

**Original Article**

Relationship between Fertility and Milk Production Traits in Pure Jersey Dairy Cows: Multitrait Analysis

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ABSTRACT

Records on 22175 pure Jersey dairy cows evaluated the genetic and phenotypic correlations. Data for this study were collected from Adea Berga dairy research farm span over 33 years (1986-2019) performance records. Five fertility; number of services per conception (NSC), days open (DO), calving interval (CI), age at first calving (AFC), age at first service (AFS), and three-milk production traits; lactation milk yield (LMY), daily milk yield (DMY), lactation length (LL) were estimated by WOMBAT software fitted a multitrait repeatability animal model. The result of present study revealed that genetic correlations among fertility traits for pure Jersey cows varied from -0.63 to 0.91 whereas the values of phenotypic correlations were found to be ranged from -0.28 to 0.98. The AFS-AFC was the highest genetic and phenotypic correlations among all fertility traits. The lowest genetic and phenotypic correlations were between AFS/AFC-CI and AFS/AFC-NSC, respectively. For milk production traits, the genetic correlations ranged from 0.86 to 0.96 whereas the values of phenotypic correlations were found in the range of -0.05 to 0.82. The LMY-LL was the highest genetic and phenotypic correlation and DMY-LL was the lowest. The genetic correlations between reproductive and milk production traits also varied from

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-0.38 to 0.42 and phenotypic correlations ranged from 0.13 to 0.48. The highest genetic and phenotypic correlations for reproductive and milk production traits were from DO-LL and LMY-CI/DO whereas the lowest was from NSC-LL and AFS-LL, respectively. Genetic correlations among the traits in the present study were higher than the corresponding phenotypic correlations among all milk production traits and the majority of fertility traits. The positive genetic correlations among traits in the present study would broaden the choice selection of more traits at one time for improvement. To improve genetic progress and breeding efficiency of Jersey dairy cows, periodic evaluation of the genetic and phenotypic relationship of dairy traits should be applied and more than one trait should be selected based on the magnitude of correlations (more correlated traits).

Keywords: Adea Berga, correlation, Ethiopia, Jersey dairy cow, fertility trait.

INTRODUCTION

In animal breeding, knowledge of the genetic properties of the traits that the breeders are interested in is the first prerequisite in establishing a selection program concerned with traits controlled by a single or few genes (Meyer, 1989). This can increase interest to know the relationships or correlations between two or more traits. Correlations are the relationship between two traits or two breeding values of traits (Roman *et al.*, 2000). A high correlation value implies a strong relationship between variables and vice versa (Bourdon, 2000). Correlations are partitioned into genetic and phenotypic. The genetic correlation expresses the extent to which two characters (traits) are influenced by the same genes or by genes located in the same chromosome. It is important when selecting for net merit involving several traits. Estimates of genetic correlation between any pair of traits suggest that selection for one trait can lead to an indirect genetic response in the other trait leading to high genetic variability (Edward *et al.*, 2013; Gebeyehu *et al.*, 2014) and the existence of high genetic variability is greatly important for genetic improvement of the existing population (Zelege, 2019). On the other hand, phenotypic correlation is the correlation between records of two traits on the same animal (searle, 1961).

Genetic and phenotypic correlations are the most common measures of the genetic parameter in livestock genetic or breed improvement (Yibrah, 2008). The development of effective genetic improvement programs requires advanced knowledge of the genetic variation of economically important traits and accurate estimates of genetic and phenotypic correlations of traits (Juma and Alkass 2006). Furthermore, the knowledge of mutual relationships between the traits is of great importance to breeding. Measures of correlations among dairy traits are the most important prerequisite to selecting more than two traits at one time. Moreover, estimation of trait relationships is commonly required to construct selection indexes, predict correlated responses, and perform efficient genetic evaluations (Ruales *et al.*,

2007). Multitrait selection of pure Jersey dairy cows in the research farm was not practiced as the correlation or relationship between those economically important (milk yield and fertility) traits were not studied well. Therefore, the objective of this study was to estimate the genetic and phenotypic correlations among fertility and milk production traits for pure Jersey dairy cows at Adea Berga dairy research farm, Ethiopia.

