International Journal of Food, Agriculture and Veterinary Sciences ISSN: 2277-209X
An Open Access, Online International Journal Available at http://www.cibtech.org/jfav.htm
2023 Vol.13, pp.10-18/ Kefale
Research Article

GENETIC PARAMETERS OF MILK YIELD AND LACTATION LENGTH TRAITS IN THE FIVE CONSECUTIVE LACTATIONS IN CROSSBRED DAIRY COWS

***Kefale Getahun**
Ethiopian Institute of Agricultural Research, Holetta Research Center
P O Box 2003 Addis Ababa or 31 Holetta, Ethiopia
**Author for Correspondence: kefalegetahun@gmail.com*

ABSTRACT

Variances, heritabilities, genetic and phenotypic correlations were estimated for lactation milk yield and lactation length traits in the first five lactations. The data set comprised 1809 first, 1411 second, 974 third, 705 fourth and 509 fifth lactation records of crossbred dairy cows. multivariate animal model that included breed and year as fixed effects and animal and error as random effects were applied. There were larger residual variances observed across lactations in both lactation milk yield and lactation length traits. The residual variances also increased in advanced lactation for both traits. Heritability across lactations for lactation milk yield were in the range of 0.11 to 0.35. Highest heritability (0.35) was observed at first lactation but declined then after. Mean estimation of heritability for lactation length in the five consecutive lactations were also found in the range of 0.035 to 0.401. Heritability of lactation length shows decreasing trend from first to third lactations. However, highest heritability (0.40) was found at fourth lactation which implies that presence of sufficient additive genetic variance. Estimated genetic correlations of first lactation milk yield to its corresponding lactation numbers were greater than 0.80 shows that the extent of common genes were large while phenotypic correlations were medium values within the range of 0.40 to 0.67. For lactation length, the genetic correlations between the different lactations were ranged from negative (-0.45) to 0.88. On the other hand, phenotypic correlations of lactation length in all lactations were positive values but lower in the range 0.03 to 0.39 which shows little relationship of phenotypic measurements among lactations. Results suggest that difference between variances, heritabilities as well as genetic and phenotypic correlations from multivariate analyses, each lactation number of lactation milk yield and lactation length should be assumed as separate traits. different lactations are not influenced by the same set of genes and environments.

Keywords: *genetic correlation, crossbred dairy cow, lactation number, variance*

INTRODUCTION

Milk yield improvement of dairy cattle is largely dependent on selection of outstand animals from the population and this is done by effective utilization of additive genetic variance. The goal of selection is to improve lifetime production of cows, which implies that taking the different lactations into account (Beaumont, 1989). Considering repeated performances of the animal (the potential for more than one lactation per cow) is important for accurate genetic evaluation. If assumed that genetic parameters are the same for all lactations when they are in fact different, genetic improvement would be decreased by introducing errors during the selection of animals (Butcher and Freeman, 1968).

For formulation of breeding plan or program, the basic prerequisite is that of the existence of total variability in the population and how much of this is caused by differences in the genetic make-up of the individuals. A quantitative measure of this is provided by heritability. The magnitude of heritability dictates the choice of the selection method and breeding system (Paul *et al.*, 2003). Ilatsia *et al*. (2007) presented that genetic improvement of effective breeding programs is highly dependent on the accuracy of selection and genetic and phenotypic parameter estimates, which include heritability, genetic and phenotypic associations among first and later lactation performance traits.

Many countries use first lactation performance for genetic evaluation because of first lactation is an ideal evaluation system to select bulls based on their daughter performances (Tong *et al.*, 1979; Strandberg and Danell, 1989; Meseret and Negussie, 2017). Additionally, Philipsson (1981) concluded that early lactation production is found to be the most reliable measures of genetic relationships. However, research on the basis of first lactation milk yield or less is not gave complete information because the physiological status of cows is changed considerably after first calving (Wiltbank *et al.*, 2006). Thus, records of second and later lactations provide more complete information on lifetime performance than those from first lactation only (Powell and Norman, 1981). As a trait which is expressed repeatedly in animals' life, the milk production performance is affected by different genetic and environmental factors. Genetic and phenotypic parameters of a trait measured in different lactations are essential to know the true heritability and relationship in different periods and used for management decision in every complete lactation stages.

