Correlation Measures among Reproductive and Milk Production Traits in Crossbred Dairy Cows at Holetta Dairy Research Farm, Ethiopia: Multitrait Analysis

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ABSTRACT

Genetic and phenotypic correlations for reproductive and milk production traits were estimated by multitrait analysis of WOMBAT software. Total of 14222 crossbred dairy cows performance records collected from Holetta dairy research farm span over 43 years (1974-2017) were used for this study. Five reproductive; age at first calving (AFC), age at first service (AFS), calving interval (CI), days open (DO) and number of service per conception (NSC) and three-milk production; lactation milk yield (LMY), daily milk yield (DMY) and lactation length (LL) traits were included for estimation. The result of present study revealed that the genetic correlations among reproductive traits were varied from -0.31±0.08 to 0.98±0.03 while phenotypic correlations were ranged from -0.03±0.001 to 0.84±0.04. Strong positive genetic and phenotypic correlations were found between AFS and AFC traits (0.98±0.03) and (0.84±0.04), respectively. For milk production traits, the genetic correlations were ranged from 0.11±0.03 to 0.77±0.12 while phenotypic correlations were in the lower range of 0.07±0.02 to 0.36±0.07. Higher genetic correlations were observed between LMY and LL (0.77±0.12). The genetic correlations among reproductive and milk production traits were also varied from -0.55±0.04 to 0.79±0.07 while phenotypic correlations were ranged from -0.55±0.22 to 0.32±0.10. The higher genetic correlation was between CI and LL (0.79±0.07). The correlation between DMY and AFC (0.32±0.10) was recorded as higher phenotypically. The positive genetic correlations among traits indicates that effective selection of one trait might be improved the other and would be given the chance of broader selection of traits in the breeding goal. Therefore, to improve genetic progress and breeding efficiency of crossbred dairy cows in the research farm, estimation and selection of correlated traits should be done periodically.

HIGHLIGHTS

⊙ Milk yield and reproductive traits are complex relationship.
⊙ This relationship can be depend on genetic and environmental variabilities.
⊙ This study was conducted to know the correlation among reproductive and milk production traits and the results are summarized in this paper.

Keywords: Crossbred, Genetic correlation, Lactation milk yield, Phenotypic correlation, Reproductive trait

In animal breeding, knowledge of the genetic properties of the traits that the breeders are interested in is the first pre-requisite in establishing a selection program concerned with traits controlled by single or few genes (Meyer, 1989). This can be increase an interest to know the relationships or correlations between two or more traits. Correlations are measures of the strength of the relationship between two traits (variables). 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 (Missanjo *et al.*, 2013; Gebeyehu *et al.*, 2014) and the existence of high genetic variation is greatly important for genetic improvement of the existing population (Zeleke, 2019). On the other hand, phenotypic correlation is the correlation between records of two traits on the same animal (Searle, 1961).

Phenotypic and genetic correlations are most common measures of genetic parameter in livestock genetic or breed improvement (Yibrah, 2008). The development of effective genetic improvement programs require advanced knowledge of the genetic variation of economically important traits and accurate estimates of genetic and phenotypic correlations of traits (Solomon *et al.*, 2002; Juma and Alkass 2006). Furthermore, knowledge of the kind and amount of genetic and phenotypic correlations among milk yield and reproductive traits in dairy cattle population can lead to design of optimum breeding plan and setup selection program. Measures of correlations among dairy traits is the most important prerequisite to select more than two traits at one time. Multi trait selection of crossbred dairy cows in the research farm was not practiced as the correlation or relationship between those economically important (milk yield and reproductive) traits were not studied well. Therefore, the objective of this study was to estimate the genetic and phenotypic correlations among reproductive and milk production traits in crossbred dairy cows at Holetta dairy research farm, Ethiopia.

MATERIALS AND METHODS

Study location and data source

This research was conducted at Holetta dairy research farm. Holetta is located in the central highland of Ethiopia at 29 km west of Addis Ababa (9° 00' N latitude and 38° 30' E longitude) with an altitude of 2400 meter above sea level. The average annual rainfall is 1100 mm and average annual temperature is 15 °C with minimum 6 °C and maximum 24 °C, respectively. Getahun *et al.* (2020) extensively discussed description of the farm, herd

management and breeding program of the research farm. Therefore, Retrospective data on crossbred cows calved from 1974-2017 were obtained from this research farm.

