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Simple Summary: The milk production performance of Jersey crossbred cattle under farmers' rearing environment in the state of Tamil Nadu, Southern India, is evaluated genetically from the monthly test-day milk yields. Genetic parameters *viz.*, heritability and genetic correlation were estimated for test-day milk yields, total milk yield and 305-day milk yield to assess whether the improvement of these traits could be made through selective breeding. The overall means of various test-day milk yields ranged between 4.98 to 9.95 kg and the mean total milk yield and 305-day milk yield were 2480.33 and 2393.71 kg respectively. The performance of Jersey crossbred cattle found in the present study indicates the suitability of the crossbreds in the State. The desirable genetic parameters observed in the study revealed an ample scope for improving milk production traits by selection. Moreover, the early and mid-lactation test-day milk yields could be favorably used for the early selection of cows under the farmers' rearing environment to improve total milk production.

Abstract: Tamil Nadu, a state in southern India, is bereft of any native milch or dual-purpose cattle breed and the state depends chiefly on crossbred cattle for milk production. As most (90 percent) of the milk production in the state was contributed by Jersey crossbred cattle, the genetic evaluation study was intended to assess the milk production traits *viz.*, test-day milk yields (TDMYs), total milk yield (TMY) and 305-day milk yield (305MY) in these crossbred cattle reared under farmers' rearing environment. Data on monthly TDMYs (TDMY1 to TDMY10) of Jersey crossbred cows (n=81,653) reared by the farmers over 24 years (1999-2022) were collected for evaluation. The influence of non-genetic factors *viz.*, location (agroclimatic zones), period and season of calving, and parity on TDMYs, TMY, and 305MY were assessed, and the variance and covariance components for genetic parameters (heritability and genetic correlation) of the traits were estimated by the method of restricted maximum likelihood (REML) under multivariate animal model and by random regression model (RRM). The overall means of various TDMYs ranged from 4.98 (TDMY10) to 9.95 kg (TDMY2) and, for TMY and 305MY the means were 2480.33 and 2393.71 kg respectively. The heritabilities estimated by animal model for TDMYs were high and ranged from 0.39 ± 0.01 to 0.47 ± 0.01 and were fairly less variable throughout the lactation while the estimates obtained by RRM were medium to high and ranged between 0.28 ± 0.01 and 0.65 ± 0.02 for different days in milk (DIMs). The heritability estimated for TMY and 305MY were 0.48 ± 0.01 and 0.49 ± 0.01 respectively.

The estimates of heritability in mid-lactation yields were comparatively little less than those at the beginning and the end of lactation. The high estimates of heritabilities for TDMYs, TMY, and 305MY obtained in the present study offered an ample scope for improving milk production through selective breeding. Genetic correlations between TDMYs estimated by animal model were positive and moderate to high, with a range between 0.47 ± 0.01 and 0.99 ± 0.00. Considerably higher estimates (0.97-0.99) were observed between adjacent TDMYs showing strong genetic associations. By RRM, genetic correlations estimated between DIMs were positive, except for a few estimates and the magnitude of genetic correlation decreased with an increase in the interval between the DIMs. The high genetic correlation observed between the TDMYs in early and mid stages of lactation with TMY and 305MY suggested that these test day yields could be used favorably for the early selection of cows for milk production which facilitates reduction in the generation interval and consequently increase the annual genetic gain for the milk production traits.

Keywords: Jersey crossbred cattle; genetic correlation; heritability; random regression; REML; test day milk yield

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1. Introduction

Tamil Nadu, a state in the southernmost part of India, is bereft of any native milch or dual-purpose cattle breed and the state depends chiefly on crossbred cattle for milk production. Out of the estimated milk production of Tamil Nadu (10.10 million tonnes as of 2021-22), about 90 percent was contributed by Jersey crossbred cattle [1]. The breeding policy of the state advocatesJersey as the breed of choice for crossing non-descript cows in the plains of the state with the level of exotic inheritance restricted to 50 percent for improving milk production because of its adaptability and thus, Jersey crossbred cattle is being widely reared.

The genetic evaluation of milk production is a demanding task in terms of time and expenses, especially under farmers' production conditions. As recording daily milk yields of a lactation is invariably difficult and expensive under such conditions, test-day milk yield (TDMY) in monthly intervals have been successfully used [2,3] to arrive at total milk yield (TMY) and 305-day milk yield (305MY) in dairy evaluations. The genetic evaluation employing TDMY records may be better than the evaluation based on the calculated TMY and 305MY. The use of TDMYs maximizes the amount of information gathered for each animal and improves the accuracy of genetic evaluation [4]. Further, more environmental variation could be removed from the phenotypic observations by considering the effects acting on TDMYs that could not be considered when modeling TMY and 305MY [5]. Besides, the available reports also narrated that selection based on some TDMYs was as efficient as on all TDMYs [6,7]. The selection based on early TDMYs would result in a reduction in generation interval, decrease in cost of milk recording, and facilitate early culling of cows and bulls with low breeding values. [8,9].

The genetic evaluation for milk production involves the assessment of the effects of non-genetic factors and the estimation of variance and covariance components for genetic parameters *viz.* heritability of the traits and genetic correlation between the traits. The use of accurate models in genetic analysis and precise estimation of genetic parameters contribute to increased efficiency of selection programs for the improvement of milk production. Among the various genetic evaluation methods, the Restricted Maximum Likelihood (REML) method with animal model is the commonly employed method to estimate variance components considering fixed and random effects simultaneously [10,11]. Nevertheless, the Random Regression Model (RRM) is an alternative approach for genetic evaluation of longitudinal trait like milk yield by considering the nature of the data having measures repeated over intervals (TDMYs) in addition to the estimation of both fixed and random effects simultaneously [12]. In RRM, the regression coefficient for each animal is estimated and the orthogonal Legendre polynomials are used popularly to fit random curves due to their ability to describe the variation along the lactation, better convergence and being normalized.