Previous genetic analysis of milk production and lactation length traits in crossbred dairy cows at Holetta dairy research farm was included >6 parities with extended lactation records (milk records more than 305 days). Such genetic evaluation system (including different lactations as repeated measures of the same trait) assuming that different lactations are influenced by the same set of genes i.e, common genetic and environmental effect (Gebreyohannes *et al.*, 2012). However, the fact is beyond the assumption and for accurate evaluation of milk yield and lactation length, parity should be treated as different, but correlated traits in a multiple-lactation analysis (Mesesret and Negussie, 2017). No studies were found in the literature regarding variances and the resulting genetic parameter (heritability and correlation) estimation in different lactation numbers for crossbred dairy cows in Ethiopia. Keeping this in view, the aims of this study were to estimate variances, heritabilities, and correlations among different lactation numbers of lactation milk yield and lactation length traits.

MATERIALS AND METHODS

Study location and data source

Long term retrospective data of lactation milk yield and lactation length with a completed lactation records through five consecutive lactations in crossbred dairy cows calved from 1974 to 2017 obtained from Holetta dairy research farm, Ethiopia, were used for genetic parameter analysis. Holetta dairy cattle research farm is located 29 km far from the capital, Addis Ababa in the western direction. The detail geographical location, environmental condition, animal management and breeding program of the study area was described by (Getahun *et al.*, 2021).

Data collection and management

Pedigree information regarding ID number of animal, sire and dam, birth date, calving dates, lactation end date and parities/lactation numbers were obtained from individual animal record sheets from crossbreeding and dairy cows genetic improvement research farm. The traits used for the study were production traits (lactation milk yield and lactation length). First, second, third, fourth and fifth lactations of lactation milk yield and lactation length are considered as different traits.

Prior to analysis, incomplete records were deleted/edited according to the following criteria 1. Lactation which was still in progress
2. Lactation length less than 100 days
3. Data with unknown sire and dam (animals with unknown pedigree were pruned)
4. Abortion and stillbirth data
5. Apparent errors associated with animal birth date, calving date, lactation end date.
6. only five consecutive lactations are used for analysis

Table 1: Number of records and average performances of lactation milk yield and lactation length in the five consecutive lactations

	Observed data in different lactations				
	1	**2**	**3**	**4**	**5**
Number of records (animals) for milk yield	790	586	442	318	239
Average milk yield	1885.96	1977.74	1872.49	1904.14	1892.61
Number of records (animals) for lactation length	1019	825	532	387	270
Average lactation length	364.6	338.8	354.4	344.8	392.8

Statistical analysis

Multi-trait analyses of correlated traits utilize information from all traits to obtain estimates for a specific trait and provide accurate estimates of genetic parameters than a single-trait genetic evaluation (Meyer, 1991). Mrode (2005) also, suggested multivariate analysis is increase the accuracy of results by better connections in the data due to residual covariance between traits. Moreover, multiple trait analysis is the only way to obtain unbiased estimates for a trait, which is observed only on animals selected based on values of a correlated trait (Thompson and Meyer, 1986; Van der Werf, 2003). In support of these ideas, multi-trait analysis of an animal model was used for estimation of (co) variance components and the resulting genetic parameters (heritabilities, genetic and environmental correlations) of lactation milk yield and lactation length across five lactation numbers with AI-REML algorithm of the WOMBAT software (Meyer, 2007). Each lactation was considered as different traits for analysis of milk yield and lactation length in the genetic evaluation. Three fixed effects (breed, year and season) were identified as fixed effects and analyzed by (SAS, 2004) to determine the level of significance. The preliminary analysis showed that breed and year were the significant source of variation in all lactations and fitted in to genetic parameter analysis. Additive genetic and residuals effects were assumed as random effects. The animal model for analysis of genetic and phenotypic (co) variances in the five consecutive lactations were described as follows:

$Y_i = X_i b_i + Z_i a_i + e_i$

For $_i$ = 1, 2, 3, 4, 5 representing the i^{th} lactation number;

Y_i, is the vector of observations (lactation milk yield and lactation length) on the i^{th} lactation number;

b_i, includes vector of fixed effects (breed and year in this case) on the i^{th} lactation number;

a_i, is random direct animal (additive) genetic effects on the i^{th} lactation number;

e_i, is the vector of random residual effects on the i^{th} lactation number; and

X_i and Z_i are matrices of the fixed and random animal (additive) genetic effects on the i^{th} lactation number, respectively.

