

Full length Research paper

Variations, Heritabilities and Correlations of Some Fertility Traits (Calving Interval and Service Per Conception) in the Five Consecutive Calving Numbers of Crossbred Dairy Cows

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Accepted 15th August, 2023.

The objectives of this study were to investigate population parameters (variances, heritabilities and correlations) in the first five calving numbers of fertility traits. Studied fertility traits were calving interval and number of service per conception. Calving and insemination records were 782 and 1062, 602 and 787, 458 and 604, 368 and 455, 277 and 366 in first, second, third, fourth and fifth lactation/calving, respectively. Crossbreed cows' data were spans over 43 years (through 1974 to 2017) recorded at Holetta dairy research farm, Ethiopia. Multivariate animal model that included breed and year (season was not significant) as fixed effects and animal and error as random effects were applied. The larger genetic and phenotypic variance for calving interval was observed at first calving (3435 and 26248 days²) but for service per conception, it was at second calving (0.66 and 0.60), respectively. The estimated heritabilities for calving interval in the five consecutive calving numbers were 0.13, 0.09, 0.18, 0.11 and 0.16. The estimated heritabilities for service per conceptions were also found to be 0.003, 0.04, 0.03, 0.11 and 0.006, respectively. Genetic correlations for calving interval in the five calving's were found to be in the range of -0.38 to 0.69 while phenotypic correlations were positive but lower in the range of 0.06 to 0.27. The genetic correlations for service per conception in different calving numbers were found in the range of -0.76 to 0.78 whereas phenotypic correlations were about -0.026 to 0.16. As the variances, heritabilities and correlations of calving interval and service per conception are different in each lactation, both fertility traits should be interpreted as different traits across lactations rather a repeated measures along lactations.

Key words: calving number; correlations; heritability; variance

INTRODUCTION

Fertility traits are the most important concern in the recent dairy production system. Good fertility in cows is important for keeping the calving interval within acceptable limits, reducing the number of services per conception and reducing culling owing to reproductive failure (Johan et al., 1989). Moreover, Improved fertility increases profit by reducing culling costs and by increasing incomes from milk sales and shorter calving intervals (Navid, 2011). On the other hand, economic losses from poor fertility are mainly due to lost total production as a result of prolonged calving intervals, increased insemination cost, reduced returns from calves born and higher replacement costs (Bagnato and Oltenacu, 1993; Olori et al., 2002). Poor health and

fertility are the main reasons for premature culling in dairy cattle (Pryce et al., 1997). Earlier studies reported that fertility failures accounted for 16% (Miller et al., 1966), 21% (Burnside et al., 1971) and 25% (Colleau and Moureaux, 1999) of all disposals of Holsteins in the United States, Canada and France, respectively due to either low reproduction rate or failure to conceive. Pryce et al. (1997, 1998) also reported failures to conceive especially was the predominant culling reason in the United Kingdom dairy cows and accounted 44% and 42% in the first and second lactation animals, respectively. The low heritability of fertility traits has largely discouraged efforts to improve the traits for decades

(Raheja et al., 1989; Pryce et al., 1998). This low heritability implies that this trait is significantly influenced by environment and management practices and little genetic improvement for reproductive performance can be expected. Despite low heritability, the trait has significant genetic variation (Weigel and Rekaya, 2000). Improvement of this trait through selection was controversial reports (Hansen, et al., 1983; Seykora and McDaniel, 1983). Genetic evaluation of fertility can be analyzed by two different approaches (1) as a repeated measure trait (Berry et al., 2003; González-Recio et al., 2006; König et al., 2008) and (2) as different traits at each lactation (Bagnato and Oltenacu, 1993; De Jong, 1998; Andersen-Ranberg et al., 2005).

The second approach assumes that changes in the regulation and expression of the responsible genes may arise along cows' life and factors affecting fertility are supposed to be of different magnitude over lactations (Tiezzi et al., 2012).

