



ESTIMATION OF GENETIC AND PHENOTYPIC PARAMETERS FOR
MILK PRODUCTION AND REPRODUCTION TRAITS IN A
DEVELOPING SYNTHETIC DAIRY CATTLE BREED AT HOLETA
AGRICULTURAL RESEARCH CENTER, ETHIOPIA

MSC THESIS

BY

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HAWASSA UNIVERSITY
COLLEGE OF AGRICULTURE

HAWASSA, ETHIOPIA

May, 2025

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DEDICATION

I dedicate this thesis manuscript to my family in appreciation of their unwavering love and tremendous sacrifice. My beloved wife Aberash Belete and my daughter Befikir Asamenew are also honored in this work for their unwavering support, unreserved prayers, and warm love and compassion throughout my life.

STATEMENT OF THE AUTHOR/DECLARATION

First, I declare that this thesis is my authentic work and that all sources of materials used for this thesis have been properly acknowledged. This thesis has been submitted in partial fulfillment of the requirements for MSc degree at the Hawassa University and is deposited at the University Library to be made available to borrowers under rules of the library. I hereby certify that this thesis has not been submitted for consideration for any academic degree, diploma, or certificate to any other institution anywhere.

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LIST OF ABBREVIATIONS OR ACRONYMS

AFC	Age at First Calving
AFS	Age at First Service
AI	Artificial Insemination
AMY	Annual Milk Yield
BV	Breeding Value
CI	Calving Interval
CSA	Central Statistical Authority
CV	Coefficient of Variation
DMY	Daily Milk Yield
EARO	Ethiopian Agricultural Research Organization
EBV	Estimated Breeding Value
F1	First Generation Crossbred
F2	Second Generation Crossbred
F3	Third Generation Crossbred
FAO	Food and Agriculture Organization of the United Nation
GLM	Generalized Linear Model
HARC	Holeta Agricultural Research Center
HF	Holstein Friesian
ID	Individual Identity
LL	Lactation Length
LDI	Livestock Development Institute
LMY	Lactation Milk Yield
LSM	Least Square Means
MASL	Meter Above Sea Level
SAS	Statistical Analysis System

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Estimation of genetic and phenotypic parameters for milk production and reproduction traits in a developing synthetic dairy cattle breed at Holeta Agricultural Research Center, Ethiopia

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ABSTRACT

This study was carried out to estimate genetic and phenotypic parameters for milk production and reproduction traits of synthetic dairy cattle breed development program being implemented at Holeta research center dairy farm. Data collected from 1995 through 2024 on lactation milk yield, lactation length, daily milk yield, age at first service, age at first calving, and calving interval from experiments targeted to develop synthetic breed at Holeta Agricultural Research Center dairy herd were used for this study. The GLM procedures of SAS software were used to estimate the effect of fixed effects such as year, season and parity while regression analysis was performed to estimate crossbreeding parameters (additive, heterosis and recombination effects). Genetic components including variance covariance estimates were analyzed using WOMBAT software. A univariate mixed model for genetic Parameters and Multiple Regression Model for crossbreeding parameters was used for data analysis. The performance of dairy cattle affected by genetic and non-genetic factors. The result of fixed effects (year and genetic group) analysis showed that a significant ($p < 0.0001$) differences in all productive and reproductive traits. Correspondingly, productive traits (LMY and DMY) and reproductive (CI) traits were also significantly ($p < 0.0001$) influenced by parity. The traits, lactation milk yield, were sensitive to seasonal variation. The overall least squares means for lactation milk yield (LMY), daily milk yield (DMY), lactation length (LL), age at first service (AFS), age at first calving (AFC) and, calving interval (CI) were $2140.61 \pm 32.92\text{kg}$, $6.89 \pm 0.07\text{kg}$, $316.54 \pm 3.31\text{days}$, $33.56 \pm 0.63\text{months}$, $42.78 \pm 0.63\text{months}$ and, $469.01 \pm 7.03\text{days}$, respectively. Additive genetic effects were much larger than for the non-significant negative value of heterosis effect of lactation milk yield ($3728 \pm 139.39\text{ kg}$ of additive and $-81.65 \pm 97.98\text{ kg}$ of heterosis). The cross breeds were $-21.51 \pm 29.19\text{ days}$, $-2.29 \pm 3.12\text{ months}$, and $-2.23 \pm 3.12\text{ months}$, reduced for CI, AFS and, AFC due to the additive effect of Friesian gene. Estimation of heritability for productive traits (LMY, DMY and LL) were 0.180 ± 1.00 , 0.235 ± 0.053 and 0.219 ± 0.077 , respectively and reproductive traits (AFS, AFC, and CI)

0.0798 ± 0.034, 0.080 ± 0.033 and 0.180 ± 0.042, in respective order. The current result indicated that repeatability values of productive traits 0.589 ± 1.00 for LMY, 0.491 ± 0.227 for DMY, 0.735 ± 0.151 for LL, and 0.23 ± 0.01 for CI. The current study indicated that the direct genetic correlation between productive traits were positive and ranged from very weak (0.141 ± 0.073) to very strong (0.854 ± 0.304) genetic correlations. From the current study high correlation was observed in between LMY and LL (0.854 ± 0.304). The current study indicated that positive genetic correlation ranged from very weak to weak genetic correlation among reproductive traits. AFS-AFC (0.228 ± 0.172), AFS-CI (0.181 ± 0.194), AFC-CI (0.063 ± 0.02). The present study indicated that the genetic correlation among productive and reproductive traits was closely related with each other in some traits. Strong genetic correlation looked between CI-LL (0.785 ± 0.074), moderate genetic correlation between CI-LMY and AFC-LL (0.428 ± 0.098, and 0.40 ± 0.107), respectively. Thus, based on the study's findings, it was feasible to draw the conclusion that proper parental line selection and crossing should be used to create next-generation calves and improve the farm's overall management system.

Key words: Additive genetic effect, Borena, crossbred dairy cattle, Ethiopia, genetic parameter, genetic trend, Holeta, productive performance, reproductive performance.

1. INTRODUCTION

Globally, there are approximately 1.5 billion cattle and 1000 recognized breeds (FAO, 2020). Ethiopia alone is home to more than 30 cattle breeds, with a national cattle population of 66 million (CSA, 2022). However, the cattle population in Ethiopia is predominantly composed of indigenous breeds, which are mainly characterized by low milk yield (1.48 kg) and shorter lactation length (approximately 7 months) (CSA, 2022). Since 1950s, crossbreeding has been practiced in Ethiopia to improve milk production. Among the exotic cattle breeds, germplasm of Holstein Friesian, Jersey and Semental have been imported for crossbreeding with the local breeds (Kebede, 1992). According to recent reports (CSA, 2022), the proportion of crossbred cattle in the country is not exceeding 3%. Currently, Holstein Friesian and Jersey breeds are mainly utilized for crossbreeding purpose Tesema *et al.* (2020). In tropical regions, this kind of crossbreeding has been frequently employed to combine the high milk production of *Bos Taurus* breeds and resistance to disease, heat stress, adaptation to poor management, and survival to low-quality feeds of indigenous breeds. The first filial generation (F1) of these crosses has a significant advantage in total output due to heterosis impacts on milk yield and reproduction traits, in addition to the additive contribution of each breed to overall performance Mackinnon *et al.* (1996). Nevertheless, additional improvement through backcrossing to the European breed produced inconsistent and frequently unsatisfactory results. According to Schuler *et al.* (2001), a number of factors influence crossbred offspring, namely direct effects, parental effects, heterosis effects like dominance and epistasis, recombination loss, and implications for combination appropriateness.

These effects, which have been theoretically outlined by Hill *et al.* (1971), rely on the breeds involved and the characteristics of interest. When there are significant trait-related variations between the parent breeds, heterosis effects are likely to be significant. For

example, among dairy cow breeds, Jersey has the greatest genetic distance from Holstein-Friesian (HF) (Basedow, 1998). A detailed review of crossbreeding schemes for dairy cattle and of heterosis estimates reported on many literatures (Sorensen *et al.* 2008). It is noted that heterosis effects are not heritable additions accompanying the combined additive effects as a bonus of a cross and decreasing in advanced generations of crosses between two breeds. On the other hand, rotation crosses result in a cyclical gene composition from generation to generation Schüler *et al.* (2001). Two breed rotations maintain 67% of F1 heterosis at equilibrium and 3 breed rotational crosses maintain 86% of F1 heterosis. A decrease in milk production from F1 to F2 (and F3) was noted by Littlewood (1933). However, this was attributed to gene segregation or loss of heterosis. Ayrshire and Friesian F2 crossings with zebu breeds (Sahiwal, Red Sindhi, and Hariana) yielded 30–35% less milk than F1 crosses (Kartha's, 1934). In a review of dairy cattle cross-breeding experiments in the tropics, Syrstad (1989) concluded that most of the decline in the productivity from F₁ to F₂ generations was due to loss of heterozygosity, i.e. dominance effects were the most important contributor to heterosis, with perhaps a small negative effect of recombination on milk yield. Milk yield increased only slightly, or even declined, fertility deteriorated and mortality increased. The lack of adaptation to tropical conditions was obvious. Breeding strategies aiming at the economic use of genetic resources require information on breed and cross breed performance, including estimates of within and between-population genetic factors (Dickerson, 1969). Nevertheless, these estimations differ significantly among breeds, production systems, estimation techniques, etc. (Kahi *et al.*, 2000; Lobo *et al.*, 2000). Crossbreeding program can be optimized by using the best breed combinations and breeding systems to maximize heterosis. Separating the additive and non-additive contributions and dividing the latter into within-locus (dominance) and between-locus (epistatic) components are the challenges in crossbreeding (Tadesse and

Tadelle, 2003). Even though Ethiopia has been upgrading or crossbreeding native cattle with exotic breeds for the past 50 years or more, breed combinations are optimized for dominance and additive genetic contribution. Selecting the best crossbreeding method for the country's milk production is still hindered by the absence of reliable estimations of crossbreeding parameters.

1.2. Statement of the research problem

Dairy cattle production in Ethiopia is a vital component of the country's agriculture, contributing significantly to the national economy. However, local breeds have limited genetic potential for milk production and reproductive performance, which hampers the growth of the dairy cattle industry. To address this, upgrading the genetic potential of local breeds through crossbreeding with exotic dairy cattle breeds, developing synthetic breeds, and promoting good management practices are essential strategies to enhancing productivity and promote sustainable dairy cattle farming in Ethiopia.

A dairy research at Holetta agricultural research center has been conducting crossbreeding experiments for five decades and evaluated different crossbreds of different exotic gene inheritance. As a result, researchers at Holetta research center initiated synthetic breed development program few years ago. Developing synthetic breeds of dairy cattle in Ethiopia holds greater long-term importance than traditional crossbreeding programs. Crossbreeding is mating local cows with exotic dairy breeds to improve milk yields, often lacks consistency and sustainability. This is due to uncontrolled breeding practices and a lack of adaptability in successive generations. In contrast, synthetic breeds are developed through systematic breeding over several generations to combine the high milk production traits of exotic breeds with the hardiness, disease resistance, and environmental adaptability of indigenous Ethiopian cattle. This approach results in a more stable and uniform breed population that can thrive in local conditions while maintaining improved

productivity. Moreover, synthetic breeds reduce reliance on the continuous importation of exotic genetics, lowering costs and preserving national biosecurity. Therefore, the current study estimated the genetic and phenotypic parameters for productive and reproductive traits of on-going synthetic dairy cattle breeding program at HARC.

1.3. Objectives

1.3.1. General objective

To assess the genetic and non-genetic factors influencing productive and reproductive traits in an ongoing synthetic breed development program, with the aim of improving breeding strategies through the estimation of genetic and crossbreeding parameters.

1.3.2. Specific Objectives

- To estimate genetic parameters for productive and reproductive traits in an on-going synthetic breed development program at Holetta Agricultural Research Center.
- Evaluate the effect of non-genetic factors affecting productive and reproductive performance traits in an on-going synthetic breed development program at Holetta Agricultural Research Center.
- To estimate crossbreeding parameters of productive and reproductive traits of an on-going synthetic breed development program at Holetta Agricultural Research Center.

2. LITERATURE REVIEW

2.1. Historical Overview of Synthetic (Composite) Cattle Breed

From the beginning New World, breeders have created synthetic taurine, taurindicine and zebu breeds. In addition, gaining in popularity is crossbreeding, which exploits the first-generation heterosis (Freyer and Sørensen, 2008). The most popular crossbreeds result from a Holstein × Jersey cross (*Kiwi* in New Zealand) or from Hereford × Angus crosses (*black baldy* in North America, breeding objectives (Felius *et al.*, 2024).

Maximum heterosis in synthetics can be calculated from the proportion of genes an individual has received from each source breed Dickerson *et al.* (1973). But breeders must be aware, that for any gene proportion, a synthetic is always inferior in performance to the source crossbreeds (Cunningham and Syrstad, 1987). Indeed, performance of F2 cows has been disappointing by higher age at first calving, longer calving intervals and significantly lower milk production (Syrstad,*et al* .,1996). The advantage of synthetics is that the population is replaced from within itself and after the initial crossing; no additional breed is needed (Mason and Buvanendran, 1982).

2.1.1. The Development of the Sunandini cattle breeds in India

The creation of new cattle breeds to increase milk production was started in India as early as 1856 when the Taylor breed was formed by crossing zebu with the Jersey breed Singh *et al* .(1951). Sunandini breed characteristics that have been fixed for the cows are Chacko *et al* .(1998), Mature body weight of 350 to 400 kg; age at first calving from 28 to 32 months; first lactation milk yield of 2 300 to 2 700 kg; overall lactation yield of 3 200 kg; milk fat percentage of 4 and productive and reproductive performances of Australian zebu breed were 2929 liters of milk in 300 days milking, 39 months of age at first calving, 52 months of calving interval and 5.5 % fat (Handbook of Australian Livestock, Australian Meat & Livestock Corporation, 1989).

2.1.2. The development of Girolando cattle breed in Brazil

In 1989 the Ministry of Agriculture together with the representing associations, drafted the standards for the breeding of Girolando to be 5/8 Holstein and 3/8 Gir. Female Girolando have physiological and morphological characteristics perfect for the production in the tropics (udder capacity and support, size of teats, factors intrinsic to the milk, pigmentation, thermo-regulatory capacity, strong hooves and legs, forage conversion, reproductive efficiency). Girolandos start producing calves at around 30 months; the peak of milk production is at 10 years and they can keep on producing till about 15 years. The interval between births is around 410 days. The average production of milk per lactation is 3,600 kg (two milkings/day) in 305 days, with 4% fat, accumulating a lifetime production over 20,000 kg of milk (www.girolando.com.br).

2.2. The theory and type of crossbreeding

Crossbreeding is the mating of individuals from different lines, breeds, or populations. There are 2 main reasons for applying crossbreeding within livestock. The first is to utilize the different additive genetic levels between breeds to generate offspring with better economic ability caused by new combinations of additive genetic components. Utilization of the different additive genetic levels between breeds is termed “specific combining abilities” (Falconer and Mackey, 1996). Second, crosses between pure lines/breeds express heterosis. Crossbred animals are more robust and economically efficient compared with the parental breeds Mäki-Tanila, *et al.* (2007). Crossbreeding is appealing to many livestock producers and has been recommended by Hansen *et al.* (2000) and Kalm *et al.* (2002).

Heterosis was first described by (Shull, 1948) and is defined as the increased performance of crossbred animals compared with the average of the purebred parental populations.

The increased performance is due to changes in non- additive genetic effects of dominance and epistasis. Thorough discussions on the theory behind crossbreeding in dairy cattle have

been given by Swan and Kinghorn *et al.* (1992). Dominance effects are caused by gene interaction within loci. In general, animals with more heterozygous loci have better performance compared with animals with more homozygous loci. Often, pure breeds have an increased degree of homozygosity due to selection and genetic drift. In crossbred animals, there is a larger chance that genes within loci are heterozygous because the genes at a locus originate from different breeds. If the parental breeds have different alleles or different allele frequencies, the offspring will show greater heterozygosity and heterosis compared with crosses between parental breeds with similar allele frequency. Therefore, in general, heterosis increases with increased genetic distance between the parental breeds (Mäki-Tanila *et al.* (2007), and with increased inbreeding in the parental breeds. The greater the chance that 2 genes within a locus originate from different breeds, the more heterosis is obtained. Heterosis due to dominance effects is therefore fully expressed in first-generation crosses (F_1), where all pairs of genes have one gene from each of the breeds.

