***Type of article:** Original research article*

"Genetic and Environmental Factors Influencing Lactation Traits in Jersey x Sahiwal Crossbred Cattle: Variance Component Estimation"

ABSTRACT

Crossbreeding programs enhance dairy productivity by combining desirable traits from different breeds. Accurate genetic evaluation is essential for improving economically important lactation traits in crossbred cattle. This study aimed to estimate genetic parameters and variance components for 305-day milk yield (305-DMY), total milk yield (TMY), lactation length (LL) and peak yield (PY) using Derivative-Free Restricted Maximum Likelihood (DFREML) method (Meyer, 1998). A total of 4,877 first lactation performance records of Jersey x Sahiwal crossbred cattle, maintained under the progeny testing program in Chittoor district of Andhra Pradesh, India were utilized for this study. Six univariate animal models were fitted for each trait by including or excluding maternal additive genetic (m^2) and permanent environmental (c^2) effects. Selection of the best-fitted model for each trait was based on AIC, BIC and log-likelihood values. The overall least-square means for 305-DMY, TMY, LL and PY were 2276.46±8.57 kg, 2300.23±9.20 kg, 283.93±0.49 days and 10.23±0.03 kg, respectively. The effect of sire, period and season of calving were highly significant ($P<0.01$) for all traits, indicating the influence of environmental factors on milk production. Direct heritability estimates were moderate to high, with values of 0.50 for 305-DMY, 0.53 for TMY, 0.42 for LL and 0.15 for PY, suggesting substantial genetic variability for selection. Maternal genetic (m^2) and permanent environmental (c^2) effects had minimal influence on 305-DMY, TMY and LL, whereas individual permanent environmental effects (c^2) accounted for 39% of the total phenotypic variance in PY, emphasizing the critical role of environmental management in improving peak yield. These findings emphasize the necessity of selecting appropriate models for accurate genetic evaluations and advocate for an integrated approach that combines genetic selection with strategic environmental management. By optimizing both genetic potential and environmental conditions, this approach ensures balanced and sustainable improvements in dairy productivity, contributing to the long-term success of crossbreeding programs.

Keywords: Lactation traits, Variance components, Genetic parameters, Maternal effects, Jersey x Sahiwal crossbred cattle

1. INTRODUCTION

The success of any breeding program hinges on accurately identifying genetically superior animals to achieve substantial genetic progress. In animal breeding, the primary goal is to maximize genetic improvement through systematic and effective selection, which relies heavily on precise evaluation of genetically superior animals (Ratwan *et al.,* 2019). In India, selection of dairy cattle primarily depends on lactation performance records, emphasizing the need for thorough assessment of lactation traits. Reliable genetic improvement requires accurate estimation of genetic parameters, forming the foundation for effective selection and enhanced genetic gains. Maternal lineage plays a pivotal role in shaping milk production traits in dairy cattle (Ratwan *et al.,* 2019). Beyond the genetic contributions, maternal effects encompass the influence of dams on their offspring through prenatal and postnatal care, as well as environmental factors. Previous research has quantified these effects, with Bell *et al.* (1985)

attributing 2% of the variation in milk yield to maternal lineage, while Huizinga *et al.* (1986) reported contributions as high as 6%.

The selection of superior animals with the highest breeding values requires knowledge of genetic parameters and variance components. The advent of restricted maximum likelihood (REML) method for the estimation of variance components has simplified the partitioning of variance into direct and maternal effects. Understanding the interplay between maternal and direct genetic effects is essential for refining selection strategies and optimizing breeding programs (Meyer, 1992). Neglecting maternal genetic effects during genetic evaluations can lead to biased heritability estimates, reducing the accuracy and efficiency of selection processes. Nasholm and Danell (1994) demonstrated that excluding maternal genetic effects leads to upwardly biased heritability estimates, compromising selection efficiency. Similarly, Meyer (1992) and Rumph *et al.* (2002) emphasized that ignoring maternal effects introduces significant errors in genetic parameter estimation, hindering genetic progress. Hazel *et al.* (1994) further pointed out that such inaccuracies could result in suboptimal selection decisions, undermining the goals of breeding programs.

Recognizing the significance of maternal effects, this study aims to estimate genetic parameters and variance components associated with direct additive genetic, maternal genetic, individual permanent environmental and maternal permanent environmental effects for key lactation traits viz., 305-day milk yield (305-DMY), total milk yield (TMY), lactation length (LL) and peak yield (PY) in Jersey x Sahiwal crossbred cattle. These findings are expected to shed light on the genetic architecture of economically important traits and provide a basis for developing effective breeding strategies to enhance the genetic potential and productivity of this crossbred population.

