



Bayesian Estimation of Heritability, Repeatability, and Genetic Correlations in Crossbred Jersey Cattle

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

In animal breeding programs, estimating genetic parameters such as heritability, repeatability, and genetic correlation is crucial for assessing breeding value, forecasting genetic progress in selection programs, and improving breeding strategies. Since both populations and environments evolve over time, genetic parameters must be updated frequently. In this study, the genetic parameters of economically significant traits in crossbred Jersey cattle were evaluated using univariate and multi-trait repeatability animal models with a Bayesian approach. The posterior mean of Heritability estimates for lactation milk yield, lactation length, calving interval, dry period, services per conception, and service period were 0.43 ± 0.21 , 0.26 ± 0.20 , 0.18 ± 0.15 , 0.23 ± 0.17 , 0.13 ± 0.10 , and 0.17 ± 0.13 respectively and estimates of repeatability for the corresponding traits were 0.75 ± 0.11 , 0.53 ± 0.17 , 0.32 ± 0.17 , 0.41 ± 0.17 , 0.23 ± 0.10 , and 0.31 ± 0.13 . Moderate heritability values for lactation milk yield and lactation length suggest that there is sufficient additive genetic variability to achieve genetic improvement through selection. The moderate repeatability estimates for traits such as lactation milk yield, lactation length, and calving interval indicate the potential for early evaluation of crossbred cattle for selection purposes. Negative genetic correlations were found between productive traits (such as lactation milk yield and lactation length) and reproductive traits (such as services per conception), with values ranging from 0.17 to 0.26. Additionally, strong negative genetic correlations were observed between lactation milk yield, lactation length, and dry period. These findings highlight the importance of giving attention to reproductive traits when selecting high-yielding crossbred Jersey dairy cattle, as the negative correlation suggests that an increase in production may adversely affect reproductive performance.

Keywords: Heritability; repeatability; genetic correlation; crossbred Jersey cattle; economic traits.

1. INTRODUCTION

The genetics of a metric character revolves around the study of its variation, as variation forms the foundation for answering key genetic questions. The primary objective in studying variation is to break it down into components attributed to different causes, which helps define the genetic characteristics of a population. By partitioning variance into its contributing factors, we can estimate the influence of various determinants on the phenotype, particularly the relative contributions of heredity (nature) and environment (nurture). The importance of each source of variation is measured by its proportion of the total phenotypic variance. Key genetic parameters, such as heritability, genetic correlation, and repeatability, are derived from these variance components (Falconer and Mackay, 1996).

In animal breeding genetic evaluation, models and algorithms play a crucial role, with Restricted Maximum Likelihood (REML) and Bayesian methods being particularly important for estimating (co)variance components and genetic parameters (Thompson 2008; Worku et al., 2021). REML is commonly employed to estimate variance components and genetic parameters for traits of economic significance in animal breeding (Neumaier and Groeneveld, 1997; Ghavi

Hosseini-Zadeh 2017; Dige et al., 2021; Ehsaninia, 2021; Choudhary et al., 2023; Koçak et al., 2024). The Bayesian method has advantages over REML, especially in handling data with small sample sizes (Carneiro Junior et al., 2007) and offering more precise heritability estimates when data do not follow a normal distribution (Jensen et al., 1994). Unlike REML, the Bayesian method does not rely on assumptions about the distribution and variance of estimators (Lopes et al., 2017). Several studies (Ødegård et al., 2010; Malhado et al., 2012; Ghavi Hosseini-Zadeh, 2017; Rajendran et al., 2022; Balasundaram et al., 2023) highlight the use of Bayesian approaches in estimating (co)variance components and genetic parameters for animal breeding. An important feature of Bayesian methods is their ability to guarantee positive variance estimates and provide interval estimates, such as the highest posterior density (HPD) region (Pretorius and van der Merwe, 2000). Moreover, the Markov Chain Monte Carlo (MCMC) method has had a significant impact on applied statistics, particularly within Bayesian frameworks, for estimating genetic parameters in linear mixed-effect models (Sorensen and Gianola, 2002; Hallander et al., 2010).

