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

ABSTRACT

A total of 4,877 first lactation performance records of Jersey x Sahiwal crossbred cattle, maintained under the progeny testing program in Chittoor district, Andhra Pradesh were utilized for this study. Variance components and genetic parameters for 305-day milk yield (305-DMY), total milk yield (TMY), lactation length (LL) and peak yield (PY) were estimated using Derivative Free Restricted Maximum Likelihood (DFREML) method (Meyer, 1998). Six univariate animal models were fitted for each trait by including or excluding maternal additive genetic (m²) and permanent environmental (c²) effects. Selection of the best-fitted model for each trait was based on AIC, BIC and log-likelihood values. Direct heritability estimates were moderate to high, with values of 0.50, 0.53, 0.42 and 0.15 for 305DMY, TMY, LL and PY, respectively. Maternal genetic (m²) and permanent environmental (c²) effects were insignificant contributors to 305-DMY, TMY and LL, whereas individual permanent environmental effects (c²) accounted for 39% of the total phenotypic variance in PY. These findings suggest the importance of including individual permanent environmental effect (c²) in selection programs for peak yield and confirm the potential for genetic improvement of lactation traits under the current environment and managemental conditions.

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%. Understanding the interplay between maternal and direct genetic effects is essential for refining selection strategies and optimizing breeding programs. 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 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

The present study utilized first lactation performance records of 4,877 daughters belonging to 176 Jersey x Sahiwal crossbred bulls, maintained under the progeny testing program in Chittoor district, Andhra Pradesh, over 10 years (2014 to 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). The characteristics of data structure for various lactation traits of Jersey x Sahiwal crossbred cattle are summarized in Tables 1.

Table 1. Characteristics of data structure for lactation traits in Jersey x Sahiwal

Items	305-days milk yield	Total milk yield	Lactation length	Peak yield
No. of records	4877	4877	4877	4877
No. of animals	4877	4877	4877	4877
No. of sires with progeny record	176	176	176	176
No. of dams with progeny record	4456	4456	4456	4456
Period of data	2014–2023	2014–2023	2014–2023	2014–2023

crossbred cattle

Statistical analysis

Variance components and heritabilities for various lactation traits were estimated by fitting six univariate animal models using the Derivative-Free Restricted Maximum Likelihood (DFREML) algorithm (Meyer, 1998). These models varied by including or excluding maternal genetic (m²) and permanent environmental (c²) effects. The best-fitted model for each trait was determined based on AIC, BIC and log-likelihood values. 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:

$y = Xb + Z_a a + e$	model 1
$y = Xb + Z_a a + Z_m m + e$	model 2
$y = Xb + Z_a a + Z_{pe} ipe + e$	model 3
$v = Xb + Z_aa + Z_mm + Z_{ne}ipe$	model 4

$$y = Xb + Z_aa + Z_mm + Z_{mpe}mpe + e model 5$$
$$y = Xb + Z_aa + Z_mm + Z_{pe}ipe + Z_{mpe}mpe + e model 6$$

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 X, Z_a, Z_m, Z_{pe} and Z_{mpe}. It was assumed that

$$V(a) = A\sigma_a^2$$
, $V(m) = I\sigma_m^2$, $V(ipe) = I\sigma_{ipe}^2$, $V(mpe) = I\sigma_{mpe}^2$ and $V(e) = I\sigma_e^2$

where, **A** is the numerator relationship matrix, **I** is the identity matrix and $\sigma_a^2, \sigma_m^2, \sigma_{pe}^2, \sigma_{mpe}^2$ and σ_e^2 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 ($h_a^2 = \sigma_a^2/\sigma_p^2$), maternal heritability ($h_m^2 = \sigma_m^2/\sigma_p^2$) and individual or maternal permanent environmental variance as a proportion of phenotypic variance ($h_{ipe}^2 = \sigma_{ipe}^2/\sigma_p^2$ or $h_{mpe}^2 = \sigma_{mpe}^2/\sigma_p^2$).

3. RESULTS AND DISCUSSION

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. Notably, no maternal genetic (m²) or permanent environmental (c²) 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. As compared to the present study, Singh and Gurnani (2004), Haile et al. (2009), Banik and Gandhi (2010), 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. These lower estimates could be due to differences in breed composition, environmental factors or genetic evaluation methodologies. No contribution of maternal genetic (m²) or permanent environmental (c²) 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 (h²) 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. Additionally, there is no contribution of maternal genetic (m²) or permanent environmental (c²) 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 (c²) effect on lactation.

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 (c²) 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 nongenetic 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		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±0.00				
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	0.29±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_{mpe}^2	-	-	-	-	0.01±0.053	0.01±0.000			
Peak yield									
σ_a^2	0.657	0.461	0.657	0.461	0.461	0.461			
σ_m^2	-	1.169	-	1.169	0.610	0.610			
σ_{ipe}^2	-	-	1.692	1.176	-	1.114			
σ^2_{mpe}	-	-	-	-	0.559	0.559			
h_a^2	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_m^2	-	0.28±0.048	-	0.28±0.048	0.14±0.003	0.14±0.003			
h_{ipe}^2	-	-	0.39±0.032	0.27±0.006	-	0.26±0.005			
h_{mpe}^2	-	-	-	-	0.13±0.048	0.13±0.048			

 σ_a^2 - direct additive genetic variance, σ_m^2 - maternal genetic variance, σ_{ipe}^2 - individual permanent environmental variance, σ_{mpe}^2 - maternal permanent environmental variance, h_a^2 - direct additive genetic heritability, h_m^2 - maternal genetic heritability, h_{ipe}^2 - individual permanent environmental heritability, h_m^2 - maternal permanent environmental heritability

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

Trait	Model	σ_a^2	σ_m^2	σ_{ipe}^2	σ^2_{mpe}	h_a^2	h_m^2	h_{ipe}^2	h_{mpe}^2
305-	1	15.035	1	-	-	0.50±0.001	-	-	-
DMY									
ТМҮ	1	16.039	-	-	-	0.53±0.001	-	-	-
LL	1	157.46	-	-	-	0.42±0.04	-	-	-
РҮ	3	0.657	-	1.692	-	0.15±0.033	-	0.39±0.032	-

4. CONCLUSIONS

The findings of this study highlight the importance of selecting appropriate models for estimating variance components and genetic parameters for lactation traits in Jersey x Sahiwal

crossbred cattle. Maternal genetic and maternal permanent environmental effects have minimal influence on the studied traits. Although, these effects were not found to significantly affect the traits, their inclusion in the models is recommended as it enhances model fitness and improves the accuracy of genetic evaluation. Individual permanent environmental effects significantly influenced peak yield, emphasizing the importance of integrating both genetic and environmental factors in breeding strategies. Direct additive genetic effects were the primary contributors to 305-DMY, TMY and LL, highlighting their significance in genetic improvement programs. Conversely, non-genetic factors significantly affected peak yield, suggesting the value of effective environmental management. These results advocate a combined approach that focuses on genetic selection for key traits while optimizing environmental conditions to maximize genetic potential, ensuring balanced and sustainable dairy productivity improvements.

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.

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