic variance		Temporary Environ. variance
	V_A	SE	VE_p	SE	V_p	SE	VE_T
TD1	1.77	0.52	8.32	0.56	12.44	0.46	2.34
TD2	1.30	0.37	7.46	0.44	11.10	0.37	2.34
TD3	1.55	0.41	8.53	0.49	12.43	0.42	2.34
TD4	1.95	0.46	7.63	0.47	11.92	0.40	2.34
TD5	2.19	0.46	6.42	0.43	10.95	0.37	2.34
TD6	2.24	0.45	5.80	0.40	10.37	0.35	2.34
TD7	2.12	0.43	5.60	0.39	10.06	0.34	2.34
TD8	1.94	0.43	5.76	0.40	10.04	0.34	2.34
TD9	1.81	0.43	6.43	0.44	10.57	0.37	2.34
TD10	1.80	0.45	7.10	0.48	11.24	0.40	2.34
TD11	2.02	0.58	6.96	0.62	11.32	0.50	2.34

reported that V_A of test-day milk yields increased at the end of lactation for first lactation milk yield in Murrah buffaloes. Jamrozik et al. (1997) reported higher magnitude of V_A and VE_p over residual variances for first lactation test-day milk yield records of Holstein cows. It was revealed from Figure 1 that the magnitude of additive genetic and permanent environment variances were higher for test-day milk yields at both ends of lactation compared to test-day milk yields in mid lactation. Roose et al. (2004) reported that the additive genetic and permanent environmental variances for test-day milk yields were higher at both ends of lactation using LP function in second and third parity of dairy cattle in the Netherlands.

Heritability estimates of test-day milk yields

The additive genetic, permanent environmental and residual variances were utilized to estimate the heritability of MTDMY records using LP function for Karan Fries cattle. Low heritability estimates by RR-TDM in comparison to paternal half sib model were observed for monthly test day milk yields are presented in Table 5. Heritability estimates for MTDMY obtained with RR-TDM ranged from 0.22 (TD-6) to 0.11 (TD-2). It was revealed that on TD-1 heritability was higher than on TD-2. Thereafter, heritability increased up to TD-6, then declined and again increased towards the end of lactation. Higher estimates of heritability during initial lactation days were also reported by many workers (Jamrozik and Schaeffer, 1997; Kettunen et al., 1998; Bignardi et al., 2009). The heritability estimates 0.20 (TD-5), 0.22 (TD-6), and 0.21 (TD-7) of MTDMY were higher in the mid-lactation compared to early and late lactation due to higher additive genetic variance in this segment of lactation curve. Similar estimates of heritability for test day milk yields by RRM were reported by many researchers (Meyer et al., 1989; Brotherstone et al., 2000; Mayeres et al., 2004; Elahi Torshizi et al., 2012) in different cattle breeds.

Table 5. Estimates of heritability for monthly test-day milk yields by random regression test day model and paternal half sib method

Test day	$h^2 \pm SE$ (RR-TDM)	$h^2 \pm SE$ (LSML)
TD1	0.14±0.04	0.14±0.05
TD2	0.11±0.03	0.20±0.06
TD3	0.12±0.03	0.26±0.07
TD4	0.16±0.03	0.17±0.06
TD5	0.20±0.04	0.23±0.06
TD6	0.22±0.04	0.34±0.07
TD7	0.21±0.04	0.27±0.07
TD8	0.19±0.04	0.21±0.06
TD9	0.17±0.04	0.22±0.06
TD10	0.16±0.03	0.21±0.06
TD11	0.18±0.04	0.11±0.05

SE, standard error; RR-TDM, random regression test-day model; LSML, least squares maximum likelihood.