2. MATERIAL AND METHODS

2.1 Study location and animals

The present study was designed to genetically evaluation lactation traits in Jersey x Sahiwal crossbred cattle under the field Progeny Testing Programme (PTP) in Chittoor district of Andhra Pradesh, India. The PTP has been implemented since 1987, aims to improve the genetic potential of Jersey x Sahiwal crossbreds. Chittoor district is situated in the Rayalaseema region of Andhra Pradesh, between the longitudes of 78°-2’-2" and 79°-41’-52" East and the latitudes of 12°-44’-42" and 13°-39’-21" North. In the eastern region, summer temperatures can reach upto 46°C, while in the western region, they hover between 36° and 38°C. During winter, the eastern portion experiences 16°C to 18°C, whereas the western portion has comparatively lower temperatures of 12°C to 14°C. Chittoor district receives an annual rainfall of 918.1 mm, with 438.0 mm coming from the southwest monsoon i.e. from June to September and 396.0 mm from the northeast monsoon i.e. from October to December. These two monsoons are the primary sources of rainfall in this area (Kumar and Subramanyachary, 2015).

2.2 Animal population and management practices

The study exclusively focused on first-generation (F1) Jersey x Sahiwal crossbred cattle with a fixed 50% Jersey x 50% Sahiwal genetic composition. There were no reciprocal crossings involved and no admixture at varying levels was present in the studied population. Over time, most cattle populations in the district have been stabilized at this inheritance level due to systematic breeding efforts under the PTP. The cattle were bred exclusively using semen from genetically evaluated Jersey x Sahiwal crossbred bulls, collected under the PTP. Natural service by bulls was eliminated, and artificial insemination (AI) was practiced. Cattle were housed in a loose housing system, allowing free movement and exercise. Depending on availability, animals were housed in either Kachcha (temporary) or Pakka (permanent) shelters, ensuring optimal ventilation and protection from adverse weather. Lactating animals were provided with a balanced diet, primarily comprising green fodder (such as maize, bajra, and anjan), dry fodder (mainly paddy straw), and concentrates. While *ad libitum* green fodder was available, concentrates were provided either separately based on milk yield or as a total mixed ration (TMR) when necessary to optimize nutrient intake.

2.3 Data and traits considered

The data utilised in this study were collected from first lactation performance records of 4,877 daughters sired by 176 Jersey x Sahiwal crossbred bulls. These records were obtained from history and pedigree sheets of Jersey crossbred progeny maintained under a progeny testing program (PTP) by selected field farmers across 24 mandals of Chittoor district over a 10-year period (2014–2023). These records were analyzed to estimate variance components and genetic parameters for key lactation traits viz., 305-days milk yield (305-DMY), total milk yield (TMY), lactation length (LL) and peak yield (PY). Data collection started once the daughters matured and completed their first lactation. Since the female progeny born during or just prior to 2014 were not available for lactation, data from 2014 to 2015 could not be included. Additionally, records affected by culling, abortion, stillbirth or other pathological conditions were also excluded.

To account for environmental influences, data were classified into four periods based on the year of calving: Period 1 (2016–2017), Period 2 (2018–2019), Period 3 (2020–2021) and Period 4 (2022–2023). Additionally, records were grouped into three calving seasons: winter (November–February), summer (March–June), and rainy (July–October). Year and season of calving were explicitly included as fixed effects in the statistical model to adjust for their potential influence on lactation traits, ensuring accurate genetic evaluations.

2.4 Statistical analysis

2.4.1 Preliminary analysis

A preliminary univariate analysis was conducted to identify fixed effects that significantly influence lactation traits. The identified significant effects were then incorporated into the model for further genetic analysis.

2.4.2 Effect of genetic and non-genetic factors on different lactation traits

Every phenotypic observation on an animal is determined by environmental and genetic factors and may be defined by the following model (Mrode R, 2013):

Phenotypic observation = environmental effects + genetic effects + residual effects

The influence of genetic and non-genetic factors on different lactation traits was analyzed using the following model, with the assumption that the factors included in the model are linear, independent, and additive.

$$Y_{ijkl} = \mu + B_i + P_j + S_k + e_{ijkl}$$

Where,

Y_{ijkl} = l^{th} 305-days milk yield/Total milk yield/Lactation length/Peak yield of cattle which is progeny of i^{th} sire, calved in j^{th} period and k^{th} season

μ = overall mean

B_i = random effect of i^{th} sire

P_j = effect of j^{th} period of calving ($j = 1,2,3,4$)

S_k = effect of k^{th} season of calving ($k = 1,2,3$)

e_{ijkl} = random error associated with each observation assumed to be NID $(0, \sigma_e^2)$

2.4.3 Estimation of variance components and genetic parameters

Variance components and heritabilities for various lactation traits were estimated by fitting six univariate animal models (for each trait) using the Derivative-Free Restricted Maximum Likelihood (DFREML) algorithm (Meyer, 1998) in WOMBAT software. These models varied by including or excluding maternal genetic (m^2) and permanent environmental (c^2) effects. The best-fitted model for each trait was determined based on Akaikes information criterion (AIC), Bayesian information criterion (BIC) and log-likelihood values. A lower AIC or BIC value indicates a better model by incorporating penalties for model complexity, preventing overfitting. In contrast, a higher log-likelihood value suggests a better fit but does not account for the number of parameters. Therefore, AIC and BIC were preferred over log-likelihood alone for selecting the best-fitting model, as they provide a more balanced comparison.The genetic parameters were then estimated using the model that provided the best-fit.