Data editing

Prior to analysis, incomplete records were edited/deleted according to the following criteria:

1. Lactation which are in progress

2. Data with unknown sire and dam (animals with unknown pedigree were pruned)

3. Abortion and still birth data was removed

4. Errors associated with animal birth date, calving date, service date.

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

1. Lactation length less than 100 days,

2. Age at first service below 10 months and above 80 months,

3. Age at first calving below 20 months and above 90 months,

4. Days open below 45 days and above 1250 days,

5. Calving interval below 330 days and above 2100 days,

6. Number of service per conception greater than 25 times,

7. Parities (lactation numbers) above 8,

Finally, 14222 crossbred dairy cows' performance data were obtained.

Data collection

Traits (LMY, DMY, LL, AFS, AFC, CI, DO and NSC) 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 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 orders and clearing any mistakes.

STATISTICAL ANALYSIS

The genetic and phenotypic correlations were estimated by using WOMBAT software (Meyer, 2012) fitted multi trait animal model (all reproductive and milk production traits were analyzed simultaneously). Fixed factors (genotype, year, season and parity) that have a significant effect were included in the model for correlation analysis. Fitting of significant fixed effects in the model are important for separation of genetic and environmental co (variances). As showed from table 1, the genotypes are 50% F_1, F_2, F_3, 75% first and 75% second generations. 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 (animal) and permanent environment for repeated records were fitted as random effects in the model.

The representation of multi trait animal model used to estimate genetic and phenotypic co (variances) for reproductive (*AFS, AFC, CI, DO* and *NSC*) and milk production (*LMY, DMY* and *LL*) traits is as follow:

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

Where;

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

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

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

X is a matrix relating records to fixed effects,

Z is an incidence matrix for direct additive genetic effect,

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 effect for *AFS* and *AFC*. Other fixed effects (genotype, year, season and parity) were significant source of variations for the rest of reproductive and milk production traits and fitted in to the model for co (variances)/correlations analysis. Parity was not included as a fixed effect for AFS and AFC traits as no observations were recorded in these traits.

From the resulting co (variance) components, 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 correlations,

rp: phenotypic correlations

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

| Traits | Genotypes | | | | |
| | 50% | | | 75 % | |
	F_1	F_2	F_3	F_1	F_2
Lactation milk yield (LMY)	1598	234	139	299	43
Daily milk yield (DMY)	1543	234	139	236	34
Lactation length (LL)	1543	234	139	236	34
Age at first service (AFS)	461	89	60	143	26
Age at first calving (AFC)	470	89	60	143	26
Calving interval (CI)	1295	162	89	167	22
Days open (DO)	1271	161	87	163	22
Service per conception (NSC)	1762	258	150	313	48
Total	**9943**	**1461**	**863**	**1700**	**255**

Table 2: Number of records on pedigree characteristics for estimation of genetic and phenotypic correlations

Number	Pedigree characteristics	Number of records
1	Number of animal IDs in the pedigree file	1095
2	Number of animal IDs in total	1299
3	Number of animals without offspring	667
4	Number of animals with offspring	535
5	Number of animals with unknown sire	376
6	Number of animals with unknown dam	413
7	Number of animals with both parents unknown	355
8	Number of sires with progeny in the data	96
9	Number of dams with progeny in the data	439
10	Number of animals with paternal grandsire	0
11	Number of animals with paternal grand dam	0
12	Number of animals with maternal grandsire	342
13	Number of animals with maternal grand dam	313

ai: additive genetic covariance betweentrait *i* and *j*,

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

$\sigma^2 ai$: additive genetic variance for trait *i*,

$\sigma^2 aj$: additive genetic variance for trait *j*, phenotypic variance for trait *i*,

$\sigma^2 pj$: Phenotypic variance for trait *j*.