MATERIALS AND METHODS

Study location and data source

This research was conducted at Adea Berga dairy research farm. Adea Berga dairy research farm is one of the sub-research centers of Holetta agricultural research center. The sub-center was founded with the objective of pure Jersey breed genetic improvement program and bull dam station for national artificial insemination (production of Jersey semen for domestic uses). The sub-research center is geographically situated in the central highlands of Ethiopia at 9° 16' N latitude and 38° 23' E longitude, 70 km West of Addis Ababa and 35 km northwest of Holetta. It lies at an altitude of 2500 m above sea level. Hunde *et al.*, (2015) extensively discussed the description of the farm, herd management, and breeding program of the sub-research farm. Therefore, retrospective data on pure Jersey cows calved from 1986 to 2019 were obtained from this research farm.

Data editing

Before analysis, incomplete records were edited/deleted according to the following criteria.

1. Lactation that is in progress.
2. Data with unknown sire and dam (animals with unknown pedigree were pruned).
3. Abortion and stillbirth data were removed.
4. Errors associated with the animal birth date, calving date, and service date.

Trait values above or below the following criteria were truncated which were considered outliers.

- NSC greater than 25 times,
- DO below 45 days and above 1250 days,
- CI below 330 days and above 2100 days,
- AFC below 17 months and above 62 months,
- AFS below 8 months and above 46 months,
- Lactation length less than 100 days,
- Parities (lactation numbers) above 8.

Finally, 22175 pure Jersey cows' performance data were obtained.

Table 1: Number of records for estimation of genetic and phenotypic correlations

Traits	Number of records
Service per conception (NSC)	4176
Days open (DO)	2930
Calving interval (CI)	2908
Age at first calving (AFC)	1161
Age at first service (AFS)	758
Lactation milk yield (LMY)	3374
Daily milk yield (DMY)	3433
Lactation length (LL)	3435
Total	22175

Data collection

Traits (NSC, DO, CI, AFC, AFS, LMY, DMY, and LL) which are used for estimation of genetic and phenotypic correlations were generated from long-term recorded breeding data (date of birth, date of calving, date of service, lactation number, date of lactation, end of lactation, etc.). A pedigree is the set of known parent-offspring relationships in a population, often displayed as a family tree diagram. To do so, animal ID, dam ID, and sire ID are important parameters exploited from the herd-recording sheet, which were used for pedigree analysis. Identity numbers (ID) were sequenced by pedigree viewer software package (version 6.5) for arranging animals' ID in chronological order and clearing any mistakes.

Table 2: Pedigree structures (characteristics) and number of records for estimation of genetic and phenotypic correlations

Number	Pedigree structure (characteristics)	Number of records
1	Number of animal IDs in the pedigree file	1284
2	Number of animal IDs in total	1671
3	Number of animals without offspring	649
4	Number of animals with offspring	635
5	Number of animals with unknown sire	368
6	Number of animals with unknown dam	498
7	Number of animals with both parents unknown	297
8	Number of sires with progeny in the data	107
9	Number of dams with progeny in the data	528
10	Number of animals with paternal grandsire	0
11	Number of animals with paternal grand dam	0
12	Number of animals with maternal grandsire	619
13	Number of animals with maternal grand dam	566

Statistical analysis

The genetic and phenotypic correlations were estimated by using WOMBAT software (Meyer, 2020) fitted multitrait repeatability animal model (all fertility and milk

production traits were analyzed simultaneously). Fixed factors (year, season, and parity) that have significant effects were fitted into the model. Fitting of significant fixed effects in the model is important for the separation of genetic and environmental co (variances). Seasons in the year were classified into three based on rainfall distribution. Dry season (October to February), short rain season (March to May), and main rain season (June to September). Additive plus permanent environmental effects due to repeated records per cow were fitted as random effects.