The following six models were fitted to account for direct additive genetic effects, maternal genetic effects, individual permanent environmental effects and maternal permanent environmental effects for each lactation trait:

$$y = Xb + Z_a a + e \qquad \text{model 1}$$

$$y = Xb + Z_a a + Z_m m + e \qquad \text{model 2}$$

$$y = Xb + Z_a a + Z_{pe} ipe + e \qquad \text{model 3}$$

$$y = Xb + Z_a a + Z_m m + Z_{pe} ipe + e \qquad \text{model 4}$$

$$y = Xb + Z_a a + Z_m m + Z_{mpe} mpe + e \qquad \text{model 5}$$

$$y = Xb + Z_a a + Z_m m + Z_{pe} ipe + Z_{mpe} mpe + e \qquad \text{model 6}$$

where **'y'** is the vector of records; **b, a, m, ipe, mpe** and **e** are the vectors of fixed, direct additive genetic, maternal genetic, individual permanent environmental, maternal permanent environmental and residual effects, respectively with association matrices $\mathbf{X}, \mathbf{Z_a}, \mathbf{Z_m}, \mathbf{Z_{pe}}$ and $\mathbf{Z_{mpe}}$. It was assumed that

$$V(a) = A\sigma^2_a,\ V(m) = I\sigma^2_m,\ V(ipe) = I\sigma^2_{ipe},\ V(mpe) = I\sigma^2_{mpe} \text{ and } V(e) = I\sigma^2_e$$

where, **A** is the numerator relationship matrix, **I** is the identity matrix and $\boldsymbol{\sigma^2_a}, \boldsymbol{\sigma^2_m}, \boldsymbol{\sigma^2_{ipe}}, \boldsymbol{\sigma^2_{mpe}}$ and $\boldsymbol{\sigma^2_e}$ are direct additive genetic, maternal additive genetic, individual permanent environmental, maternal permanent environmental and residual variances, respectively. Estimated variance components were used to obtain direct heritability ($h^2_a = \sigma^2_a/\sigma^2_p$), maternal heritability ($h^2_m = \sigma^2_m/\sigma^2_p$) and individual or maternal permanent environmental variance as a proportion of phenotypic variance ($h^2_{ipe} = \sigma^2_{ipe}/\sigma^2_p$ or $h^2_{mpe} = \sigma^2_{mpe}/\sigma^2_p$).

3. RESULTS AND DISCUSSION

The least-squares mean along with standard errors and effect of genetic and non-genetic factors for different lactation traits under this study are presented in Table 1. The overall least-squares mean for 305DMY, TMY, LL and PY were observed to be 2276.46±8.57 kg, 2300.23±9.20 kg, 283.93±0.49 days and 10.23±0.03 kg, respectively. The effect of sire, period of calving and season of calving were found to have highly significant (P≤0.01) effect on all the lactation traits studied. Effects of different environmental factors on considered lactation traits were in agreement with the findings of Bhutkar *et al.* (2014), Japheth *et al.* (2015), Ratwan *et al.* (2016) and Verma *et al.* (2016).

Table 1: Least-squares mean (±SE) for different lactation traits of Jersey x Sahiwal crossbred cattle

EFFECTS	**305DMY**	**TMY**	**LL**	**PY**
Overall mean	2276.464±8.576 (4877)	2300.239±9.208 (4877)	283.934±0.495 (4877)	10.239±0.036 (4877)
SIRE	**	**	**	**
PERIOD	**	**	**	**
Period - 1 (2016-2017)	2255.042±23.456^{c} (436)	2423.499±25.185^{b} (436)	280.287±1.354^{a} (436)	11.078±0.099^{d} (436)
Period - 2 (2018-2019)	2242.171±11.429^{c} (1974)	2302.489±12.272^{a} (1974)	285.618±0.660^{b} (1974)	10.284±0.048^{c} (1974)
Period - 3 (2020-2021)	2168.963±12.142^{a} (1672)	2224.020±13.038^{a} (1672)	289.422±0.701^{c} (1672)	9.681±0.051^{a} (1672)
Period - 4 (2022-2023)	2230.679±18.669^{b} (795)	2250.949±20.046^{a} (795)	280.410±1.078^{a} (795)	9.912±0.079^{b} (795)
SEASON	**	**	**	*
Season - 1 (Winter)	2307.844±15.924^{b} (1344)	2337.262±17.098^{b} (1344)	287.530±0.919^{c} (1344)	10.320±0.067^{a} (1344)
Season - 2 (Summer)	2300.839±13.000^{b} (2205)	2314.980±13.958^{ab} (2205)	282.981±0.751^{a} (2205)	10.098±0.055^{ab} (2205)
Season - 3 (Rainy)	2220.709±15.471^{a} (1328)	2248.476±16.612^{a} (1328)	281.292±0.893^{b} (1328)	9.299±0.066^{b} (1328)

Figures in parenthesis represent number of observations

Means with different superscripts differ significantly from each other

** - Highly significant (P≤ 0.01); * - Significant (P≤ 0.05)

Estimates of variance components and genetic parameters for lactation traits of Jersey x Sahiwal crossbred cattle analyzed using six different models are detailed in Table 2.

