

Genetic Analysis of Lifetime Traits of Crossbred Dairy Cattle in the Central Highland of Ethiopia

Sileshi Tefera^{1*}, Kefelegn Kebede², Direba Hunde³, and Million Tadesse³

¹Metu Woreda Livestock and Fishery Office Expert

²Haramaya University, School of Animal and Range Sciences, P.O. Box 138, Dire Dawa, Ethiopia

³Holetta Agricultural Research Centre P.O. Box 31, Holetta, Ethiopia

Abstract: Data collected from 1974 to 2015(42 years) on crossbred dairy cows maintained at Holetta Agricultural Research Centre were used to estimate genetic parameters for lifetime traits. These traits were total life, herd life, productive life, lifetime milk yield, lifetime calf crop, lifetime milk yield per total life (LTMYTL), lifetime milk yield per productive life (LTMYPL), and lifetime milk yield per herd life (LTMYHL). The VCE (6.0.2) and PEST (4.2.5) software were employed for genetic parameter estimations. The heritability estimates for lifetime traits observed in the present study were medium to high ranging from 0.19 ± 0.04 to 0.62 ± 0.06 . The estimates of heritability for total life, productive life, herd life, lifetime milk yield, LTMYTL, LTMYPL, LTMYHL and lifetime calf crop were 0.25 ± 0.05 , 0.20 ± 0.04 , 0.19 ± 0.04 , 0.21 ± 0.04 , 0.31 ± 0.05 , 0.31 ± 0.06 , 0.27 ± 0.07 and 0.62 ± 0.06 , respectively. The genetic correlation estimates between traits vary in magnitude ranging from 0.02 between lifetime calf crop and LTMYPL to 0.94 between LTMYTL and lifetime milk yield. Similarly, the phenotypic correlation estimates between the traits also vary from lower to high, ranging from 0.02 between lifetime calf crop and LTMYHL to 0.94 between herd life and total life. It can be noted from estimated heritability values that including the lifetime trait in the selection program can bring genetic progress to the herd. The genetic and phenotypic correlations among the total life, productive life, herd life, and lifetime milk yield were high and imply that selection on total life and lifetime milk yield would bring positive improvement on most of the lifetime traits. From the study it was concluded that including the lifetime trait in the selection program can bring genetic progress in this herd through choosing the best young sire. Based on the conclusion it was recommended that TL and LTMY need to be considered as important trait in cross breed dairy selection program.

Keywords: *Borana, Crossbred dairy cows, Genetic correlation, Heritabilities, Phenotypic correlation, Lifetime traits*

Introduction

In the tropics, longevity traits, lifetime milk and calf productivities are of high interest to the dairy cattle producers and crossbreeding has brought substantial change in lifetime performances of dairy cattle. Several research reports revealed that 50% crossbred cattle had between 1.4–2.6 times higher lifetime milk yield (LTMY) and 1.2 times more lifetime calf (LTC) than the indigenous cattle breeds (Gebeyehu, 2005; Singh, 2005; Galukande *et al.*, 2013; Kefena *et al.*, 2013; Sileshi *et al.*, 2020). Moreover, the 50% and 75% *Bos Taurus* crossbreeds had a longer lifespan, stay in the herd with more number of lactation with the highest LTMY and had more lifetime calf crop than 87.5 or 93.7% of crossbred cows (Galukande *et al.*, 2013). Furthermore, later generation (F2) crosses were inferior in all the lifetime traits (Kefena *et al.*, 2013; Sileshi *et al.*, 2020). The main preferred selection criteria for longevity traits in the medium-scale crossbreed producers were the number of lactation (39%), herd life (32%), and (29%) length of a productive lifetime (Amare *et al.*, 2019).

Genetic variation existing in a population is a chief source of the genetic improvement for a given trait. Variation in the inheritance of particular traits in a

population of a given environment is measured by heritability estimates at a given time (Gebeyehu, 2014; Lodhi *et al.*, 2016). Hence, the role of heritability is very prominent in predicting the genetic worth as well as in predicting the genetic improvement expected in any selection program. Genetic and phenotypic correlations are necessitated as they aid in the prediction of response to selection in one trait due to selection in another. Variance and covariance are of prime importance to the breeder for estimating the genetic parameters and then utilizing these estimates for the selection of animals (Lodhi *et al.*, 2016). Therefore, the importance of knowing genetic parameter estimates is undeniable and aids in deciding the appropriate selection method and mating system.