According to FAO breeding strategy guideline (2010), crossbreeding program can be categorized in to three. The first is sustained crossing which involve a group of livestock keepers who produce females of a specific breed or breed combination that will be mated to sires of another breed to produce cross-bred progeny. The second is upgrading program which practices a continuous backcrossing to one parental breed. The third breeding program is creating new breed (often called synthetic breed) through long term crossing to fix the genotype at desirable level.

2.3. Crossbreeding under European situations

Concluding from the above, it appears that crossbreeding indeed has distinct advantages for functional traits such as survival and fertility. However, all results mentioned with the exception of the special case of New Zealand, were obtained from comparisons of F_1 -

animals with purebreds. However, for dairy breeders and producers who normally intend to breed their own replacements, an important question is how to go on from F1 -animals. Backcrossing to Holstein will reduce heterosis effects and thus may not be advisable. Rotational crosses would require sophisticated breeding strategies within each herd, and up to now no results exist from experiments under European or North American conditions Swalve *et al.* (2007).

The distinct advantages of F1 -animals can only be fully exploited in a hierarchical system with specialized breeding and production tiers. Commercial milk producers would then buy F1-animals and replace them regularly, concentrating on producing milk. Under present conditions, there is no way for breeding herds to produce their own replacements and F1 -animals for sale. This could only be envisaged if semen sexing would become common practice. Up to now, only a limited amount of sexed semen is available at high price and low expected pregnancy rates, but it may find increasing acceptance, especially for inseminating virgin heifers in well managed herds, until further refinements of the procedure of sexing semen are achieved. In view of the current demand and attractive price for purebred Holstein breeding stock, breeders are more likely to stick to the Holstein breed as first choice for well managed herds Swalve, *et al.* (2007).

The indication of specific combining ability of individual bulls will not surprise plant or animal breeders. But it should be taken as a note of caution against recommending crossbreeding as an easy solution to current problems. Systematic crossbreeding would require a long-term breeding plan to progeny test young bulls for purebred and crossbred performance. In contrast to chickens or pigs, the information from sisters will be limited due to low reproductive rates .Crossbreeding Sinhala cattle with Jersey and Friesian in Ceylon review that, the lactation lengths of the Fi breed groups are larger than their

corresponding F2 breed groups but the repeatability of lactation length is generally low Wijeratne *et al.* (1970).

2.4. History of dairy cattle crossbreeding and vision of synthetic breed formation in Ethiopia

Ethiopia's dairy cattle improvement initiatives began with the introduction of pure temperate cow breeds during the Italian occupation Staal *et al.* (2008). Following the initial importation of pure temperate cow breeds during the Italian occupation, various governmental and non-governmental organizations in Ethiopia engaged in crossbreeding programs utilizing both native and temperate breeds. In the early 1970s, formal breed improvement research was initiated at the Bako, Melka Werer, Adami Tulu, and Holetta Agricultural Research Centers. These centers focused on crossbreeding three indigenous breeds—Barça, Borena, and Horro—with three temperate breeds—Jersey, Simmental, and Friesian (EARO, 2001; Haile, 2006). However, these efforts faced several challenges, including organizational, social, and technical limitations, which hindered their success. The objective of crossbreeding is to combine desirable traits from two or more different breeds to produce offspring that outperform the parent breeds in certain characteristics. These can include: Increased productivity (e.g. more milk, meat), improved disease resistance, Better adaptability to environmental conditions, Enhanced fertility and reproductive performance, Hybrid vigor (heterosis) – improved performance of crossbred animals over purebreds.

A breeding objective is a clearly defined goal that outlines the specific traits or characteristics a breeder wants to improve in a population. It guides decision-making in selecting parents and planning breeding programs Falconer & Mackay (1996) and Bourdon (2000). However, most breeding programs lacked clearly defined objectives and comprehensive performance documentation.

Several studies have assessed the performance of crossbred cattle, though many do not compare them directly with indigenous breeds under similar management conditions. Evaluating both crossbred and indigenous cattle under identical management conditions is crucial for obtaining accurate and comparable data on their performance. Such comparative studies allow researchers to isolate the effects of genetic differences from environmental and management factors, leading to more reliable conclusions. (Tadesse and Dessie ,(2003) found that the F1 cross between Holstein Friesian and Barka cattle produced over three times more milk—an increase of 1,644 kg—and had a lactation period that was 47 days longer than that of pure Barka cattle. Similarly, Haile *et al.* (2009) reported that the F1 cross between Holstein Friesian and Boran cattle yielded four times more milk during lactation and daily milking, and the lactation period was extended by 97 days compared to pure Boran cattle.

Similarly, the F1 cross between Holstein Friesian and Zebu cattle produced 1,423 kg more milk per lactation than pure Zebu cattle and had a lactation period that was 75 days longer Kiwuwa *et al.* (1983). The F1 cross between Holstein Friesian and Arsi cattle yielded 1,168 kg more milk per lactation than pure Arsi and Zebu cattle, with a lactation period extended by 84 days compared to pure Arsi cattle. In contrast, the Jersey x Arsi cross produced 905 kg more milk per lactation than pure Arsi cattle, and the lactation period was 62 days longer than that of pure Arsi cattle Kiwuwa *et al.* (1983). In addition to increased milk production, several studies have highlighted the positive effects of crossbreeding indigenous breeds with Jersey and Holstein Friesian cattle on reproductive traits, such as age at first calving and calving interval (Negussie *et al.*, 1998; Demeke *et al.*, 2004; Roschinsky *et al.*, 2015). However, Beyene. (1992), reported that the reproductive performance, milk yield, growth, and survival rates of calves resulting from inter se mating of F1 temperate-Zebu crosses were relatively poor. This decline is attributed to

recombination losses in second or later generations. Therefore, utilizing F1 crossbreds is preferable in terms of fitness and productivity, as they benefit from superior additive and non-additive gene contributions. Under smallholder management systems, Holstein Friesian crossbreds produced approximately $2,123 \pm 65.6$ liters per lactation over 325 days, while indigenous cattle yielded about 403 ± 90 liters over 204.3 days Kumar *et al.* (2014). Similarly, Holstein Friesian \times Gurage Highland crosses produced an average of $2,430 \pm 154$ kg over 313 days, and Jersey \times Gurage Highland crosses yielded $2,364 \pm 85$ kg over 270 days Ayalew *et al.* (2018). Crossbreeding also reduced age at first calving and calving interval by 1.6 and 1.1 years, respectively Roschinsky *et al.* (2015). These findings suggest that crossbreeding enhances both production and reproductive performance by harnessing additive and non-additive genetic effects. When combined with alternative feed sources and improved health services, crossbreds can better express their genetic potential, thereby improving the livelihoods of smallholder farmers.

In fact, synthetic breed formation is a special form of crossbreeding dairy cattle. Hence, synthetic breed formation could be considered in the case of Ethiopian dairy sector development; in doing so, the exotic gene in heritage to be fixed after a minimum of eight generation (Jembere *et al.*, 2021).

2.5. Productive Traits

Dairy cattle's lactation performance is typically assessed by measuring the total milk produced during a lactation period or annually, the average daily milk production, and the duration of lactation (Zewudu *et al.*, 2013). In general, the reproductive performance and lactation performance of dairy cattle are closely linked to one another. Breeding failure directly impacts milk production and farm profitability, playing a significant role in the long-term viability of a dairy operation (Alem *et al.*, 2021). The level of milk production and the consistency of lactation are essential factors in establishing the suitable calving

interval. According to Arbel *et al.* (2001), breeding failure adversely affects milk yield and farm profitability, ultimately impacting the long-term sustainability of a dairy farm. The levels of milk production and the consistency of lactation are key factors in establishing the optimal calving interval.

2.5.1. Lactation Milk Yield (MY/L)

The performance of dairy cows can be assessed based on the amount of milk they produce over a designated lactation period. The milk production performance of dairy cows is influenced by the animal's genetic makeup as well as environmental conditions. Among these environmental factors, the amount and quality of available feed resources play a significant role (Getahun *et al.*, 2022). Ethiopian breeds produce significantly less milk during lactation compared to exotic breeds, with this variation influenced by factors such as the number of calving, milking frequency, and the consistency of milk production Alem *et al.* (2021). The milk production during lactation in Ethiopian breeds is quite low in comparison to exotic breeds, and this is depending on such as the number of calving's, milking frequency, and the consistency of milk yield. According to Ayeneshet *et al.* (2018), the primary reason for differences in lactation physiology is linked to particular genes and how they interact with non-genetic factors.

2.5.2. Lactation Length (LL)

Lactation length is the duration from the beginning of milk secretion following calving until the cow is dried off. It is a significant production trait because it affects the overall amount of milk produced. In most advanced dairy farms; a lactation period of 305 days is commonly regarded as the standard benchmark. The lactation length of crossbred dairy cows is influenced by various factors, including the breed type, nutritional management, and other non-genetic elements (Getahun *et al.*, 2022). Kumar *et al.* (2014) also noted that 75% Frisian crosses (bred with Barca and Horro) exhibited longer lactation periods

compared to other genotypes. Additionally, lactation length was significantly affected by factors such as season and parity. Beneberu *et al.* (2020) reported that pure Jersey cows had an average lactation length of 344.89 ± 3.81 days. Variations in lactation duration among dairy cows could be attributed to differences in genotype and management practices.

2.5.3. Daily milk yield (DMY)

The daily milk yield is a key trait of dairy cows, representing the quantity of milk produced by a cow each day, usually measured in liters or kilograms. This feature is crucial because it has a direct impact on the profitability of a dairy operation. The daily milk production of crossbred dairy cows is influenced by the breed type and management conditions. As noted by Abera *et al.* (2016), Holstein Frisian crossbred cows produced an average of 11.8 liters of milk per day under farm conditions, which is higher than the findings of Getahun *et al.* (2020), who reported an average daily milk yield of 6.7 ± 0.10 liters for HF×Boran crossbreds in on-station management. The higher milk yields observed in on-farm crossbred cows compared to those in controlled station environments may be attributed to differences in feeding and breeding practices, with farm animals experiencing less stress during these management activities Getahun *et al.* (2022).

Gizaw *et al.* (2017) in Northwest Ethiopia reported that 50% crossbred cows produced an average of 7.3 ± 3 liters of milk per day, while 75% crossbred cows yielded approximately 8.8 ± 2 liters daily. And the average daily milk yield performance of 50% HF×Zebu crossbred cows yielded approximately 6.7 ± 0.10 Getahun *et al.* (2020).

Table 1: Productive performance of crossbred dairy cows with different genetic group in Ethiopia

No	Genotype	LMY (Lit)	LL (days)	DMY(Lit)	Study sites	Sources
1	50% F1	2366.85	332.25	7.13	On station	Birhanu <i>et al.</i> (2015)
2	50%F2	1624.34	298.00	5.43	On station	Birhanu <i>et al.</i> (2015)
3	75%F1	2280.77	325.84	6.87	On station	Birhanu <i>et al.</i> (2015)
4	50% F1	512.7 ± 156	322.4 ± 47	5.6 ± 2	On farm	Gizaw <i>et al.</i> (2017)
5	75% F1	595.3 ± 105	304.6 ± 40	7.30 ± 2	On farm	Gizaw <i>et al.</i> (2017)
6	50% F1	2203.23±38.13	343.62 ± 3.56	6.69 ± 0.08	On station	Getahun <i>al.</i> (2018)
7	50% F2	1697.09±71.82	319.42 ± 6.68	5.66 ± 0.16	On station	Getahun <i>et al.</i> (2018)
8	50% F3	1522.67±90.07	319.25 ± 8.37	5.02 ± 0.19	On station	Getahun <i>et al.</i> (2018)
9	50%HF×Bor	2203.2±38.00	343.6±6.40	6.7±0.10	On station	Getahun <i>et al.</i> (2020)
10	50% F1	2257.9±29	340.8±3	-----	On station	Hunde <i>et al.</i> (2022)
11	75% F1	3043.8±54	376.0±6	-----	On station	Hunde <i>et al.</i> (2022)
12	75% F1	2957.46±72.98	374.05 ± 7.24	8.70 ± 0.17	On station	Getahun <i>et al.</i> (2018)
13	75% F2	2027.16±152.5	303.12± 15.73	6.72 ± 0.37	On station	Getahun <i>et al.</i> (2018)
14	Pure jersey	2166.10±26.7	344.89±3.81	6.37±0.05	On station	Beneberu <i>et al.</i> (2020)
15	Crossbreed	-----	9.04±0.31 Month	5.9±0.17	On station	A dugna <i>et al.</i> (2022)
16	50%HF×Bor	2264.0±41.20	312.0±3.16	-----	On station	Tadesse <i>et al.</i> (2022)
17	Cross=>75%	2676.5±86.33	311.3±3.04	8.5±0.25a	On farm	Zenebe <i>et al.</i> (2024)

Note: LMY: Lactation Milk Yield; LL: Lactation length; DMY: Daily milk yield; HF: Holstein Friesian; F2: 2nd filial generation; F3: 3rd filial generation; Fg: 1 st generation for 75% crosses; Sg: 2nd generation for 75% crosses.

2.6. Reproductive traits

Reproductive performance of cows and heifers is one of the most important factors that influence the profitability of the dairy sector. The lifetime productivity of a cow is influenced by its reproductive performance traits Beneberu *et al.* (2023). To improve the reproductive performance of dairy cows under different production there should be improved nutrition, Proper heat detection, health care, timely insemination Abera *et al.*(2023). The performance of reproduction parameters of improved dairy cattle reports

was inconsistently varied across breed types, blood levels, dairy farms, study areas and seasons, and production environment systems Mesele *et al.* (2024).

Reproductive Traits, including age at first calving, calving interval, days open, and service per conception, are essential for improving reproductive efficiency and overall farm profitability.

2.6.1. Age at first service (AFS)

AFS (Age at First Service) refers to the age when heifers achieve the proper body condition and sexual maturity necessary for their initial breeding. According to Sisay *et al.* (2017), it is also regarded as the age at puberty. Hence, it is a key factor determining a heifer's productive and reproductive performance by influencing the length of her calving lifespan calf crop, as stated by Adugna *et al.* (2022). According to Abera *et al.* (2016), the average age at first service (AFS) for improved dairy cattle in Europe and Zebu-type dairy heifers ranges from 8 to 10 months and 17 to 27 months, respectively. Mesele *et al.* (2024) noted that there were no significant differences ($P>0.05$) in the mean AFS values among improved dairy cattle breeds in Ethiopia. According to Adugna *et al.* (2022), the age at first service (AFS) is affected by various factors, including feeding and nutrition, housing, health management, breeding (both sire and dam), the season of birth, climatic conditions, and the agro-ecological environment. With this regard, the environment in which the farm is located and the farm management practices employed play a crucial role in determining the AFS of improved dairy cattle. These factors influence prepubertal growth rates, the development of reproductive organs, the onset of puberty, and fertility, as noted by Hunde *et al.* (2022).

According to Mesele *et al.* (2024), the overall AFS performance of improved dairy cattle in Ethiopian conditions is relatively low. However, this can be improved through proper management strategies, such as providing better nutrition to dams before calving,

implementing effective care and management practices for calves, and maintaining good management at the heifer stage. These measures can lead to improved reproductive traits and increase the replacement rate of the dairy farm herd.

2.6.2. Age at first calving (AFC)

Age at first calving (AFC) marks the start of a cow's reproductive cycle and milk production. It influences both the productive and reproductive life of the female Adugna *et al.* (2022). The recommended body weight of Holstein at the first service is 340 kg. Holstein cattle reach puberty at approximately 37.21 months of age Abera *et al.* (2016) than their crosses with zebu which reach puberty at about 24.8 months of age Mekonnin *et al.* (2015). Based on Mesele *et al.* (2024), in Ethiopia, the review study analyzing collected metadata of improved dairy cattle indicated significant differences in age at first calving (AFC) across different breed types at a 5% significance level. However, the mean AFC values and assessments of exotic blood levels were found to be relatively similar. Mesele *et al.* (2024) Exotic blood level rating showed that 38.5 ± 5.5 , 38.4 ± 4.1 , 37.9 ± 5 , 37.7 ± 4.2 , and 35.2 ± 5.1 months of the average AFC for 50%, pure exotic (100%), 50–75, 75–100, and <50% exotic blood levels in descending order, respectively. Jalata *et al.* (2023) identified several factors influencing the age at first calving (AFC) in improved dairy cattle, including management aspects such as feeding, heat detection, breed selection, inseminator expertise, timing of insemination, health care, and other husbandry practices. Mesele *et al.* (2024) reported that the age at first calving (AFC) of improved dairy cattle in Ethiopia is quite inconsistent and varies significantly across different breed types and blood levels. They suggest that these variations in AFC performance are primarily attributed to differences in genetic traits and how these genetics interact with the production environment.

