

Genetic Effects on Production and Reproductive Traits of Jersey Cattle at Wolaita Sodo Dairy Farm, South Ethiopia

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Abstract: This study was conducted to estimate genetic parameters for milk production and reproductive traits of Jersey cattle. Animal model was considered to calculate the variance component using VCE-6 version 6.0.2 & PEST 4.2.5 software. The data was obtained from a state farm, located in Wolaita Sodo, south Ethiopia. Heritability estimated in the present study was generally low to medium having the values of 0.19 ± 0.02 , 0.02 ± 0.05 , 0.16 ± 0.03 , and 0.18 ± 0.04 for daily milk yield (DMY), lactation length (LL), age at first calving (AFC), and calving interval (CI), respectively. Estimated genetic correlation (r_g) between daily milk yield and lactation length was positive and high (0.88), moderate (0.45) between lactation length and calving interval, and low but positive (0.23 and 0.24) between the traits of daily milk yield and calving interval, and daily milk yield and age at first calving, respectively. The results of this study suggest that improvement of the performance of the pure Jersey cattle population at Wolaita Sodo dairy farm is possible through selection and better management of production and reproduction traits, and for sustainable herd improvement better data management system should be in place.

Keywords: *Genetic parameters, Jersey cattle, Production, Reproductive*

Introduction

The estimation of variance and covariance of multivariate data analysis in a dairy herd is helpful to assess the magnitude of genetic correlations among breeding goal traits that enable to set up a total merit index for the accurate evaluation of the genetic merit of animals in the herd (Amaya *et al.*, 2021). The implementation of earlier breeding plans and selection procedures in Ethiopia have also been running without detailed analysis of genetic parameters for milk production and important reproductive traits that are essential to make evidence-based recommendations while planning dairy cattle breed improvement programs (Ayalew *et al.*, 2017). Accurate estimation of the genetic parameters of tropical herds is very important to plan and implement effective breeding programs (Birhanu, 2023).

Evaluation of genetic parameters are required in animal improvement research as adequate knowledge of which is the basis in implementing sound dairy cattle breed improvement programs. Furthermore, the development of effective genetic improvement programs require advanced knowledge of the genetic variation of economically important reproductive and production traits and accurate estimates of genetic and phenotypic correlations of economically important traits (Solomon *et al.*, 2002, Juma and Alkass, 2006).

Even though much information has been generated on the various genetic effects on the major production and reproductive parameters of the Jersey cattle breed across several countries in the world, there is limited

information on genetic parameters, genetic and phenotypic correlations among reproductive and milk production traits of pure exotic Jersey breed in general in the country and in particular in the study area. The Wolaita Sodo Jersey Cattle Dairy Farm has been keeping records of production and reproductive performances of Jersey cattle herds managed in the farm for the past decades. However, the study of genetic effect on productive and reproductive traits of Jersey herd in Wolaita dairy farm was scanty in the past decade. Therefore, this study was conducted to estimate the genetic parameters for production and reproductive traits of Jersey cattle.

Materials and Methods

Description of the Study Area and Population

The study was conducted at the Wolaita Sodo Jersey Cattle Dairy Farm in the Wolaita district in southern Ethiopia, which is located at $6^{\circ}49'N$ latitude and $39^{\circ}47'E$ longitude (WZFEDD, 2012). The farm is located at an altitude of 1990 meters above sea level. The average annual temperature in the area is $19^{\circ}C$; the mean annual rainfall is 1014 mm (NMA, 2012). The rainfall pattern is characterized by a bimodal, which includes a short dry season from October to February and a long rainy (wet) season that in most cases runs from March to September. The Wolaita Sodo Jersey Cattle Dairy Farm was established by the Wolaita Agricultural Development Unit (WADU) in 1971, with imported 90 Jersey heifers and a bull by the Ministry of Agriculture (Habtamu *et al.*, 2009) in an area of 115 hectares, which

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had different structures of farmland and cultivated forage crops. Feeding management involves grouping animals according to age, sex, and production patterns. Except for calves and bulls, all animals graze out on the fields for seven hours during the day. The cows are milked by hand in the barn twice a day (morning and evening). The study population was raised on the farm for the past 50 years. Existing retrospective data on various production and reproduction parameters were used and the influence of genetic factors were evaluated. Among them, the data available and the traits considered include daily milk yield (DMY), lactation length (LL), calving interval (CI), and age at first calving (AFC); and the independent variables, such as calving year, calving season, and parity were taken into account.