Life-time traits are difficult traits for direct selection in dairy cow breeding, due to their low heritability and different influencing factors and the indicators traits were used to select and breed for the lifetime traits of dairy cows (Dallago *et al.*, 2021). The lifetime traits measure the whole lifespan of a cow and can be measured only after the disposal of a cow. The multiple-trait estimation combining indirect measures of longevity with direct measures is helpful to improve

*Corresponding Author. E-mail: sileshitefera95@gmail.com

the accuracy of evaluations. However, there is a lack of research reports on the estimation of genetic parameters for the lifetime traits of crossbred dairy cows in Ethiopia. Therefore, this study aimed to estimate the genetic parameters for lifetime traits of crossbred dairy cows in the central highland of Ethiopia.

Materials and Methods

Study Area

The research was carried out at the Holetta Agricultural Research Centre. Holetta is located 35 km west of Addis Ababa (3°24'N to 14°53'N latitude and 33°00'E to 48°00'E longitude) in Ethiopia's central highlands, at an altitude of 2400 meters above sea level. The average annual temperature in the area is 15°C, with lows of 6°C and highs of 24°C. A bimodal rainfall pattern exists. With an average annual rainfall of 1100 mm, the short-wet period lasted from March to May, and the long rainy period lasted from July to October (Yohannes *et al.*, 2017; Fikadu, 2020; Kefale *et al.*, 2020).

Data Source and Animal Management

Data for the study was obtained from the long-term (1974 to 2015) crossbreeding research on a herd of Ethiopian Borana x Friesian dairy crossbred cattle maintained at the Holetta research station and therefore, records of Borana breed and different blood levels of Friesian crossbred dairy cows were used for the study. This centre is the largest and oldest dairy research center conducting studies on crossbreeding in Ethiopia. In addition, the center serves as a source of crossbred bulls for crossbreeding carried out on smallholder farmer's dairy cattle. The initial aims of the farm were to evaluate crossbred cattle with different exotic inheritances (Friesian and Jersey breed with indigenous breeds). Then it was intended to stabilize crossbred inheritance at 50%. This breeding program was interrupted after 10 years and shifted to stabilize the crossbred inheritance at 75% Friesian inheritance since 2009.

The animals were herded based on breed group, stage of pregnancy, lactation stage, sex, and age. For all animals in each category, uniform feeding and management practices were used. The main feed sources are natural grazing, hay, and concentrate supplements. Animals were allowed to graze during the day from early morning 8 a.m. until 4 p.m. During the evenings, supplementary feed was delivered in the form of natural pasture hay. Depending on their body weight, productivity, and physiological category, a concentrate mixture of wheat middling (32%), wheat bran (32%), noug (*Guizocia abyssinica*) cake (34%), and salt (2%) was supplied. Milking cows, heifers, and calves were supplemented with concentrate mixture at a rate of 4, 1-1.5, and 0.25-1kg per day, respectively depending on the availability of supplemental feed. The cows had free access to clean water all the time.

Calves were allowed to suckle their dam immediately after birth for about four days to get sufficient colostrum; thereafter they were taken into a calf rearing pen and continued to be fed 260 kg of whole milk for 98 days through bucket feeding. Birth weight was recorded and an ear tag was applied within 24 hours after birth. Weaned calves were transferred to other pens and kept in-door until 6 months of age. Milking was done by hand early in the morning and evening, until 2001 and after that a milking machine was introduced. Culling was practised on the farm on criteria of old age, health, body condition, and milk yield. Culled animals were auctioned off. A major disease that is prevalent in the area is treated and immunized in the animals.

Breeding Program

The Borana cattle used as a dam line for crossbreeding were obtained from Borana pastoralists in southern Ethiopia (their homeland) and grown on the station before being randomly inseminated to create the required generations. Seasonal breeding was practised until the year 2000. After 2000, however, the mating method was changed to year-round use of natural mating with locally recruited crossbred bulls or insemination with AI. The main source of semen for crossbreeding research was National Artificial Insemination Centre (NAIC) and the farm has also been using WWS (worldwide sire) Friesian semen for F1 and ¾ crossbred productions since 2009. When animals with AI became repeat breeders, natural mating was also used. Teaser bulls were raised with cows to sense heat. Cows that were found to be in heat were artificially inseminated. Cows that were not seen in heat after 45-60 days of being serviced were assumed to be pregnant. To produce F₁, Borana dams were mated with Friesian sperm. Then mating of the F₁ with 75% Borana x Friesian or 100% Friesian semen to produce 62.5% and 75% generation, respectively. The later generations F₂ (50% F₁ dam x 50% F₁ sire), F₃ (F₂ dam x F₂ sire), and 75% second generations were produced by inter se mating using 50% and 75% Friesian genotypes.