Pervious genetic analysis of crossbred dairy cows at Holetta dairy research farm, Ethiopia has been undertaken by considering fertility traits as a repeated measure and the results were reported by (Getahun et al., 2020). The present genetic evaluations of fertility traits were considering each lactation/calving as a different trait which aims to identify and determine the amount and magnitude of genetic and environmental effects of fertility traits (calving interval and service per conception in different lactation/calving number).

MATERIALS AND METHODS

Breeding information of crossbred dairy cattle from 1974 to 2017 were obtained from Holetta dairy research farm, Ethiopia. The following data were obtained from individual animal card history and from the center database for analysis;

- ✓ Identification number of each animal, sire and dam.
- ✓ Date and year of calving of the animal
- ✓ Calving interval and service per conception
- ✓ calving number and genotype (breed) of cows

The lower and upper limit records for calving interval were 330 and 1500 while 1 and 13 for service per conception. Lactation/calving numbers from 1 to 5 were used for analysis.

Statistical analysis

Multi-trait analysis of an animal model was used for estimation of (co) variance components and the resulting genetic parameters (heritabilities, genetic and phenotypic correlations) of calving interval and service per conception across five calving numbers with AL-REML algorithm of the WOMBAT software (Meyer, 2007).

Each lactation was considered as different traits for analysis of both fertility traits in the genetic evaluation. Three fixed effects (genotype/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 variations in all calving and fitted in to genetic parameter analysis. Additive genetic and residual effects were assumed as random effects. The animal model for analysis of genetic and phenotypic (co) variances in the five consecutive calving 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} calving number;

Y_i , is the vector of observations (calving interval and service per conception) on the i^{th} lactation /calving number;

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

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

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

X_i and Z_i are matrices of the fixed and random animal (additive) genetic effects on the i^{th} calving, 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 calving number i and j of calving interval or service per conception,

σ_{pij} : phenotypic covariance between calving number i and j of calving interval or service per conception,

$\sigma^2 ai$: additive genetic variance for calving number i of calving interval or service per conception,

$\sigma^2 aj$:additive genetic variance for calving number j of calving interval or service per conception,

$\sigma^2 pi$: phenotypic variance for calving number i of calving interval or service per conception,

$\sigma^2 pj$:Phenotypic variance for calving number j of calving interval or service per conception.

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

$$h^2 = \frac{\sigma_a^2}{\sigma_p^2}$$

RESULT AND DISCUSSIONS

Table 1 shows numbers of records, means and standard errors of the traits in the first five lactations. Calving interval and service per conceptions were longer/higher in first lactation animals than second or third lactation animals. Detail descriptive statistics and fixed effect analysis for performance evaluation of both traits were published earlier by (Getahun et al., 2019).

Heritabilities and variances of calving interval across lactations

Table 1. Number of records and average performances of calving interval and service per conception in the five consecutive lactations/calving numbers

	Observed data in different lactations/calving numbers				
	1	2	3	4	5
Number of records (animals) for calving interval	782	602	458	368	277
Average calving interval	529.8	493.2	469.8	479.7	471.5
Number of records (animals) for service per conception	1061	787	604	455	366
Average service per conception	1.84	1.77	1.78	1.75	1.90

Table 2. Pedigree structure of calving interval and service per conception for genetic analysis in different calving numbers

Animal pedigree	Calving interval	Service per conception
Original number of animals	1007	1299
Number of animals after pruning	895	1202
Number of animals w/out offspring	498	667
Number of animals with offspring	397	535
Number of animals with unknown sire	344	376
Number of animals with unknown dam	385	413
Number of animals with both parents' unknown	321	355
Number of sires with progeny in the data	79	96
Number of dams with progeny in the data	318	439
Number of animals with paternal grandsire	0	0
Number of animals paternal granddam	0	0
Number of animals maternal grandsire	194	342
Number of animals maternal granddam	171	313