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

σ_{aij}: additive genetic covariance between parity i and j of milk yield or lactation length trait,

σ_{pij}: phenotypic covariance between parity i and j of milk yield or lactation length trait,

$\sigma^2 ai$: additive genetic variance for parity i of milk yield or lactation length trait,
$\sigma^2 aj$: additive genetic variance for parity j of milk yield or lactation length trait,
$\sigma^2 pi$: phenotypic variance for parity i of milk yield or lactation length trait,
$\sigma^2 pi$: Phenotypic variance for parity j of milk yield or lactation length trait.

Heritability is the proportion of additive genetic variance to total phenotypic variance and calculated as the following formula;

$$h2 = \frac{\sigma a\ 2}{\sigma p\ 2}$$

Table 2: Pedigree structure of lactation milk yield and lactation length for genetic analysis in the five consecutive lactations in crossbred dairy cows

Pedigree of animals	Lactation milk yield	Lactation length
Original number of animals	1184	1137
Number of animals after pruning	1042	997
Number of animals w/out offspring	591	568
Number of animals with offspring	451	429
Number of animals with unknown sire	315	309
Number of animals with unknown dam	401	395
Number of animals with both parents' unknown	300	158
Number of sires with progeny in the data	91	89
Number of dams with progeny in the data	360	340
Number of animals with paternal grandsire	0	0
Number of animals paternal granddam	0	0
Number of animals maternal grandsire	268	236
Number of animals maternal granddam	223	194

RESULTS AND DISCUSSION

Number of records and other descriptive statistics are summarized in Table 1. Performances of lactation milk yield and lactation length for crossbred dairy cows were studied and published earlier (Kefale *et al.*, 2020). Thus, no further discussion is needed about Table 1. The aim of this study was to evaluate variances, heritabilities and correlations of lactation milk yield and lactation length traits in different lactation numbers.

Variances and heritabilities of lactation milk yield in different lactations

Genetic, residual (error) as well as phenotypic variances of lactation milk yield in the five consecutive lactation numbers are presented in Table 3. Additive genetic variance was highest in lactation number 1 then declined to third lactation but variable then after. On the other hand, residual (error) variances were increased steadily across lactations. Residual variances were larger than additive genetic variance for all lactations on lactation milk yield indicating that both known and unknown environmental effects were higher impact on the variation of milk yield across lactations. Tong *et al*. (1979) suggested that the increases in error variance in later lactations may be attributed to additional sources of variation, such as dry periods, which do not influence the first lactation. The existence of prolonged dry or open period, repeat breeder of cows, udder health like mastitis which could not include in the model might be partially accounts for the increase of residual variances.