Data Analysis

The mixed model was used to estimate genetic parameters by considering both fixed and random variables. Before estimation of a genetic parameter, the data were adjusted for different significant fixed effects (genetic group, year, and season). The seven genetic groups identified were Borana, 50%F₁, 50%F₂, 50%F₃, 62.5%F, 75% F₁, and 75% F₂ Holstein Friesian inheritance in the study.

After clearing the data of 1136 animals for consistency of pedigree information a final data set comprising of 757,756,755,743,697,733,714 and 757 records of TL, PL, HL, LTMY, LTMYTL, LTMYPL, LTMYHL and LTC respectively, were used for the study. Genetic parameters (heritability, genetic and phenotypic correlation) of lifetime traits were

estimated, using the PEST Ver. 4.2.5 (Groeneveld, 2006) and VCE, version 6 (Groeneveld *et al.*, 2010). The following statistical model was used to estimate genetic parameters:

$$Y = Xb + Zu + e,$$

Where; Y is a vector of observations for the traits of interest (total life, herd life, productive life, lifetime milk yield, milk production per day of total life, milk yield per day of herd life, milk yield per day of productive life, and lifetime calf crop); b is a vector of fixed effects (breed group, year, and season); u is a vector of random individual additive (heterotic) effects; X, matrices relating records to fixed effects; Z, matrices relating records to incidence random individual additive effects and e, a vector of random residual effects.

Results and Discussion

Heritability Estimates of Lifetime Traits

Heritability is the proportion of variation in a trait due to genetic factors, which are measured in numbers ranging from 0.0 to 1.0, with higher numbers being more heritable. The more heritable the trait the faster genetic progress can be made by selecting for that trait (Young, 2017). The direct heritability estimates for lifetime traits observed in the present study were medium to high and ranged from 0.19 ± 0.04 to 0.62 ± 0.06 (Table 1).

Total Life (TL) and Lifetime Milk Yield (LTMY)

The heritability estimated for TL was 0.25 ± 0.05 (Table 1) which was lower than 0.38 (Chhaya, 2013) for HF x Deoni crossbred cows, 0.31 (Gebeyehu, 2014) for Holstein Fresian breed, and 0.28 (Kathiravan *et al.*, 2009) for Sahiwal cattle. The lower value of the present estimate might be due to, the difference in environment, breed and breed composition, and methods of estimation used for the study. However, it is higher than the value reported by Singh *et al.* (2008), Abou-Bakr (2009), Kern *et al.* (2014), Vintohraj *et al.* (2016), and Ambhore *et al.* (2017) for the Sahiwal cross (0.10), HF (0.18), Red Sindhi x Jersey (0.09) and Synthetic breed (0.10), respectively. Moderate heritability is a result of optimum additive genetic and environmental variance.

The estimated heritability for LTMY and milk Yield per day of total life was found to be 0.21 ± 0.04 and 0.31 ± 0.05 , respectively. It is following the estimate of Abou-Bakr (2009) for HF (0.24). The result of the present estimates was higher than the report of Singh *et al.* (2008), Kathiravan *et al.* (2009), Kern *et al.* (2014), and Ambhore *et al.* (2017). However, it was lower than the 0.79 (Chhaya, 2013) for HF x Deoni crossbred cows and 0.36 (Lodhi *et al.*, 2016) for crossbred cows. The current lower estimate is due to, the increase of phenotypic variance than additive variance of this trait. Besides to, the more uniform feeding and management practices careful measuring of a trait can increase the estimate of h^2 . Moderate heritability of the present study implied that LTMY had an optimum additive

genetic variance for selection to act along with production and reproductive traits.