2.6.3. Calving interval (CI)

The calving interval (CI) is the period between two consecutive calvings and is a crucial indicator of reproductive performance that influences dairy productivity. Under optimal management practices, its ideal duration is generally considered to be between 360 and 390 days, Abera *et al.* (2022). Gebreyohanes *et al.* (2021) and Adugna *et al.* (2022) indicate that a longer calving interval is generally associated with a decline in annual production cycles and milk yield performance. Conversely, a longer calving interval can be advantageous for milk production if proper management practices are in place, including adequate nutrition, which enables farmers or cooperatives to purchase sufficient quantities of milk for the market, as suggested by Toure *et al.* (2020).

According to Mesele *et al.* (2024), the average calving intervals (CI) for various improved dairy cattle breeds in Ethiopia showed significant differences ($P < 0.05$). Specifically, the shortest CIs were observed in Jersey-crossed Arsi breed (407 days), Jersey-crossed Barka breed (415 days), and Jersey crossbred with other breeds (421.7 days). In contrast, the longest CIs were recorded in HF-crossed Barka breed (460.6 days), Jersey-crossed Borena breed (456 days), and HF-crossed Borena breed (452.4 days). Toure *et al.* (2020) suggest that a longer calving interval can be advantageous for milk production if proper management practices are in place, including adequate nutrition, which enables farmers or cooperatives to purchase sufficient quantities of milk for the market.

Table 2: Reproductive performance of crossbred dairy cows with different genetic group in Ethiopia.

No	Breeds	AFS (Months)	AFC (Months)	CI (Days)	Sources
1	HF	32.71±0.69	42.13±0.70	413.04±7.31	Mengistu <i>et al.</i> (2016)
2	HF	-----	40.83±0.46	---	Gebeyehu <i>et al.</i> (2014)
3	HF x Boran	-----	40.23	461.34	Tadesse <i>et al.</i> (2014)
4	HF x Boran	26.80±0.34	37.42±0.35	476.35±3.91	Getahun <i>et al.</i> (2018)
6	HF x Boran	30.47±0.85	39.49±0.83	476.36±4.73	Wassie <i>et al.</i> (2015)
7	HF x Arsi	33.62±0.71	42.84±0.84	475.48±4.08	Wassie <i>et al.</i> (2015)
8	Jersey	22.93±0.22	32.95±0.22	494.16±3.68	Beneberu <i>et al.</i> (2020)
9	3/4HF*1/4Borena	-----	-----	476.78±10.49	Tadesse <i>et al.</i> (2019)
10	HF	30.5 ± 0.60	39.76 ± 0.67	446.1 ± 6.80	Kassa <i>et al.</i> (2020)
11	50% F1	-----	32.37±97.5	426.25±22.52	Yesuf <i>et al.</i> (2020)
12	3/4F:1/4B (F1)	-----	42.2±0.7	520.5±9	Hunde <i>et al.</i> (2022)
13	Cross breed	20.95 ±0.06	30 ±0.05	16±0.38(Month)	Adugna <i>et al.</i> (2022)
14	Cross=>75%	22.2±0.54	31.5±.54	13.8±0.46 (Month)	Zenebe <i>et al.</i> (2024)

HF=Holstein Friesian, AFS=Age at First Service, AFC=Age at First Calving, CI=Calving Interval

2.7. Genetic parameter

Genetic parameters are essential for genetic improvement programs, as they enable the estimation of breeding values for selection candidates, guide mating plan decisions, and help predict the response to selection (Montaldo *et al.*, 2010). The extent to which a trait can be genetically improved largely depends on the genetic variation present within the population. Understanding the genetic makeup of a population involves assessing the relative influence of hereditary and environmental factors that impact individual performance. Having detailed and accurate information on genetic parameters is crucial for designing effective selection and breeding strategies aimed at genetic enhancement programs Goshu *et al.*(2014).

Research on estimating genetic parameters in Ethiopian cattle is limited, likely due to the absence of comprehensive pedigree data and farm records. Nonetheless, some studies have reported estimates of genetic parameters such as heritability, repeatability, and genetic and phenotypic correlations related to milk production traits (Effa *et al.*, 2018; Beneberu *et al.* 2020; Hunde *et al.* 2022).

2.7.1. Estimates of Heritability for Production and Reproduction traits

Environmental conditions constrain the ability of superior animals to fully express their genetic potential. Since climate, feed, disease, and other environmental factors have a more significant impact on performance in subtropical and tropical areas compared to temperate regions, and heritability may be reduced in tropical regions (Chrulukovian, 2006). Estimates of heritability of Ethiopian Boran and their crosses with Holstein Friesian were 0.30 ± 0.00 , 0.18 ± 0.02 for lactation milk yield and lactation length, respectively Hunde *et al.* (2022). Getahun *et al.* (2018) reported a heritability value of 0.25 ± 0.01 , 0.28 ± 0.05 , and 0.12 ± 0.04 for lactation milk yield, daily milk yield, and lactation length, respectively.

Many reproductive traits are largely affected by variations in herd management and environmental conditions rather than genetics. However, sire selection can still have a significant impact on the long-term reproductive performance of herds (Yosef, 2006). Estimates of heritability of Ethiopian Boran and their crosses with Holstein Friesian were 0.22 ± 0.08 , 0.30 ± 0.08 , 0.071 ± 0.03 for age at first service, age at first calving, and calving interval respectively Getahun *et al.* (2018). The study by Hunde *et al.* (2022) showed that heritability estimates of Frisian with Boran crosses were 0.19 ± 0.06 , and 0.09 ± 0.03 for age at first calving and calving interval, respectively. Heritability estimate may vary depending on the breed, management practices, and geographical location associated with the data collection.

2.7.1.1. Heritability

Heritability refers to the proportion of observable variation that result from additive genetic variance. Heritability, as a measure that reflects and quantifies the average effect of additive genes, is a key characteristic of quantitative traits, especially in the development of genetically superior cattle populations (Beneberu, 2023). Heritability is essential for the effective selection of polygenic traits. According to Javed *et al.* (2001), low heritability is caused not only by a low genetic variance but also by a higher phenotypic variance due to the small size of the herd and random or unidentified environmental factors.

Table.3. Heritability of productive and reproductive traits for some Ethiopian dairy cattle

Traits	Breed	$h^2 \pm SE$	Sources
LMY	HF x Bor	0.25 ± -1	Getahun <i>et al.</i> (2018)
	Pure jersey	0.14	Beneberu <i>et al.</i> (2020)
	HF x Bor	0.30±0.00	Hunde <i>et al.</i> (2022)
DMY	HF x Bor	0.28±0.05	Getahun <i>et al.</i> (2018)
	Pure jersey	0.12± 0.04	Beneberu <i>et al.</i> (2020)
LL	HF x Bor	0.27±0.03	Tadesse <i>et al.</i> (2014)
	HF x Bor	0.12±0.04	Getahun <i>et al.</i> (2018)
	HF x Bor	0.18±0.02	Hunde <i>et al.</i> (2022)
	Pure jersey	0.04±0.02	Beneberu <i>et al.</i> (2020)
AFS	HF x Boran	0.22 ± 0.08	Getahun <i>et al.</i> (2018)
	Pure jersey	0.05±0.08	Beneberu <i>et al.</i> (2020)
AFC	HF x Boran	0.30±0.08	Getahun <i>et al.</i> (2018)
	Pure jersey	0.05±0.05	Beneberu <i>et al.</i> (2020)
	HF x Boran	0.19±0.06	Hunde <i>et al.</i> (2022)
CI	HF x Boran	0.071±0.03	Getahun <i>et al.</i> (2018)
	Pure jersey	0.03±0.02	Beneberu <i>et al.</i> (2020)
	HF x Boran	0.09±0.03	Hunde <i>et al.</i> (2022)

LMY=Lactation Milk Yield, DMY=Daily Milk Yield, LL=Lactation Length, AFS=Age at First Service, AFC=Age At First Calving, CI=Calving Interval, h^2 =Heritability, SE=standard error.

2.7.1.2. Repeatability

In dairy cattle, the repeatability estimate reflects the degree of correlation between repeated measurements of a trait within a population, which can be used to evaluate the true productive potential of individual cows (Olawumi and Salako, 2010). The repeatability value exceeds the heritability estimate because it encompasses both the permanent environmental variance and the additive genetic variance component. When repeatability is high, it indicates that a single performance measurement for an animal typically provides a reliable estimate of that animal's overall productive capacity. When repeatability is low, relying on a single phenotypic measurement doesn't give a reliable indication of an animal's true producing ability or future performance.

Getahun *et al.* (2018) investigated the repeatability estimates for milk production traits in Frisian-Boran crossbred dairy cows in Ethiopia. The study reported repeatability values of 0.46 ± 0.0 for daily milk yield (DMY), 0.23 ± 0.02 for lactation length (LL), and 0.50 ± 1 for 305-day milk yield (LMY). Whereas repeatability values of 0.17, 0.54, and 0.70 for lactation milk yield, daily milk yield, and lactation length Haile *et al.* (2009).

2.7.2. Genetic and Phenotypic Correlation

Correlations play a crucial role in predicting how selecting for one trait can influence another trait through correlated responses. These correlations are divided into three types: phenotypic, genetic, and environmental. A correlation measures the degree of association between two variables. A higher correlation indicates a stronger relationship between them; while a lower correlation suggests a weaker connection Bourdon. (2000). Genetic correlation estimates between two traits indicate that selecting for one trait may result in an indirect genetic change in the other trait Goshu *et al.* (2014). According to Haile *et al.* (2009), in Ethiopian Boran cows, DMY (Daily Milk Yield) with LL (Lactation Length)

was 0.786 ± 0.12 . In Holstein Frisian crossbred cows, DMY with LL was 0.436 ± 0.14 , and LMY (Lactation Milk Yield) with LL was 0.556 ± 0.12 .

2.7.3. Breeding Value

Breeding value is defined as the genetic contribution of an individual to its offspring, representing the additive genetic value or parental worth in passing on genes to the next generation. According to Mohammed, (2004), breeding value refers the value of an individual assessed based on the average performance of its offspring. Breeding values can be estimated through various sources of information, including the individual's own performance, the performance of its progeny and/or parents, or even the breeding values for other traits of the animal or its relatives.

In dairy cattle, genetic improvement of productive and reproductive traits is often constrained in females due to the limited availability of replacement stock. Conversely, intensive selection is more feasible for males, as only a few males are needed for breeding purposes Lodhi *et al.* (2016).

2.8. Crossbreeding Parameters

Crossbreeding, whether it involves terminal or rotational crossing, the development of synthetic breeds, or breed replacement, is commonly recommended as a cost-effective method to enhance farmers' earnings by improving the productivity of indigenous cattle breed.

The two main methods for genetic enhancement are within-breed selection (pure breeding) and crossbreeding, which utilizes either local or exotic genetic germplasm. In contrary to pure breeding, crossbreeding does not produce genetic progress by itself (i.e. in the sense that the additive genetic merit of the crossed animals is equal to the mean of the breeds involved), but has different merits such as using the complementarity between traits and

heterosis effects Leroy *et al.* (2016). Since the late 19th and early 20th centuries, efforts have been made in developing countries to replace or develop new breeds. The outcomes of these initiatives have varied greatly and largely depended on local conditions Madalena *et al.* (2002). The lack of adaptation of crossbreds to harsh production environments: such as extreme climate conditions, high disease pressure, and limited feed availability, coupled with insufficient socio-economic support, has raised concerns about the long-term sustainability of crossbreeding in certain regions or within specific breeding systems.

One of the main reasons for estimating crossbreeding parameters is to predict the genotypes not include in the original data set without actually producing the animals, in order to make a choice of breeding systems for the benefit of producers.

2.8.1. Additive Genetic Effect

Several authors reported that the individual additive genetic breed difference for milk production traits were significant Taddele *et al.* (2015); Tadesse *et al.* (2019) and Hunde *et al.* (2022). Getahun *et al.* (2018) evaluated the additive genetic difference of Friesian against local Borena and reported 2674.05 ± 252.8 , 7.1 ± 0.6 and 88.4 ± 26.6 days for LMY, DMY and LL, respectively.

Cunningham and Syrstad (1987) reviewed reports from 25 tropical countries on dairy cattle crossbreeding and found that the Friesian breed generally provides high breed additive contributions to milk production traits. This indicates that incorporating Friesian genetics into crossbreeding programs can effectively enhance milk yield in tropical dairy cattle populations. This may be attributed to the lower milk production capacity of indigenous tropical breeds relative to the Friesian breed. For example, the Borena breed exhibits a lower additive genetic contribution to milk production potential compared to other milking-type tropical indigenous cattle, such as the Sahiwal. The Sahiwal is frequently

utilized in various crossbreeding studies due to its comparatively higher milk production traits (Cunningham and Syrstad, 1987).

Getahun *et al.* (2018) presented the negative value of additive genetic effects Ethiopian Borena and Holstein Friesian reported -373.9 ± 114.8 , -337.1 ± 112.6 - 105.7 ± 54.2 for, AFS, AFC, and CI respectively. In contrary, Taddele *et al.* (2015) reported Ethiopian Borena and Holstein Friesian for AFC and CI were positive value of additive genetic effects.

2.8.2. Non-Additive (Heterosis) Effect

Heterosis is a key theoretical principle in hybrid breeding, where hybrid species demonstrate increased robustness and vigor in growth and yield compared to their purebred parent breeds. This phenomenon, often referred to as hybrid vigor, plays a crucial role in enhancing productivity and performance in various agricultural and livestock breeding programs Fujimoto *et al.* (2018). According to the heterosis theory, hybrid breeding serves as a powerful genetic approach for joining predominantly non-additive gene actions, which include dominance and epistasis effects. This strategy allows breeders to exploit the interactions between different alleles to achieve improved traits such as higher yield, increased vigor, and enhanced strength.

2.8.3. Direct Recombination

Recombination loss in F1 crosses generally has a negative impact on milk production traits because it can disrupt favorable gene combinations that were optimized within pure breeds. Conversely, for traits related to fertility and health, recombination loss tends to be either neutral or may even have some favorable effects, as suggested by studies such as Konstantinov *et al.* (2006) and Dechow *et al.* (2007).

Additionally, when crossing different pure breeds, there is a risk of breaking apart these beneficial gene combinations, a phenomenon known as recombination loss. This can lead to a reduction in the overall performance of the hybrid animals for certain traits, especially those that rely heavily on specific gene interactions established within the pure breeds.

Most authors have reported that the direct recombination effect on milk production traits tends to have negative values. This suggests that recombination often disrupts favorable gene combinations related to milk production, potentially leading to decreased performance in crossbred animals for these traits. Hunde *et al.* (2022) reported the direct recombination genetic effects for Ethiopian Borena and Holstein Friesian breeds as -1496.6 ± 143 and -64.2 ± 15 , for lactation milk yield and lactation length, respectively. Different authors have reported negative values indicating recombination loss as a significant effect on total lactation milk yield. Birhanu *et al.* (2015) reported a value of -586.44 ± 162.02 liters, Tadesse *et al.* (2019) reported -2984.73 ± 883 liters, Hunde *et al.* (2022) found -1496.6 ± 143 liters, and Getahun *et al.* (2018) reported -1902.3 ± 200 liters. The negative value of recombination on total lactation milk yield is associated with a reduction in heterosis dominance effects observed in F₂, F₃, 75% F, and 62.5% F generations, as reported by Taesew *et al.* (2015).