Genetic and permanent environment correlations between test-day milk yields

The genetic and permanent environment correlations between different test-day milk yields were estimated based on the genetic and permanent environmental variance and covariances using LP (Table 6). The estimates of genetic correlations between different test-day milk yields ranged 0.01 (TD-1 and TD-11) to 0.99 (TD-4 and TD-5). It was observed that the genetic correlation estimates of first test-day milk yield (TD-1) with TD-7 and onwards were negative (-0.05 to 0.04) and with last test day i.e. TD-11 was positive (0.01). It was revealed from the results that the magnitudes of genetic correlations between test-day milk yields decreased as the interval between test-days increased and adjacent test-day had higher correlations. Other authors have reported the same trend, with positive estimates that are higher between adjacent test-days (Rekaya et al., 1999; Kettunen et al., 2000; Lidauer et al., 2003; Geetha et al., 2006; Cobuci et al., 2011; Elahi Torshizi et al., 2012). The estimates of permanent environment correlations of all

Table 6. Genetic (below diagonals) and permanent environment correlations (above diagonals) among monthly test day milk yields estimated using RR-TDM

Test day	TD1	TD2	TD3	TD4	TD5	TD6	TD7	TD8	TD9	TD10	TD11
TD1	1	0.69	0.45	0.39	0.40	0.42	0.43	0.42	0.39	0.37	0.42
TD2	0.82	1	0.94	0.86	0.73	0.56	0.42	0.36	0.35	0.37	0.39
TD3	0.49	0.89	1	0.96	0.84	0.65	0.47	0.35	0.30	0.29	0.28
TD4	0.25	0.75	0.96	1	0.94	0.8	0.62	0.46	0.33	0.27	0.23
TD5	0.10	0.63	0.91	0.99	1	0.94	0.80	0.63	0.44	0.308	0.24
TD6	0.004	0.55	0.86	0.96	0.99	1	0.94	0.80	0.60	0.41	0.31
TD7	-0.05	0.50	0.82	0.94	0.98	0.99	1	0.94	0.78	0.60	0.44
TD8	-0.08	0.46	0.79	0.91	0.96	0.98	0.99	1	0.94	0.80	0.62
TD9	-0.08	0.44	0.77	0.89	0.94	0.96	0.98	0.99	1	0.95	0.79
TD10	-0.04	0.46	0.76	0.87	0.92	0.94	0.96	0.98	0.99	1	0.91
TD11	0.01	0.5	0.77	0.87	0.91	0.93	0.95	0.96	0.98	0.99	1

RR-TDM, random regression test-day model.

MTDMY ranged from 0.23 to 0.96. Similar trend were reported by Kettunen et al. (1998) and Zavadilova et al. (2005) using RR-TDM in Finish Ayrshire and Czech Holstein cattle respectively.

In conclusion, the TDM can be used in future for the analysis of test-day milk yield records of Karan Fries cattle instead of using 305 day lactation milk yield resulting in early and high genetic gain, high intensity and accuracy of selection. This paper discussed the use of RRM for the estimation of genetic parameters for first lactation MTDMY. The heritability estimates of MTDMY were higher in the mid-lactation compared to early and late lactation due to higher additive genetic variance observed in this segment of lactation curve. The estimates of heritability by RR-TDM were in general, lower than least squares maximum likelihood (LSML) but were more precise due to lower standard errors. The magnitudes of genetic correlations between adjacent test-day milk yields were higher for mid lactation and decreased as the interval between test-days increased. There is an inverse relationship between the VE_P and V_A across the trajectory of lactation curve estimated by RR-TDM. The VE_P has a higher magnitude in the beginning and at the end of lactation and relatively lower value in the mid-lactation while the V_A shows the reverse trend. Thus, RRM allows an animal to be evaluated on the basis of only single test-day or on any number of test-day records. However, because of technical complexity of RR-TDM, these are not much in use in India and proposed for the first time for the analysis of test-day milk yield records in Karan Fries cattle.

CONFLICT OF INTEREST

We certify that there is no conflict of interest with any financial organization regarding the material discussed in the manuscript.

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