Herd Life (HL) and Milk Yield per day of Herd Life (LTMYHL)

The heritability estimates for HL were 0.19 ± 0.04 (Table 1) which is comparable to 0.18 reported by Abou-Bakr (2009). But lower than 0.47 (Chhaya, 2013) for HF x Deoni crossbred cows and 0.32 (Gebeyehu, 2014) for Holstein Fresian breed, respectively. The lower estimates of the present study indicated that the HL had lower additive genetic variance.

The heritability estimates for LTMYHL were 0.27 ± 0.07 , which was higher than the values reported else were in the tropics (Chhaya, 2013; Vintohraj *et al.*, 2016; Dash *et al.*, 2018) whereas; lower than the report of Singh and Dubey (2005) and Chhaya (2013).

Productive Life (PL) and Milk Yield per day of Productive Life (LTMYPL)

The estimate of heritability of PL is 0.20 ± 0.04 which is lower than the report of Lodhi *et al.* (2016) who's found 0.38 for crossbred cows in India. However, it highly deviates from 0.04 - 0.137 values obtained by some of the authors (Singh *et al.*, 2008; Kern *et al.*, 2014; Vintohraj *et al.*, 2016; Ambhore *et al.*, 2017; Salem and Hammoud, 2019). The difference between our estimate with other studies could be due to the difference in data size used, presence of different missing values and difference in the method of data analysis employed. Even though, evaluation of productive life is after the animal is disposed; however, possible to improve the lifetime traits by using early age indicator traits at an early age due to strong association between lifetime traits and early life indicators (Age at first calving and management of calf at early age and etc.). Dallago *et al.* (2021) reported the association of age at first calving with the ability of cows to remain in the herd and avoid culling, since animals that calved for the first time at a young age are less likely to be culled early during the productive life. Moreover, housing and feeding of calves, health events in early life and inbreeding are associated with cow longevity (Dallago *et al.*, 2021) and the age at which the animal first consumed 0.91 kg/day of grain was positively associated with the age when removed from the herd (Heinrichs and Heinrichs, 2011). For instance, the housing automatically fed calves in small groups (6 to 9 calves) had a higher growth rate than larger groups (12 to 18) calves (Svensson and Liberg, 2006) with the higher average daily weight gain in different ages before the first calving which causes the younger the age at first calving (Vacek *et al.*, 2015). Furthermore, the animals with an inbreeding coefficient of 6.25 to 12.5% were 1.14 times more likely to have a shorter length of productive life, with the likelihood increasing as high as 1.51 times with an inbreeding coefficient $\geq 25.0\%$ (Sewalem *et al.*, 2006).

The heritability estimates for LTMYPL were 0.31 ± 0.06 (0.31 ± 0.05) which are similar to heritability

estimate of LTMYTL. The present estimates of heritability for LTMYPL were higher than some other studies (VanRaden *et al.*, 2006; Chhaya, 2013; Vintohraj *et al.*, 2016).

Lifetime Calves Crop (LTC)

The highest estimated heritability (0.62 ± 0.06) for LTC was higher than 0.29, 0.40, 0.11, 0.09, 0.116, and 0.116 reported in the tropical country by Sadek *et al.* (2009), Oudah *et al.* (2013), Gebeyehu (2014), Kern *et al.* (2014), Vintohraj *et al.* (2016) and Salem and Hammoud (2019) for Holstein Fresian and Jersey x Red Sindh crossbred cows, respectively. The higher heritability of the present study showed that the lifetime calf crop had enough additive genetic variance in the herd for

selection. The current higher heritability value of LTC indicates the improvement of this trait by crossbreeding experiment carried out on the farm; however, the standard heritability value (0.10) for LTC was lower (Cassell, 2001).

These wide ranges of various heritability estimates reported by different authors may be attributed to variation in environment, breed composition, breeds, management practices, the structure of the data set, and analytical models employed. Therefore, the heritability estimates from some countries tend to be different from those in other countries for cattle breeds with the same traits. Moreover, the heritability estimates were changed with the methods, models, and software used for estimating genetic parameters.

Table 1. Estimates of Heritability \pm s.e (on diagonal in bold), genetic (above diagonal) and phenotypic (below diagonal) correlations among lifetime traits.