3.1 305-days milk yield

Direct heritability estimates for 305-DMY based on the model used varied from 0.24 to 0.50. For this trait, ignoring both maternal genetic and permanent environmental effects (Model 1) produced higher heritability (h_a^2) of 0.50 for direct additive genetic effect compared to other models, whereas including either maternal genetic (Model 2) or an individual permanent environmental effect (Model 3) reduced the heritability from 0.50 to 0.32. The heritability estimates for maternal genetic (Model 2) or individual permanent environmental effects (Model 3) were found to be 0.26, with corresponding decrease in the direct heritability value to 36%. When both maternal genetic and individual permanent environmental effects were included (Model 4), the heritability value (h_a^2) decreased to 0.28. Similarly, fitting maternal genetic and maternal permanent environmental effects (Model 5) resulted in heritability similar to that of Model 4. The heritabilities for maternal genetic (models 4 and 5), individual permanent environmental (model 4) and maternal permanent environmental (model 5) effects accounted for 23%, 20% and 20% of phenotypic variance, respectively, with a corresponding decrease in the direct heritability value to 44%. Finally, when maternal genetic, individual permanent environmental and maternal permanent environmental effects were all included (Model 6), the heritability value (h_a^2) dropped to 0.24, the lowest value among six models. The corresponding estimates for h_m^2, h_{ipe}^2 and h_{mpe}^2 were found to be 0.17, 0.14 and 0.16, respectively, with a decrease in direct heritability (h_a^2) to 52%.

The direct heritability estimate for 305-DMY was found to be 0.50 under the most suitable model i.e. model 1 in the present study (Table 3). This finding aligns closely with the value of 0.55 reported by Ratwan *et al.* (2015) in Jersey crossbred cattle. However, Lee and Han (2004), Amimo *et al*. (2007), Ankuya *et al.* (2016), Kumar *et al.* (2017) and Kaur *et al.* (2023) reported lower heritability values of 0.25, 0.12, 0.40, 0.32 and 0.30, respectively in various cattle breeds and its crosses. Additionally, Banik and Gandhi (2010) and Roman *et al.* (2000) reported lower heritability estimates of 0.22 and 0.26 in purebred Sahiwal and Jersey cattle, respectively. This discrepancy is likely due to a combination of additive genetic effect, heterosis and potentially reduced environmental variance, depending on adaptability to local conditions. Notably, no maternal genetic (m^2) or permanent environmental (c^2) effects contributed to the total phenotypic variance of 305-DMY, suggesting that the trait is predominantly influenced by direct genetic effect rather than by maternal or permanent environmental effects. However, Lee and Han (2004), Khattab *et al.* (2005) and Ratwan *et al.* (2019) reported maternal genetic (m^2) contributions of 4.5, 1 and 9%, respectively to the phenotypic variance of 305-DMY in Holstein, Friesian and Jersey crossbred cattle. Similarly, Ojango and Pollot (2001), Khattab *et al.* (2005) and Amimo *et al*. (2007) reported permanent environmental (c^2) contributions of 5, 13 and 26% in various dairy cattle breeds.

3.2 Total milk yield

Direct heritability estimates for TMY ranged from 0.25 to 0.53 across the six models. Model 1, which ignored maternal genetic and permanent environmental effects, produced the highest heritability (h_a^2) of 0.53 for direct additive genetic effect, while introducing either maternal genetic (Model 2) or an individual permanent environmental effect (Model 3), decreased the heritability (h_a^2) value from 0.53 to 0.38. The heritability estimates for maternal genetic (Model 2) or individual permanent environmental effects (Model 3) were found to explain 29% of total phenotypic variance, with corresponding decrease in direct heritability to 28%. Model 4, which included both maternal genetic and individual permanent environmental effects, further reduced the heritability to 0.30. Similarly, including maternal genetic and maternal permanent environmental effects (Model 5) resulted in heritability similar to that of Model 4. The heritabilities for maternal genetic (Models 4 and 5), individual permanent environmental (Model 4) and maternal permanent environmental (Model 5) effects were found to be 0.23, 0.21 and 0.21, respectively. Model 6, which included maternal genetic effect along with both individual and maternal permanent environmental effects, resulted in the lowest heritability of 0.25. The corresponding estimates for h_m^2, h_{ipe}^2 and h_{mpe}^2 were found to explain 19, 16 and 17% of total phenotypic variance, respectively.