Table 3. Heritabilities and variances of calving interval trait in crossbred dairy cows across lactations

parameters	Lactation/calving numbers				
	1	2	3	4	5
h^2	0.13±0.08	0.09±0.09	0.18±0.12	0.11±0.15	0.16±0.17
σ_a^2	3435.8±2071	2151.5±1884.7	3046.2±2193.8	1616±2400	3001±3316
σ_e^2	22812±2190	19710.4±2160	14280.8±2218	13859.8±2448	16228.4±3430
σ_p^2	26248±1390	21710.9±1312	17327±1225.9	15476±1228	19229±1803

Heritabilities, additive genetic and phenotypic variations with its standard errors for calving interval trait in different calving numbers are presented in Table3. Higher additive genetic variance was found at first calving (3435.8 days²) and higher than Aziz et al. (2014) who reported 276 days² in the first calving of Brown Swiss cattle. Makgahlela et al. (2008) found lower estimates of additive genetic variances of calving interval in the four consecutive calving (103, 131, 136 and 82 days²). Error/residual and phenotypic variances were high at first lactation but decreased then after. Heritabilities of calving interval trait considered across lactations were relatively low with values in the range of 0.09 to 0.18.

Across lactation heritabilities were not stable and varied. High heritabilities were obtained at third, first and fifth lactations compared to the rest of lactations, respectively as a result of fairly high additive genetic components.

The low heritabilities across lactations were expected and might be due to the high proportion of error variances implies that calving interval is highly influenced by different breeding managements as the

trait is a function of open period, service period, service repetition, gestation length, dry period and lactation period during different lactations which finally inflates the known or unknown environmental variances. Navid (2011) reported lower heritabilities of calving interval in the three lactations of Iranian Holstien cows. Muir et al. (2004) and Aziz et al. (2014) also reported lower value of heritability in the first lactation of Canadian Holstein and Turkish Brown Swiss cattle (0.07). Heritabilities of calving interval in the four consecutive calving reported by Makgahlela et al. (2008) were in the range of 0.03 to 0.04 which were lower than the present study. Ilatsia et al. (2007) also found 0.05, 0.02 and 0.03 heritabilities in the first three consecutive calving of Kenyan Sahiwal cattle.

The literature difference might be breed, management, environment and data and statistical procedure for analysis.

Heritabilities and variances of service per conception across lactations

The variances and heritabilities of service per

Table 4. Heritabilities and variances of service per conception trait in crossbred dairy cows in different lactations

parameters	Lactation/calving numbers				
	1	2	3	4	5
h^2	0.003±0.04	0.04±0.06	0.03±0.08	0.11±0.1	0.006±0.1
σ_a^2	0.53±0.07	0.66±0.1	0.55±0.15	0.15±0.15	0.13±0.3
σ_e^2	1.69.1±0.0	1.6±0.13	1.74±0.17	1.32±0.17	2.15±0.33
σ_p^2	1.69±0.07	1.66±0.07	1.79±0.1	1.48±0.1	2.16±0.17

Table 5. Genetic (above diagonal) and phenotypic (below diagonal) correlations of calving interval trait in crossbred dairy cows across lactations

Calving numbers	Lactation/calving numbers				
	1	2	3	4	5
1		0.6±0.55	0.058±0.46	-0.2±0.70	0.67±0.61
2	0.12±0.04		0.69±0.64	-0.38±0.98	0.06±0.75
3	0.13±0.05	0.11±0.05		0.24±0.71	0.04±0.64
4	0.15±0.05	0.11±0.06	0.11±0.06		0.59±0.84
5	0.27±0.06	0.06±0.07	0.16±0.07	0.27±0.07	

conceptions assessed by treating different lactations as different traits are given in Table 4. The additive genetic variance for service per conception was increased till third lactation and the trend was agreed with earlier study by (Raheja et al., 1993). Heritability of service per conception trait varied from 0.003 to 0.11 and no constant trend across lactations. The present low heritabilities implies that the contribution of genetic variability in each lactation is negligible and management practices of the animals were outshined. Therefore, care should be taken in estrus detection and timing of insemination, semen quality, efficiency of technician and nutritional status of the animal in different lactations. literature estimates of heritabilities for service per conception in different lactations ranged from 0.03-0.06 (Hansen et al., 1983; Van Raden et al., 1987; Raheja et al., 1993).