Data Source

A study was carried out based on retrospective data on the production and reproductive performance of Jersey cattle as affected by genetic factors. The retrospective data collected from the Wolaita Sodo Jersey Cattle Dairy Farm for 17 years (2000-2016) were used for this study and only data from cows with complete information were.

The major production and reproductive performances for which data was collected include parity, calving date, calving season, and daily milk yield recorded during the reference years. Screening of data was made to avoid errors during data entry. Seventeen years reliable data were filtered, cleaned, and organized using a Microsoft Excel spreadsheet (Table 1). Such clean and organized data were then used to analyse the effects of genetic factors on major reproductive and production traits that are age at first calving (AFC), calving interval (CI), daily milk yield (DMY), and lactation length (LL).

Table 1. Average final number of records for each trait used for analysis.

	Traits			
	DMY	LL	AFC	CI
No of records	3495	3495	795	2480

DMY= Daily milk yield; LL= Lactation length; AFC = Age at first calving; CI = Calving interval.

Model for Genetic Parameters

The genetic parameters estimated were heritability and genetic and phenotypic correlation among traits. They were estimated using the VCE-6 version 6.0.2 & PEST 4.2.5 software program for the estimation of the variance components (Groeneveld, 2012). The analysed traits are assumed to be continuous and have a multivariate normal distribution. Variance components and heritability were estimated using a multivariate animal model, which uses a model that adjusts direct additive effects to random effects and fixed effects. Using the available data in the farm, the following model equation was used to calculate genetic factors for DMY, LL, AFC, and CI:

$$\text{Model } Y = Xb + Za + e;$$

Where, Y = record vector; b = vector of fixed effects; X = correlation matrix of fixed effects a = sum of vectors of direct additive genetic effects Z = incidence matrix of direct additive genetic effects; e = random error vector. Permanent environmental effect was considered in the error term. This model was also used to estimate the correlation between different traits (genetic and phenotype) from multivariate analysis.

Results and Discussion

Genetic Parameters Estimate

The genetic composition of a population can be studied by considering the relative importance of genetic and environmental factors that affect the performance of individuals in the population. Estimation of genetic parameters helps to determine selection methods, predict direct and selection-related responses, select breeding systems for future improvements, and estimate genetic benefits. The genetic source of variation includes all the differences that can be attributed to heredity. This study was focused on estimating heritability, genetic, and phenotypic correlations.

Heritability (h^2) estimates for reproduction traits:

The rate of genetic gain that could be made by selection depends on the heritability of the trait, therefore, the higher the heritability of traits the higher their response to selection. Estimation of the heritability of the traits is an essential genetic parameter required for animal breeding programs.

Age at first calving (AFC): Heritability of age at first calving is generally low and observed to be 0.16 ± 0.03 (Table2). This implies that there were higher environmental influences or lower additive genetic effect in the population of the farm. The higher environmental influence may be temporary and permanent of any kind and as a denominator it could influence the value of heritability. This finding was comparable with the value of 0.19 reported by Hadi *et al.* (2021) for Iranian Holstein. However, it was lower than the heritability value of 0.40 reported by Deb *et al.* (2008) and 0.62 observed by Yosef (2006) for Jersey cows. The heritability value recorded in the current study is higher than 0.04 reported for Sahiwal (Ilatsia *et al.*, 2007) and Kenyan Boran (Wasike *et al.*, 2009). The study by Cassell (2001), on the other hand, reported a habitability value of 0.14 for age at first calving for Holstein cattle; while Haile-Mariam and Kassa-Mersha (1994) reported habitability values of 0.06 and 0.07 for Ethiopian Boran cattle using original and selected data, respectively. The heritability variation observed with other literatures might be due to the difference in additive genetic effect, farm management and population size between farms.