Direct heritability estimate for TMY was observed as 0.53 under model 1, which was closely consistent with the estimate of 0.50 reported by Ratwan *et al.* (2015) in Jersey crossbred cattle. However, Dubey and Singh (2005) reported higher heritability value of 0.69 in Jersey x Sahiwal cattle. As compared to the present study, Singh and Gurnani (2004), Haile *et al*. (2009), Saha *et al*. (2010) and Gorbani *et al.* (2011) reported relatively lower heritability values, ranging from 0.10 to 0.41 across various dairy cattle breeds. Similarly, Banik and Gandhi (2010), Javed *et al*. (2001) and Singh and Singh (2016) reported lower heritability estimates of 0.10, 0.013 and 0.25 in purebred Sahiwal cattle. These lower estimates could be due to differences in breed composition, environmental adaptability and methodological differences in genetic evaluations. No contribution of maternal genetic (m^2) or permanent environmental (c^2) effects to the total phenotypic variance of total milk yield was observed in this study. However, Boujenane (2002) reported 5% contribution of the permanent environmental (c^2) effect to the phenotypic variance of total milk yield in Holstein Friesian cattle.

3.3 Lactation length

Estimates of direct heritability for lactation length based on the model used varied from 0.23 to 0.42. Model 1, which ignored both maternal genetic and permanent environmental effects, produced the highest heritability (h_a^2) of 0.42 for direct additive effect. Fitting either maternal genetic effect (Model 2) or an individual permanent environmental effect (Model 3) decreased the heritability (h_a^2) value from 0.42 to 0.23 and 0.24, respectively. Models 2 and 3 yielded estimates of h_m^2 and h_{ipe}^2 that explained only 5% and 35% of the phenotypic variance, respectively. Model 4, which accounted for both maternal genetic and individual permanent environmental effects, did not significantly improve the heritability compared to models 2 and 3. Similarly, introducing maternal genetic and maternal permanent environmental effects in Model 5 did not lead to significant improvement in heritability values. The heritabilities of maternal genetic (models 4 and 5), individual permanent environmental (model 4) and maternal permanent environmental (model 5) effects were found to explain only 3, 32 and 1% of phenotypic variance, respectively. Model 6, which included maternal genetic as well as individual and maternal permanent environmental effects, produced estimates similar to those from models 2, 3, 4 and 5 with no significant improvement in the heritability of the direct additive genetic effect. Consequently, the estimates for maternal genetic, individual permanent environmental and maternal permanent environmental effects from model 6 were nearly identical to those from the other models.

Direct heritability (h^2) value for lactation length was noted to be 0.42 under the best-fitted model (model 1), indicating a moderate genetic influence on this trait. In comparison to the present study, Ojango and Pollot (2001), Lakshmi *et al.* (2010) and Al-Samarai *et al.* (2015) reported significantly lower heritability estimates of 0.08, 0.06 and 0.06 for lactation length in different breeds of dairy cattle. Similarly, Banik and Gandhi (2010) and Javed *et al*. (2001) noted very low heritability values of 0.09 and 0.06 in purebred Sahiwal cattle. Additionally, there is no contribution of maternal genetic (m^2) or permanent environmental (c^2) effects to the phenotypic variance of lactation length, suggesting that direct genetic factors are the primary drivers of this trait in the current population. In contrast, Ojango and Pollot (2001) found 3% contribution of permanent environmental (c^2) effect on lactation length in Holstein Friesian cattle.

3.4 Peak yield

Depending on the model used, direct heritability estimates for peak yield ranged from 0.11 to 0.15. Model 1, which ignored both maternal and permanent environmental effects, produced higher estimates of σ_a^2 and h_a^2 compared to other models. When maternal genetic effect was included (Model 2), it significantly explained 28% of the total phenotypic variance, causing direct heritability value to decrease to 0.11. In model 3, an individual permanent environmental effect accounted for 39% of the total phenotypic variance, but did not significantly change the heritability (h_a^2) value compared to model 1. Model 4, which included both maternal genetic and individual permanent environmental effects, did not significantly improve the heritability value compared to model 2. Adding maternal genetic and maternal permanent environmental effects (Model 5) also gave no significant improvement in the heritability estimate compared to models 2 and 4. The heritabilities of maternal genetic effect in models 4 and 5 were estimated as 0.28 and 0.14, respectively, whereas for an individual permanent environmental (model 4) and maternal permanent environmental (model 5) effects, they were found to explain only 27 and 13% of phenotypic variance, respectively. Model 6, which included maternal genetic as well as both individual and maternal permanent environmental effects, produced results similar to models 2, 4 and 5, with no significant improvement in the direct heritability value. Consequently, the estimates of h_m^2, h_{ipe}^2 and h_{mpe}^2 from model 6 were almost similar to those from models 4 and 5.