When both the additive genetic and permanent environmental components are modeled by Legendre polynomial coefficients over time, the estimate of variance components becomes more accurate [13].

The genetic evaluation of performance for milk production under farmers' conditions of rearing will be helpful to assess the performance as well as to identify the ways and means to improve its potential. Such genetic evaluation studies on milk production of crossbred Jersey cattle under the farmers' production system in Tamil Nadu are scanty. Hence, the present study was intended to assess genetically the milk production traits *viz*., TDMYs, TMY, and 305MY by estimating the variance and covariance components and genetic parameters (heritability and genetic correlation) in Jersey crossbred cattle under farmers' production system in Tamil Nadu.

2. Materials and Methods

Records on monthly test day milk yields of 81,653 Jersey crossbred cows, covering a period of 24 years from 1999 to 2022 were obtained from the field performance recording programme of Tamil Nadu Co-operative Milk Producers' Federation of Tamil Nadu.Under the farmers' production system, the test day milk yields were recorded from several herds and the herd size was invariably small. The crossbreds studied had about 50 per cent of Jersey inheritance and the remaining being from non-descripts or a mixture of non-descript and indigenous milch breeds.A test-day milk yield (TDMY) is the quantity of milk produced by a cow over 24 hours. The traits considered were 10 monthly test-day milk yield records (TDMY1 to TDMY10) obtained between day 5 to day 305 of lactation. The milk yields that were less than 50 percent of the previous TDMY and the values beyond three standard deviations from the mean) for each test day yield was excluded from the analyses as outliers. The TMY and 305MY were computed from the TDMYs by the Test Interval method as recommended by the International Committee for Animal Recording [14].

The data was subjected initially to descriptive analysis and then the method of least squares under General Linear Model (GLM) for the milk yield traits was carried out by the IBM SPSS Statistics package [15] to assess the effect of fixed factors. The fixed factors considered were agroclimatic zones (North Eastern, North Western, Western, Cauvery Delta, and Southern zones); period of calving (six periods of 4 years each); season of calving [Summer (Mar-May), Southwest monsoon (Jun-Sep), Northeast monsoon (Oct-Dec) and Winter (Jan-Feb)], and parity (1st, 2nd, 3rd, 4th, 5thand above 5th). The pedigree detailsand data structure of performance records of Jersey crossbred cows are given in Tables 1 and 2 respectively.

Table 1. Pedigree details of Jersey crossbred cows under farmers' production system.

Total number of animals	82406
Number of sires with progeny record	505
Number of animals with known sire	29793
Average number of progeny per sire	58.96
Number of animals with known dam	14368
Number of animals with unknown dam	68038
Number of dams with progeny record	11923

Table 2. Data structure of performance records of Jersey crossbred cowsunder farmers' production system.

Fixed factor	Sub-class	No. of records
Agro-climatic zone	North Eastern	32787
	North Western	18328
	Western	27216

	Cauvery Delta	3674
	Southern	803
Period of calving	Period 1 (1999 to 2003)	435
	Period 2 (2004 to 2007)	2046
	Period 3 (2008 to 2011)	2981
	Period 4 (2012 to 2015)	26772
	Period 5 (2016 to 2019)	32489
	Period 6 (2020 to 2022)	18085
Season of calving	Winter	14105
	Summer	24231
	Southwest Monsoon	26485
	Northeast Monsoon	17987
Parity	First	39098
	Second	16926
	Third	12757
	Fourth	7837
	Fifth	3915
	Above fifth	2275

Multivariate analysis of TDMY data, total milk yield (TMY), and 305-day milk yield (305MY) was carried out by fitting animal model to estimate the variance and covariance components for heritability, genetic, and phenotypic correlations. All the fixed non-genetic factors were found as significant ($P \leq 0.05$) sources of variation under GLM, and hence, all the fixed factors (fixed effects) and direct animal genetic effect (random effect) were included in the multivariate analysis.The mixed model for single trait analysis used in the present study is given below:

$$Y_{ijklm} = \mu + C_i + P_j + S_k + N_l + A_n + e_{ijklm}$$

where, Y_{ijklm} is mth observation in ith zone, jth period and kth season and lth parity, μ is the overall mean, $C_i$is the effect of ithagro-climatic zone ($i = 1$ to 5), P_j is the effect of jth period of calving ($j = 1$ to 6), S_k is the effect of kth season of calving ($k = 1$ to 4), N_l is the effect of lth parity ($l = 1$ to 6), A_n is the random animal effect and e_{ijklm} is the residual effects.

The following animal model was used for multivariateanalyses of all the traits studied.

$$y_i = X_i b_i + Z_i a_i + e_i,$$

In matrix notation:

$$\begin{bmatrix} y_1 \\ : \\ y_6 \\ : \\ y_{12} \end{bmatrix} = \begin{bmatrix} X_1 & .. & 0 & .. & 0 \\ : & : & : & : & : \\ 0 & .. & X_6 & .. & 0 \\ : & : & : & : & : \\ 0 & .. & 0 & .. & X_{12} \end{bmatrix} \begin{bmatrix} b_1 \\ : \\ b_6 \\ : \\ b_{12} \end{bmatrix} + \begin{bmatrix} Z_1 & .. & 0 & .. & 0 \\ : & : & : & : & : \\ 0 & .. & Z_6 & .. & 0 \\ : & : & : & : & : \\ 0 & .. & 0 & .. & Z_{12} \end{bmatrix} \begin{bmatrix} a_1 \\ : \\ a_6 \\ : \\ a_{12} \end{bmatrix} + \begin{bmatrix} e_1 \\ : \\ e_6 \\ : \\ e_{12} \end{bmatrix}$$

where $y_i$is the vector of observations for trait i [$i = 1$ to 12(TDMY1 to TDMY10, LMY and 305MY)],X_i is the incidence matrix relating the fixed effects (b_i) to the vector of observations (y_i); Z_i is the incidence matrix relating the vector of direct additive genetic effects (a_i) to y_i and e_i is the vector of random residual effects assumed to be NID (0, σ^2_e) associated with y_i.