Table.4. Crossbreeding parameter estimates (Direct Additive, Direct Heterosis, and Direct Recombination) with standard errors for productive and reproductive traits of different genotype in Ethiopia

Traits	Breed	Direct Additive	Direct Heterosis	Direct Recombination	Resources
LMY	HF x Bor	2040.19±256.01	899.02±132.68	-586.44±162.02	Taddele <i>et al.</i> (2015)
	HF x Bor	2674.05 ± 252.8	423.9 ± 128.7	-1902.3 ± 200	Getahun <i>et al.</i> (2018)
	HF x Bor	3852.83±937	-54.08±195	-2984.73±883	Tadesse <i>et al.</i> (2019)
	HF x Bor	3985.2±150	-150.6±76	-1496.6±143	Hunde <i>et al.</i> (2022)
DMY	HF x Bor	5.18±0.62	2.78±0.32	-0.61±0.40	Taddele <i>et al.</i> (2015)
	HF x Bor	7.1 ± 0.6	1.25 ± 0.3	-4.2 ± 0.5	Getahun <i>et al.</i> (2018)
LL	HF x Bor	85.95±27.75	43.05±14.38	-25.47±17.56	Taddele <i>et al.</i> (2015)
	HF x Bor	88.4 ± 26.6	-0.1±9.3	-91 ± 20.8	Getahun <i>et al.</i> (2018)
	HF x Bor	257.51±25	4.33±12	-177.06±54	Tadesse <i>et al.</i> (2019)
	HF x Bor	166.3±16	-7.3±8	-64.2±15	Hunde <i>et al.</i> (2022)
AFS	HF×Boran	-9.16±2.88	-----	-----	Birhanu <i>et al.</i> (2014)
	HF×Boran	-----	-2.83±1.63	-----	Birhanu <i>et al.</i> (2014)
	HF x Bor	-373.9 ± 114.8	-117.6 ± 61.3	129.2 ± 97.2	Getahun <i>et al.</i> (2018)
AFC	HF x Bor	385.30±208.92	-354.47±129.6	-62.60 ±138.41	Taddele <i>et al.</i> 2015)
	HF x Bor	-337.1 ± 112.6	-207.9 ± 59.8	70.5 ± 95.2	Getahun <i>et al.</i> (2018)
	HF x Bor	-0.2±2	-4.7±1	7.1±2	Hunde <i>et al.</i> (2022)
CI	HF x Bor	55.01±54.51	-70.14±27.88	-17.34±33.97	Taddele <i>et al.</i> (2015)
	HF x Bor	55.01±54.51	-70.14±27.88	-17.34±33.97	Birhanu <i>et al.</i> (2015)
	HF x Bor	-105.7 ± 54.2	2 ± 27.5	-113.6 ± 43	Getahun <i>et al.</i> (2018)
	HF x Bor	3.9±5	-38.46±26	-124.60±136	Tadesse <i>et al.</i> (2019)
	HF x Bor	52.9±25	-88.7±13	-26.5±26	Hunde <i>et al.</i> (2022)

LMY=Lactation Milk Yield, DMY=Daily Milk Yield, LL=Lactation Length, AFS=Age At First Service, AFC=Age At First Calving, CI=Calving Interval.

3. MATERIALS AND MHODS

3.1. Description of the Study Area

The study was conducted at Holetta Agricultural Research Center (HARC). It is located at 9°30' N and 38° 30' E and 35 km west of Addis Ababa on the way to Ambo. The topography where the center is located consists of section of central Ethiopia, which represents cool tropical highland area that covers about 30% of land mass of Ethiopia and more than 70% of the population of the country. In the area where the center is located, the topography can be expressed by the existence of some scattered hills and mountains ranging between altitudes of 2250 m to 2500m above sea level. The area receives an average annual rainfall of around 1,200 mm. The region's average yearly temperature is 18°C, with relative humidity averaging 60% throughout the year.

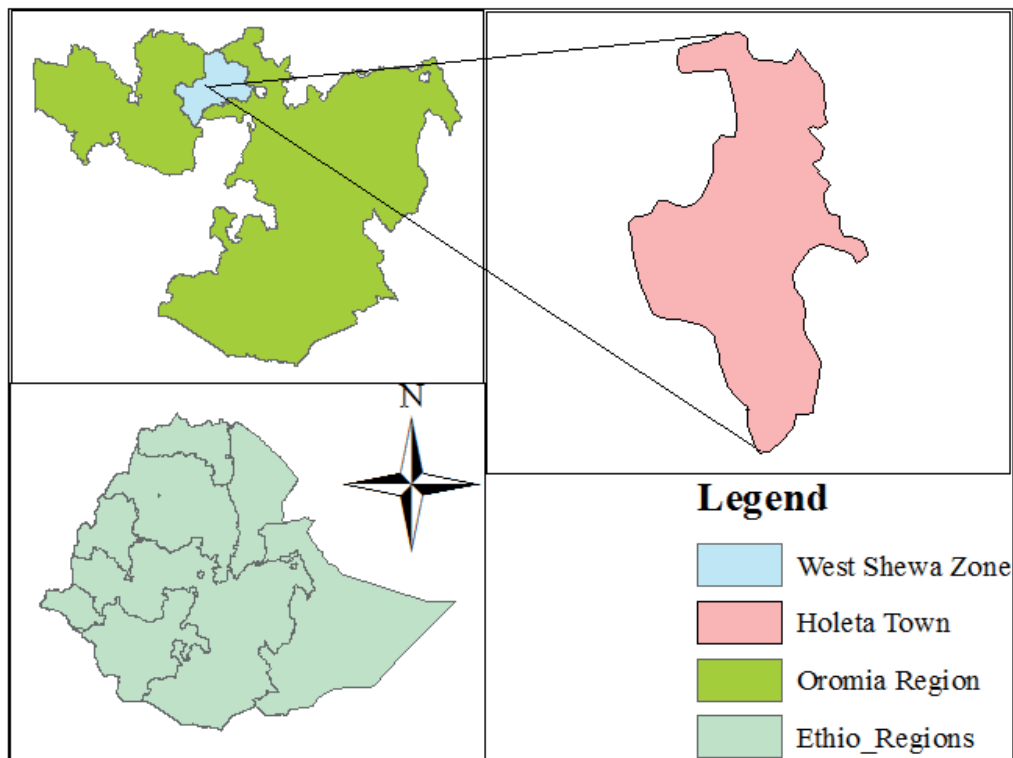


Figure 1: Map of study area

3.2. Data Source and Data Collection

Data recorded from 1995 through 2024 at Holetta Agricultural Research Center (HARC) were used for this study. The Borana cow breed was used as a foundation stock to produce 50% F1 crosses. Whereas, 50% F1, F2 and F3, 75%F₁, and 75%F₂ were different genotypes resulted from subsequent crossing

The following data were recorded in a database:

- Identification number of animals
- Date of birth
- Date of first service
- Date of First calving
- Daily milk yield,
- lactation length and
- lactation milk yield
- Parity
- genetic group
- Sire of cow and dam of cow.

3.3. Animal Management

The animals were managed according to their breed group, pregnancy stage, lactation period, sex, and age. Consistent feeding and management protocols were applied to all animals within each specific category. During the daytime, animals were allowed to graze starting from early morning until evening. Concentrate mixture composed of wheat bran (64%), noug (*Guizocia abyssinica*) cake (35%), and salt (1%) was supplemented for heifers up to 2 years age, 69 % wheat bran 39% noug cake, and salt 1% for pregnant cows and calves supplemented with concentrate mixture at a rate of 0.25-1 kg per day/animal. The animals had free access to clean tap water. Calves were permitted to suckle their dam immediately after birth for approximately four days to ensure they received sufficient colostrum. Weighting and ear tagging are applied within 24 hours after birth. After four days, they were moved to a calf rearing pen and provided with a dry diet and whole milk. Over 98 days, 260 kg of whole milk was administered via bucket feeding except the F₁

calves which suckled their dams until weaning. Weaned calves were transferred to another pen and kept in-doors until 6 months of age.

Cows were milked with a milking machine twice daily (early morning and evening) since 2002. Since 2005; animal selection was conducted through estimated breeding value and physical appearance. All herds in the research farm were vaccinated against for major transmittable diseases (Anthrax, Blackleg, Foot and Mouth Disease (FMD), and Lamp Skin Disease (LSD) were vaccinated on a regular schedule. Management system (feeding) of the herd might vary with seasons depending on availability of feed and other inputs.

3.4. Overview of Dairy Cattle Research at Holetta Agricultural Research Center

Holetta Research Center was established in 1966. The dairy cattle research started two years later after the establishment of the center. In the beginning, preliminary characterization and milk production and reproductive performances of selected indigenous cattle breeds were evaluated at four experimental stations (Holetta, Horo, Melka-Werer and Adamitulu). Indigenous breeds such as Begait, Borana and Horro were evaluated for milk production. As a result, these indigenous breeds produced an overall total lactation yield of 550 kg over a lactation period of 6 months. However, due to lower milk yield of indigenous cows and high demand for milk and milk products associated with alarming human population growth, crossbreeding was proposed in 1972 by G. Winner FAO consultant.

The first preliminary results of the long-term dairy cattle crossbreeding experiments in Ethiopia were reported Sendros, (1987), 20 years after the start of the experiment. The results indicated that first generation (F₁) crossbred dairy cows in general produce three to five times more milk than indigenous cows. Kebede, (1992) conducted a comprehensive

study and identified milk production as one of the breeding program's target goals, achieving significant success.

The F1 (50%) and $\frac{3}{4}$ crosses produced 3 to 5-fold higher daily milk yield than their contemporary local cow groups. The F2 and F3 genotypes resulted from the inter se mating, however, produced somewhat lower milk yield due to loss of hybrid vigor compared to $\frac{1}{2}$ F1 and $\frac{3}{4}$ F1 crosses. Moreover, it was also concluded that Jersey crosses produce higher milk yield per metabolic body weight than Friesian and Simmental crosses reflecting higher efficiency of Jersey crosses for milk production under low-input low-output dairy production systems. Likewise, crossbred calves were found to have higher birth weight and growth rate to reach at puberty earlier as compared to local calves.

The second approach was the extension on the conclusive results obtained from the first national dairy cattle cross breeding program. The aim of this approach was to develop 50% synthetic dairy breed around the milk sheds of Addis Ababa with nucleus herd planned to be established at Holetta Agricultural Research Center. A community-based open nucleus breeding scheme was suggested and the program was designed to span over a period of 10 years (1995-2005). However, this strategy was unsuccessful and finally failed due to absence of on-farm dairy cattle performance recording schemes.

Due to fluctuations in exotic gene inheritance among crossbreds animals produced as a result of crossing and lack of an appropriate breeding program, efforts are underway to develop a 75% synthetic/composite dairy breed at Holeta Agricultural Research Center (HARC). The current on-going synthetic breed development program has already attained fourth generation. Subsequent crossing will be continued until 9th generation is achieved, where gene segregation will be fixed and stabilized at this stage.

3.5. Mating Design

The Borana cattle used as a foundation stock for crossbreeding were brought from Borena pastoralists in the southern Ethiopia. Pure Borena dams mated with pure Holstein Friesian (HF) semen to produce 50% F1 crosses while the 50% F1 is back crossed with pure Friesian semen to produce the 75% (HF X Borana) first generation. The later generations (F2 and F3) were produced by *inter se* mating of 75% (HF X Borana) male with 75% (HF X Borana) female to produce synthetic breed of 75% HF and 25% Borena gene inheritance. The mating design used to produce synthetic breed in the farm is indicated in Figure 1.

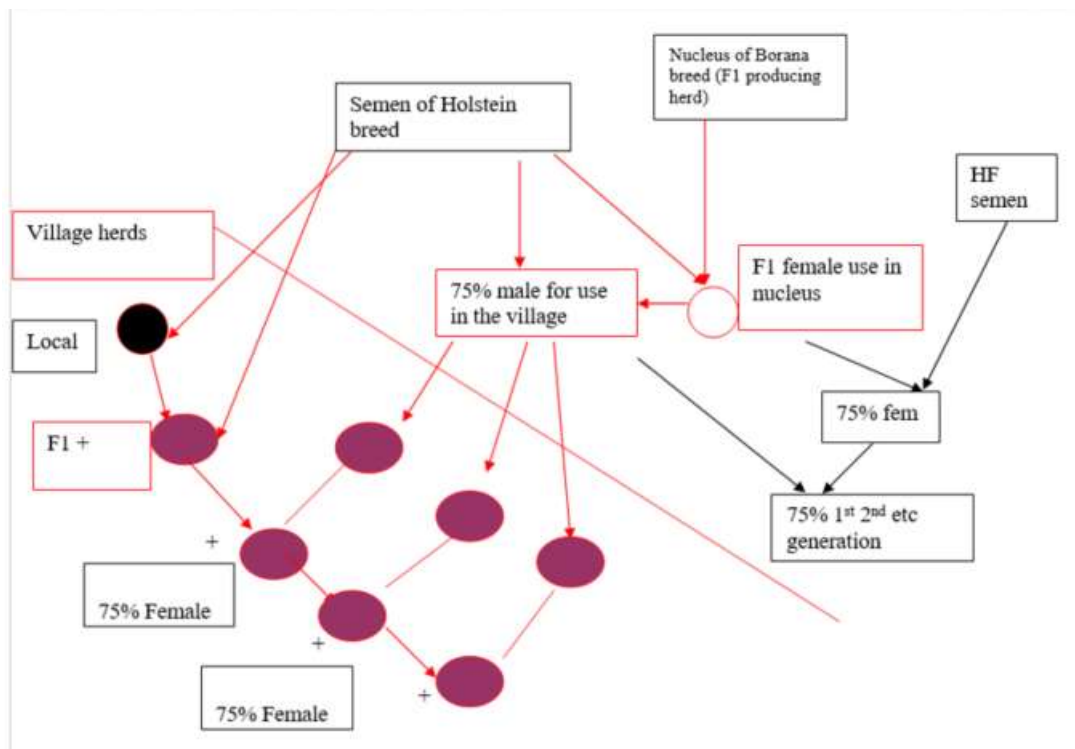


Figure 2: Schematic presentation of breeding program at Holeta agricultural research center

(Source: Adopted by Philipsson (2011)).

Mating was undertaken throughout the year using artificial insemination. Semen of 75% (HF X Borana) sourced from NAIC, Kality, Addis Ababa. In cases where cows/heifers became repeat breeders following AI, natural service was occasionally used. Bulls born on

the farm were selected for breeding based on the milk performance of their dams and physical conformation. These selected bulls were used for on-station breeding activities after their semen was collected and evaluated in collaboration with NAIC. A careful attention paid to avoiding genetic relatedness during bull selection. Heat detection in cows was carried out daily by herd attendants and a teaser bull kept together with female herd. Cows exhibiting standing heat were artificially inseminated by qualified technicians. Cows that did not exhibit signs of heat after service were diagnosed for pregnancy at 45 days post-insemination.

3.6. Data management

Data cleaning was done to avoid too many missed observations, outliers and incorrectly recorded observations. Lactation lengths less than 100 days were eliminated from the data set. Age at first service (AFS) below 10 months and above 80 months as well as age at first calving (AFC) below 20 months and above 90 months, were removed from the data set. Parities above 7 were few in number and grouped as parity 7.

The average gestation time for cows is 285 days, and they have a 45-day voluntary waiting period (330 days CI) following calving. Cows with a calving interval (CI) of less than 330 days were eliminated from the analysis.

Table 5: Records used for analysis of genetic and crossbreeding parameters for different trait

Genotypes	Milk production Traits			Reproduction Traits			Total
	LMY	DMY	LL	CI	AFS	AFC	
Pure Boran	240	240	132	205	44	51	912
50% F1	1665	1665	1665	1329	828	828	7980
50% F2	236	236	236	156	158	158	1180
50% F3	142	142	142	84	131	131	772
75% F1	436	436	436	304	515	515	2642
75% F2	85	85	85	35	126	126	542
Total	2804	2804	2696	2113	1802	1809	14,028

LMY=Lactation Milk Yield, DMY=Daily Milk Yield, LL=Lactation Length, CI=Calving Interval, AFS =Age At First Service, AFC=Age At First Service

Table 6: Number of observations in pedigree records

No.	Pedigree data	N
1	No. of animals with unknown sire	401
2	No. of animals with unknown dam	406
3	No. of animals with both parents unknown	378
4	No. of sires	438
5	No. of animals with paternal grandsire	1031
6	No. of animals with paternal grand dam	1067

N=Number of observations

3.7. Method of Data Analysis

Data analysis on non-genetic factors was performed using SAS software (SAS, 2004). General linear model (GLM) of this software was employed to the effect of genetic group, parity, season and year on age at first service (AFS), age at first calving (AFC), calving interval (CI), lactation milk yield (LMY), daily milk yield (DMY), and lactation length (LL)

The genetic groups considered in the model were 50% HFXB and 75% HFXB). No selection and improvement have been undertaken on Borena breed since it has only been used as dam line for F1 generations. Therefore, performance evaluation of pure Borena breed was not the objective of this study and excluded from fixed effect analysis. However, their genetic contribution for further generation was immense (25% and 50%) in the present study and the breed was fitted in to the genetic and genotypic models to calculate their contribution.

For season of birth and calving, months in a year were classified into 3 seasons based on rainfall distribution. October to February is the dry season; March to May is a short rainy season; and June to September is the main rainy season.