Direct heritability estimate for peak yield was identified as 0.15 under model 3, indicating relatively low genetic influence on this trait. This value was in accordance with the finding of 0.16 reported by Lakshmi *et al.* (2010) in HF x Sahiwal cattle. In contrast, Rekaya *et al*. (2000), Dhaka *et al.* (2002), Deb *et al*. (2008) and Ratwan *et al.* (2019) found considerably greater heritability values, varying from 0.26-0.41 in various breeds of dairy cattle. Individual permanent environmental (c^2) effect was observed to be an important component while estimating heritability for peak yield and contributed 39% to the total phenotypic variance of this trait. This substantial contribution highlights the influence of non-genetic factors like management practices and environmental stability on peak yield. Recognizing the significant role of permanent environmental effect on peak yield could inform breeding and management strategies to optimize peak yield while considering both genetic potential and environmental stability.

Table 2. Estimates of variance components and genetic parameters for 305-day milk yield, total milk yield, lactation length and peak yield in Jersey x Sahiwal crossbred cattle

Traits	Model 1	Model 2	Model 3	Mod	Model 5	Model 6
305-day milk yield						
σ_a^2	15.035	13.505	13.505	13.505	13.505	14.546
σ_m^2	-	10.973	-	10.973	10.973	10.244
σ_{ipe}^2	-	-	10.973	9.646	-	8.485
σ_{mpe}^2	-	-	-	-	9.646	9.698
h_a^2	0.50±0.001	0.32±0.001	0.32±0.001	0.28±0.001	0.28±0.001	0.24±0.001
h_m^2	-	0.26±0.001	-	0.23±0.001	0.23±0.001	0.17±0.000
h_{ipe}^2	-	-	0.26±0.001	0.20±0.000	-	0.16±0.001
h_{mpe}^2	-	-	-	-	0.20±0.001	0.16±0.001
Total milk yield						
σ_a^2	16.039	16.078	16.078	16.078	16.078	16.157
σ_m^2	-	12.059	-	12.059	12.059	12.059
σ_{ipe}^2	-	-	12.059	11.054	-	10.049
σ_{mpe}^2	-	-	-	-	11.054	11.054
h_a^2	0.53±0.001	0.38±0.001	0.38±0.001	0.30±0.001	0.30±0.001	0.25±0.001
h_m^2	-	0.29±0.001	-	0.23±0.001	0.23±0.000	0.19±0.000
h_{ipe}^2	-	-	0.29±0.001	0.21±0.001	-	0.16±0.001
h_{mpe}^2	-	-	-	-	0.21±0.001	0.17±0.001
Lactation length						
σ_a^2	157.46	192.39	195.17	190.71	190.76	190.69
σ_m^2	-	44.418	-	24.154	13.545	12.435
σ_{ipe}^2	-	-	286.62	265.15	-	251.18
σ_{mpe}^2	-	-	-	-	12.416	11.398
h_a^2	0.42±0.043	0.23±0.041	0.24±0.041	0.23±0.041	0.23±0.041	0.23±0.041
h_m^2	-	0.05±0.053	-	0.03±0.053	0.02±0.000	0.01±0.053
h_{ipe}^2	-	-	0.35±0.008	0.32±0.059	-	0.31±0.059

h^2_{mpe}	-	-	-	-	0.01±0.053	0.01±0.000
Peak yield						
σ^2_a	0.657	0.461	0.657	0.461	0.461	0.461
σ^2_m	-	1.169	-	1.169	0.610	0.610
σ^2_{ipe}	-	-	1.692	1.176	-	1.114
σ^2_{mpe}	-	-	-	-	0.559	0.559
h^2_a	0.15±0.033	0.11±0.027	0.15±0.033	0.11±0.027	0.11±0.027	0.11±0.027
h^2_m	-	0.28±0.048	-	0.28±0.048	0.14±0.003	0.14±0.003
h^2_{ipe}	-	-	0.39±0.032	0.27±0.006	-	0.26±0.005
h^2_{mpe}	-	-	-	-	0.13±0.048	0.13±0.048

σ^2_a - direct additive genetic variance, σ^2_m - maternal genetic variance, σ^2_{ipe} - individual permanent environmental variance, σ^2_{mpe} - maternal permanent environmental variance, h^2_a - direct additive genetic heritability, h^2_m - maternal genetic heritability, h^2_{ipe} - individual permanent environmental heritability, h^2_{mpe} - maternal permanent environmental heritability

Table 3. Estimated parameters from the best model for lactation traits of Jersey x Sahiwal crossbred cattle

Trait	Model	σ^2_a	σ^2_m	σ^2_{ipe}	σ^2_{mpe}	h^2_a	h^2_m	h^2_{ipe}	h^2_{mpe}
305-DMY	1	15.035	-	-	-	0.50±0.001	-	-	-
TMY	1	16.039	-	-	-	0.53±0.001	-	-	-
LL	1	157.46	-	-	-	0.42±0.04	-	-	-
PY	3	0.657	-	1.692	-	0.15±0.033	-	0.39±0.032	-

4. CONCLUSIONS

The findings of this study emphasize the necessity of selecting appropriate models for accurately estimating variance components and genetic parameters associated with lactation traits in Jersey x Sahiwal crossbred cattle. While maternal genetic and maternal permanent environmental effects had minimal influence on the studied traits, their inclusion in the models improved overall model fitness and enhanced the accuracy of genetic evaluations.