For Random Regression Model (RRM) analysis, a single trait linear mixed RRM was applied to TDMY records. A homogenous (constant) residual variance along days in milk (DIM) was considered on an assumption that residual effects on different DIM were uncorrelated both within and between cows. In this analysis, the direct genetic (additive) effects and permanent environmental effects were modeled by Legendre polynomials of order three [16]. The RRM used in the analysis is described below:

$$Y_{ijklmn} = C_i + P_j + S_k + N_l + \sum_{q=1}^{n} \beta_q Z_{mnq} + \sum_{q=1}^{n} a_{mq} Z_{mnq} + \sum_{q=1}^{n} pe_{mq} Z_{mnq} + e_{ijklmn}$$

where Y_{ijklmn} is the nth observation of cow m of ith zone, jth period and kth season and lth parity, C_i is the effect of ith agro climatic zone (i = 1 to 5), P_j is the effect of jth period (j = 1 to 6), S_k is the effect of kth season (k = 1 to 4), N_l is the effect of lth parity (l = 1 to 6), β_q is the set of q regression coefficients to model average trajectory of thepopulation, Z_{mnq} is the fixed covariate of Legendre polynomial according to DIM, a_{mq} is the set of q additive genetic random regression coefficients for cow m, pe_{mq} is the set of q permanent environmental random regression coefficients for cow m and e_{ijklmn} is the random residual effect associated with Y_{ijklmn}.

The variance structure for the random effects of the model was

$$V \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{pmatrix} G \otimes A & 0 & 0 \\ 0 & I \otimes P & 0 \\ 0 & 0 & R \end{pmatrix}$$

where I is the Identity matrix, A is the matrix of additive genetic relationship among the animals, ⊗is the Kronecker product function, P and G are covariance matrices for permanent environmental and additive genetic effects, respectively. R is the diagonal matrix of the form $I\sigma^2_e$ and σ^2_e is the residual variances.

The multivariate analysis and the RRM were carried out usingthe method of restricted maximum likelihood (REML) in WOMBATsoftware [17].

3. Results

The results of the descriptive statistical analysis are presented in Table 3.The mean TDMYs ranged from 4.66 to 9.53 kg and the coefficient of variation ranged from 27.54 to 39.83 per cent.The overall least-squares means of various TDMYs ranged from 4.98 (TDMY10) to 9.95 kg (TDMY2) and are depicted in Figure 1.The trend for TDMYs showed that milk yield was slightly lower at the beginning of lactation, and then it peaked at TDMY2 (9.95 kg) after which the yield displayed a gradual but consistent decline to the end of lactation. The GLM analysis revealed that all the fixed factors under study were significant ($P \le 0.05$) and, therefore, were included in the multivariate (animal model) and RRM analyses. The overall mean estimated for TMY and 305MY in this study were 2480.33 and 2393.71 kg respectively, which is a real indicator of the performance potential of Jersey crossbreds in Tamil Nadu, as it is based on the farmers' production system with considerable data size.

Table 3. Descriptive statistics of test day milk yields (kg) of Jersey crossbred cows under farmers' production system.

Trait	n	Min	Max	Mean	SD	Var	CV (%)
TDMY1	89005	1.40	16.88	8.92	2.51	6.32	28.18
TDMY2	88563	1.62	17.49	9.49	2.61	6.84	27.54
TDMY3	88113	1.60	18.04	9.53	2.80	7.82	29.33
TDMY4	87622	1.47	18.14	9.29	2.92	8.50	31.38
TDMY5	87101	1.25	17.56	8.84	2.88	8.28	32.53
TDMY6	86420	1.03	16.43	8.23	2.70	7.29	32.81
TDMY7	85431	0.72	15.00	7.49	2.46	6.06	32.87
TDMY8	81725	0.72	13.42	6.66	2.21	4.88	33.17
TDMY9	76608	0.61	11.85	5.70	1.99	3.96	34.93
TDMY10	66288	0.53	10.42	4.66	1.85	3.44	39.83

TDMY – Test-day milk yield, n – number of records, min – minimum, max – maximum, SD – standard deviation, Var – variance, CV – coefficient of variation.

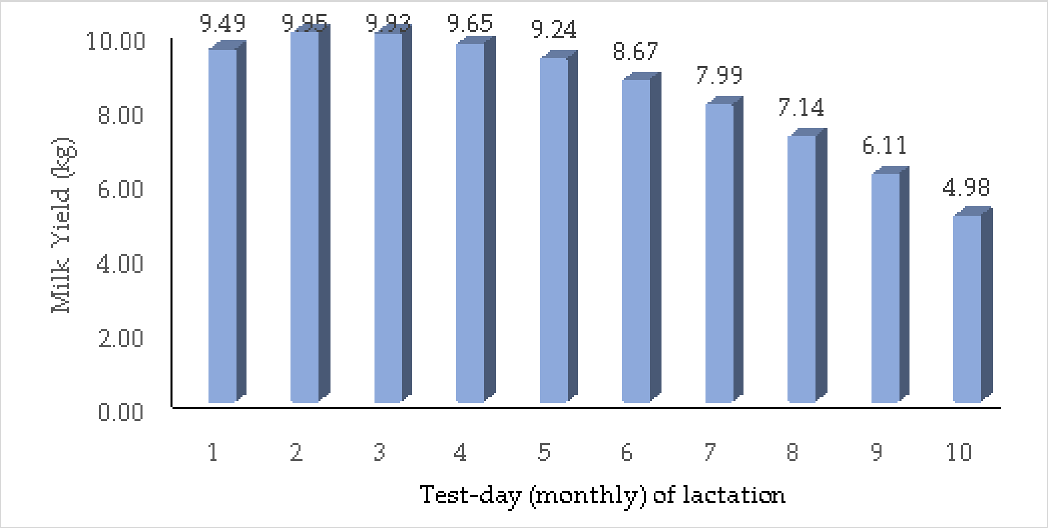

Figure 1. Least-squares mean of test day milk yields in Jersey crossbred cattle.