In animal breeding, estimating genetic parameters is crucial. Understanding the genetic

mechanisms of traits of interest, including additive and potentially non-additive genetic variances, enables breeders to make informed decisions. Furthermore, estimates of genetic and phenotypic variances and covariances are essential for predicting breeding values (using methods like the selection index and BLUP) and forecasting the genetic response to selection in breeding programs (Bourdon 2000). In dairy cattle breeding, traits like lactation milk yield, lactation length, calving interval, dry period, services per conception, and service period are economically valuable. These traits are relatively easy to measure, have heritability ranging from low to high, and respond well to selection. To improve these traits through selection, reliable genetic parameter estimates for the population are needed. This information is particularly important in designing breeding programs for crossbred Jersey cattle, which are crucial for milk production in southern India, where there is a scarcity of pure milch breeds. Southern Indian states, especially Tamil Nadu, rely heavily on crossbred Jersey cattle for dairy production, and a state breeding policy encourages farmers to rear these cattle. However, there are limited studies on crossbred Jersey cattle (Jersey x nondescript) in the region (Vijayakumar et al., 2019; Vijayakumar et al., 2021; Kasiviswanathan et al., 2023). Therefore, this investigation aimed to estimate heritability, repeatability, and genetic correlation in crossbred Jersey dairy cattle using a univariate and multi-trait repeatability animal model with a Bayesian approach.

2. MATERIALS AND METHODS

2.1 Herd Structure and Farm Management Practices

This study was conducted at the Dairy Unit of the Livestock Farm Complex at the Veterinary College and Research Institute in Salem, Tamil Nadu, India, involving crossbred Jersey cows (Jersey x nondescript). The exact genetic composition of these crossbred cows, in terms of the Jersey and nondescript inheritance levels, is not known, but the population includes varying levels of inheritance from both. All animals were managed under the same environmental conditions and followed a consistent management system. They were kept in an intensive management system, receiving a daily diet of 20-30 kg green fodder, 5-7 kg dry fodder, and 2 kg of concentrate feed, with an additional 400 g of feed per kg of milk production. Milking occurred twice daily at 12-hour intervals, and

periodic disease screenings and vaccinations were routinely carried out. Estrus detection was monitored, and artificial insemination was performed 12 hours after the first signs of estrus.

2.2 Data Analysis

Data for the study were collected from farm records over a three-year period (2021-2024), including 47 records from 25 crossbred Jersey cattle. Records that were incomplete due to death or disposal were excluded from the analysis. To ensure a normal distribution, outliers exceeding two standard deviations from the mean were removed. The study focused on six economic traits: lactation length (days), lactation milk yield (liters), calving interval (days), services per conception, dry period (days), and service period (days). Two non-genetic factors were analyzed: the season of calving (divided into four seasons: cold weather, summer, southwest monsoon, and northeast monsoon) and parity (divided into six groups: first, second, third, fourth, fifth, and sixth or more). A general linear model analysis was conducted using the IBM SPSS Statistics package to determine the effects of non-genetic factors on the production and reproduction traits. Significant non-genetic factors were then incorporated into the model as fixed effects.

Variance and covariance components for the studied traits were estimated using both univariate and multi-trait repeatability animal models, applying a Bayesian approach. The general description of the models in matrix forms is given below:

$$Y = X\beta + Za + Wp + e$$

where Y is a vector of observed traits, X, Z, and W are incidence matrices related to fixed, additive genetic, and permanent environmental effects, respectively, while, β , a, p, and e are vector of fixed effects, vector of additive genetic random effects, vector of random animal permanent environmental effects and vector of random residual effects, respectively. The fully conditional posterior distributions for genetic, permanent environmental, and residual matrices were assumed to be an inverted Wishart distribution (Sorensen and Gianola, 2007). The permanent environmental effect due to the repeated records per animal was considered as additional random effects for the analysis of lactation length, lactation milk yield, calving

interval, services per conception, dry period, and service period.

The genetic analysis of data was carried out using the BLUPF90 family of programs (Misztal et al., 2015). The dataset was first renumbered and processed through RENUMF90. For estimating the posterior densities of variance and covariance components, the Gibbs sampler method was employed. A single long chain of 100,000 iterations was run, with the first 20,000 iterations discarded as burn-in. After this burn-in phase, every 10th iteration was stored for subsequent analysis. To assess the convergence of the Gibbs chains, graphical inspections (trace-plots) of selected parameters were performed. These plots confirmed that the burn-in period was sufficient to achieve convergence for all estimated parameters. A total of 8,000 effective samples were generated and used for the calculation of variance components. Estimates of heritability, repeatability, and correlations (both genetic, and permanent environmental) were computed using the GIBBS3F90 and POSTGIBBSF90 programs (Misztal et al., 2015).

3. RESULTS AND DISCUSSION

Polygenic traits are influenced by so many genes that it is nearly impossible to pinpoint the effects of specific loci or alleles. As a result, identifying an individual's exact genotype for such traits is not feasible. Instead, the practical approach is to assess the overall impact of the individual's many genes on the trait, which involves measuring the individual's performance and estimating their breeding value, along with other related genetic values. This assessment relies on statistical tools and concepts, such as heritability and repeatability, to quantify and predict the genetic contribution to the trait's variation (Bourdon, 2000).