Due to limited number of records available per calving year, the years were categorized into 5 groups: 1995-1999 (year 1), 2000-2005 (year 2), 2006-2011(year 3), 2012-2017 (year 4), 2018-2024 (year 5).

Lactation milk yield (LMY) is the mammary gland secretes and yields milk throughout a single lactation period.

Daily milk yield (DMY) is the amount of milk produced by the cow each day in the morning (AM) and evening (PM).

Lactation length (LL) refers to the time of period from when a cow starts to secrete milk after parturition to the time of drying off.

The calving interval (CI) is the period between two consecutive parturitions and one of the major components of reproductive performances that influences livestock production systems.

Age at first service (AFS) is defined as the age at which heifers reach sexual maturity and attain body condition and sexual maturity for accepting service for the first time.

Synthetic breeds are developed by combining two or more different breeds, aiming to take advantage of hybrid vigor while maintaining a stable population without the need for further crossbreeding (Bourdon, 2000).

3.7.1. Model was used for fixed effect analysis:

Model 1: For production traits (LMY, DMY, and LL) and for reproductive trait (CI)

$Y_{ijkln} = \mu + Y_i + S_j + G_k + P_l + e_{ijkln}$, Where;

Y_{ijkln} = n^{th} record of, i^{th} year, j^{th} season, k^{th} genetic group and l^{th} parity

μ = overall mean

Y_i = effect of i^{th} Year of Calving S^j = effect of j^{th} Season of Calving dry (October to February), short rain season (March to May), and long rain season (June to September).

G_k = effect of k^{th} Genetic group (50% F1, F2, F3 and 75% F1, F2)

P_l = effect of l^{th} Parity of Dam (1, 2, 3, 4, 5, 6, 7)

e_{ijkln} = random error associated with each observation

Model 2: Reproductive traits (AFS and AFC) were analyzed the main model without the effect of parity.

$Y_{ijkn} = \mu + Y_i + S_j + G_k + e_{ijkn}$

Where, Y_{ijkn} = n^{th} record of, i^{th} year, j^{th} season, k^{th} genetic group

μ = overall mean

Y_i = effect of i^{th} year of birth

S_j = effect of j^{th} season of birth

G_k = effect of k^{th} genetic group ($i= 75\% \text{HF} \times \text{BoF1}, 75\% \text{HF} \times \text{BoF2}, 75\% \text{HF} \times \text{BoF3}$)

e_{ijkn} = random error associated with each observation

3.7.2 Genetic Parameter Analysis

Variance and covariance components, heritability, repeatability, genetic correlations were estimated by using WOMBAT software version 01-11-2011. Univariate and multivariate analysis were applied for genetic parameter estimation.

The following animal model was applied,

$Y = Xb + Za + Wd + e$. where;

Y , is a vector of observations for the traits of interest

b , is a vector of fixed effects (genetic group, calving year, calving season and parity).

a , is a vector of random individual additive effects

d , is a vector of permanent environmental effects

X , matrices relating records to fixed effects

Z , incidence matrices relating records to individual animal effect

W , matrices of permanent environmental effects

e , vector of random residual effect

The model assumed the expected mean of zero and variances σ_a^2 , σ_c^2 and σ_e^2 , respectively. Pedigree data as the software already recognized the formula as follows;

$\sigma_p^2 = \sigma_a^2 + \sigma_c^2 + \sigma_e^2$ σ_p^2 ; is phenotypic variance (total variance)

$h^2 = \sigma_a^2 / \sigma_p^2$ σ_a^2 ; additive genetic variance

$r^2 = \sigma_c^2 + \sigma_e^2 / \sigma_p^2$ σ_c^2 ; permanent environmental variance

$A_i = h^2 \times P$ σ_e^2 ; residual variance

3.7.3. Crossbreeding Parameter Analysis

The regression analysis was performed using the Generalized Linear Model (GLM) procedure in SAS version 9.0 (2004) was used to analyze the productive (LMY, DMY, and LL) and reproductive (AFS, AFC, and CI) performance traits on crossbreeding parameters. Crossbreeding effects were decomposed into breed additive effects, heterosis, and recombination loss coefficients. These components were fitted as covariates in the model to estimate the breed additive (g_i), heterosis (h_{ij}), and recombination loss (r_{ij}) coefficients, following the methodologies outlined by Dickerson et al. (1969) and Akbaş et al. (1993). The genetic model used for estimation of crossbreeding parameters is indicated as follows;

$$Y = X_1b_1 + X_2b_2 + \beta\alpha. \text{ Where;}$$

Y, is a vector of observations for the traits of interest.

b_1 , is a vector of fixed effects other than genotype.

b_2 , genetic effect (breed additive difference, heterosis and recombination coefficients).

B is the matrix of expected genetic contribution (breed additive, heterosis and recombination loss)

α is a vector of the estimated corresponding parameters including overall mean

X_1 , matrices relating records to fixed effects.

X_2 is a matrix of coefficients relating fixed breed additive, heterosis and recombination effects to the individual trait record.

The equation uses to calculate breed additive (g^j), heterosis (h_{ij}) and recombination loss (r_{ij}) effects will as follows:

$$\text{Breed additive } (g^j) = \frac{1}{2} (\alpha_i^s + \alpha_i^d),$$

$$\text{Heterosis } (h_{ij}) = \alpha_i^s \alpha_j^d + \alpha_j^s \alpha_i^d \text{ and}$$

Recombination loss (r_{ij}) = $4\alpha_i^s \alpha_j^d - h_{ij}$ (Wolf et al., 1995 cited by Demeke et al., 2004a, b)

where α_i^s and α_i^d denote the gene proportion of breed i in the sire and dam of the cow, respectively.

Table 7: The proportions of Holstein Friesian genes, individual and maternal heterosis and individual recombination coefficients used in prediction of performance of different genetic group

Breed and Genetic group (sire x dam)	Genetic coefficient		
	g^I	h^I	r^I
Pure Borena	0	0	0
50 % F1 (HF*Bo)	0.5	1	0.5
F2 (HF*Bo) *(HF*Bo)	0.5	0.5	0.5
F3 (((HF*Bo)*(HF*BO))*((HF*Bo)*(HF*BO)))	0.5	0.5	0.5
75 % F1 HF * (HF*Bo)	0.75	0.5	0.25
F2 ((HF * (HF*Bo) * (HF * (HF*Bo)))	0.75	0.375	0.375

g^I ; individual additive genetic, h^I ; individual heterosis, r^I individual recombination effect
Bo; Borena, HF; Holstein Friesian.

4. RESULTS AND DISCUSSION

4.1. Productive Performance

4.1.1. Lactation Milk Yield

Results of the least square mean and standard errors for fixed effects of genetic group, calving year, calving season and parity are summarized in Table 8. The overall lactation milk yield, daily milk yield and lactation length in the present study was 2140.61 ± 32.92 kg, 6.89 ± 0.07 kg and 316.54 ± 3.31 days, respectively. Our present results are slightly lower than those reports by Zenebe *et al.* (2024), which showed values of 2676.5 ± 86.33 for Local x HF crosses in Smallholder Farmers, and Kassa *et al.* (2018), with values of 2305.2 ± 32.15 for Holstein Friesian Dairy Herd at ELFORA Cheffa Dairy Farm. Comparable with the current result was reported by Getahun *et al.* (2018) with values of 2204.05 ± 21.12 for Borena x HF crosses at Holeta Research Center dairy farm. Lower values were reported (Effa *et al.*, 2011, and Ashutosh *et al.*, 2013) with values, 1798 ± 25 for Borena x HF crosses, 2088.7 ± 29.4 for Borena x HF crossbred in the central highlands of Ethiopia, and 1506.75 ± 71.37 for HF x local in Bangladesh, respectively. By contrast, higher LMY results for Holstein–Friesian cows, with amounts of 3349.1, 3084.0, and 3604.0, liters, were reported by Yosef *et al.* (2006) in Holleta dairy farms, and by Gebeyehu *et al.* (2014), and Wondwossen *et al.* (2015) at the Holleta Bull Dam, respectively. The difference might be attributed to breed/genetic makeup, management, feeding practice and climate factors in which animals were managed.

Lactation milk yield was significantly ($p < 0.0001$) affected by genetic group. The least square mean of lactation milk yield was increased when exotic gene inheritance increased from 50% to 75% HF crosses since the management level of high-grade cows increased. The 75% F1 crossbred cows produced significantly ($P < 0.05$) the highest lactation milk yield. Mean lactation milk yield was significantly decreased by 25% in the F2 generation

of inter-se genotype (75% F2). The findings in the present study agree with the previous reports Million *et al.* (2010), who suggested upgraded crossbred cows produce higher lactation milk yield than 50% crosses. However, cows need to be managed well as the level of exotic gene inheritance is continuously upgraded. Likewise, Hirooka and Bhutyan (1995) reported high milk yield is recorded by exotic breeds in tropics when they are well-fed and managed, signifying that the genetic potential of an animal is partly the reflection of management. Milk yield decreased in the inter se mated individuals in the subsequent generations, as a result of loss of heterosis due to gene segregation.

Calving year markedly ($P < 0.0001$) affected lactation milk yield. The lactation milk yield decreased over years. The highest lactation milk yield obtained in the year 1995-1999 (2397.85kg) while the lowest milk yield was attained in the year group 2018-2024 (Figure 2). The difference could be explained by the availability of feed across years.

The lactation milk yield was significantly ($P < 0.0003$) affected by calving season. Higher lactation milk yield was obtained in both dry and main rainy seasons, the reason might be in the dry season, harvesting hay by bell forms and supplementing green forage in the rainy season, but milk yield was lowest in the short rainy season. Quality of feed mainly varies over seasons, which perhaps affects the performance of animals, where strategic supplementation might enhance the productivity of animals in feed shortage periods (in rainy season).

Parity had significant ($p < 0.05$) effect on lactation milk yield. In this study lactation milk yield sharply increased from first to fourth parity and became plateau towards 5th parity. Most literature support our present finding, for instance, Goshu and Mekonnen (1997) reported similar higher milk yield for the first four lactations for Fogera-Friesian crosses around Gonder city. However, some reports reveal that lactation milk yield decreases after the third parity for crossbred cows Mackinnon *et al.* (1996), Getahun *et al.* (2018). The

gradual increase in milk yield from first to four lactations might be attributed to development of secretory tissues of the udder due to recurring pregnancies.

4.1.2. Daily Milk Yield (DMY)

Daily milk yield was markedly ($P < 0.05$) affected by genetic group, calving year, season of calving and parity (Table 8). The daily milk yield increased as the exotic blood level of cows upgraded from 50% F1 to 75% F1. In line with our finding, the level of heterosis certainly enhanced in advanced generations. Though, the significant difference observed in this study is not in agreement with studies Gebregziabher *et al.* (2013) who reported that upgrading from 50% to higher Friesian fractions for HF X indigenous crosses have shown no significant differences for milk yields. The variation between the present and the previous study might be associated with management difference and number of records considered in a data set. The 75% F1 produced 24 and 23.7% more daily milk yield than 50% F1 and 75% F2 generations, respectively. 50% F1 and 75% F2 genetic groups gave same amount of milk yield/day ($P > 0.05$). The mean daily milk yield decreased from the 1st generation to 50% F2 and F3 inter mated generations. It is clear and frequently mentioned in much literature that heterosis declines in the inter se mated progeny, which favours recombination loss during further crossing, process.

4.1.3. Lactation Length

The overall least square means and standard errors for lactation length in HF × Boran genetic groups are presented in Table 6. The 75% F1 cows exhibited the longest lactation length (335 days), followed by the 50% F1 crossbred cows (329 days). The lactation lengths observed in this study are relatively close to the standard lactation length of 305 days. Previous studies, such as those by Haile *et al.* (2009a), Kumar *et al.* (2014), and Dash *et al.* (2015), have reported similar values of 325 ± 3 days, 325.12 ± 61.28 days, 326.69 ± 2.03 days, and 326.57 ± 2.60 days, respectively. On the other hand, longer lactation lengths

were reported by Suhban *et al.* (2000) and Effa *et al.* (2006), with corresponding estimates of 503.0 ± 6.36 days and 360.76 ± 6.11 days, respectively. In contrast, a shorter lactation length of 204 ± 27.8 days was reported by Djoko *et al.* (2003). Despite the substantial milk production associated with longer lactation lengths, the number of calves produced per cow would inevitably decrease. Several factors may contribute to variations in lactation length, including differences in breed type, nutrition, health status, and overall management practices. A balanced compromise in lactation length is essential in dairy cattle breeding practices to ensure that neither milk yield nor calf crop production is adversely affected.

Lactation length exhibited a decreasing trend over time, as shown in Table 8. Over the past 30 years, lactation length declined by approximately 28 days. Similar findings were reported in the same farm in earlier periods Haile *et al.* (2009a) and Effa *et al.* (2006b). This downward trend in lactation length may be attributed earlier drying-off practices, shifts in breeding schedules, or nutritional adjustments aimed at optimizing other performance traits. Understanding these factors is crucial for developing informed breeding and management decisions that balance milk production with overall herd reproductive efficiency.

Table 8: Least square means and standard errors (LSM±SE) of lactation milk yield, daily milk yield and lactation length

Effects	N	LMY (lit)	DMY (lit)	LL (days)
Overall	2564	2140.61 ± 32.92	6.89 ± 0.07	316.54 ± 3.31
CV (%)		37.92	25.89	27.23
Genetic group		****	****	****
50% F1	1665	2280.06 ^b ± 32.74	7.03 ^b ± 0.07	329.07 ^a ± 3.28
50% F2	236	1719.34 ^c ± 61.99	5.85 ^c ± 0.13	307.85 ^b ± 6.21
50% F3	142	1546.64 ^c ± 77.79	5.30 ^d ± 0.17	300.06 ^b ± 7.79
75% F1	436	3030.305 ^a ± 52.44	9.26 ^a ± 0.11	335.20 ^a ± 5.25
75% F2	85	2126.71 ^b ± 96.86	7.01 ^b ± 0.21	310.52 ^{ab} ± 9.75
Year group of calving		****	****	****
1995-1999	95	2299.19 ^{ab} ± 103.54	6.19 ^c ± 0.22	386.34 ^a ± 10.37
2000-2005	569	2301.18 ^a ± 44.23	7.096 ^b ± 0.09	326.19 ^b ± 4.43
2006-2011	712	2162.22 ^b ± 43.85	7.19 ^{ab} ± 0.09	299.50 ^c ± 4.39
2012-2017	817	2104.517 ^b ± 46.16	7.37 ^a ± 0.10	287.75 ^{cd} ± 4.63
2018-2024	371	1835.95 ^c ± 53.44	6.59 ^c ± 0.11	282.91 ^d ± 5.37
Calving season group		***	****	ns
Dry season	1179	2214.76 ^a ± 37.43	7.02 ^a ± 0.08	321.31 ± 3.75
short rain season	703	2047.08 ^b ± 42.69	6.49 ^b ± 0.09	313.96 ± 4.28
Main rain season	682	2159.99 ^a ± 43.35	7.01 ^a ± 0.09	314.34 ± 4.35
Parity		****	****	ns
1	718	1894.13 ^b ± 41.43	5.92 ^c ± 0.09	320.38 ± 4.15
2	566	2048.24 ^a ± 44.26	6.35 ^b ± 0.10	324.90 ± 4.44
3	437	2162.03 ^a ± 48.00	7.11 ^a ± 0.10	309.56 ± 4.81
4	320	2225.43 ^a ± 54.53	7.09 ^a ± 0.12	319.62 ± 5.46
5	236	2202.23 ^a ± 61.57	7.12 ^a ± 0.13	316.40 ± 6.17
6	170	2206.44 ^a ± 71.20	7.18 ^a ± 0.15	314.71 ± 7.16
7	117	2245.77 ^a ± 84.44	7.49 ^a ± 0.18	310.19 ± 8.45

LMY=Lactation Milk Yield, DMY=Daily Milk Yield, LL=Lactation Length LSM=Least Square Mean, SE=standard error, N= Number of observations*Different superscripts (a, b, c, d) in the same fixed effect indicate differences among sample means. ns=non-significant, **** highly significant.

4.2. Reproductive Traits

Reproductive traits are vital for milk production, herd replacement, and the overall profitability of dairy farming. Among the various factors influencing livestock production, the reproductive performance of female animals is the most critical consideration.