Individual permanent environmental effects significantly influenced peak yield, underscoring the critical role of environmental factors in determining milk production potential. Direct additive genetic effects emerged as the primary contributors to 305-DMY, TMY and LL, reinforcing their significance in genetic improvement programs. Conversely, non-genetic factors played a crucial role in influencing peak yield, highlighting the need for an integrated breeding strategy that not only focuses on genetic selection but also prioritizes environmental optimization.

These results advocate for an integrated approach that combines genetic selection for economically important traits with strategic environmental management. By optimizing both genetic potential and environmental conditions, this approach ensures balanced and sustainable improvements in dairy productivity, contributing to the long-term success of crossbreeding programs.

ETHICAL STATEMENT

The data for this study were collected from dairy cattle managed under the Progeny Testing Program (PTP) of the Andhra Pradesh Livestock Development Agency (APLDA) in compliance with ethical guidelines for the care and use of farm animals. No experimental interventions or invasive procedures were conducted, and all data were obtained from routine performance records. Standard dairy farm management protocols were strictly followed to ensure animal welfare and ethical handling.

DISCLAIMER (Artificial Intelligence)

Author(s) hereby declare(s) that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

REFERENCES

Al-Samarai F R, Abdulrahman Y K, Mohammed F A, Al-Zaidi F H and Al-Anbari N N. (2015). Comparison of several methods of sire evaluation for total milk yield in a herd of Holstein cows in Yemen. *Open Veterinary Journal*, 5(1), 11-17.

Amimo J O, Wakhungu J W, Inyangala B O and Mosi R O. (2007). The effects of non-genetic factors and estimation of genetic and phenotypic parameters and trends for milk yield in Ayrshire cattle in Kenya. *Livestock Research for Rural Development,* 19(1), 13.

Ankuya K J, Pareek N K, Patel M P, Rathod B S, Prajapati K B and Patel J B. (2016). Genetic analysis of first lactation production traits in Kankrej cattle. *Veterinary world,* 9(6), 672.

Banik S and Gandhi R S. (2010). Estimation of genetic parameters in Sahiwal cattle using single and multi-trait restricted maximum likelihood method. *Indian Journal of Animal Sciences,* 80(3), 266–268.

Bell B R, McDaniel B T and Robison O W. (1985). Effect of cytoplasmic inheritance on production traits of dairy cattle. *Journal of Dairy Science*, 68, 2038–2051.

Bhutkar S S, Thombre B M and Bainwad D V. (2014). Effect of non-genetic factors on production traits in Deoni cows. *IOSR- Journal of Agriculture and Veterinary Science (IOSR-JAVS)*, 7(12), 9-14.

Boujenane I. (2002). Estimates of Genetic and Phenotypic Parameters for Milk Production in Moroccan Holstein-Friesian cows. *Revue d'Elevage et de Medicine Veterinaire des Pays Tropicaux*, 55(1), 63-67.

Deb GK, Mufti MM, Mostari MP and Huquel KS. (2008). Genetic Evaluation of Bangladesh Livestock Research Institute Cattle Breed-1: Heritability and Genetic Correlation. *Bangladesh Journal of Animal Sciences,* 37(2), 25-33.

Dhaka S S. (2002). Genetic Studies on Production Efficiency Traits in Hariana Cattle. *Asian-Australasian Journal of Animal Sciences (AJAS),* 15(4), 466-469.

Dubey PP and Singh CV. (2005). Estimates of genetic and phenotypic parameters considering first lactation and lifetime performance traits in Sahiwal and crossbred cattle. *Indian Journal of Animal Sciences*. 75(11), 1289-1294.

Gorbani A, Salamatdoust Nobar R, Mehman Navaz U, Gyasi J, Agdam Shahryar H and Nazer Adl, K. (2011). Heritability and Repeatability Estimation in Iranian Brown Swiss Crossbred Dairy Cattle Population. *International Journal of Animal and Veterinary Advances,* 3(4), 335-337.

Haile A, Joshi B K, Ayalew W, Tegegne A and Singh A. (2009). Genetic evaluation of Ethiopian Boran cattle and their crosses with Holstein Friesian in central Ethiopia: milk production traits. *Animal – An International Journal of Animal Bioscience,* 3(4), 486-493.

Harvey W R. (1990). Guide for LSMLMW, PC-1 Version, mixed model least squares and maximum likelihood computer programme. Mimeograph Ohio State University, USA.