The representation of the animal model used to estimate genetic and phenotypic co (variance) for fertility/reproductive (NSC, DO, CI, AFC, AFS and) and milk production (LMY, DMY, and LL) traits are as follows:

Model: $Y = Xb + Za + W_d + e$

Where;

Y is a vector of records/ observations for the traits of interest (NSC, DO, CI, AFC, AFS LMY, DMY, and LL),

b , is a vector of fixed effects that had a significant (year, season, and parity),

a , is a vector of random individual direct additive genetic effects (animal),

d is a vector of permanent environmental effect,

X is a matrix relating records to fixed effects,

Z is an incidence matrix for direct additive genetic effect,

W is an incidence matrix for permanent environmental effects,

e , is a vector of random residual effect (error term).

Non-significant effects were not included in the model of analysis. For example, Season was not significant for LMY, DMY, LL, and DO traits and, parity was not significant for CI for pure Jersey cows. Other fixed effects (year, season, and parity) were a significant source of variations for the rest of the fertility and milk production traits and were included in the correlations analysis model. Parity was not included as a fixed effect for AFS and AFC traits as no parity was recorded in these traits.

The genetic and phenotypic correlations were calculated by using the following formulas;

$$rg = \frac{\sigma_{aij}}{\sqrt{\sigma^2_{ai} \sigma^2_{aj}}}$$

$$rp = \frac{\sigma_{pij}}{\sqrt{\sigma^2_{pi} \sigma^2_{pj}}}$$

Where;

rg : genetic correlation,

rp : phenotypic correlation

σ_{aij} : additive genetic covariance between trait i and j ,

σ_{pij} : phenotypic covariance between trait i and j ,

σ^2_{ai} : additive genetic variance for trait i, σ^2_{aj} : additive genetic variance for trait j,
 σ^2_{pi} : phenotypic variance for trait i,
 σ^2_{pj} : Phenotypic variance for trait j.

RESULTS AND DISCUSSION

Genetic and phenotypic correlations

The estimates of direct genetic and phenotypic correlations among five fertility (NSC, DO, CI, AFC, and AFS) and three milk production (LMY, DMY, and LL) traits are summarized in table 3.

Genetic and phenotypic correlations among fertility traits

The genetic correlations among fertility traits ranged from highly positive to negative. The correlation between AFS and AFC was higher followed by CI and DO traits. The number of services per conception was also a medium positive correlation with CI and DO which are favorable in the selection process. Age at first service and age at first calving was negatively correlated (unfavorable) with CI, DO, and NSC. The present 0.84 genetic correlation between CI-DO was agreed with the report by (Dubey and Singh, 2005; Dhal *et al.*, 2016; Beneberu *et al.*, 2021). However, Dhal *et al.*, (2016) reported a higher genetic correlation between CI-NSC and DO-NSC and, a positive correlation between AFC-DO traits, which were deviated from the present finding.

The phenotypic correlations among fertility traits for Jersey dairy cows are indicated in table 3 below diagonal. Except for NSC with AFS and AFC traits, other phenotypic correlations among fertility traits were positive in which estimates of phenotypic correlations and their correlated responses under this study were important to find out simultaneous improvement in the planning of more than one trait. Furthermore, the gene and environment geared the relationship among fertility traits in a favorable direction. The highest phenotypic correlation was observed between AFS and AFC traits (0.98) followed by CI-DO (0.89), NSC-CI (0.75), and NSC-DO (0.74). The lowest correlations were recorded between NSC and AFS/AFC traits (-0.28). The sign and magnitude of the phenotypic correlations among the majority of reproductive traits in the present study were agreed with the study by (Dubey and Singh, 2005; Sreedhar *et al.*, 2013; Dhal *et al.*, 2016; Beneberu *et al.*, 2021).