Traits	TL	PL	HL	LTMY	LTMYTL	LTMYPL	LTMYHL	LTC
TL	0.25\pm0.05	0.73	0.85	0.67	0.48	0.19	0.11	0.40
PL	0.85	0.20\pm0.04	0.92	0.92	0.82	0.35	0.36	0.26
HL	0.94	0.92	0.19\pm0.04	0.85	0.76	0.28	0.17	0.46
LTMY	0.79	0.93	0.85	0.21\pm0.04	0.94	0.68	0.59	0.17
LTMYTL	0.61	0.82	0.69	0.91	0.31\pm0.05	0.74	0.61	0.14
LTMYPL	0.34	0.40	0.33	0.56	0.69	0.31\pm0.06	0.90	0.02
LTMYHL	0.13	0.35	0.13	0.47	0.64	0.83	0.27\pm0.07	0.03
LTC	0.07	0.07	0.10	0.05	0.06	0.04	0.02	0.62\pm0.06

TL= Total life; PL= Productive life; HL= Herd life; LTMY= Lifetime milk yield; LTMYTL= Lifetime milk yield per total life; LTMYPL= Lifetime milk yield per productive life; LTMYHL= Lifetime milk yield per herd life; LTC= Lifetime calf crop production.

Correlation Estimates of Lifetime Traits

The genetic correlation of 1 implies that all of the genetic influences on the two traits are identical, whereas the genetic correlation of 0 implies that the genetic effects on one trait are independent of the other (Falconer and Mackay, 1996). The genetic correlation describes how the genetic values for two traits associate whereas phenotypic correlations describe animals with high values for one phenotype also tending to have high or low values for another phenotype. The present estimates of both genetic and phenotypic correlation were all positive and ranged from 0.02 to 0.94 (Table 1).

The genetic correlation estimates between the traits vary in magnitude from lower to high, ranging from 0.02 between LTMYPL and LTC to 0.94 between LMYTL and LTMY. The genetic correlation of total life (TL) with productive life (PL), herd life (HL), and lifetime milk yield (LTMY) ranged from 0.67 to 0.92. Also, the genetic correlation of productive life and herd life with the LTMYTL were 0.82 and 0.76, respectively, whereas genetic correlations of LTMY with the lifetime milk production efficiency traits were from 0.59 to 0.94. Similarly, the genetic correlation of LTMYTL with LTMYPL, and LTMYHL ranged from 0.61 to 0.90. A similar higher value was observed for the genetic correlation of HL and LTMY with PL (0.92) and TL with HL and HL with LTMY (0.85), which indicated that selection for TL and LTMY will have a positive genetic response for other lifetime traits.

Moreover, a higher association between the longer herd life and the productive life of dairy cows is useful to obtain more productive cows in the herd. Although the higher association between a productive life and lifetime milk production of a dairy cow is useful to obtain more economic productivity. Furthermore, a higher association between the longer lifespan and herd life of dairy cows is useful to obtain genetically improved high producer cows in the herd and the increase in the number of lactation indicate the genetic merit of cows. Dallago *et al.* (2021) reported the increase of cow longevity by reducing involuntary culling would cut health costs, increase cow lifetime profitability, improve animal welfare, and could contribute to a more sustainable dairy industry while optimizing dairy farmers' efficiency in the overall use of resources available.

There is a low to moderate genetic correlation (0.02-0.46) estimates of lifetime calf crop with other lifetime traits. The number of lactation increase indicates the genetic merit of cows but it is genetically less correlated with lifetime traits due to, the genetic effects on lifetime calf are different from the other traits (lifetime calf crop has high genetic value whereas the other lifetime traits are moderate genetic value). The genetic correlation of lifetime calf crop with TL (0.40) and HL (0.46) was moderate and implied that selection for lifetime calf crop could have a minor effect on TL and HL. To utilize this higher heritability of LTC with its low genetic correlation using genomic selection the

marker-assisted selection strategy is efficient to improve prediction accuracy for moderate heritability of traits due to improved precision in poorly estimated low to moderate genetic correlations of the present study. The positive and strong genetic association within the above traits implied the possibility that selecting one trait will increase the genetic values of the other traits. Abou-Bakr (2009), Ambhore *et al.* (2017), and Dash *et al.* (2018) also reported highly positive genetic correlations among lifetime traits in Holstein cows, Phule Triveni synthetic cows, and Karan Fries cattle, respectively. Genetic correlations among traits arise from the pleiotropic effects of genes on multiple traits and/or linkage disequilibrium among distinct loci.