RESULTS AND DISCUSSION

Genetic and phenotypic correlations

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

Genetic correlations among reproductive traits

The present study showed that negative and small to high positive genetic correlations among reproductive traits. There were negative correlations between AFS and DO (-0.001±0.003), AFC and DO (-0.05±0.01), AFS and NSPC (-0.02±0.01), AFC and NSPC (-0.29±0.06) and CI and NSPC (-0.31±0.08). The negative genetic correlation of these traits reported here were unfavorable in the sense that selection of one or two traits in the favorable direction would be discouraged the other traits. However, these can

be reverted/improved by broader selection of reproductive traits set as a breeding goal. Strong and positive genetic correlation (0.98±0.03) was found between AFS and AFC traits. The positive genetic correlations might be arises due to the pleiotropic effect of gene and some linkage among genes. However, moderate positive (0.36±0.04) genetic correlation was observed between CI and DO. The correlation between AFS and AFC with DO and NSPC in this study was not agreed with the finding of Haile *et al*. (2009b) who reported 0.51 for AFS and DO, 0.19 for AFC and DO, 0.38 for AFS and NSPC and 0.65 for AFC and NSPC, respectively. Other study carried out by Gutterez *et al*. (2002) found comparatively higher correlation (0.23) between AFC and CI for beef crossbred. Tadesse (2014) reported strong positive genetic correlation (0.99±0.00) between CI and DO. However, a perfect positive genetic correlation (1.00) between AFS and AFC and CI and DO for Fogera crosses were reported by (Belay *et al*., 2016). These differences might be due to variation in size of the data set, geographical location and management, breed difference, estimation procedure and analysis type.

Genetic correlations among milk production traits

The genetic correlations among milk production traits for crossbred cows in the present study were positive and ranges from low (0.11±0.03) to slightly high (0.77±0.12). High genetic correlation was observed between LMY and LL (0.77±0.12). This value was closely similar with the

Table 3: Estimates of genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for reproductive and milk production traits in crossbred dairy cows

Parameters	AFS	AFC	CI	DO	NSPC	LMY	DMY	LL
AFS	*	0.98±0.03	0.001±0.001	-0.001±0.003	-0.02±0.01	0.29±0.05	0±0.0	-0.11±0.09
AFC	0.84±0.04	*	0.05±0.05	-0.05±0.01	-0.29±0.06	0.17±0.10	-0.55±0.04	0.04±0.02
CI	-0.03±0.001	-0.02±0.10	*	0.36±0.04	-0.31±0.08	0.42±0.07	0.16±0.02	0.79±0.07
DO	-0.03±0.0	-0.02±0.001	0.25±0.02	*	0.08±0.04	0.30±0.06	0.51±0.2	0.68±0.2
NSPC	-0.01±0.0	0.09±0.04	0.19±0.06	0.07±0.06	*	0.24±0.10	0.39±0.01	0.01±0.002
LMY	0.23±0.11	0.08±0.03	0.14±0.06	0.13±0.02	0.08±0.08	*	0.11±0.03	0.77±0.12
DMY	0±0.0	0.32±0.10	0.05±0.02	0.08±0.01	0.09±0.03	0.07±0.02	*	0.54±0.12
LL	-0.19±0.001	-0.001±0.0	0.18±0.01	-0.55±0.22	0.15±0.09	0.36±0.07	0.18±0.05	*

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.

study by Gebregziabhere *et al*. (2013) who reported 0.73 correlations between LMY and LL. Ashutosh *et al*. (2013) reported an estimated lower correlation between LMY and LL (0.31) and between LMY and DMY (0.30). The correlation between LMY and LL was higher than DMY and LL. However, Haile *et al.* (2009a) reported different from the present result and genetic correlation between LMY and LL was lower (0.55±0.12) than DMY and LL (0.78±0.12) from univariate analysis. Tadesse (2014) also reported higher genetic correlation between LMY and LL (0.99) than DMY and LL (0.59) from bivariate analysis. The difference in correlation estimation would be arose from statistical procedures that the authors followed.

Genetic correlations among reproductive and milk production traits

The genetic correlations among reproductive and milk production traits were also examined in this study and there were closely associated with each other between majority traits. Accordingly, slightly higher genetic correlations were observed between CI and LL (0.79±0.07) and between DO and LL (0.68±0.2). AFS and AFC were negative genetic correlations (-0.11±0.09 and -0.55±0.04) with LL trait, respectively. Genetically, AFS and DMY were uncorrelated, which was zero value. The correlation between CI with LL and LMY estimated for this study was similar in magnitude but statistically different from the report of Tadesse (2014) who found correlations of 0.81±0.06 and 0.59±0.06, respectively. Gutterez *et al*. (2002) reported a negative genetic correlation between

CI and LL that was completely different from the present study. This study was also deviated from Ashutosh *et al*. (2013) who reported correlations of -0.14, 0.12, 0 and 0.03 between AFC and LMY, CI and LMY, AFC and LL and CI and LL, respectively for Bangladesh Holstein Friesian crosses with Sahiwal and local breeds. The positive genetic correlations among traits (LMY with DMY, LL with DMY, LMY with CI, and AFS with AFC and DMY with DO) in the present study indicated that selection of one trait might be important for the improvement program of other traits. However, traits which showed negative or zero correlations (AFS with DO, AFC with NSPC, CI with NSPC and AFS with DMY) in the present study is considered as antagonistic or uncorrelated of each other and the result of independent gene action.