Genetic and phenotypic correlations among milk production traits

Genetic correlations among milk production traits for pure Jersey cows were all positive and highly correlated. A strong correlation was found between LMY and LL (0.97) following LMY and DMY (0.96). These values would be a good prediction for increasing milk yield through a selection of single or multiple traits. The genetic correlations among milk production traits were higher than the phenotypic counterpart. The present genetic correlation between LMY-LL was very similar to

Wahinya *et al.*, (2020) who found the range of 0.84-0.96 in different production systems from multiple breed evaluation. Roy and Katpatal (1988) also found a higher genetic correlation between LMY-LL in the first lactation records in Jersey breed. The high genetic associations among milk production imply that the same genes govern all milk traits. As observed in Table 3, the LMY was a higher correlation with LL and DMY. This correlation was also repeated in milk composition traits reported by (Roman and Wilcox, 2000; Edward *et al.*, 2013; Hugo *et al.*, 2017). However, what made them different in their reports was a phenotypic correlation of milk yield-milk composition had a higher than genetic correlation.

The phenotypic correlation was higher between LMY-LL (0.82) and lower between LMY-DMY, which was negative. The negative correlation could be due to the influence of non-measurable environmental factors in each animal in addition to measurable factors (year, season, and lactation difference).

Genetic and phenotypic correlations between fertility and milk production traits

The genetic correlations between fertility and milk production traits for Jersey cows in the present study showed mixed results in the range of weak positive between DO and LL (0.42) to negative between NSC-LL (-0.38). The result showed that AFS, AFC, and NSC were negatively correlated with LMY, DMY, and LL, which were favorable in the selection process. These indicated that the increased milk-producing cows associated with longer LL would be reduced the AFS, AFC, and NSC. These results were in agreement with the finding of Wahinya *et al.*, (2020) who reported the negative genetic correlation of AFC and positive genetic correlation CI with milk traits, respectively. The present 0.17 genetic correlation between LMY-CI traits agreed in magnitude and sign with those of (Camops *et al.*, 1994; Pritchard *et al.*, 2012). An earlier study by (Berger *et al.*, 1981; Janson and Andearsson, 1981; Hansen *et al.*, 1983; Faust *et al.*, 1989; Pritchard *et al.*, 2012) reported a substantial antagonistic relationship between reproductive and milk production traits, which means that selection for increasing milk production traits would be extended the reproductive efficiency of dairy cows. These authors suggested that these antagonistic relationships could be partly explained because of the negative energy balance of high-yielding cows and the accompaniment of reduced feed intake at calving time. Nevertheless, genetic correlations of specific traits in dairy cows are different in a different investigators. Badinga *et al.*, (1985) reported a positive correlation (0.38) between milk yield and NSC, which had inconsistent with the present study. Hugo *et al.*, (2017) reported -0.71 correlation between AFC-LMY. Roy and Katpatal (1988) found 0.1 correlation between LMY-CI for Jersey breed, which was consistent with the present result. The genetic association between milk yield and fertility traits might depend on the potential of milk production of dairy cows.

Table 3: Estimates of genetic correlations (above diagonal) and phenotypic correlations (below diagonal) among fertility and milk production traits for pure Jersey dairy cows

Parameters	AFS	AFC	CI	DO	NSPC	LMY	DMY	LL
AFS	*	0.91±0.07	-0.63±0.08	-0.65±0.09	-0.65±0.11	-0.03±0.10	0.053±0.30	-0.20±0.42
AFC	0.98±0.002	*	-0.63±0.08	-0.65±0.09	-0.65±0.11	-0.06±0.26	-0.02±0.27	-0.19±0.38
CI	0.18±0.03	0.19±0.04	*	0.84±0.05	0.48±0.16	0.17±0.29	0.08±0.30	0.28±0.37
DO	0.18±0.04	0.20±0.03	0.89±0.01	*	0.46±0.15	0.27±0.23	0.11±0.24	0.42±0.28
NSPC	-0.28±0.04	-0.28±0.06	0.75±0.03	0.74±0.02	*	-0.36±0.34	-0.35±0.33	-0.38±0.49
LMY	0.18±0.03	0.20±0.03	0.48± 0.02	0.48±0.02	-	*	0.96±0.07	0.97±0.72
DMY	0.15±0.05	0.18±0.05	0.28±0.04	0.26±0.04	-	0.48±0.02	*	0.86±0.26
LL	0.13±0.04	0.15±0.03	0.47±0.02	0.47±0.02	-	0.82±0.01	-0.05±0.02	*