The phenotypic correlation estimates between the traits vary in magnitude from lower to high, ranging from 0.02 between LTC and LTMYHL to 0.94 between HL and TL. The low phenotypic correlation between LTC and LTMYHL is due to, the low genetic influences on the two traits (the nature of variables which didn't govern by the same set of genes in additive manners) which implies that selection of traits in designing crossbreeding program based on either of the traits has an adverse effect on the other. The phenotypic correlation of total life (TL) with productive life (PL), herd life (HL), lifetime milk yield (LTMY), and LTMYTL ranged from 0.61 to 0.94 which indicates that selection on TL and LTMY is sufficient to bring improvement on HL and PL.

Also, the phenotypic correlation of LTMYHL with the LTMYTL and LTMYPL were 0.64 and 0.83, respectively, whereas, correlation of LTMYPL with LTMYTL was 0.69. A similar higher value (0.85) was observed within the phenotypic correlation of PL with TL and LTMY with HL. The genetic and phenotypic correlation of HL and PL (0.92), HL and LTMY (0.85), and LTMYTL and PL (0.82) was similar which implies that possible to estimate the genetic value through phenotypic expression of these traits. However, phenotypic correlation estimates were slightly higher than the genetic correlation for TL and PL, HL and TL, and LTMY and TL. This higher phenotypic correlation than genetic correlation implied that those traits had high possibilities for the existence of high yielder animals through selection and culling of unproductive animals in the herd. There is a lower phenotypic correlation (0.02-0.10) estimate of lifetime calf crop with other lifetime traits.

Genetic and phenotypic correlation estimates between lifespan with the length of herd life, productive life, and lifetime milk production performance were all positive and slightly lower than the report of El-Saied (2008), Dash *et al.* (2018), Ambhore *et al.* (2017) and Salem and Hammoud (2019). On the other way, the present estimate disagrees with the report of Tiwari *et al.* (2010). The authors indicated the negative genetic and phenotypic correlations of LTMYPL with HL, PL, and TL and the negative correlation between HL and LTMY. The negative correlation might be due to, higher additive genetic

variance in one trait and lower in the other trait and vice versa. Sadek *et al.* (2009) and Salem and Hammoud (2019) reported the high genetic and phenotypic correlation between LTC and LTMY, LTC and TL, and LTC and PL, which disagree with the current low to moderate correlation of these traits. Disagreement of the result might be due to, the difference in genetic value and environmental effects on these traits in different environments and different genotypes and hence the difference in traits responses to existing environmental conditions was reflected.

Conclusion

The heritability estimates for lifetime traits observed in the present investigation were medium to high in the range between 0.19 ± 0.04 and 0.62 ± 0.06 . The estimate of h^2 in LTC is much better than other lifetime traits. The present estimates of both genetic and phenotypic correlation were all positive and ranged from 0.02 to 0.94. The high genetic and phenotypic correlation between TL, PL, HL, and LTMY implies that selection on TL and LTMY would bring positive improvement to most of the lifetime traits in this herd. The low correlation between LTC and other lifetime traits is due to, the low genetic influences on the two traits which reflects that selecting either of the traits has an adverse effect on the others in designing of appropriate crossbreeding program. From the study it was concluded that including the lifetime trait in the selection program can bring genetic progress in this herd through choosing the best young sire. Based on the conclusion it was recommended that TL and LTMY need to be considered as important trait in cross breed dairy selection program.

Acknowledgments

The Bill and Melinda Get Foundation Project (BMGP) funded this research as a scholarship grant to the first author, and the author expresses his gratitude to them. The authors would also like to express their gratitude to the Ethiopian Institute of Agricultural Research for allowing us to use their data.

Conflict of Interests

The authors declare that they have no competing interests.