Low estimates of heritability for AFC can be an indication of the importance of environmental factors on the trait. Therefore, improvements in nutrition and reproductive management would likely have an apparent impact on reducing AFC (Vergara *et al.*, 2009). It was noted that due to the low heritability of reproduction

traits, selection for improving these traits in dairy cattle would not worthwhile (Kadarmideen, 2004; Makgahlela *et al.*, 2008). Therefore, genetic improvement for this trait through selection should be accompanied by increasing the amount of information used for genetic evaluation and better husbandry management.

Calving interval (CI): A decrease in CI would reduce the cost of herd replacement and maximize the longevity and the productive life of a cow. The estimated value of calving interval in this study was 0.18 ± 0.04 (Table 2). This result was higher than the heritability value (0.03) reported by Million and Tadelle (2003) for the first calving interval in Holstein dairy cattle. Other studies by Ojango and Pollot (2001), Haile-Mariam *et al.* (2003), Demeke *et al.* (2004), and Yosef (2006) reported 0.1, 0.4, 0.08, and 0.08 heritability values for Kenyan, Holstien, Boran, and Holstien breed in Ethiopia, respectively. Other studies (Gogoi *et al.*, 1992; Rahumathalla *et al.*, 1993; Gebeyehu, 2014) also estimated higher heritability values for CI that include 0.28, 0.25, and 0.37 on Holstein Friesian cattle in Ethiopia, for Jersey×Sindhi crossbreds and Jersey×Tharporker in India, respectively. The differences in the estimated heritability in the present study and that of other investigations might be due to variations in environmental conditions such as feeding as well as the method of estimation used, small sample size, and poor data recording system (pedigree information). Therefore, in the current study, calving interval is influenced more by environmental factors and within short period of time it is possible to improve CI by management and environmental improvements whereas, long-time of selection in the population is required to get genetic improvement on this trait. Thus, improving the feeding and fertility management for the herd is critical to reduce CI.

Generally, as a standard on a comparison of heritability estimates, the estimated value of reproductive traits is lower than that of production traits. This is because the environment affects more reproductive traits than production traits. This means that the reproductive performance of cattle can be improved better by manipulating the production environment compared with that through selection (Wasike, 2006). In different populations or for populations at different times, different estimates of heritability can be found for the same trait.

Heritability (h^2) Estimate for Production Traits

Daily milk yield (DMY): The estimated heritability for daily milk yield for this study was 0.19 ± 0.02 (Table 2). This value was in line with 0.19 reported by Demeke *et al.* (2004) for Friesian×Boran crosses. However, this result was higher than the estimated heritability value of 0.13 reported by Aynalem *et al.* (2008) for Ethiopian Boran, Arendonk *et al.* (1987) for Dutch Friesian cows (0.04), and 0.12 by Kefale *et al.* (2020) for Jersey cattle in Ethiopia.

However, this value (0.19) observed in the present study was lower than the report of Gebregziabher *et al.*

(2014) for Jersey x Boran cross, 0.25 for Friesian cows in large-scale Kenyan farms (Ojango and Pollot, 2001), and 0.25 for lactation milk yield in tropical dairy breeds (Lôbo *et al.*, 2000). The variation with other studies might be due to environmental effects (nutrition) and breed differences.

Lactation length (LL): The estimated value of lactation length was 0.02 ± 0.01 (Table 2), which is similar with 0.02 reported by Yosef (2006) for Jersey cows in the central Shoa, Ada'a berga dairy farm. The present estimate is also close to 0.06 reported by Mohiuddino *et al.* (1994), and 0.03 reported by Gandhi and Gurani (1995) for Indian Sahiwal breed in Pakistan and India.