4.2.1. Age at First Service (AFS)

The least square means and standard errors for age at first service (AFS) are summarized in Table 9. The overall mean AFS was 33.56 ± 0.63 months. In this study, the highest and lowest AFS values recorded were 37.01 and 27.23 months, respectively. The mean AFS observed in the current study is lower than the 36.8 ± 0.8 months reported by Gebeyehu *et al.* (2005) for Fogera \times Holstein Friesian (HF) crosses. However, it is higher than the values reported by Haile *et al.* (2009b) and Birhanu *et al.* (2014), which were 29 ± 0.7 months for Borena \times HF crosses and 29.30 ± 0.21 months for Borena \times HF \times Jersey crosses, respectively. These variations in AFS among different studies may be attributed to differences in breed composition, environmental conditions, and management practices, all of which significantly influence reproductive performance in dairy cattle.

A highly significant effect of genetic group on age at first service (AFS) was observed ($P < 0.0001$); (Appendix Table IV), consistent with the findings of Wssie *et al.* (2015). The 50% F1 group had the shortest AFS (30.33 ± 0.46 months), while the 50% F2 group exhibited the longest (37.92 ± 1.00 months), indicating a 6.5-month increase from 50% F1 to 75% F1. This suggests that traits influenced by hybrid vigour may show reduced performance in backcrosses, depending on the additive genetic merit of the parental breeds (Cunningham & Syrstad *et al.* (1987), Arthur *et al.* (1999). No significant differences ($p > 0.05$) were observed among 50% F2, 50% F3, and 75% F1, nor between 50% F1 and 75% F2. Additionally, calving season had no significant ($p > 0.05$) effect on AFS, implying that the season of birth did not influence the onset of puberty in heifers. Nonetheless,

timely breeding—aligned with periods of optimal forage quality may help achieve earlier first service through better nutritional management.

4.2.2. Age at First Calving (AFC)

Age at first calving (AFC), a critical factor influencing the cost of raising dairy replacements. AFC showed a highly significant ($P < 0.0001$) variation across genetic groups and birth years (Table 9). The overall mean AFC in this study was 42.78 ± 0.63 months, aligning with findings by Damissu *et al.* (2013) and Wassie *et al.* (2015), but higher than values reported by Getahun *et al.* (2018), Suhban *et al.* (2000), and Hafez *et al.* (2013). Among the genetic groups, 50% F1 crosses had the lowest AFC (38.44 ± 0.46 months), while 50% F2 exhibited the highest (45.94 ± 1.05 months). No significant differences ($p > 0.05$) were found among 50% F2, 50% F3, and 75% F1 or between 50% F1 and 75% F2. The differences in AFC across studies may be attributed to breed composition, environmental conditions, feeding and management practices, heat detection efficiency, and health care. Additionally, animals born between 2015 and 2020 had significantly lower AFC compared to those born in 2005–2009, while birth season had no significant ($p > 0.05$) effect on AFC.

Table 9: The least square means and standard error (LSM±SE) of AFS and AFC

Effects	N	AFS (month)		AFC (month)	
		LSM	SE	LSM	SE
Overall	1758	33.56	± 0.63	42.78	± 0.63
CV (%)		34.22		26.89	
Genetic group		***		***	
50% F1	828	29.17 ^b	± 0.59	38.44 ^b	± 0.59
50% F2	158	36.64 ^a	± 1.05	45.94 ^a	± 1.05
50% F3	131	35.54 ^a	± 1.15	44.64 ^a	± 1.15
75% F1	515	35.67 ^a	± 0.82	44.93 ^a	± 0.82
75% F2	126	30.763 ^b	± 1.26	39.95 ^b	± 1.26
Year group of calving		****		****	
1995-1999	232	34.49 ^b	± 0.86	43.78 ^b	± 0.86
2000-2004	674	33.86 ^b	± 0.58	43.00 ^{bc}	± 0.58
2005-2009	522	37.01 ^a	± 0.55	46.43 ^a	± 0.55
2010-2014	306	35.01 ^{ab}	± 0.83	44.25 ^{ab}	± 0.83
2015-2020	24	27.23 ^c	± 2.42	36.46 ^c	± 2.42
Calving season group		ns		ns	
Dry season	808	33.69	± 0.68	42.93	± 0.68
short rain season	582	33.33	± 0.73	42.53	± 0.73
Main rain season	368	33.65	± 0.84	42.8	± 0.84

AFS=Age at First Service, AFC=Age at First Calving, LSM=Least Square Mean, SE=Standard error

4.2.3. Calving Interval (CI)

The calving interval (CI), defined as the period between successive calving, averaged 469.01 ± 7.03 days in this study, aligning closely with findings from Getahun *et al.* (2011), Wassie *et al.* (2015), Belay *et al.* (2014), and Getahun *et al.* (2018), who reported CI values ranging from 468 to 476 days for different crossbred dairy cattle in Ethiopia. However, this result was notably lower than the 612 ± 4.6 days reported by Suhban *et al.* (2000) for Pakistani crossbreds. Year of calving significantly influenced CI ($p < 0.0001$),

consistent with studies by Yosef *et al.*(2006), Hunde *et al.*(2012), and Getahun *et al.* (2018), suggesting the impact of management practices, location, and genetic background. Interestingly, calving season did not significantly affect CI, echoing earlier reports by Million and Tadelle (2003a), Haile *et al.* (2009b), and Belay *et al.* (2014)

Genetic and non-genetic factors influenced the calving interval, with the exception of season. Among genetic groups, 50% F2 crosses had the longest CI at 507.17 ± 15.10 days, while 50% F1 crosses had the shortest at 449.12 ± 6.15 days. This variation is likely due to heterosis, recombination effects, and differences in lactation length. Parity also had a significant impact, with the longest CI observed in first parity and the shortest in fourth parity, aligning with reports by Getahun *et al.* (2018) and Gojam *et al.* (2016). The trend suggests a decrease in CI with increasing parity, potentially due to improved uterine recovery and adaptation to parturition and lactation stress as cows mature.

Table 10: Least square means and standard error of (LSM±SE) Calving Interval (CI)

Effects	N	CI
Overall	1977	469.01 ± 7.03
CV (%)		29.14
Genetic group		****
50% F1	1329	449.12 ^b ± 6.15
50% F2	156	507.17 ^a ± 15.10
50% F3	84	455.65 ^b ± 12.99
75% F1	304	463.23 ^b ± 9.94
75% F2	35	469.89 ^{ab} ± 23.49
Year group of calving		****
1995-1999	83	469.014 ^{ab} ± 18.85
2000-2005	401	471.66 ^{ab} ± 8.77
2006-2011	556	453.76 ^b ± 9.18
2012-2017	653	452.47 ^b ± 9.49
2018-2024	215	498.14 ^a ± 11.57
Calving season group		ns
Dry season	900	474.62 ± 7.64
Short rain season	504	472.03 ± 8.66
Main rain season	504	460.37 ± 8.82
Parity		****
1	539	519.315 ^a ± 8.29
2	441	493.69 ^{ab} ± 8.62
3	325	462.54 ^{bc} ± 9.39
4	244	451.11 ^c ± 10.40
5	173	451.91 ^c ± 11.95
6	119	464.51 ^c ± 13.75
7	67	439.98 ^c ± 17.94

N=number of observation CI=Calving Interval, LSM= Least Square Mean, SE=Standard error

4.3. Estimation of Crossbreeding Parameters

4.3.1. Crossbreeding parameter estimates for production traits

Estimates of individual breed additive, individual heterosis and individual recombination for lactation milk yield, daily milk yield and lactation length are shown in Table 11. Individual breed additive effects were large and highly significant ($p < 0.001$) for lactation milk yield and daily milk yield, but not significant for lactation length. Relative to the mean value of the Borena cows, the individual additive contribution of Holstein Friesian cows was 3728 ± 139.39 for lactation milk yield, 10.89 ± 0.30 daily milk yields and 48.95 ± 14.77 days for lactation length. Individual heterosis effect was not-significant for lactation milk yield, daily milk yield and lactation length.

The breed additive difference for lactation milk yield in the present study (Table 11) was higher than the breed additive difference of 2674.05 kg reported for crosses between Boran x HF in the central highlands of Ethiopia reported by Getahun *et al.* (2018) and breed additive difference of 2220 kg lactation milk yield for crosses between Holstein Friesian and Barca breed at Debre Zeit Agricultural Research Center in Ethiopia Tadesse *et al.* (2010).

The estimate of individual heterosis with respect to Holstein Friesian and Borena breed genes was negative -81.65 ± 97.98 , positive 0.44 ± 0.21 and negative (-18.72 ± 10.38) for lactation milk yield, daily milk yield and lactation length, respectively (Table 11). Non-significant and negative heterosis estimates by Tadese *et al.*, (2019) reported estimates of average lactation milk yield in crossbreeding between Boran and HF. The current study on the estimate of individual heterosis slightly differs from the value reported by Million *et al.* (2019), which was -54.08 ± 195 kg for milk yield in the crossbreeding of Boran cattle with Holstein Friesians in the central highlands of Ethiopia. The current study aligns with the findings of Getahun *et al.* (2018), who reported a significant negative effect of

recombination on lactation milk yield (LMY), daily milk yield (DMY), and lactation length (LL). A small negative and highly significant individual heterosis for lactation milk yield (LMY) was reported by Abolfazl *et al.* (2012) in Iran for Holstein Friesian crosses with local breeds. In contrast, Hunde *et al.* (2022) reported a significant and higher negative individual heterosis value of 150.6 ± 76 . Differences in heterosis estimates between crossbred cattle can arise from various factors, including the genetic diversity of the parent breeds, the specific traits being measured, and environmental influences. Additionally, non-additive gene effects and the degree of genetic compatibility between the breeds can significantly impact heterosis outcomes. The Friesian breed has undergone selection for many generations primarily to enhance milk production per cow. Consequently, beneficial epistatic relationships among genes across various loci may have evolved. Therefore, when the Friesian is crossed with the unselected Borena, these interactions could be disrupted due to recombination.

Table 11: Crossbreeding parameters estimates and their associated standard errors for productive traits.

Crossbreeding parameters	LMY	DMY	LL
Breed additive genetic	$3728 \pm 139.39^{***}$	$10.89 \pm 0.3^{***}$	48.95 ± 14.77^{ns}
Individual heterosis	-81.65 ± 97.98^{ns}	0.44 ± 0.21^{ns}	-18.72 ± 10.38^{ns}
Individual recombination	$-1440.92 \pm 152.25^{***}$	$-2.55 \pm 0.33^{***}$	$-75.15 \pm 16.13^{***}$

LMY=lactation milk yield, DMY=daily milk yield, LL=lactation length

ns: non-significant; ** significant ; *** highly significant

4.3.2. Crossbreeding parameter estimates for reproduction traits

Genetic parameter estimates of the individual additive, heterosis and recombination effect on reproductive traits in the present study are summarized in Table 12. The additive effect of individuals had no significant negative impact on age at first service (AFS), age at first calving (AFC), and calving interval (CI) traits. Getahun *et al.* (2018) reported a significant

negative estimate of -373.9 ± 114.8 , -337.1 ± 112.6 days for AFS and AFC traits, respectively.

The genetic estimate for individual heterosis in the current study was a small significant negative and desirable for AFC and a non-significant negative effect for AFS. This result was similar to the findings of Hunde *et al.*, (2022) and Getahun *et al.*, (2018). However, CI was positive and non-significant. A significant estimate was reported by Demeke *et al.* (2004b) (-3.5months, -50 days for AFC and CI, respectively).

The recombination effect in the current study was non-significant and positive for AFS, AFC and CI traits. Friesian crosses with Borena about 2.95 ± 3.15 months and 2.91 ± 3.15 months delay in AFS and AFC, which could be attributed to the recombination loss.

Table 12: Crossbreeding parameters estimates and their standard errors for reproductive traits.

Crossbreeding parameters	CI	AFS	AFC
Breed additive genetic	-21.51 ± 29.19^{ns}	-2.29 ± 3.12^{ns}	-2.23 ± 3.12^{ns}
Individual heterosis	5.33 ± 19.79^{ns}	-8.79 ± 2.69^{ns}	$-8.84 \pm 2.71^*$
Individual recombination	81.01 ± 32.71^{ns}	2.95 ± 3.15^{ns}	2.91 ± 3.15^{ns}

CI=calving interval AFS=age at first service AFC=age at first calvingns: non-significant; ** significant ; *** highly significant.

4.4. Estimates of Genetic and Phenotypic Parameters

4.4.1. Estimates of variance components and heritability

4.4.1.1. Heritability and variance component of productive traits

Heritability is important among several factors determining how much genetic improvement can be made in any trait Haile, *et al.* (2006).

In tropical and sub-tropical regions environment, disease, feed were higher effects on the performance of the animal as result heritability might be low Dechow *et al.*, (2001) and Wasike *et al.*, (2006).

Variance component heritability (h^2) repeatability (r) and permanent environment effects (Vc) of productive traits are presented in Table 13. The current study was presented that the productive traits of heritability LMY (0.180 ± 1.00), DMY (0.235 ± 0.053), and LL (0.219 ± 0.077) and repeatability LMY (0.589 ± 1.00), DMY (0.491 ± 0.227), and LL (0.735 ± 0.151).

Estimated heritability value for lactation milk yield (LMY) was 0.180 ± 1.00 . The current study is similar with value corroborated by Demeke *et al.* (2004a) for various crossbred breeding in Ethiopia and 0.18. Ashutosh *et al.* (2013) reported comparable value for Holstein X Sahiwal crossbred cattle. However, the present heritability estimate is lower than that reported by Getahun *et al.* (2018) for Holstein Friesian \times Boran crosses and Gebregziabher *et al.* (2013), which were 0.25 ± -1 and 0.30 ± 0.04 for multi-breed cattle, respectively. In contrast, Tadesse *et al.* (2014) reported a higher value of 0.57 ± 0.02 for Ethiopian Holstein Friesian \times Boran crosses. The wide variation among these studies might be resulted from the type of model used for the analysis and number of records

Daily milk yield (DMY): The heritability estimate from this study was 0.24 ± 0.05 . This result is comparable to the findings of Getahun *et al.* (2018) at 0.28 ± 0.05 for Holstein Friesian \times Boran crosses in the central highlands of Ethiopia and Gebregziabher *et al.* (2014) at 0.26 ± 0.08 for various crossbreds. In contrast, lower estimates were reported by Demeke *et al.* (2004a) at 0.19 ± 0.03 for various crossbreds and Beneberu *et al.* (2020) at 0.12 ± 0.04 for pure Jersey breeds. Higher values were reported by Tadesse *et al.* (2014) at 0.52 ± 0.02 for Ethiopian Holstein Friesian \times Borena crosses

Lactation length (LL): The heritability estimate was 0.22 ± 0.1 , which is comparable to the previous findings of Haile *et al.* (2009a) for Ethiopian Boran \times Holstein Friesian (HF) crosses (0.26 ± 0.03) and Tadesse *et al.* (2014) for the same cross (0.27 ± 0.03). In contrast, a higher heritability value of 0.63 ± 0.02 was reported by Haile *et al.* (2009a) for

HF × local breeds, while lower estimates were documented by Getahun *et al.* (2018) at 0.12 ± 0.04 for HF × Boran crosses and Beneberu *et al.* (2020) at 0.04 ± 0.02 for pure Jersey breeds.

Table 13: Estimate of variance components, heritability ($h^2 \pm se$) and repeatability ($r \pm se$) for milk production traits from univariate analysis.

Traits	δ^2_e	δ^2_a	δ^2_p	δ^2_c	h^2	R
LMY	315455	138225	769134	315454	0.180 ± 1.00	0.589 ± 1.00
DMY	2.727	1.258	5.359	1.374	0.235 ± 0.053	0.491 ± 0.227
LL	164135	135519	619251	319597	0.219 ± 0.077	0.735 ± 0.151

δ^2_a = additive variance, δ^2_c = permanent environmental variance, δ^2_e = error variance, δ^2_p = phenotypic variance, h^2 =heritability and r = repeatability, LMY=lactation milk yield, DMY=daily milk yield, LL=lactation length.

4.4.1.2. Estimation of heritability for reproductive traits

Estimation of for variance component, heritability (h^2) and repeatability (r) for AFS, AFC and CI are showed in Table 14. The current finding has shown that heritability values of reproductive traits were low.