References

- Abou-Bakr, S. (2009). Genetic and phenotypic parameters of some lifetime and longevity traits in Holstein cows of a commercial farm in Egypt. *Egyptian Journal of Animal Production*, 46: 11-18.
- Amare Berhe, Kefena Effa, Yesihak Yusuf & Million Tadesse (2019). Selection criteria for Holstein Friesian and crossbreed dairy cattle objective traits in Ethiopia. *Open Journal of Animal Sciences*, 9: 429-460. <https://doi.org/10.4236/ojas.2019.94034>.
- Ambhore, G. S., Singh, A., Deokar, D. K., Singh, M., Sahoo, S. K. & Divya, P. (2017). Genetic evaluation

- of lifetime performance of Phule Triveni cows by univariate and multivariate methods. *Indian Journal of Animal Sciences*, 87 (2): 177–181.
- Cassell, B. (2001). Using heritability for Genetic improvement. *The Cattle Site, Featured article*. Retrieved from: <https://www.thecattlesite.com/articles/699/using-heritability-for-genetic-improvement>.
- Chhaya, T. Sh. (2013). Studies on lifetime milk production performance of HF x Deoni (HOLDEO) half-bred. *Indian Journal of Animal Sciences*, P2873-TH6879, [http://krishikosh.egranth.ac.in/...](http://krishikosh.egranth.ac.in/)
- Dallago, G. M., Wade, K. M., Cue, R. I., McClure, J. T., Lacroix, R., Pellerin, D. & Vasseur, E. (2021). Keeping dairy cows for longer: A critical literature review on dairy cow longevity in high milk-producing countries. *Animals*, 11: 808. <https://doi.org/10.3390/ani11030808>.
- Dash, S. K., Gupta, A. K., Manoj, M., Kumar, V., Shivhare, P. R. & Valsalan, J. (2018). Analysis of lifetime performance in Karan Fries Cattle. *Indian Journal of Animal Research*, 52 (5):761-767. <https://arccjournals.com/journal/indian-journal-of-animal-research/B-3283>.
- El-Saied, U.M. (2008). Lifetime performance traits for Holstein Friesian cattle raised in Egypt. *Egyptian Journal Animal Production*, 45:11-20.
- Falconer, D. S. & Mackay, T. F. C. (1996). Introduction to quantitative genetics. *Longman Group*, Essex, UK.
- Fikadu Wodajo (2020). Phenotypic and genetic parameters estimation for growth traits of Holstein Friesian x Boran crossbred dairy cattle at Holetta agricultural research centre, Ethiopia, M.Sc. Thesis, Bahir Dar University, Ethiopia.
- Galukande, E., Mulindwa, H., Wurzinger, M., Roschinsky, R., Mwai, A. O. & Sölkner, J. (2013). Cross-breeding cattle for milk production in the tropics: Achievements, challenges, and opportunities. *Animal Genetic Resources*, 52: 111-125.
- Gebeyehu Goshu (2005). Breeding efficiency, lifetime lactation and calving performance of Friesian-Boran crossbred cows at Cheffa farm, Ethiopia. *Livestock Research for Rural Development*, 17: 73.
- Gebeyehu Goshu (2014). Genetic studies on replacement rate and first lactation traits in Holstein Friesian cattle at Holetta bull dam station, Ethiopia, PhD Dissertation, College of Veterinary Medicine and Agriculture, Addis Ababa University, Ethiopia.
- Groeneveld, E. (2006). PEST user's manual. *Institute of Animal Science press, Neustadt*. Available at: <ftp://ftp.tzv.fal.de/pub/pest/doc/pest-manual-Apr-2006.pdf>.
- Groeneveld, E., Kovac, M. & Mielenz, N. (2010). VCE User's Guide and Reference Manual, version 6.0. Institute of Farm Animal Genetics; Neustadt, Germany.
- Heinrichs, A. J. & Heinrichs, B. S. (2011). A prospective study of calf factors affecting first-lactation and lifetime milk production and age of cows when removed from the herd. *Journal of Dairy Science*, 94: 336–341.
- Kathiravan, P., Sachdeva, G.K., Gandhi, R.S., Raja, T.V. and Singh, P.K. (2009). Genetic evaluation of first lactation production and reproduction traits in Sahiwal cattle. *Journal of livestock Biodiversity*, 1: 51-55.
- Kefale Getahun, Million Tadesse, Direba Hunde & Yosef Tadesse (2020). Productive performances of crossbred dairy cattle. *Ethiopian Journal of Agricultural Science*, 30 (2): 55-65.
- Kefena Effa, Diriba Hunde, Molla Shumiye & Roman H. Silasie (2013). Analysis of longevity traits and lifetime productivity of crossbred dairy cows in the tropical highlands of Ethiopia. *Academic Journals*, 7 (11): 138-143.
- Kern, E. L., Cobuci, J. A., Costa, C. N., McManus, C. M. & Neto, J. B. (2014). Genetic association between longevity and linear type traits of Holstein cows. *Science of Agriculture*, 72 (3): 203-209.
- Lodhi, G., Singh, C. V., Barwal, R. S. & Shahi, B. N. (2016). Genetic and phenotypic parameters of first lactation and lifetime traits in crossbred cattle. *International Journal of Agricultural Policy and Research*, 4 (8): 143-148.
- Oudah, E. Z. M., Shalaby, N. A., El Barbary, A. S. A. & Helmy, M. (2013). Estimation of genetic parameters and breeding values for longevity traits for Friesian cattle in Egypt. *The 4th International Conference on Sustainable Animal Agriculture for developing countries*, 27-31, Lanzhou Universities, Lanzhou, China, July 2013.
- Sadek, M. H., Halawa, A. A., Ashmawy, A. A. & Abdel Glil, M. F. (2009). Phenotypic and genetic parameters estimation of the first lactation, lifetime yield and longevity traits in Holstein cattle. *Egypt Journal of Genetic Cytology*, 38: 127-136.
- Salem, M. M. I. & Hammoud, M. H. (2019). Genetic evaluation of some productive lifetime traits of locally Born Friesian cows in Egypt. *Egyptian Journal of Animal Production*, 56 (2): 39-45.
- Sewalem, A., Kistemaker, G. J., Miglior, F. & Van Doormaal, B. J. (2006). Analysis of inbreeding and its relationship with functional longevity in Canadian dairy cattle. *Journal of Dairy Science*, 89: 2210–2216.
- Sileshi Tefera, Direba Hunde, Kefelegn Kebede & Million Tadesse (2020). Analysis of lifetime traits for crossbred dairy cattle in the central highland of Ethiopia. *East African Journal of Veterinary and Animal Sciences*, 4 (2): 31-38.
- Singh, A. (2005). Crossbreeding of cattle for increasing milk production in India: A review. *Indian Journal of Animal Sciences*, 75 (3): 383–390.
- Singh, C. V. & Dubey, P. P. (2005). Estimates of genetic and phenotypic parameters considering first lactation performance traits in Sahiwal cattle and crossbred cattle. *Indian Journal of Animal Sciences*, 75 (11): 1289-1294.
- Singh, V. K., Singh, C. V., Kumar, D. & Sharma, R. J. (2008). Genetic parameters for first lactation and