3.1 Heritability

The core concept in studying variation involves breaking it down into components linked to various causes. The relative magnitude of these components determines the genetic properties of the population, in particular the degree of resemblance between relatives (i.e., the heritability). Heritability is one of the most crucial characteristics of a quantitative trait, reflecting the proportion of total variance attributed to

additive genetic variance, which influences familial resemblance. Its main role in genetic studies is predictive, as it indicates how accurately phenotypic values can predict breeding values. While phenotypic values are directly observable, breeding values determine an individual's impact on the next generation. Therefore, a breeder's success in altering population traits depends on the degree to which phenotypic values correspond to breeding values, a relationship measured by heritability. Defined as the ratio of additive genetic variance to phenotypic variance, heritability is a key factor in nearly all breeding-related calculations and decisions (Falconer and Mackay, 1996). High heritability means phenotypic values reliably reflect breeding values, making phenotypic selection effective, whereas low heritability weakens this correlation and makes phenotypic selection less effective.

Heritability estimates of calving interval estimated in this study was 0.18 ± 0.15 (Table 1). This was in concordance with heritability estimates reported by Ratwan et al. (2019a) in Sahiwal cattle. Vinothraj et al. (2016) and Vijayakumar et al. (2021) reported higher estimates of heritability in Jersey crossbred cattle. Ali et al. (2019), Worku et al. (2021), Ratwan et al. (2024) and Roy et al. (2024) reported lower heritability estimates for calving intervals in different dairy cattle breeds. The heritability estimates for services per conception (0.13 ± 0.10) of crossbred Jersey herd (Table 1) are higher than the earlier reports of Roy et al. (2024) and Sarma et al. (2024). However, Ratwan P et al. (2019a) reported higher estimates of heritability (0.24) for services per conception in Sahiwal cattle.

The service period is an important trait of dairy animals and directly impacts the calving interval period. The estimated heritability of the service period is 0.17 ± 0.13 (Table 1), which was in close agreement with the results of Ratwan P et al. (2019a) for Sahiwal cattle. However, higher estimates of heritability were reported for Jersey crossbreds (Vijayakumar et al., 2021; Sarma et al., 2024). Heritability is not constant; it varies across populations and environments. Each trait has a distinct heritability in a specific population, and while similar traits may show similar heritability across populations, environmental and genetic differences can cause significant variation.

Table 1. Posterior means of variance components, heritability, and repeatability for various production and reproduction traits in crossbred Jersey cattle

Traits	σ^2_a	σ^2_{Eg}	σ^2_e	σ^2_p	$h^2 \pm PSD$	c^2	$r \pm PSD$
Lactation milk yield	345490	266290	200440	812220	0.43 \pm 0.21	0.328	0.75 \pm 0.11
Lactation length	1688.3	1795.3	3115.5	6599.1	0.26 \pm 0.20	0.272	0.53 \pm 0.17
Dry period	2588.8	2139.6	6679.5	11407.9	0.23 \pm 0.17	0.188	0.41 \pm 0.17
Services per conception	0.30539	0.22451	1.7352	2.2651	0.13 \pm 0.10	0.099	0.23 \pm 0.10
Calving interval	2850	2212	10999	16061	0.18 \pm 0.15	0.138	0.32 \pm 0.17
Service period	2859	2214.4	11270	16343.4	0.17 \pm 0.13	0.135	0.31 \pm 0.13

σ^2_a -additive genetic variance; σ^2_{Eg} - general environmental variance; σ^2_e - residual variance; σ^2_p -phenotypic variance; h^2 -heritability; r -repeatability; PSD-posterior standard deviation, c^2 -permanent environmental variance proportion (ratio of the permanent environmental variance to total variance)

The present study lactation milk yield heritability estimate was 0.43 \pm 0.21 for crossbred Jersey herd, which is higher than the earlier report of Vijayakumar et al. (2021) for crossbred Jersey cattle. However, Hadge et al. (2012), Worku et al. (2021), Ratwan et al. (2024) and Sarma et al. (2024) reported a lower heritability estimate of dairy cows. Previous works of the literature showed that heritability estimates of the lactation milk yield ranged widely from 0.06 to 0.69 (Dubey and Singh, 2005; Cilek and Sahin, 2009; Hadge et al., 2012; Singh and Singh, 2016; Ali et al., 2019).