Generally, the positive genetic correlations among traits in the present study indicates that effective selection of one trait would be important for the improvement of other correlated traits. Beside these, the presence of high genetic correlations are due to the phenomenon of a single gene affecting more than one trait and due to the occurrence of two or more loci that affect the same trait on the same chromosome (Bourdon, 2014). However, traits that showed negative genetic correlations indicates that as selection of one trait to favor, the other trait tends to disfavor.

Phenotypic correlations among reproductive traits

Strong phenotypic correlation was observed between AFS and AFC. Like the genetic correlations, AFS and AFC phenotypically showed negative correlation with CI and

DO. The positive and negative phenotypic correlation of reproductive traits in the present study were somewhat similar in the direction but strongly disagreed statistically with the finding of Tadesse (2014) a n d Belay *et al*. (2016) who found very strong phenotypic correlation between CI and DO (0.99 and 0.99) for crossbred and indigenous Fogera cows, respectively from bivariate analysis. The variation of the present study from others literature might be due to breed difference, number of observation studied and software procedure used for analysis.

Phenotypic correlations among milk production traits

The estimated phenotypic correlations among milk production traits were very low (0.07±0.02 between DMY and LMY), low (0.18±0.05 between DMY and LL) and moderately low (0.36±0.07 between LMY and LL). The phenotypic correlation between LMY and LL was in agreement with the report of (Ashutosh *et al*., 2013). Relative to the present study, Tadesse (2014) found higher phenotypic correlations between DMY and LL (0.39), DMY and LMY (0.86) and LMY and LL (0.76) for crossbred dairy cattle.

Phenotypic correlations among reproductive and milk production traits

The phenotypic correlations among reproductive and milk production traits were positive but small in which environment and management would be accounted for majority of this relationship. Lactation length was negatively correlated with AFS, AFC and DO traits. However, this trait was positive genetic correlation with AFC and DO traits. This shows that the presence of large environmental variance changed the magnitude of positive genetic correlations into negative phenotypic correlations. Nevertheless, the highest phenotypic correlation was between DMY and AFC (0.32). There was no phenotypic correlation between DMY and AFS. The present study indicates that both random environmental and genetic (additive and non- additive) effects could be influence phenotypic correlations of the studied traits. The negative phenotypic correlation between AFC and LL in the present study was agreed with the finding of (Ashutosh *et al*., 2013). The estimated phenotypic correlations among

reproductive and milk production traits in the present study were lower than genetic correlations.

In general, both environmental and genetic effects would b e influence g e n e t i c a n d phenotypic correlations of the reproductive and milk production traits.

CONCLUSION

The present study showed complex correlations (relationships) among all reproductive and milk production traits. Traits that showed positive genetic correlations showed negative phenotypically and vice versa. However, majority of reproductive and milk production traits for crossbred cows were positive genetic and phenotypic correlations indicates that selection of these traits would be effective. The negative genetic or phenotypic correlated traits can be overcome by applying broader selection of traits in the breeding goal. In other word, to improve the genetic and phenotypic correlations of reproductive and milk production traits, the breeder must understand the complex interactions of milk production and reproduction, genetics, environment and management of the herd. Genetic correlations among 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 of genetic and phenotypic correlations of dairy cow traits are specific to geographical location, breed, animal management, data set and analysis procedures. In many countries, traits related to milk production, reproduction, longevity and health are included in breeding programs of dairy cattle in order to maximize improvement of a breeding goal involving traits related to income and costs. However, in Ethiopia mild selection is only applied for milk yield trait. Therefore, to improve genetic progress and breeding efficiency of crossbred dairy cows at Holetta dairy research farm, genetic parameter (correlations) should be accurately estimated and more than one traits should be selected based on the magnitude of correlations (more correlated).

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