3.1. Variance Components

The variance components estimated by multivariate animal model for TDMYs, TMY and 305MY (Table 4) showed that the estimates of additive genetic variance (V_A) ranged from 1.64 (TDMY10) to 2.62 (TDMY1) and the variance decreased gradually as the lactation advanced (Figure 2). The estimates of residual variance (V_E) were ranged between 2.10 (TDMY10) and 3.70 (TDMY4) and phenotypic variance (V_P) were dispersed from 3.73 (TDMY10) to 6.12 (TDMY4) indicating higher estimates in the mid-lactation. Both V_E and V_P exhibited a similar trend of increasing from TDMY1 to TDMY4 and decreasing towards the end of lactation while the proportionate contribution of V_A to V_P decreased marginally for TDMYs as the lactation advances until TDMY8 and then it increased a little. The estimates of V_A and V_P for TMY and 305MY were high in the present study.

Table 4. Estimates of variance components for test day milk yields (TDMY), total milk yield (TMY) and 305-day milk yield (305MY) of Jersey crossbred cattle from multivariate animal model.

Trait	Additive variance (V_A)	Residual variance (V_E)	Phenotypic variance (V_P)
TDMY1	2.62 (0.07)	2.92 (0.07)	5.54 (0.03)
TDMY2	2.50 (0.08)	3.30 (0.07)	5.80 (0.03)
TDMY3	2.52 (0.08)	3.52 (0.07)	6.04 (0.03)
TDMY4	2.42 (0.08)	3.70 (0.07)	6.12 (0.03)
TDMY5	2.31 (0.08)	3.52 (0.07)	5.83 (0.03)
TDMY6	2.04 (0.07)	3.26 (0.07)	5.30 (0.03)
TDMY7	1.86 (0.06)	2.87 (0.06)	4.73 (0.02)
TDMY8	1.65 (0.06)	2.62 (0.05)	4.28 (0.02)
TDMY9	1.67 (0.06)	2.30 (0.05)	3.97 (0.02)
TDMY10	1.64 (0.06)	2.10 (0.05)	3.73 (0.02)
TMY	156250	166590	322840
305MY	155440	164530	319970

Figures within the parentheses indicate the Standard Error.

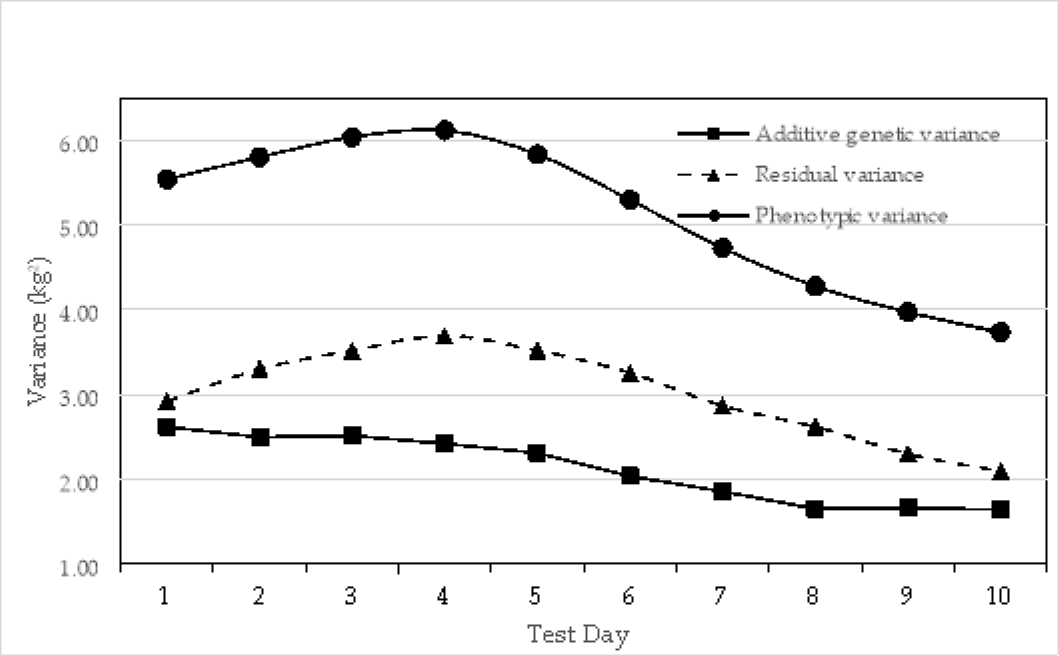

Figure 2. Estimates of variance components for test day milk yields (TDMY) of Jersey crossbred cattle frommultivariate animal model.

In RRM, the variance components for various TDMYs were estimated using the variance-covariances structure among random regression coefficients and covariate of the functions of RRM,and are presented in Table 5 and depicted in Figure 3. The residual variance was assumed constant (homogeneous) throughout the lactation. The highest V_A was observed for DIM 305 (18.18) and the lowest was observed for DIM 65 (1.67). The permanent environmental variance (V_{EP}) was the highest for DIM 305 (7.22) and lowest (1.75) for DIM 65. The magnitude of V_A and V_{EP} decreased from DIM 5 up to DIM 65 and then increased gradually till the end of lactation (Figure 3). The phenotypic variance (V_P) was higher at the beginning and end of the lactation as compared to the mid-lactation.

Table 5. Estimates of variance components for days in milk (DIM) of Jersey crossbred cattle from random regression model.