The present study lactation length heritability estimate was 0.26 \pm 0.20 for crossbred Jersey herd, which was in concordance with the results of Sarma et al. (2024) for Frieswal cattle. However, Worku et al. (2021), and Ratwan et al. (2024) reported a lower heritability estimate of lactation length for Indian Karan-Fries and Sahiwal cows. In the present study, the heritability of dry period was 0.23 \pm 0.13. Similar estimates of heritability were observed by Vinothraj et al. (2016) in Jersey crossbred cattle. Ali et al. (2019) and Sarma et al. (2024) reported 0.11 \pm 0.124 and 0.08 \pm 0.06 heritability estimates of dry period which are comparatively lower than present result. Hadge et al. (2012) observed higher estimates of heritability of dry period in Sahiwal x Jersey crossbred cows.

3.2 Repeatability

Repeatability measures the strength of the relationship between repeated records (or phenotypic values) of a trait within a population. When multiple measurements can be taken for a character from the same individual, phenotypic variance can be split into two parts: within-individual variance and between-individual variance. The within-individual variance is

entirely environmental, stemming from temporary environmental changes between performances. The between-individual variance is partly genetic and partly environmental, with the environmental component arising from long-term influences. The temporary within-individual environmental variance is called special environmental variance (V_{Es}), while the permanent, between-individual environmental variance is called general environmental variance (V_{Eg}). Repeatability is then defined as the ratio of between-individual variance to total phenotypic variance, expressed as $r=(V_G+V_{Eg})/V_P$. The repeatability has three main functions: (1) determining the value of repeated measurements, (2) setting an upper limit for both the degree of genetic determination (V_G/V_P) and heritability (V_A/V_P), and (3) predicting future performance from past records (Falconer and Mackay, 1996). Repeatability is often easier to estimate than genetic determination or heritability and can be useful even when these other ratios are unknown. While heritability is usually lower than repeatability, the latter still provides helpful insight, especially when heritability data is unavailable. Understanding repeatability can guide decisions like culling based on an animal's performance records (Bourdon 2000).

The posterior mean of repeatability estimates for lactation milk yield (0.75 \pm 0.11) and lactation length (0.53 \pm 0.17) were moderately repeatable (Table 1). In contrast, Thakkar et al. (2019), Worku et al. (2021) and Ratwan et al. (2024) were reported lower repeatability estimate for total milk yield in dairy cattle. Repeatability varies based on the trait's nature, the population's genetics, and environmental conditions. The moderate repeatability estimates found for lactation milk yield and lactation length of the current study implies that information from first parity could be used for early prediction of

estimated breeding value and selection. Knowing repeatability helps assess the potential improvement in accuracy from multiple measurements. If repeatability is high, repeated measurements offer little additional value; if it is low, more measurements significantly improve accuracy.

In the current study, the posterior mean of repeatability estimates for calving interval was 0.32 ± 0.17 , whereas, for service period was 0.31 ± 0.13 (Table 1). Besides, Vinothraj et al. (2016) reported lower repeatability estimates for calving interval and service period were 0.234 ± 0.06 and 0.219 ± 0.06 in Jersey crossbred cattle respectively. The repeatability of services per conception was 0.23 ± 0.10 in crossbred Jersey cows. The low repeatability estimate obtained in this study suggests the influence of temporary environmental factors on services per conception of crossbred Jersey cows. With respect to dry period, the repeatability estimate was 0.41 ± 0.17 . Our result in line with estimates of repeatability for dry period was 0.420 ± 0.06 for crossbred Jersey dairy cattle in tropical environment (Vinothraj et al., 2016). In contrast, Thakkar et al. (2019) reported higher repeatability estimate (0.48 ± 0.04) for dry period in Kankrej cattle.

3.3 Genetic Correlation

Correlated characters refer to the relationships between two measurable traits, particularly those that show either a positive or negative correlation within individuals of a population. The covariance between two traits is divided into genetic and environmental components, corresponding to the genetic and environmental correlations. Genetic correlation refers to the correlation between breeding values, while environmental correlation includes both environmental deviations and non-additive genetic effects. In genetic studies, it is important to distinguish between the genetic and environmental causes of these correlations. The genetic correlation is primarily due to pleiotropy, where a single gene influences multiple traits, though linkage can also cause temporary correlations (Falconer and Mackay, 1996). The studying the correlated characters are of interest for the understanding the effects of selection, as improving one trait can lead to simultaneous changes in other traits (Bourdon, 2000).