Hazel L N, Dickerson G E and Freeman A E. (1994). Symposium: Selection index theory; The selection index – then, now, and for the future. *Journal of Dairy Science,* 77, 3326–51.

Japheth K P, Mehla R K, Imtiwati and Bhat S A. (2015). Effect of non-genetic factors on various economic traits in Karan Fries crossbred cattle. *Indian Journal of Dairy Science*, 68(2), 163-169.

Javed K, Mohiuddin G and Akhtar P. (2001). Heritability estimates of some productive traits in Sahiwal cattle. *Pakistan Veterinary Journal*, 21(3), 114-117.

Kaur S, Ghosh A K and Shahi B. (2023). Assessment of genetic parameters for first lactation production traits in crossbred cattle in India. *Journal of Animal Research,* 13(1), 33-41.

Khattab A S, Atil H and Badawy L. (2005). Variances of direct and maternal genetic effects for milk yield and age at first calving in a herd of Friesian cattle in Egypt. *Archives Animal Breeding,* 48(1), 24-31.

Kumar S R and Subramanyachary P. (2015). Major agricultural crops in Chittoor district. *PARIPEX–Indian Journal of Research*, *4*(5).

Kumar S. (2017). Productive and Reproductive Performance of Jersey x Sahiwal Crossbred progeny under Progeny Testing Programme in Chittoor district of Andhra Pradesh. M.V.Sc. Thesis submitted to Sri Venkateswara Veterinary university, Tirupati, Andhra Pradesh, India.

Lakshmi S B, Gupta B R, Prakash M G, Sudhakar K and Sharma S. (2010). Genetic analysis of the production performance of Frieswal cattle. *Tamilnadu Journal of Veterinary and Animal Sciences,* 6(5), 215-222.

Lee D H and Han K J. (2004). Genetic Parameters of Milk Yield and Milk Fat Percentage Test Day Records of Iranian Holstein Cows. *Asian-Australasian Journal of Animal Sciences (AJAS),* 17(2), 153-158.

Meyer K. (1992). Variance components due to direct and maternal effects for growth traits of Australian beef cattle. *Livestock Production Science,* 31, 179–204.

Mrode, R. (2013). *Linear models for the prediction of animal breeding values* (3rd ed.). CABI publishing.

Nasholm A and Danell O. (1994). Maternal genetic effects on lamb weights. Proceedings of the Fifth World Congress on Genetics Applied to Livestock Production, Guelph, Canada. Pp 163– 166.

Ojango J M K and Pollot G E. (2001). Genetics of milk yield and fertility traits in Holstein-Friesian cattle on large scale Kenyan farms. *Journal of Animal Sciences,* 79(7), 1742-1750.

Ratwan P, Kumar M, Chakravarty A K and Mandal A. (2019). Estimation of direct and maternal (co) variance components for lactation traits in Jersey crossbred cattle at an organized farm. *Indian Journal of Animal Sciences*, 89(2), 193-199.

Ratwan P, Mandal A, Kumar M, Kumar A and Chakravarty A K. (2016). Genetic analysis of lactation traits in Jersey crossbred cattle. *Indian Journal of Dairy Science*, 69(2), 1-4.

Ratwan P. (2015). Genetic analysis of lactation traits of crossbred cattle. M.V.Sc. Thesis submitted to ICAR-National Dairy Research Institute, Karnal (Haryana), India.

Rekaya R, Carabano M J and Toro M A. (2000). Bayesian analysis of lactation curves of Holstein-Friesian cattle. *Journal of Dairy Science,* 83(11), 2691–2701.

Roman R M, Wilcox C J and Martin F G. (2000). Estimates of repeatability and heritability of productive and reproductive traits in a herd of Jersey cattle. *Genetics and Molecular Biology*, 23(1), 113-119.

Rumph J M, Koch R M, Gregory K E, Cundiff L V and Van Vleck L D. (2002). Comparison of models for estimation of genetic parameters for mature weight of Hereford cattle. *Journal of Animal Science,* 80, 583–590.

Saha S, Joshi B K and Singh A. (2010). Generation wise genetic evaluation of various first lactation traits and herd life in Karan Fries cattle. *Indian Journal of Animal Sciences,* 80(5), 451-456.

Singh J and Singh CV. (2016). Genetic and Phenotypic Parameters of First Lactation and Life Time Traits in Sahiwal Cows. *Journal of Veterinary Science and Technology*, 7(4), 1-3.

Singh M K and Gurnani M. (2004). Performance Evaluation of Karan Fries and Karan Swiss Cattle under closed Breeding System. *Asian-Australasian Journal of Animal Sciences,* 17(1), 1-6.

Verma M K, Sachdeva G K, Yadav A K, Gautam S, Ali M M and Bindal S. (2016). Effect of genetic and non-genetic factors on milk yield and milk constituents on Sahiwal cattle. *Indian Journal of Animal Research*, 50(5), 808-810.