Estimates of heritabilities and their standard errors in different lactations for lactation milk yield are given in Table 3. A summary estimates for all five lactations were 0.35, 0.27, 0.11, 0.22 and 0.13 respectively. This shows that milk yield was more heritable in the first lactation than other subsequent lactations. Due to the difference of additive and environmental (error) variances across lactations, the values of heritability in each lactation were also different. Heritability decreased as lactation increased but no consistent trends from third to fifth lactation numbers. Management regime difference, selection or culling in latter lactations and strength of pedigree relationship of cows in the data in each lactation number might be cause of the heritability variances in each lactation. High producing heifers in low management herds are unable to recover properly after first lactation, and therefore, do not realize their full potential during second or later lactations, thus reducing the genetic variance and heritability of multiparous cows (Weller *et al.*, 1987). If culling takes place on performance in previous lactations, the parameter estimates on later lactations will be bias (Visscher and Thompson 1992). As shows in Table 1, 26%, 44%, 60% and 70% of animals were lost in second, third, fourth and fifth lactations, respectively due to no records as compared to the original first lactation record. These became presence of small population in the later lactations. Weller *et al*. (1987) Heritability estimates will decrease if population was small. Other important sources of variance like open days, dry period and other factors which could not include in the model might be affected the heritability and variances of later lactations. Urioste *et al.* (2003) demonstrated that including adjustment for heterogeneous variance and effect of reproductive traits such as dry period and days open in model result in increasing heritability of production traits in later lactations. Tong *et al*. (1979) suggested that the increases in error variance in later lactations may be attributed to additional sources of variation, such as dry periods, which do not influence the first lactation. Statistically lower values but the decreasing trend from first to third lactations were agreed with the findings of many authors (Tong *et al.*, 1979; Powell and Norman, 1981; Weller, 1986; Johan *et al.,* 1989; Visscher and Thompson, 1992; Albuquerque *et al.*, 1996; Shokri *et al.*, 2019). Other authors (Nistor *et al.*, 2011; Osman *et al.*, 2013) reported increasing trend of heritability as lactation increases. Pryce *et al.* (1998) found highest heritability in the first lactation compared to second and third lactations (0.47, 0.50 and 0.22), respectively. Ali *et al.* (2018) found similar heritability to the present study in the three lactations of Girolando cattle. The difference of this study to other authors might be genetic parameter estimations are breed, location and time specific. Additionally, differences in management, feeding conditions and statistical methodology as well, may offer different results. Number of data obtained and pedigree structure of the animals in each lactation would be other factors of differences in the heritability and variance components. Thomas *et al.* (2000) reported that data errors which leads to missing pedigree information and incorrectly assigned relationships can cause larger bias in estimates of heritability and variance components. Urioste *et al.* (2003) found low heritability influenced by the weak structure of the pedigree information. In the present study about 12% of animals were pruned (no records and genetic relationship) in the population and 49.9 % had records but no genetic relationships. However, Meyer (2003) suggested that any individual without records connected to only one another animal in the pedigree does not add any information.

Table 3: variances and heritabilities of lactation milk yield in the five consecutive lactation numbers

parameters	**Lactation numbers of lactation milk yield trait**				
	1	2	3	4	5
σa^2	186819±156	182756±215	72608.7±179	134497±149	75731.8±133
σe^2	354140±279	508446±396	575780±786	470489±651	508967±632
σp^2	540958±796	691202±927	648389±911	604986±909	584699±884
h^2	0.35±0.001	0.27±0.001	0.112±0.001	0.22±0.001	0.13±0.001

σa^2=additive genetic variance, σe^2= residual variance, σp^2=phenotypic variance, h^2=heritability

Variances and heritabilities of lactation length trait in different lactations

The heterogeneity of additive and residual (error) variances as well as heritability of lactation length from different lactations numbers were observed in Table 4. The error variances were increased until third lactation and decreased at fourth lactation. Lowest additive genetic variance was found at third lactation. This variability would be associated with length of lactation period which are influenced by management, parity, age at calving within parity, season of calving, inadequate milk yield in late lactation and poor fertility. Tiezzi *et al.* (2012) suggesting that extended lactations may be a consequence of poor fertility in year-round calving confinement systems ultimately suppress the genetic expression of length of lactation. Highest heritability of lactation length was found at fourth lactation which implies that presence of sufficient additive genetic variance. Guo *et al.* (2002) reported short lactations had lower heritabilities, which could be due to the extension procedure that introduced extra residual variation.

Table 4: variances and heritabilities of lactation length trait in the five consecutive lactation numbers

parameters	Lactation numbers of lactation length trait				
	1	2	3	4	5
σa^2	1300.7±462.6	1459±689.4	230.6±733.5	2908.2±1351.7	1008.7±1289.8
σe^2	4034.4±0.0	5104.6±674.0	6354±844.0	4329.9±1211	5563.4±1326
σp^2	5335±294.6	6563.6±423.1	6584.7±487.3	7237.6±658.3	6572.8±670.3
h^2	0.244±0.082	0.222±0.101	0.035±0.11	0.401±0.17	0.152±0.19

σa^2=additive genetic variance, σe^2= residual variance, σp^2=phenotypic variance, h^2=heritability

Genetic and phenotypic correlations of lactation milk yield in different lactations