AFS= age at first service, AFC= age at first calving, CI= calving interval, DO= days open, NSPC= number of services per conception, LMY= lactation milk yield, DMY= daily milk yield and LL lactation length

For example, Berger *et al.*, (1981) reported the highest genetic correlation between measures of reproductive performance and 305 days milk yield in the range of (0.48-0.62) and lower correlations for 180 days and 60 days milk yield with reproductive traits.

The phenotypic correlation between fertility and milk production traits was also studied and all are small positive values in the ranges from 0.13 between AFS-LL to 0.48 between CI/DO-LMY. The gene interaction with management and environment that the correlation between milk production and fertility traits were found to be in the unfavorable directions. However, fertility traits are mostly influenced by a managerial decisions like voluntary waiting, conception rate, efficiency of estrus detection, skill of inseminator, etc. several authors reported a positive phenotypic correlation between LMY and reproductive traits. These relationships are antagonistic and the increasing level of milk production would be increased the fertility status of dairy cows. Badinga *et al.*, (1985) found a positive (0.21) correlation between milk yield and DO traits. Hugo *et al.*, (2017) reported a weak phenotypic correlation between LMY and CI traits in overo Colorado Chilean dairy breeds. Pritchard *et al.*, (2012) also reported a positive relationship between LMY-CI and LMY-DO. Nebel and Mcgilliard (1993) stated that the correlation between milk yield and reproductive traits indicates that highly associated phenotypically but not genetically and an important similarity is that management and environment account for the majority of the variation. . Due to the nature of the data and simultaneous analysis of more traits, the phenotypic correlation of NSC with LMY, DMY and LL was not estimated.

CONCLUSION

The present study showed complex relationships among all fertility and milk production traits. Traits that showed positive genetic correlations showed negative phenotypically and vice versa. However, the majority of reproductive and milk production traits for pure Jersey cows were positive genetic and phenotypic correlations indicating that selection of these traits would be effective. The negative genetic or phenotypic correlated traits can be overcome by implementing a selection index of traits in the breeding goal and improving the environment and management of the herd. In other words, to improve the genetic and phenotypic correlations of fertility (reproductive) and milk production traits, the breeder must understand the complex interactions of milk production and fertility, genetics, environment, and management of the herd. Genetic correlations among the majority traits in the present study were higher than the corresponding phenotypic correlations, which is an acceptable and important consideration in the breeding plan. The deviation of the present study to other findings might be because genetic and phenotypic correlations of dairy cow traits are specific to geographical location, breed/genotype, animal management, data set, and analysis procedures. In many countries, traits related to

milk production, milk composition, fertility, and health are included in breeding programs of dairy cattle to maximize the improvement of a breeding goal involving traits related to income and costs. However, in Ethiopia mild selection is only applied for milk yield traits. Therefore, to improve genetic progress and breeding efficiency of Jersey dairy cows, genetic correlations should be accurately estimated and selection of more than one trait should be considered.

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CONFLICT OF INTERESTS

The authors declare no potential conflict of interest is reported regarding the subject matter of this manuscript either for financial, commercial, or intellectual purposes.

AUTHORS' CONTRIBUTION

1. First author contributed to the idea generation, data retrieving, data analysis, data interpretation, and manuscript drafting (writing) and, was approved for submission.
2. The second and third authors contributed to reviewing and writing the introduction and literature, manuscript drafting (writing), and approved for submission.

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