Days in milk (DIM)	Additive variance (V_A)	Permanent environmental variance (V_{EP})	Residual variance (V_E)	Phenotypic variance (V_P)
5	6.36 (0.27)	4.71 (0.24)	2.46 (0.01)	13.54 (0.11)
35	2.64 (0.09)	2.38 (0.08)	2.46 (0.01)	7.49 (0.04)
65	1.67 (0.05)	1.75 (0.05)	2.46 (0.01)	5.88 (0.02)
95	1.99 (0.06)	2.00 (0.06)	2.46 (0.01)	6.45 (0.02)
125	2.61 (0.10)	2.57 (0.09)	2.46 (0.01)	7.64 (0.04)
155	3.04 (0.12)	3.07 (0.11)	2.46 (0.01)	8.57 (0.05)
185	3.24 (0.14)	3.37 (0.13)	2.46 (0.01)	9.07 (0.05)
215	3.68 (0.17)	3.54 (0.15)	2.46 (0.01)	9.70 (0.07)
245	5.29 (0.24)	3.86 (0.21)	2.46 (0.01)	11.62 (0.10)
275	9.49 (0.41)	4.85 (0.35)	2.46 (0.01)	16.80 (0.17)
305	18.18 (0.76)	7.22 (0.65)	2.46 (0.01)	27.87 (0.31)

Figures within the parentheses indicate the Standard Error.

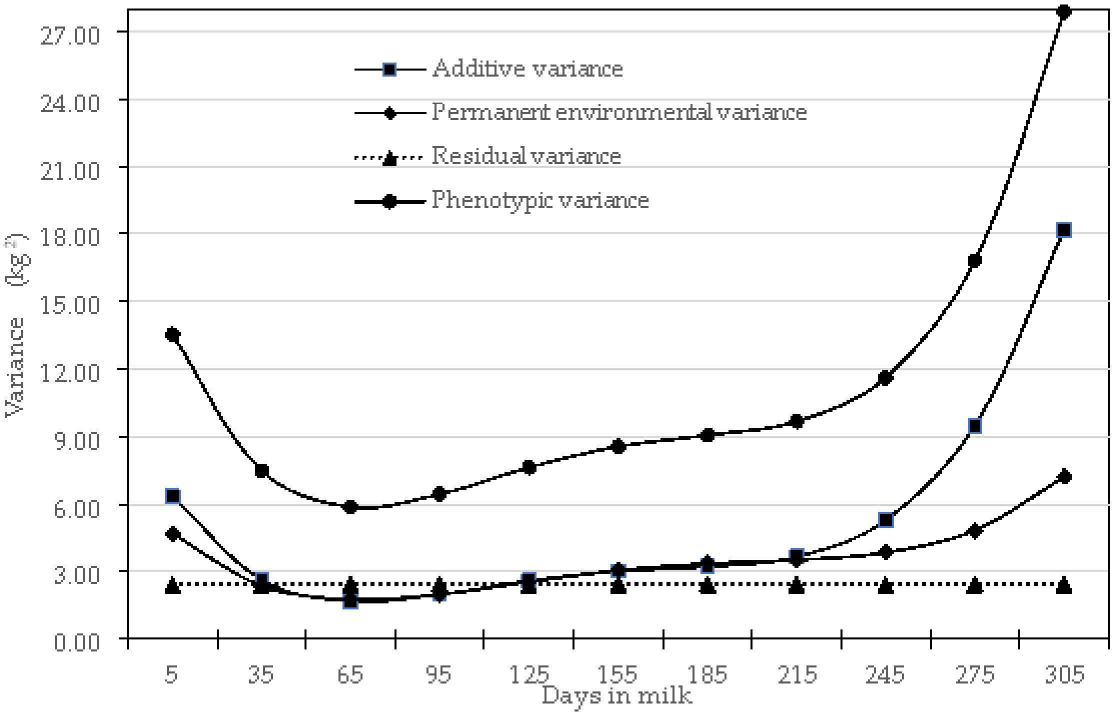

Figure 3. Estimates of variance components of Jersey crossbred cattle from random regression model.

3.2. Heritability

The estimates of heritability, the proportion of additive variance to phenotypic variance, for various TDMYs by animal model was high (>0.3) and ranged from 0.39 ± 0.01 to 0.47 ± 0.01 (Table 6) and were fairly less variable throughout the lactation (Figure 4).

Table 6. Estimates of heritability (diagonal), genetic (below the diagonal) and phenotypic (above the diagonal) correlations between TDMY, TMY and 305MY in Jersey crossbred cattle from multivariate animal model.

Trait	TDMY1	TDMY2	TDMY3	TDMY4	TDMY5	TDMY6	TDMY7	TDMY8	TDMY9	TDMY 10	TMY	MY305
TDMY1	**0.47** (0.01)	0.83 (0.00)	0.72 (0.00)	0.63 (0.00)	0.56 (0.00)	0.51 (0.00)	0.47 (0.00)	0.44 (0.00)	0.38 (0.00)	0.32 (0.00)	0.71 (0.00)	0.71 (0.00)
TDMY2	0.98 (0.00)	**0.43** (0.01)	0.87 (0.00)	0.77 (0.00)	0.69 (0.00)	0.63 (0.00)	0.57 (0.00)	0.52 (0.00)	0.44 (0.00)	0.36 (0.00)	0.80 (0.00)	0.80 (0.00)
TDMY3	0.92 (0.01)	0.98 (0.00)	**0.42** (0.01)	0.88 (0.00)	0.79 (0.00)	0.72 (0.00)	0.65 (0.00)	0.58 (0.00)	0.47 (0.00)	0.37 (0.00)	0.85 (0.00)	0.85 (0.00)
TDMY4	0.84 (0.01)	0.91 (0.01)	0.97 (0.00)	**0.40** (0.01)	0.89 (0.00)	0.81 (0.00)	0.70 (0.00)	0.57 (0.00)	0.44 (0.00)	0.41 (0.00)	0.87 (0.00)	0.87 (0.00)
TDMY5	0.77 (0.01)	0.85 (0.01)	0.94 (0.01)	0.99 (0.00)	**0.40** (0.01)	0.89 (0.00)	0.81 (0.00)	0.70 (0.00)	0.57 (0.00)	0.44 (0.00)	0.87 (0.00)	0.87 (0.00)
TDMY6	0.73 (0.01)	0.82 (0.01)	0.90 (0.01)	0.96 (0.00)	0.99 (0.00)	**0.39** (0.01)	0.89 (0.00)	0.79 (0.00)	0.65 (0.00)	0.51 (0.00)	0.87 (0.00)	0.87 (0.00)
TDMY7	0.69 (0.02)	0.77 (0.01)	0.84 (0.01)	0.90 (0.01)	0.94 (0.01)	0.98 (0.00)	**0.39** (0.01)	0.87 (0.00)	0.74 (0.00)	0.61 (0.00)	0.86 (0.00)	0.86 (0.00)