Age at first service (AFS): The heritability estimate for AFS was 0.079 ± 0.034 , which is consistent with the findings of Beneberu *et al.* (2020), who reported a value of 0.05 ± 0.08 for pure Jersey breed. This result is significantly lower than the estimates reported by Getahun *et al.* (2018) at 0.22 ± 0.08 for Holstein Friesian × Boran crosses and Belay *et al.* (2014) at 0.26 for Fogera × Holstein Friesian crosses. Conversely, higher heritability values were reported by Haile *et al.* (2009b) at 0.61 ± 0.15 for Boran × Holstein Friesian crosses and Berhanu and Ashim (2014) at 0.51 ± 0.10 for Ethiopian Boran × Holstein Friesian crosses.

Age at first calving (AFC): The heritability estimate for AFC derived from the univariate analysis was 0.080 ± 0.033 . This finding is consistent with the results reported by Beneberu *et al.* (2020), who documented a heritability estimate of 0.05 ± 0.05 for pure

Jersey breeds, indicating a relatively low genetic influence on this trait. However, this estimate is lower than that reported by Yosef *et al.* (2006), who found a heritability of 0.16 ± 0.06 for Jersey breeds, suggesting a moderate genetic component in that population. In contrast, significantly higher heritability estimates were reported by Haile *et al.* (2009b) for Ethiopian Boran \times Holstein Friesian crosses at 0.7 ± 0.16 and by Gebeyehu *et al.* (2014) for Holstein breeds at 0.53 ± 0.116 . These higher values imply a stronger genetic influence on AFC in these populations, which may be attributed to selective breeding practices and genetic variability within the respective breeds

Calving interval (CI): The heritability estimate obtained in the present study was 0.180 ± 0.042 . This result is comparable to that reported by Tadesse *et al.* (2014), who found a heritability of 0.16 ± 0.031 for Ethiopian Boran \times Holstein Friesian crosses. Additionally, the current estimate is higher than the value reported by Getahun *et al.* (2018), which was 0.071 ± 0.03 for Holstein Friesian \times Boran crosses. Notably, a significantly higher heritability estimate of 0.499 was reported by Mohamed *et al.* (2007) for Holstein and Jersey crosses with local breeds. It is important to note that the length of the calving interval is influenced by various factors, including the herd's reproductive management practices, which can significantly affect the genetic expression of this trait. These different estimates of heritability may be due to sample size used, genetic group/breed and analysis methods Assemu *et al.* (2015).

Table 14: Estimate of variance components, heritability ($h^2 \pm se$) and repeatability ($r \pm se$) for milk reproductive traits from univariate analysis.

Trait	δ^2_e	δ^2_a	δ^2_p	δ^2_c	h^2	r
AFS	129.01	11.1	139.054	-	0.0798 \pm 0.034	-
AFC	129.65	11.2	139.36	-	0.080 \pm 0.033	-
CI	19007.4	4443.44	24730.0	1279.16	0.180 \pm 0.042	0.23 \pm 0.01

δ^2_a = additive genetic variance, δ^2_c = permanent environmental variance, δ^2_e = residual variance, δ^2_p = phenotypic variance, h^2 = heritability r = repeatability AFS = age at first service, AFC = age at first calving, CI = calving interval.

4.4.2. Estimation of repeatability (r) for productive traits

The repeatability estimates for productive traits of lactation milk yield (LMY), daily milk yield (DMY), and lactation length (LL) were 0.589 ± 1.00 , 0.491 ± 0.227 , and 0.735 ± 0.151 , respectively (Table 14). These high repeatability values indicate that cow performance is a reliable indicator across successive lactations, supporting culling decisions based on individual productivity. The results suggest the presence of substantial additive genetic and permanent environmental variance contributing to trait consistency. The repeatability estimate for LMY in this study is consistent with Getahun *et al.* (2018), who reported 0.50 ± 1 for Holstein Friesian \times Boran crosses, and Ghorbani *et al.* (2011), who reported 0.505 for Iranian Holstein Friesian crosses. However, it exceeds the 0.33 reported by Beneberu *et al.* (2020) for pure Jersey breeds and the lower estimate of 0.17 by Haile *et al.* (2009a) for Holstein Friesian \times Boran crosses.

The repeatability estimate for daily milk yield (DMY) in the present study was 0.46 ± 0.02 , aligning with Getahun *et al.* (2018) for Holstein Friesian \times Boran crosses, and exceeding the 0.334 reported by Ghorbani *et al.* (2011) for Iranian Holstein Friesian crosses. However, lower repeatability values of 0.30 ± 0.02 were documented by Demeke *et al.* (2004b) for Holstein Friesian \times Boran and Jersey \times Boran crosses.

Repeatability for lactation length observed in this study approximated 0.70 as reported by Haile *et al.* (2009a) for Holstein Friesian × Boran crosses and was higher than the 0.23 ± 0.02 value reported by Getahun *et al.* (2018) for the same crossbreeds. In contrast, Tadesse *et al.* (2019) reported a notably lower repeatability estimate of 0.050 ± 0.07 for Holstein Friesian × Boran crosses.

Regarding reproductive performance, the repeatability estimate for calving interval (CI) in this study was 0.23 ± 0.01 . This value is lower than the 0.359 ± 0.06 reported by Million *et al.* (2019) for Holstein Friesian × Boran crosses but higher than values reported by Beneberu *et al.* (2020) at 0.09 ± 0.02 for pure Jersey breeds and by Getahun *et al.* (2018) at 0.17 ± 0.02 for the same crossbreeds. The comparatively low repeatability observed here likely reflects a pronounced impact of transient environmental factors on individual records, thereby increasing within-animal variability and reducing trait consistency across repeated measurements.

4.4.3. Genetic and phenotypic correlations

Direct genetic and phenotypic correlations for productive traits of lactation milk yield (LMY), daily milk yield (DMY), and lactation length (LL) and reproductive traits (age at first service (AFS), age at first calving (AFC), and calving interval (CI) were estimated using multivariate analysis, as shown in Table 15. The results indicated that direct genetic correlations were generally higher than phenotypic correlations for most traits, with some exceptions among reproductive traits. Direct genetic correlations reflect the influence of shared genetic factors, while phenotypic correlations encompass both genetic and environmental effects, as noted by Zeleke *et al.* (2019). The study found that traits with positive phenotypic correlations, such as CI and DMY, often aligned with genetic correlations, while other traits exhibited negative or antagonistic correlations.

4.4.3.1. Genetic correlations

The genetic correlation between productive traits were positive and the coefficients ranged from weak (0.14 ± 0.07) to very strong (0.93 ± 0.03). High correlation observed between LMY and DMY (0.926 ± 0.032). This signifies that the two traits are governed by the same gene. Similar to our finding Beneberu *et al* (2020) a high correlation coefficient of (0.98 ± 0.07) between LMY and DMY. On the other hand, Tadesse (2014) reported moderate to very strong genetic correlation (0.589, 0.956 and 0.998) between DMY and LL, LMY and DMY and LMY and LL, respectively. However, weak genetic correlation obtained in the work of Ashutosh *et al.* (2013) i.e., 0.31 for LMY and LL and 0.30 for LMY and DM, respectively.

Genetic correlation coefficients between reproductive traits in the present were weak but positive. AFS-AFC (0.228 ± 0.172), AFS-CI (0.181 ± 0.194), AFC-CI (0.063 ± 0.02). In agreement with this finding, Belay *et al.* (2014) found a perfect positive genetic correlation (1) between AFS and AFC for Fogera cattle crosses. However, higher genetic correlation between reproductive traits was reported by Beneberu *et al.* (2020) for AFC and CI (0.30 ± 0.61) and AFS and AFC (0.89 ± 0.11) for pure Jersey breed.

Strong genetic correlation looked between CI-LL (0.785 ± 0.074), moderate genetic correlation between CI-LMY and AFC-LL (0.428 ± 0.098 , and 0.40 ± 0.107), respectively, very weak genetic correlation values were CI-DMY, AFC-LMY and AFS-LMY (0.142 ± 0.073 , 0.024 ± 0.001 , 0.129 ± 0.056), respectively and finally negative genetic correlation were appeared between AFC-DMY (-0.206 ± 0.072), AFS-DMY (-0.196 ± 0.148) and AFS-LL (-0.020 ± 0.078). The negative genetic correlation AFC-DMY (-0.206 ± 0.072) and AFS-LL (-0.020 ± 0.078) similar with the report of Getahun *et al.* (2018) AFC-DMY (-0.55) and AFS-LL (-0.11).

In general, a positive direct genetic correlation between traits in the current study showed that selection of one trait might be a vital for the improvement of other traits. Also, these high genetic correlation results 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 *et al.* (2014). Nevertheless, traits which have shown negative direct genetic correlations in the present study indicates that as one trait increases, the other trait tends to decrease which might be favorable or unfavorable depending on the combination of traits considered.

4.4.3.2. Phenotypic correlations

The phenotypic correlations estimated for production traits were positive very weak (0.017 ± 0.024) between DMY-LL strong (0.670 ± 0.012) between DMY-LMY and very strong (0.890 ± 0.078) between LMY-LL. The phenotypic correlation between LMY-LL in this study was similar with the report of Beneberu *et al.* (2018) (0.82 ± 0.01) for pure jersey breed and Tadesse *et al.* (2014) (0.862) for Boran. The variation of the present study from others might be due to breed, number of observations and analysis methods.

The phenotypic correlation among reproductive traits as indicated in Table.15, were positive very weak (0.011 ± 0.026) between AFS-AFC and (0.051 ± 0.055) AFS-CI and negative (0.014 ± 0.001) between AFC-CI. Similar results was reported by Getahun *et al.* (2018) negative phenotypic correlation AFS- CI (-0.03) .The present study was positive and negative phenotypic correlation of these traits are strongly disagreed with the finding of Belay (2014) who found very strong phenotypic correlation between AFS and AFC (0.85463).

The current study vary from others might be due to breed, number of observation studied and software procedure used for analysis.

The phenotypic correlation between productive and reproductive traits was ranged from moderate positive to negative values. The present study lactation length was a negative phenotypic correlation with AFS and AFC. However, positive correlation was showed between AFS-LMY (0.017 ± 0.031), AFS-DMY (0.041 ± 0.032), AFC-LMY (0.002 ±0.037), LL-CI (0.447 ± 0.019), LMV-CI (0.215 ±0.023) and (0.017 ± 0.024).The phenotypic correlation among LL-CI in the current study similar with the report of Beneberu *et al.* (2020) 0.41±0.02 for pure jersey and higher than the report of Getahun *et al.* (2018) 0.18 for HF x Boran.The negative value of LL-AFS similar with the finding of Getahun *et al.* (2018) and Ashutosh *et al.* (2013).

Table 15: Estimates of genetic correlations (below diagonal) and phenotypic correlations (above diagonal) between reproductive and production traits

Parameters	AFS	AFC	CI	LMY	DMY	LL
AFS		0.011 ± 0.026	0.051±0.055	0.017± 0.031	0.041±0.032	-0.017±0.056
AFC	0.228 ±0.172		-0.014±0001	0.002 ±0.037	-0.122±0.036	-0.0062±0.018
CI	0.181 ±0.194	0.063 ±0.02		0.215 ±0.023	0.017± 0.024	0.447 ± 0.019
LMY	0.129 ±0.056	0.024 ± 0.001	0.428± 0.098		0.670± 0.012	0.890 ± 0.078
DMY	-0.196±0.148	-0.206 ±0.072	0.142± 0.073	0.926 ± 0.032		0.017 ± 0.024
LL	-0.020±0.078	0.40 ±0.107	0.785± 0.074	0.854 ± 0.304	0.141± 0.073	

AFS=Age at First Service, AFC=Age at First Calving, CI=Calving Interval, LMV=Lactation Milk Yield, DMY=Daily Milk Yield, LL=Lactation Length.

4.4.4. Estimates of Breeding Values

The total genetic ability of an animal for a given trait is called breeding value (BV).Estimates of breeding value mentions the value of an animal's additive genetic effects in breeding programm for a specific trait of interest. Breeding value were estimated for reproductive and production traits of HF crosses with different genotypes at Holeta Research Center, since the trait of interest at the center is to improve the reproductive and milk production performance of the breed through improving their genetic performance.

4.4.4.1. Breeding value estimates of cows for productive traits

Average breeding values for the estimated lactation milk yield (21.89 Liters), daily milk yield (0.060 Liters), and lactation length (0.06 days) were summarized (Figure 2, 3, 4) respectively.

Average estimated breeding values across the year of birth group for milk production traits were varying across birth year groups. The highest estimated average breeding value (182.97 Liters) for lactation milk yield was observed in 2000-2005 year whereas the lowest estimated average breeding value (-159.45) was observed in 1995-1999. The genetic trend for lactation milk yield from the year of 2000-2005 in this study showed an increasing trend. The average estimated breeding value for daily milk yield ranged from -0.105 to 0.1851 Liters whereas the average estimated breeding value for lactation length was between -0.018 and 0.093 days.

The declining trend indicates inefficiency in selection and proper culling of unproductive cows for milk production traits and also implies that the inefficiency in selection methods based on phenotypic performance.

The positive improvements of genetic trend for lactation milk yield, daily milk yield and lactation length traits on some year groups might be due to the better management, feed availability, number of observations and proper selection of cows based on their phenotypic performance.

Upward and downward trends of breeding values for milk production traits across year groups might be due to the presence of high and low producing cows with the absence of culling, environmental stresses (heat stress, low quality and quantity of feed), inefficiency in selection methods based on phenotypic performance.

Summary of estimating breeding value (EBV) for Productive traits (LMY, DMY, LL)

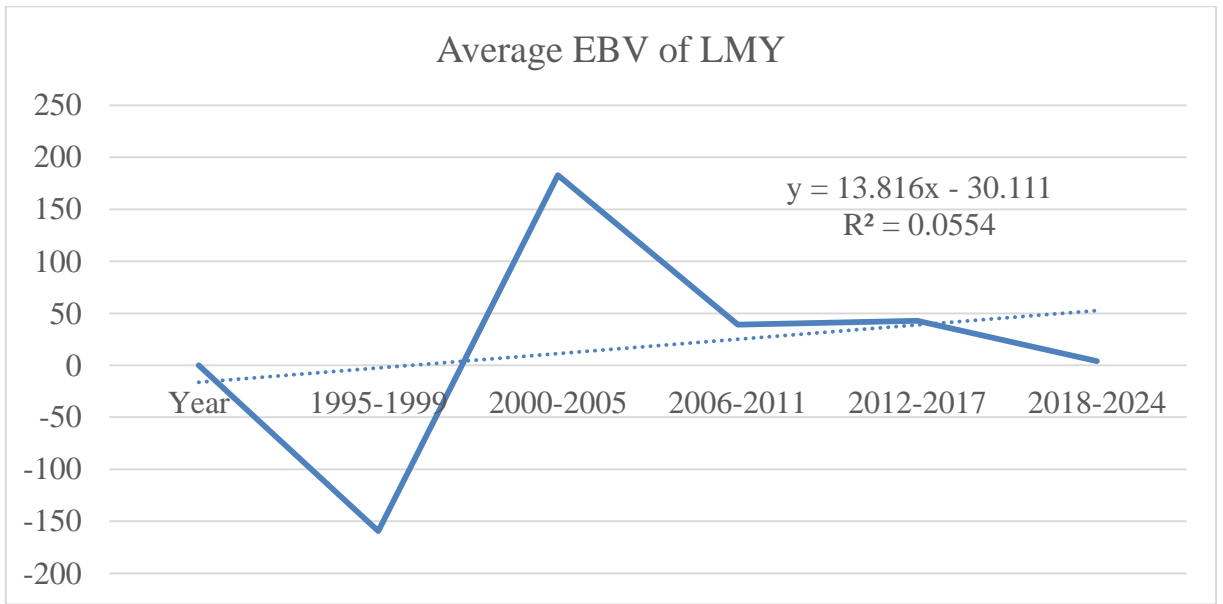


Figure 3: Estimated genetic trend of lactation milk yield (LMY) based on birth year group