However, this finding (0.02) is lower than the report of Aynalem *et al.* (2008) for Ethiopian Boran x HF cross (add value) and Tadesse (2014) for Ethiopian Boran x HF cross (0.27). Low to moderate heritability of 0.16, 0.44, and 0.11 were also reported respectively by Reddy and Nagarcenkar (1989), Pundir and Raheja (1994), and Ahmed *et al.* (2001). However, this result was lower than the findings of Bakir *et al.* (2004), Chander *et al.* (2008), and Effa *et al.* (2011) who reported heritability estimates of 0.27, 0.14, and 0.25 in Turkey, India, and Ethiopia, respectively. The difference might be attributed to the effect of the environment (farm husbandry practices and climate) on the trait and genetic variation between the herds.

The low heritability estimates of production traits in this study indicate that there is low additive genetic variation or high environmental variation in the study population. For the better expression of heritability in the population the environmental influence should be minimal to optimal. This indicates that the observed phenotypic variation is largely due to environmental influences. In other words, the low heritability in both traits indicate low additive genetic expression due to high environmental variance. The lower heritability value for production traits may be related with method of analysis, modelling, higher environmental effect and others. Hence, for improvement of production traits in the current population both selection and better management and environment is suggested.

Heritability estimates of production traits show a high degree of variability. This change is the result of the difference in the herd structure providing the data, sample size, and the environment from which the data were obtained. This shows that heritability value is dependent on place of the population and time of analysis undertaken. Hence, the use of estimates should be for that specific population and its use for other populations should be treated with caution (Wasike, 2006).

Genetic (r_g) and Phenotypic (r_p) Correlations

The genetic correlation shows how both traits are influenced by a common set of genes of an animal while the phenotypic correlations evaluated the influence of both common genetic and environmental effects of two

traits (Tamboli *et al.*, 2022). Genetic and phenotypic correlations for reproductive and milk production traits were estimated from a multivariate animal model considering four traits (Table 2). The genetic

correlations between traits in the present study were higher than the corresponding phenotypic correlations except for except between AFC and LL.

Table 2. Heritability ($h^2 \pm SE$) (the diagonal), genetic correlation (r_g) (above the diagonal), and phenotypic correlation (r_p) (below the diagonal) between the study traits for Jersey cows.

Traits	DMY	LL	AFC	CI
DMY	0.19 ± 0.02	0.88	0.24	0.23
LL	0.02	0.02 ± 0.01	-0.09	0.44
AFC	0.04	0.01	0.16 ± 0.03	0.45
CI	0.04	-0.01	0.05	0.18 ± 0.04

DMY = Daily milk yield; LL = Lactation length; AFC = Age at first calving; CI = Calving interval.

Genetic correlation (r_g): Genetic correlation indicates the degree to which two traits are affected by the same gene, which is important when selecting values that involve multiple traits. Estimates of genetic correlation between any pair of traits indicate that the selection of one trait leads to an indirect genetic response to another trait (Missanjo *et al.*, 2012; Gebeyehu, 2014).

Genetic correlations between milk production traits were strongly positive. The strong positive genetic correlation is 0.88 between DMY and LL (Table 2). This implies that the low expression of heritability value in both traits may be related with low additive genetic effect. This is comparable with Beneberu *et al.* (2021), who found 0.93 heritability value for Jersey breed in the central Shoa of Ethiopia. The strong genetic correlation between milk production traits was the result of pleiotropy (Falconer and Mackay, 1996). This means that genetic improvement of one trait could result in a highly positively correlated response in the correlated trait. Generally, the very high correlation between these two traits is indicative of the fact that using DMY can be sufficient to meet selection for lactation length.

The genetic correlations between LL and AFC (-0.09) are weak and negative (Table 2). This is lower than 0.297 (± 0.232) reported in India (Tamboli *et al.*, 2022). On the contrary, relatively higher and positive (0.54) genetic correlations (r_g) were reported for Jersey dairy cattle in central Shoa, Ethiopia (Beneberu *et al.*, 2021). The very low negative genetic correlation between LL and AFC indicates that the genes which affect the LL trait is neutral to affect AFC. The low negative direct genetic correlations of these traits showed that genes were influenced these traits separately or the values of these traits were the result of separate gene action.