TDMY8	0.64 (0.02)	0.71 (0.01)	0.76 (0.01)	0.80 (0.01)	0.85 (0.01)	0.91 (0.01)	0.97 (0.00)	**0.39** (0.01)	0.87 (0.00)	0.74 (0.00)	0.83 (0.00)	0.83 (0.00)
TDMY9	0.56 (0.02)	0.60 (0.02)	0.62 (0.02)	0.65 (0.02)	0.70 (0.02)	0.79 (0.01)	0.88 (0.01)	0.97 (0.00)	**0.42** (0.01)	0.87 (0.00)	0.76 (0.00)	0.76 (0.00)
TDMY10	0.47 (0.02)	0.49 (0.02)	0.49 (0.02)	0.49 (0.02)	0.54 (0.02)	0.64 (0.02)	0.76 (0.01)	0.89 (0.01)	0.98 (0.00)	**0.44** (0.01)	0.66 (0.00)	0.65 (0.00)
TMY	0.86 (0.01)	0.91 (0.01)	0.94 (0.00)	0.94 (0.00)	0.94 (0.00)	0.96 (0.00)	0.95 (0.00)	0.93 (0.01)	0.84 (0.01)	0.73 (0.01)	**0.48** (0.01)	1.00 (0.00)
MY305	0.86 (0.01)	0.91 (0.01)	0.94 (0.00)	0.95 (0.00)	0.95 (0.00)	0.96 (0.00)	0.95 (0.00)	0.93 (0.01)	0.84 (0.01)	0.73 (0.01)	1.00 (0.00)	**0.49** (0.01)

Figures within the parentheses indicate the Standard Error.

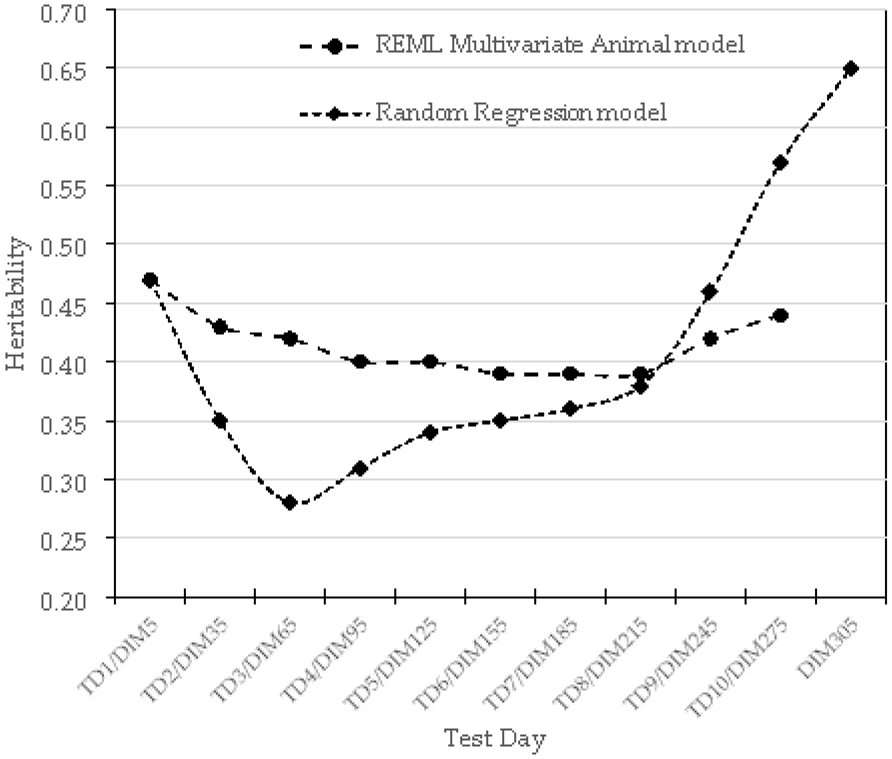

Figure 4. Estimates of heritability for test day (TD) milk yields from multivariate animal model and days in milk (DIM) from random regression model of Jersey crossbred cattle.

The heritability estimates for TMY and 305MY were 0.48 ± 0.01 and 0.49 ± 0.01 respectively (Table 6). The heritability estimates from RRM (Table 7) were moderate to high for different DIMs ranged from 0.28 ± 0.01 to 0.65 ± 0.02, showed a trend of decrease from DIM 5 (0.47) to DIM 65 (0.28) and then gradually increasing till the end of lactation (Figure 4).

Table 7. Estimates of heritability (diagonal), genetic (below the diagonal) and phenotypic correlations (above the diagonal) between days in milk (DIM) of Jersey crossbreds from random regression model.