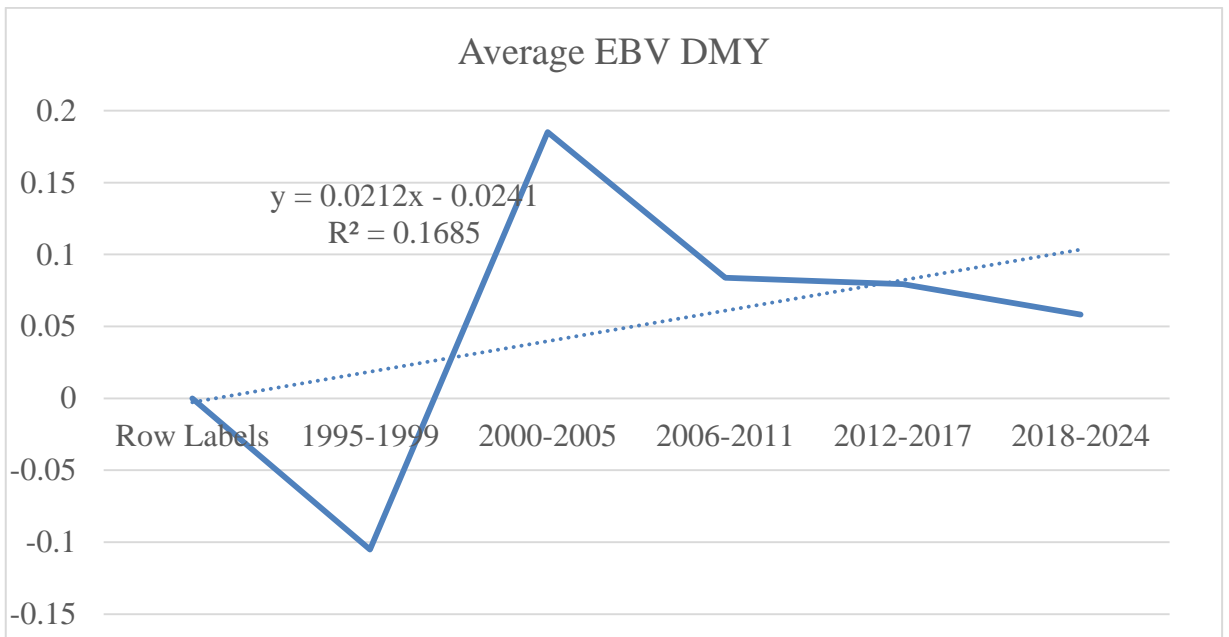


Figure 4: Estimated genetic trend of daily milk yield (DMY) based on birth year group

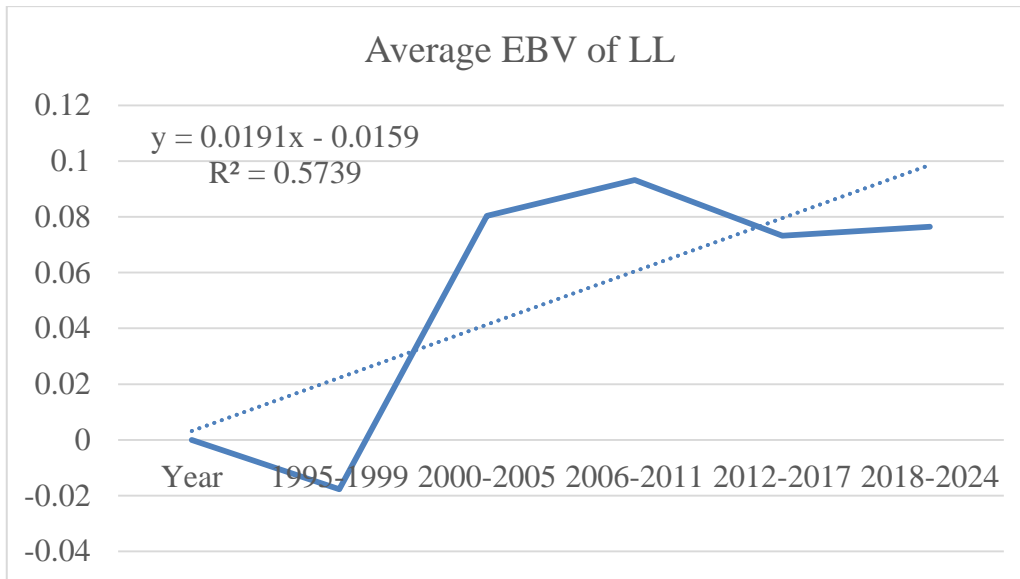


Figure 5: Estimated genetic trend of lactation length (LL) based on birth year group

4.4.4.2. Breeding value estimates of cows for reproductive traits

The current study was showed that the average estimated breeding values for AFS (-0.012 months with AFC (-0.017 months) Figure (5), and CI (-1.565 days) Figure (6) were summarized. The current study was showed negative trend for reproductive traits (AFS, AFC and CI) might be efficient breeding programs, efficiency in selection methods based on phenotypic performance and proper culling of unproductive cows.

Estimates of genetic trends AFS with AFC, and CI traits over the years are showed Figure 5, and 6, respectively.

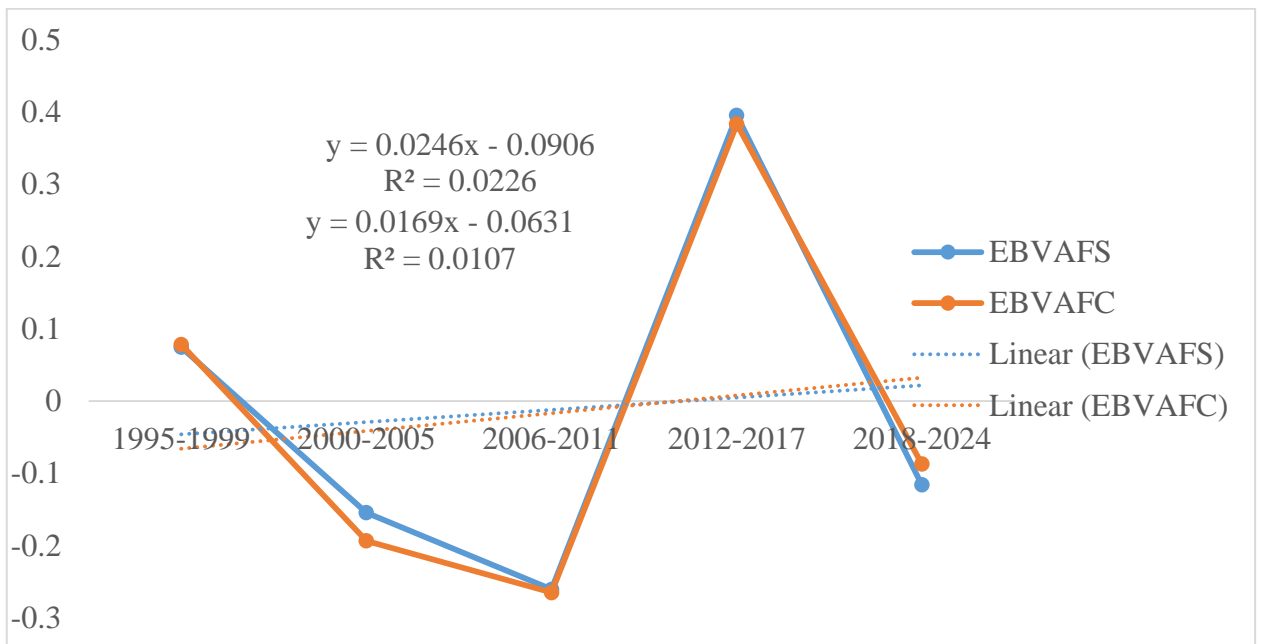


Figure 6: Estimated genetic trends of age at first service (AFS) and age at first calving (AFC) based birth year group

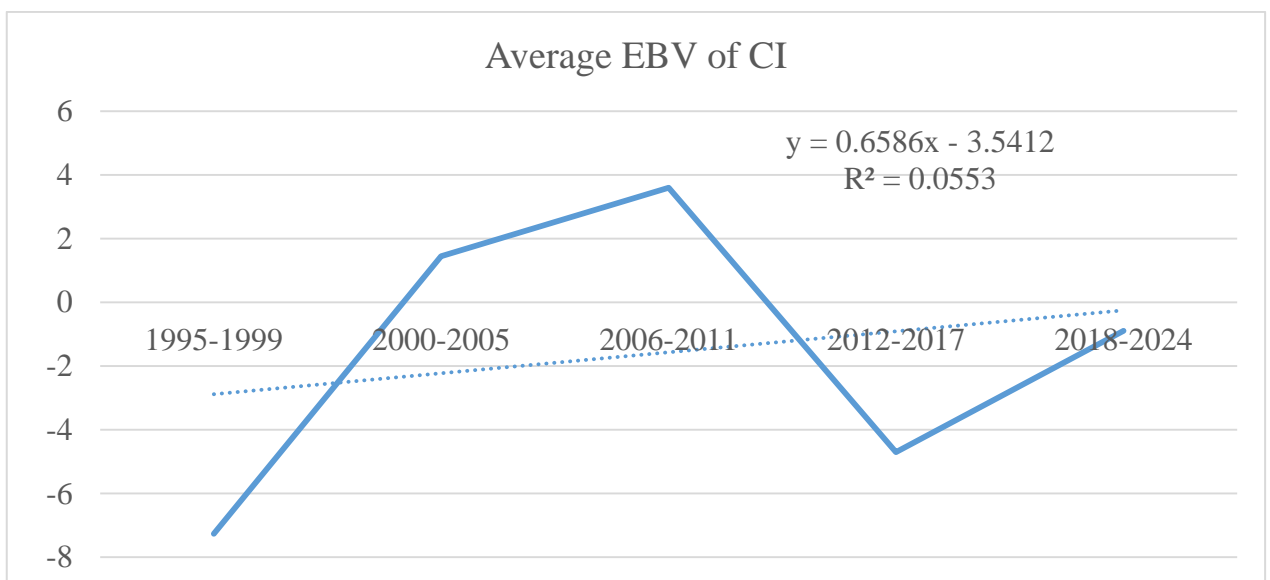


Figure 7: Estimated genetic trend of calving interval (CI) based on birth year group

5. CONCLUSIONS AND RECOMMENDATIONS

5.1. CONCLUSIONS

The current study was specifically designed to estimate the performance of Friesian and Borena crossbreds with various genotypes in a synthetic breed developing at Holeta Agricultural Research Center. With this regards during the period 1995-2024 were used for this study.

Genetic and non-genetic factors influenced the productive and reproductive performance of Friesian and Borena crossbreds.

Season of birth group, and season of calving group, had not significant effect on reproductive traits (AFS, AFC, and CI) and productive traits (DMY and LL). However, season of calving group had significant effect on LMY. The other significant variations were found in the measured reproductive and productive traits between genetic groups, birth year groups, calving year groups, and parity. This suggests that strict selection and improved management choices can result in a notable improvement.

First-generation crosses produced more milk than second-generation crosses. Performance among 50% F1, F2, and F3 and 75%F1, and F2 significantly declined, which indicated the importance of retaining heterosis. 75% F1 had produced superior milk per lactation and the breed of choice for milk production trait compared with other genetic groups.

Among 75% of crosses, mean lactation milk yield was significantly decreased by 25% for the inter-se mating breed group (75% females mated with 75% males) compared to 75% F1 or first generation.

The higher milk yield of first generation (50% F1 and 75% F1) crosses from its contemporary group was also associated with longer lactation length.

The 50% F1 genetic group was also characterized by better reproductive performance and the 75% F1 cross was poor in reproductive and high productive traits. As well as, the 50% second and third generation were belonged with their poor reproductive performances. It might be the breakdown of hybrid vigor occurs when gene interactions (epistasis) that benefited the F1 generation are disrupted in the F2 or F3 generations, leading to poorer performance and recombination loss.

The year and parity significantly influenced reproductive and productive traits due to the unpredictable changes in the environment, management practices, herd structure, and lactation stages that occurred annually.

Trend analysis has shown that the highest milk yield was recorded in the station the year from 2000-2005.

The non-significant heterosis effect of crossbred for lactation milk yield, and daily milk yield in the current study showed that the higher milk yield of these crosses were only due to breed additive of Friesian sire gene and the recombination loss were significant in all productive traits except lactation length. This might be due to unfavorable epistatic allele's interaction.

While the individual recombination effect was significant, it had an unfavorable, large, and negative impact on lactation milk yield, daily milk yield, and lactation length. In contrast, the individual breed additive effect of these three traits was more important than the individual heterosis effect.

Except AFC on heterosis, all reproductive traits in the present study indicated that the negative value and non-significant on the additive, heterosis, and recombination due to the additive effect of Friesian gene.

The values of heritability and repeatability both productive and reproductive traits were none zero values and ranges from low to higher.

Highest heritability estimate value was 0.235 ± 0.053 for DMY and the lowest was 0.180 ± 1.00 for LMY whereas highest LL (0.735 ± 0.151) and lowest DMY (0.491 ± 0.227) repeatability values were obtained. However, the current study shows that Low heritability and repeatability indicates that comparatively high environmental variance.

The genetic correlations between the traits in the current study were higher than the corresponding phenotypic correlations among all traits.

Knowing that all of the productive and reproductive traits in this study have only positive genetic correlations, it is likely that similar genes control them all. This indicates that selecting for one trait will improve other correlated traits in the desired direction, which will aid in the breeding process overall by improving all of the traits that are correlated with one another.

The phenotypic correlation between productive traits was ranges from very weak to strong correlation. Strong phenotypic correlation was observed between LL and LMY. However, negative correlation was observed among AFC and LL.

Upward and downward trends of breeding values for milk production traits across year groups might be due to the presence of high and low producing cows with the absence of culling, environmental stresses (heat stress, low quality and quantity of feed), inefficiency in selection methods based on phenotypic performance.

5.2. RECOMMENDATIONS

From this study the following recommendations were forwarded;

- Improved management is required to minimize the genetic recombination effect on lactation milk yield and daily milk yield.
- Continuous selection is important among crossbred animals to exploit the advantage of heterosis in inter se mated crossbreds.
- More data required to evaluate subsequent generations in the upcoming periods so as to produce composite breed
- It is a vital to consider a huge segregating population with sufficient genetic variability, avoiding any possibility of increasing the rate of inbreeding.

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7. APPENDICES

Appendix Table 1: Analysis of variance for lactation milk yield (LMY)

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ANIMALGROUP	4	303961455.9	75990364.0	103.13	<.0001
PARITY	6	39134338.9	6522389.8	8.85	<.0001
CALVINGSEASON	2	12591345.7	6295672.9	8.54	0.0002
CALVINGYEAR	4	39962010.5	9990502.6	13.56	<.0001

Appendix Table 2: Analysis of variance for daily milk yield (DMY)

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ANIMALGROUP	4	2042.712580	510.678145	146.72	<.0001
PARITY	6	668.772083	111.462014	32.02	<.0001
CALVINGSEASON	2	69.984369	34.992184	10.05	<.0001
CALVINGYEAR	4	216.743957	54.185989	15.57	<.0001

Appendix Table 3: Analysis of variance for lactation length (LL)

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ANIMALGROUP	4	351050.248	87762.562	11.48	<.0001
PARITY	6	76000.119	12666.686	1.66	0.1276
CALVINGSEASON	2	34545.796	17272.898	2.26	0.1046
CALVINGYEAR	4	1000231.460	250057.865	32.71	<.0001

Appendix Table 4: Analysis of variance of age at first service (AFS)

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ANIMALGROUP	4	14970.33022	3742.58255	27.94	<.0001
CALVINGSEASON	2	47.61073	23.80536	0.18	0.8372
CALVINGYEAR	4	4204.66513	1051.16628	7.85	<.0001

Appendix Table 5: Analysis of variance of age at first calving (AFC)

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ANIMALGROUP	4	14892.78718	3723.19679	27.77	<.0001
CALVINGSEASON	2	58.56457	29.28228	0.22	0.8038
CALVINGYEAR	4	4325.43154	1081.35789	8.07	<.0001

Appendix Table 6: Analysis of variance of calving interval (CI)

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ANIMALGROUP	4	299229.242	74807.310	4.07	0.0028
PARITY	6	1350672.928	225112.155	12.24	<.0001
CALVINGSEASON	2	67325.300	33662.650	1.83	0.1607
CALVINGYEAR	4	386595.209	96648.802	5.25	0.0003

BIOGRAPHICAL SKETCH

The author was born on March 1987 in South west region of Ethiopia, Sheka Zone, Yeki district, Tepi town. He attended his elementary education at Shay primary school from 1993 to 1998. He continued his secondary education in Tepi secondary high school from 1999 to 2004. And then he joined Wolaita Sodo Agricultural College and awarded a Diploma in Animal Science in 2007. Soon after graduation he was employed by Ministry of Agriculture at Yeki (Tepi) District and had been served as animal production expert for three years and Tepi agricultural research center as technical assistance for seven years. After that he has joined Ambo University to pursue his BSc degree and awarded with BSc in animal production in 2019. Then after, the author returned and continued his work at the Ethiopian Institute of Agricultural Research in Holeta Agricultural Research center as a researcher. After two years and six months of service, he joined the School of post Graduate Studies at Hawassa University in October 2021.