The mild positive genetic correlation between CI and LL (0.44) in this study was comparable with 0.41 for the Boran breed reported by Tadesse (2014). Similarly, the mild positive genetic correlation between DMY and CI (0.32) was found on Jersey breed in Ethiopia (Beneberu *et al.*, 2021) but higher and positive genetic correlations of 0.54 between LMY and CI was reported for the same breed in Ethiopia (Yosef, 2006). This shows that increasing milk yield by selection would increase calving interval and this in turn affect profitability of the farm by decreasing life time calf production. Hence, selection

should be undertaken at optimum level for milk production to reduce its effect on CI.

In this study, mild positive (0.45) genetic correlations between AFC and CI were observed (Table 2). This mild positive genetic correlation between reproductive traits indicates that the improvement of one trait has a positive impact on the other trait. This is in close agreement with genetic correlation of 0.55 found by Zambrano and Echeverri (2014) and 0.48 by Ghiasi *et al.* (2011). The mild positive genetic correlation in the present study indicates the evidence of common genetic controlling those traits. Generally, the mild positive direct genetic correlations between reproductive traits in the present study indicated that selection of one trait might be important for the improvement of other traits.

However, traits that have shown weak negative direct genetic correlations in the present study indicate that as one trait increases, the other trait tends to be neutral which might be no correlation of traits considered and in this case, both traits should be included in the selection index.

Phenotypic correlation (r_p): Phenotypic correlations between two traits are a function of genetic and environmental correlations between them. In this study, phenotypic correlations between milk productions and reproductive traits were weak positive (Table 2). The weak positive correlation between LL and AFC, DMY and LL, DMY and AFC, DMY and CI, and CI and AFC were 0.01, 0.02, 0.04, 0.04, and 0.05 respectively. This explains that selection based on phenotypic data may not bring genetic progress in the herd. The phenotypic correlation between DMY and LL (0.02) was in agreement with the report of Tadesse (2014). The current result is in contrast with Beneberu *et al.* (2021), who stated that phenotypic correlations among milk production traits was moderate for DMY-LMY (0.49 \pm 0.01) and high for LMY-LL (0.82 \pm 0.01). The phenotypic correlation between DMY and AFC (0.04) was in agreement with the report of 0.026 (\pm 0.037) by (Tamboli *et al.*, 2022). The variation of the present study from other literature might be due to breed genetic potential, population size, and data structure.

Phenotypic correlations between LL and CI were in general weak and negative (-0.01). This result agreed

with phenotypic correlations between LL and CI was 0.01 (0.00) as reported by (Manal, 2014).

A weak genetic and phenotypic correlation for two traits indicates a necessity to include both traits in the selection index for genetic improvement and both traits should be considered during environment improvement. Phenotypic correlation between production and reproduction traits were weak, suggesting that selection for one trait group will not affect the other (independent of one to the other) whereas, genetic correlations between production and reproduction traits were positive and moderate which shows the requirement of finding optimum production level of one trait to avoid its negative influence. Therefore, there is sufficient evidence that selection based on increased milk yield leads to decrease reproductive traits and selection based on LL may lead to a higher response in milk production.

Conclusion

The results showed that the heritability value of production and reproduction traits was below twenty percent. Genetic correlation between two production traits was high and between production and reproduction traits was moderate whereas, phenotypic correlation between production traits and between production and reproduction traits was low. This study recommended that for moderate and positive genetic correlations between production and reproduction traits, selection for one trait should consider its negative impact on the other trait. The weak phenotypic correlation between production and reproduction traits necessitates to implement an appropriate productive and reproductive management and further investigation of environmental factors controlling the traits.

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Conflict of Interests

The authors declare that they have no competing interests.

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