The genetic correlations (r_g) between production and reproduction traits ranged from high to low, 0.93 ± 0.15 between lactation milk yield and

lactation length, 0.48 ± 0.60 between service period and services per conception, 0.45 ± 0.64 between dry period and services per conception, 0.34 ± 0.69 between calving interval and services per conception, 0.39 ± 0.66 between calving interval and lactation length, 0.29 ± 0.69 between calving interval and dry period, and 0.28 ± 0.68 between calving interval and milk yield (Table 2). Specifically, a strong positive genetic correlation between lactation milk yield and lactation length (0.93 ± 0.15) suggests a pleiotropic effect, where genes that enhance milk yield also extend lactation length. This means that cows with longer lactation periods tend to produce more milk, a finding supported by earlier studies (Goshu et al., 2014; Ratwan et al., 2019b; Ayalew et al., 2017; Ali et al., 2019; Worku et al., 2021; Roy et al., 2024). Favourable genetic correlations among production traits have also been observed in prior research (Ayalew et al., 2017; Goshu et al., 2014; Gebreyohannes et al., 2013; Worku et al., 2021). However, moderate positive genetic correlations between service period, and calving interval (0.48 ± 0.60) suggest an antagonistic relationship, indicating competition between fertility and production traits for body resources, consistent with previous findings (Strucken et al., 2012). When traits exhibit low heritability, the phenotypic correlation is predominantly influenced by environmental factors, whereas with high heritability, the genetic correlation plays a larger role.

Negative correlations were found between production traits (lactation milk yield and lactation length) and the dry period, as well as between production traits and services per conception, echoing unfavourable correlations reported in other studies (Makgahlela et al., 2007; Ratwan et al., 2019b; Ali et al., 2019; Worku et al., 2021; Ratwan et al., 2024; Roy et al., 2024). These findings suggest that improving environmental conditions and management practices, along with enhancing genetic potential, could be effective strategies for boosting milk production (Ali et al., 2019).

Permanent environmental correlations (r_{pe}) varied from low to high, ranging from 0.07 to 0.95. Lactation length showed a high permanent environmental correlation (0.95) with lactation milk yield and a moderate correlation (0.47) with calving interval. Meanwhile, the permanent environmental correlation between production traits and the dry period was moderate and negative. In some cases, genetic and environmental correlations may differ in

Table 2. Posterior mean of genetic correlations \pm posterior standard deviation (above diagonal) and permanent environmental correlations \pm standard error (below diagonal) for production and reproduction traits in crossbred Jersey cattle

Traits	Services per conception	Calving interval	Dry period	Lactation length	Lactation milk yield	Service period
Services per conception		0.34 \pm 0.69	0.45 \pm 0.65	-0.27 \pm 0.69	-0.17 \pm 0.70	0.19 \pm 0.72
Calving interval	0.24 \pm 0.66		0.29 \pm 0.69	0.39 \pm 0.66	0.28 \pm 0.68	0.48 \pm 0.60
Dry period	0.35 \pm 0.61	0.18 \pm 0.66		-0.77 \pm 0.40	-0.73 \pm 0.43	0.12 \pm 0.71
Lactation length	-0.13 \pm 0.67	0.47 \pm 0.58	-0.74 \pm 0.40		0.93 \pm 0.15	0.17 \pm 0.70
Lactation milk yield	-0.03 \pm 0.67	0.28 \pm 0.62	-0.66 \pm 0.46	0.95 \pm 0.12		-0.07 \pm 0.70
Service period	0.11 \pm 0.67	0.51 \pm 0.56	0.07 \pm 0.67	0.40 \pm 0.60	0.20 \pm 0.66	

magnitude or even direction, though they are usually similar in both magnitude and sign. A significant difference in direction suggests distinct physiological mechanisms influencing these traits.

4. CONCLUSION

This study aimed to estimate genetic parameters for production and reproduction traits in crossbred Jersey cattle using a univariate and multivariate Bayesian approach. The moderate heritability estimates for lactation milk yield, lactation length, and dry period suggest that these traits can be effectively used for genetic improvement through selection within the herd. However, the low heritability values for reproductive traits such as services per conception, calving interval, and service period indicate limited potential for genetic improvement of these traits, with greater emphasis needed on management and environmental factors. Moderate to high repeatability estimates for lactation milk yield, lactation length, and calving interval suggest a significant influence of permanent environmental factors. Consequently, a cow's first lactation can serve as a reliable predictor of its future lactation yields and overall lifetime production, allowing for more effective selection after the first lactation. Additionally, negative genetic correlations between production and reproduction traits highlight the need to carefully consider reproduction traits when selecting high-yielding animals. While the genetic parameters estimated for productive and reproductive traits in this study were based on a relatively small sample size, larger datasets are

needed for more precise genetic parameter estimation.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare 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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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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