- lifetime performance traits in crossbred cattle. *Indian Journal of Animal Sciences*, 78 (5): 497-500.
- Svensson, C. & Liberg, P. (2006). The effect of group size on health and growth rate of Swedish dairy calves housed in pens with automatic milk-feeders. *Preventive Veterinary Medicine*, 73: 43–53.
- Tiwari, M., Kumar, D., Singh, C. V., Singh, B. & Gupta, H. P. (2010). Estimation of genetic parameters of first lactation and lifetime traits in Sahiwal and its crossbreds. *Indian Veterinary Journal*, 87 (6): 572-574.
- Vacek, M., Krpálková, L., Syru cek, J., Štípková, M. & Janecká, M. (2015). Relationships between growth and body condition development during the rearing period and performance in the first three lactations in Holstein cows. *Czech Journal of Animal Science*, 60: 417–425.
- VanRaden, P. M., Tooker, M. E., Cole, J. B., Wiggans, G. R. & Megoniga, J. H. (2007). Genetic evaluations for mixed-breed populations. *Journal of Dairy Science*, 90: 2434-2441.
- Vinothraj, S., A., Subramanian, R., Joseph, V.C. & Sivaselvam, S. N. (2016). Lifetime production performance of Jersey x Red Sindhi crossbred cows. *Livestock Resource International*, 4: 59-62.
- Yohannis Gojam, Million Tadesse, Kefena Effa & Diriba Hunde (2017). Performance of crossbred dairy cows suitable for smallholder production at Holetta Agricultural Research Centre. *Ethiopian Journal of Agricultural Science*, 27 (1): 121–131.
- Young, A. (2017). Genetics for the everyday dairy herd. University of Wisconsin-Extension Dodge County, (920). Retrieved from: <https://fyi.extension.wisc.edu/dairy/files/2017/06/Genetics-for-the-Everyday-Dairy-Herd.pdf>.