Days in milk	**5**	**35**	**65**	**95**	**125**	**155**	**185**	**215**	**245**	**275**	**305**
5	**0.47** (0.02)	0.69 (0.00)	0.40 (0.00)	0.12 (0.00)	-0.05 (0.01)	-0.12 (0.01)	-0.11 (0.01)	-0.03 (0.01)	0.12 (0.01)	0.27 (0.01)	0.39 (0.01)
35	0.93 (0.00)	**0.35** (0.01)	0.53 (0.00)	0.34 (0.00)	0.20 (0.00)	0.14 (0.00)	0.12 (0.00)	0.15 (0.00)	0.20 (0.00)	0.26 (0.01)	0.29 (0.01)
65	0.55 (0.02)	0.83 (0.01)	**0.28** (0.01)	0.54 (0.00)	0.47 (0.00)	0.43 (0.00)	0.39 (0.00)	0.35 (0.00)	0.30 (0.00)	0.22 (0.00)	0.15 (0.00)
95	0.10 (0.03)	0.47 (0.02)	0.88 (0.01)	**0.31** (0.01)	0.63 (0.00)	0.61 (0.00)	0.57 (0.00)	0.49 (0.00)	0.37 (0.00)	0.21 (0.00)	0.07 (0.00)
125	-0.12 (0.03)	0.25 (0.03)	0.74 (0.02)	0.97 (0.00)	**0.34** (0.01)	0.68 (0.00)	0.66 (0.00)	0.58 (0.00)	0.43 (0.00)	0.24 (0.00)	0.06 (0.01)
155	-0.18 (0.03)	0.17 (0.03)	0.66 (0.02)	0.92 (0.00)	0.99 (0.00)	**0.35** (0.01)	0.71 (0.00)	0.65 (0.00)	0.51 (0.00)	0.32 (0.01)	0.14 (0.01)
185	-0.11 (0.03)	0.19 (0.03)	0.62 (0.02)	0.85 (0.01)	0.92 (0.00)	0.97 (0.00)	**0.36** (0.02)	0.71 (0.00)	0.61 (0.00)	0.45 (0.00)	0.28 (0.01)
215	0.07 (0.03)	0.28 (0.03)	0.56 (0.02)	0.70 (0.01)	0.76 (0.01)	0.84 (0.01)	0.94 (0.00)	**0.38** (0.02)	0.72 (0.00)	0.62 (0.00)	0.49 (0.00)
245	0.31 (0.03)	0.39 (0.03)	0.45 (0.02)	0.45 (0.02)	0.48 (0.02)	0.58 (0.02)	0.75 (0.01)	0.93 (0.00)	**0.46** (0.02)	0.78 (0.00)	0.70 (0.00)
275	0.48 (0.03)	0.45 (0.02)	0.32 (0.02)	0.20 (0.02)	0.19 (0.03)	0.30 (0.03)	0.50 (0.02)	0.75 (0.01)	0.95 (0.00)	**0.57** (0.02)	0.85 (0.00)
305	0.59 (0.02)	0.48 (0.02)	0.23 (0.02)	0.02 (0.02)	-0.02 (0.03)	0.08 (0.03)	0.29 (0.03)	0.59 (0.02)	0.85 (0.01)	0.98 (0.00)	**0.65** (0.02)

Figures within the parenthesis indicate the Standard Error.

3.3. Genetic and Phenotypic Correlations

Genetic correlations between TDMYs estimated by animal model were positive and moderate (0.4-0.6) to high (>0.6), ranged between 0.47 ± 0.01 and 0.99 ± 0.00 (Table 6). Considerably higher estimates (0.97-0.99) were observed between adjacent TDMYs showing strong genetic association. The genetic correlation estimates were medium (0.4-0.6) between distant test days particularly for TDMY1 to TDMY5 with TDMY10. By RRM, genetic correlations estimated between DIMs were positive, except a few estimates (Table 7). The phenotypic correlations from animal model between different TDMYs were positive and medium to high, ranged from 0.32 ± 0.00 to 0.89 ± 0.00 (Table 6). Phenotypic correlations tended to decrease as the time interval between test days increased. Besides, positive and moderate to high phenotypic correlations were found for TDMYs with TMY and 305MY (Table 6). The phenotypic correlations estimated between TDMYs by RRM (Table 7) were positive except a few estimates with DIM5.

4. Discussion

The estimates of the TDMYs in the present study (Figure 1) were in the lower range compared to the values (4.70 to 10.89 kg) reported for Jersey crossbred cattle under organized farm conditions in West Bengal [18] and the values (5.41 to 10.71 kg) reported for first lactation of crossbred cattle in Kerala under field conditions [19]. Similar findings were also reported for TDMYs in crossbred cattle in Uttarakhand [20] and Holstein Friesian x Sahiwal crossbred cattle in Punjab [21]. The peak yield which was observed in the TDMY1 for Jersey crossbred cattle in West Bengal [18], which then declined till the end of lactation.

The earlier studies in Tamil Nadu had reported mean values lower than this study for TMY and 305MY in Jersey x Red Sindhi crosses [22], Jersey x Sahiwal [23] and Jersey x Tharparkar [24] crossbred cattle, and for TMY in Jersey crossbred cattle [25] in organized farms while comparable values were reported under farmers' rearing environment [26]. Higher values were reported for TMY in Jersey x Tharparkar (or) Red Sindhi crossbreds in West Bengal [27,28] and in Jersey x Sahiwal crossbred cattle in Uttarakhand [29,30]. Several researchers reported estimates lower than the present study for both TMY and 305MY in Jersey x Red Sindhi crosses in Himachal Pradesh [31,32] and for TMY in Jersey x Sahiwal crossbreds in Maharashtra [33], Jersey x Red Sindhi in Uttarakhand [34]. The difference in the mean yields between the present study and the earlier reports could possibly be due to varying levels of inheritance of Jersey and differences in rearing environment and many of the studies in subtropical environment. The superior performance of Jersey crossbreds in the present study could be considered as a testimony to the adaptability of the genetic group to conditions prevailing in Tamil Nadu. Hence, the advocated breeding policy [35]of crossing of Jersey in the plains of the state is vindicated and could be continued in future for the milk production.