The present heritabilities in the second and third lactations were similar but significantly lower at the first lactation compared to finding of (Yamazaki et al., 2014) in Japanese Holstein cows. Tiezzi et al. (2012) reported high heritability of 0.046 and 0.045 in the first and second lactations in Brown Swiss dairy cows relative to the present study.

study by Aziz et al. (2014) the heritability of service per conception in the first calving for Turkish Brown Swiss dairy cattle had 0.03 which was higher than the present study. Bagnato and Oltenacu (1993) found constant trend of heritability in the three-calving number (0.1) whereas, Ilatsia et al. (2007) found a constant values of 0.3 in the three consecutive calving of Sahiwal cattle in Kenya.

Genetic and phenotypic correlations of calving interval across calving numbers

Genetic and phenotypic correlations for calving interval in the first five consecutive lactation numbers are shown in Tables 5.

Some of the additive genetic correlations were lower even negative. Thus, calving interval in different

lactations may be influenced by different sets of genes. Medium to high genetic correlations were between first and second, first and fifth, second and third and, fourth and fifth lactations.

This result indicated that selection of calving interval considering different lactations in single trait could not be possible as large differences of genetic correlations among calving numbers were observed. Additive genetic correlations of calving interval reported in the literature were higher than the present study (Navid, 2011; Makgahlela et al., 2008) who reported in the range of 0.67-0.98 across lactations. Olori et al. (2003) reported high genetic correlation between first and second (0.94), first and third (0.85) and second and third (0.90) calvings.

This difference might be associated with data structure, number of observations, genetic profile and physiological status of the animal and, environmental and managerial situations. The phenotypic correlations were lower and positive which reflects the important of managerial and environmental factors related with this trait.

Genetic and phenotypic correlations of service per conception across lactations

The genetic and phenotypic correlations of service per conception for the five lactations are presented in Tables 6. The magnitude and direction of genetic correlation across lactations were high (0.94) between first and second and negative between fifth and the rest of lactations.

phenotypic correlations were significantly low and positive. Compared to the present result, Bagnato and Oltenacu (1993) found greater genetic correlations in the first and second, first and third and, second and third calving of service per conception (0.78, 0.49 and 0.92) but the phenotypic differences were negligible. No obvious trends in the value of the genetic and phenotypic correlations with increasing lactation were detected.

Table 6. Genetic (above diagonal) and phenotypic (below diagonal) correlations of service per conception trait in crossbred dairy cows across lactations

Lactation numbers	Lactation/calving numbers				
	1	2	3	4	5
1		0.94±0.02	-0.15±0.1	0.44±0.01	-0.76±0.03
2	0.09±0.04		0.08±0.01	0.67±0.0	-0.7±0.03
3	0.06±0.05	0.11±0.04		0.78±0.04	0.58±0.05
4	0.1±0.06	-0.026±0.05	0.15±0.05		-0.04±0.05
5	0.11±0.06	0.006±0.06	0.16±0.06	0.14±0.06	

CONCLUSION

The heritabilities of the studied fertility traits were not much heritable in the five consecutive lactations as the traits were sensitive to different environmental and management factors. The present low heritability of calving interval and service per conception traits implicated that the genetic tendency of dairy cows would be approached to other dairy traits like milk production traits. Phenotypic and genetic correlations of fertility (calving interval and service per conception) measures also changed across different lactations. Herd management has a big influence on fertility and should therefore be considered in deciding how much emphasis to put on fertility in a breeding program. Therefore, improvement must be brought about by improving management conditions. However, it is not to say that genetic improvement (increasing heritability) is not possible as increasing the genetic variances. As the variances, heritabilities and correlations of calving interval and service per conceptions are different in each lactation, both fertility traits should be interpreted as different traits across lactations rather a repeated measures along lactations. Even though, the heritabilities across lactations in both fertility traits were low, enough evidence was found to consider these traits in the selection/genetic improvement program, but slow genetic gain/progress will be expected.

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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