Genetic and phenotypic correlations of lactation milk yield traits in the first five lactations are presented in Table 5. Genetic correlations among the first five lactations for milk yield trait of crossbred cows were high ranged from 0.6 to 0.99. Estimates in the first lactation differed from estimates in later lactations. The correlations tend to increase slightly as the lactation number increased. Tong *et al.* (1979) found similar genetic correlation between first and second (0.89), first and third (0.85) and second and third (0.89) parities of lactation milk yield in Canadian Holstein and suggested that treating different lactations as the same trait genetically is justified. However, the use of different error variances for each lactation may be advisable. this study confirms that genetic correlations among different lactations of milk yield trait are high (≥0.8) but correlation between third and fourth lactation was medium (0.6). High genetic correlations between first and later lactations were reported, generally around 0.8 (Tong *et al.*, 1979; Strandberg and Danell, 1989). First and second and, first and fifth lactations seem to be more closely connected than other adjacent lactations which would be expected from the biological relationship among lactation numbers. The phenotypic correlations varied, on average from 0.40 to 0.67. In general, medium values but lower than the corresponding genetic values. However, all correlations were positive and favorable.

Table 5: Genetic (above diagonal) and phenotypic (below diagonal) correlations of lactation milk yield in the five consecutive lactations

Lactation numbers	Lactation numbers				
	1	**2**	**3**	**4**	**5**
1		0.89	0.83	0.88	0.99
2	0.51		0.71	0.82	0.84
3	0.50	0.65		0.60	0.83
4	0.40	0.52	0.56		0.86
5	0.46	0.60	0.67	0.51	

Genetic and phenotypic correlations of lactation length trait in different lactations

The genetic and phenotypic correlations among records from different lengths of lactation in crossbred dairy cows were vary and are presented in Table 6. The genetic correlations among the different lactations were ranged from negative (-0.45) to 0.88. Genetic correlations were positive in the early and adjacent lactations then low and became negative in later lactation numbers (distant lactations). The strongly high and positive genetic correlations among different lactations were evidence for common genetic and physiological mechanism controlling these traits. Nonetheless, direction and magnitude of genetic correlations of fifth lactation to its first, second and fourth lactations were unfavorable (negative). This shows that the influence of genes in the fifth lactation would be different from first, second and fourth lactations indicated a weak relationship between them. On the other hand, phenotypic correlations of lactation length in all lactations were all positive values but lower in the range 0.03 to 0.39 which shows little relationship of phenotypic measurements among lactations. this lower range was corresponded with those reported by (Navid Ghavi Hossein-Zadeh, 2012). Genetic and phenotypic correlations were high between short lactations in different parities compared with correlations between short and long lactations (Guo *et al.*, 2002). The two possible explanations forwarded by these authors are that some genes are primarily expressed in the beginning of the lactation or that the estimation procedure tends to underestimate short lactations, generating a covariance between records of short lactations.

Table 6: Genetic (above diagonal) and phenotypic (below diagonal) correlations of lactation length in the five consecutive lactations

Lactation numbers	**Lactation numbers**				
	1	**2**	**3**	**4**	**5**
1		0.74±0.2	49±0.9	0.4±0.3	-0.245±0.5
2	0.36±0.04		0.67±0.0	0.88±0.3	-0.37±0.6
3	0.26±0.05	0.39±0.04		0.49±0.9	0.45±0.0
4	0.14±0.06	0.29±0.06	0.23±0.06		-0.47±0.6
5	0.18±0.07	0.03±0.08	0.17±0.07	0.16±0.08	

CONCLUSION

Genetic parameters (variances, heritabilities and genetic and phenotypic correlations) for milk yield and lactation length across the first five lactations were estimated. Estimates of residual variances were higher than genetic variances in all the five lactation numbers and increased across lactations. Heritabilities were highest for first lactation and then decreased for all traits in later lactations owing to increasing residual (error) variances but at fourth lactation heritability increased as a result of sufficient additive genetic variance in both milk yield and lactation length traits. The present results shows that difference between variances, heritabilities as well as genetic and phenotypic correlations from multivariate analyses, each lactation number of lactation milk yield and lactation length are separate traits. However, the extent of genetic relationships was larger but not unity in majority of lactations numbers for milk yield. In conclusion, different lactations are not influenced by the same set of genes and environments.

ACKNOWLEDGEMENT

The author is grateful to Holetta dairy research staff in their contribution of raw data supply.

Conflict of interest

No potential conflict of interest is reported regarding the subject matter of this manuscript.

Funding

The author declares no fund or finance received from any organization for doing this study.

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