4.1. Variance Components

The initial increase in the magnitude of V_A followed by a decrease till the end of lactation observed in the present study was also reported in Sahiwal cattle in Kenya [36] and in Karan Fries cattle in India [37]. Though the study is based on the farmers' production system the prevailed common environmental effects at the beginning and end of lactation could possibly be the reason for high V_{EP}. Similar values of higher V_{EP} at the beginning and at the end of lactation were also reported in primiparous Holstein cattle in Brazil [38] and in primiparous Holstein Friesian cows in Ethiopia [39].

4.2. Heritability

The estimates of heritability in mid-lactation were comparatively lower than those in the beginning and the end of lactation and it might be attributed to the relatively larger V_{EP}. The high estimates of heritability observed for TDMYs at the extremes of lactation might be due to relatively higher contribution from additive action of genes to phenotypic variation. Overall, the estimates of heritability obtained in this study for TDMYs were on the higher side. The study is based on farmers' production system with several herds of small size in a progeny testing scheme.Moreover, the heterogenous nature of such a smallholderpopulation resulted in more variations due to genes and limited relationships traced from the pedigree through NRM. This results in high estimates of additive genetic variance and,consequently high heritability. The heritability estimates for TDMYs observed in this study by animal model were comparable with the estimates (0.42 to 0.60) reported earlier in Jersey crossbred cattle [18], however, they were higher than those reported in Sahiwal cattle which ranged between 0.25 and 0.30 [36] and in crossbred cattle (0 to 0.36) [19]. The heritability for TDMYs estimated by RRM in this study was higher than the reports in Karan Fries cattle (0.17 to 0.29) [37].

For TMY and 305MY similar higher estimates of heritability were reported for Jersey crossbred cattle in West Bengal [28,40] and in Tamil Nadu for TMY [25]. However, heritability estimates observed in this study were higher than those reported in Jersey crossbred cattle reared in the organized farms [22,23,29,31,34].

The high heritability estimates obtained in this study for TDMYs, TMY and 305MY in Jersey crossbred cattle indicate the presence of high genetic potential for these traits which could be improved through selective breeding under farmers' production systems in Tamil Nadu. Genetic variation identified in a population as in the present study indicates the advantage of a field progeny testing programme as compared to the usual Farm based genetic evaluations, where the base population is low and the scope of improvement is also less. Nevertheless, in such field studies, the nature of data is unique in that relationship among animals could go unexplored, due to the availability of data from a lesser number of generations. Continuing the field progeny testing programme would help in a good response to selection which in turn is dependent upon the heritability of the trait.

4.3. Genetic and Phenotypic Correlations

The genetic correlations of TDMYs with TMY and 305MY fromanimal model estimation were positive and considerably high indicating that the selection of animals based on early TDMYs for TMY and 305MY would be efficient. The high genetic correlation between TDMYs and 305MY found in this study agreed with the reports in Sahiwal cattle [41] and Karan Fries cattle [42]. In RRM, it was observed that the magnitude of genetic correlations decreased with increase in the interval between the DIMs. This type of a heterogenous and correlated covariance structure indicated the use of mixed models or RRM more appropriately.

Overall the magnitudes of genetic correlations estimated by animal model between TDMYs decreased as the interval between test days increased, which agreed with the findings [18] in Jersey crossbred cattle under organized farm conditions in West Bengal. Similar to the present study by RRM, negative estimates of genetic correlations were reported for Karen Fries cows between TDMY1 with TDMY7 to TDMY9 [37]. Similarly, the observed higher genetic correlations between DIMs that were closer to each other agreed with that reported in Karen Fries cattle [37] and in Sahiwal cattle [41]. The medium to high genetic correlations between TDMYs found for Jersey crossbred cattle in this study indicated a significant association between the additive genetic values between the traits studied. High and positive genetic correlations of TDMYs of early stages of lactation with TMY and 305MY found in this study suggested the selection of cows based on earlier TDMYs to improve TMY and 305MY.

Considerably high and positive phenotypic correlations and trend similar to the present study was observed in Jersey crossbred cattle in West Bengal [18]. The decreasing estimates of phenotypic correlations with the increase in test day interval might be attributed to the decrease in the association between the traits at different stages of lactation.

5. Conclusions

The performance of Jersey crossbred cattle observed in the present study under farmers' production conditions was comparable and even better than earlier reports indicating the suitability of Jersey crossbreeds in the state and it recommends for the continuance of crossing of Jersey for the milk production as appropriate. The study favors the use of the test-day model on account of ease in data recording and also offers a successful alternative for genetic evaluation under farmers' production system where recording of entire lactation of a large number of animals of small holders' herd is almost impossible. The test-day model also provides scope for the correction of environmental factors specific for the day of recording. This study on genetic evaluation could provide parameter estimates for a heterogeneous field performance recording system. As the permanent environmental variance is modeled and estimated by RRM, the RRM could be exploited advantageously over the simple animal model for the estimation of heritability and genetic correlations. The covariance structure identified warranted RRM for efficient genetic evaluation studies. The genetic variability for milk production was high in the farmers' production system and the high heritability obtained in this study offers better scope for improvement of milk production through selective breeding under the farmers' production system in Tamil Nadu. Such evaluations in the farmers' production system are representative of large scale breeding programs, proven as sustainable models in developing countries. The estimates, though on a higher side, considering the nature of large datasets under a farmers' production system, the overall variation expected in such data are worth documentation as very few studies on such datasets are available.Further, the high genetic correlation between the TDMYs in early and mid stages of lactation with 305MY and TMY suggested that these TDMYs could be favorably used for the early selection of cows, which facilitates reduction in the generation interval and consequently increases the annual genetic gain for the milk production traits, besides minimizing the cost of milk recording. Moreover, the presence of desirable genetic association suggested that the multi-trait combined selection using early lactation TDMYs would be explored for the genetic improvement of these traits.

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