# EVALUATION OF NON-GENETIC AND CROSSBREEDING PARAMETERS ON THE PERFORMANCE OF BORANA AND BORANA-FRISIAN CROSSBRED DAIRY CATTLE AT HOLETTA AGRICULTURAL RESEARCH CENTER

**MSc. THESIS**

**BY**

**JEMAL UMAR**

**JUNE 2024**

**JIMMA, ETHIOPIA**

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**M.Sc. THESIS**

Submitted to the School of Graduate Studies Jimma University, College of Agriculture and Veterinary Medicine in Partial Fulfillment of the Requirements for the Degree of Master of Science in Agriculture (Animal Breeding and Genetics)

By

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**Evaluation of Non-Genetic and Crossbreeding Parameters on the Performance of Borana and Borana-Frisian Crossbred Dairy Cattle at Holetta Agricultural Research Center**

I have incorporated the suggestions and modifications given by during the internal defense and got the approval of my advisors. Hence, I hereby kindly request the Department to allow me to submit my thesis for external thesis defense.

JEMAL UMAR ________________ ________________

Name of student Signature Date

We, the thesis advisors have evaluated the contents of the thesis and found it to be satisfactory, accomplished according to the approved proposal, written according to the standards and formats of the University and is ready to be submitted. Hence, we recommend the thesis to be submitted.

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Decision or suggestion of the Department of Graduate Council (DGC)

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Chair person, DGC Signature Date

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# DEDICATION

To dairy farmers and breeders around the world, thank you for your hard work and dedication to providing food on the table.

# STATEMENT OF THE AUTHOR

I hereby declare that this thesis is my bona fide work and that all sources of materials used for this thesis have been duly acknowledged. This thesis has been submitted in partial fulfillment of the requirements for M.Sc. degree at Jimma University and is deposited at the University Library to be made available to borrowers under the rules of the library. I solemnly declare that this thesis is not submitted to any other institution anywhere for the award of any academic degree, diploma or certificate.

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# BIOGRAHPIGAL SKETCH

The author was born in West Arsi Zone Gedab Hasassa Woreda on September 12, 1997 GC. He attended his elementary school at Mujama Elementary School, and he took Ethiopian grade 8 ministry exam in 2014GC at this School. Then after he attended his secondary school at Selam Shashemenne Secondary School and he took Ethiopian General Secondary Education Certificate Examination (EGSECE) in 2016GC and he passed to preparatory school. Unfortunately, he obligated to return to his birth place Gedab Hasassa due to, family problem after that he continued his education at Gedab Hasassa Preparatory School and he took Ethiopian grade 12 University entrance exams in 2018GC and he succeeded. He then joined Wolaita Sodo University in 2019GC and graduated with a B.Sc. degree in Animal and Range Science in 2021. Soon after, he was employed by Wolaita Sodo University as graduate assistance 1, and then he joined Jimma University for postgraduate study in Animal Breeding and Genetics in 2022.

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## LIST OF ABBREVIATION AND ACRONOMY

| | |
|---|---|
| AFC | Age at First Calving |
| AI | Artificial Insemination |
| ANOVA | Analysis of variance |
| CI | Calving Interval |
| CSA | Central Statistical Agency |
| DMY | Daily Milk Yield |
| EIAR | Ethiopian Institute of Agricultural Research |
| ESA | Ethiopian Standards Agency |
| FAO | food and Agricultural organization of United Nation |
| GLM | General Linear Model |
| HFxBor | Holstein-Friesian crosses Borana |
| Kg | kilogram |
| LMY | Lactation Milk Yield |
| LDI | Livestock Development Institution |
| NARS | National Agricultural Research System |
| NSC | Number of Services per Conception |
| SAS | Statistical Analysis System |
| SD | Standard Deviation |
| SE | Standard Error |
| SNF | Solid Not Fat |
| WWS | World Wide Sire |

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***EVALUATION OF NON-GENETIC AND CROSSBREEDING PARAMETERS ON THE PERFORMANCE OF BORANA AND BORANA-FRISIAN CROSSBRED DAIRY CATTLE AT HOLETTA AGRICULTURAL RESEARCH CENTER***


## ABSTRACT

*Genetic improvement of indigenous dairy cattle through crossbreeding is a crucial way to increase productivity, as it exploits both additive and non-additive genetic effect. This study was designed to evaluate non-genetic and crossbreeding parameters on the performance of Borana and Borana-Frisian crossbred dairy cattle at Holetta Agricultural research center. Retrospective type of data was used to evaluate productive and reproductive traits and laboratory based investigation was done to evaluate milk composition. The trait studied were lactation milk yield (LMY),lactation length (LL), daily milk yield (DMY), age at first calving (AFC), calving interval (CI), number of service per conception (NSC), fat, protein, lactose and solid not-fat (SNF) contents. General linear model (GLM) procedure of the SAS, version 9; 2003 was used and least square mean separation was done by Tukey Kramer test based on ANOVA result. The overall result for LMY, LL, DMY, AFC, CI, NSC, fat, protein, lactose and SNF were 1841.80±34.02kg, 317.15±3.10days, 5.79±0.08kg, 41.40±0.48 months, 487.71±5.20days, 1.69±0.04, 3.85±0.14%, 3.29±0.14%, 4.73±0.06%, 8.63±0.14% respectively. The estimate for additive breed effect of Friesian relative to Borana were; 3939.55±156.18kg, 154.73±14.07days, 8.89±0.35kg for LMY, LL and DMY respectively; whereas it was 19.32±2.23 months, 33.59±22.53days and 0.15±0.18 for AFC, CI and NSC respectively. The estimate of heterotic effect of crossing Friesian with Borana were 241.36±80.34kg, -17.41±7.2days, 0.26±18kg for LMY, LL and DMY respectively; whereas it was -1.32±1.36 months, 72.06±11.59days and -0.31±0.11 for AFC, CI and NSC respectively. The loss due to recombination of Friesian and Borana were 1547.34±149.26kg, 76.01±13.45days and -2.65±0.33kg for LMY, LL and DMY respectively; whereas it was 19.32±2.23 months, 23.01±23.23days and -0.34±0.18 for AFC, CI and NSC respectively. Result of fixed effect revealed that all studied trait were significantly ($p<0.05$) affected by genetic group except NSC; accordingly, 75%F1perform higher in LMY and DMY while 50%F1 perform better in AFC, CI and milk composition. It can be noted from analysis of crossbreeding parameters that the improvement brought in production performance was through breed additive and heterotic effect while, it was brought through heterotic effect in reproduction performance. The result suggests that combination of breed additive and heterosis effects plays significant role in shaping the performance of crossbred animals if strategically applied.*



**Key words**: *Borana, Crossbreeding, Genetic, Holetta, Holstein-Friesian, Non-genetic*

# 1. INTRODUCTION

## 1.1. Background of the study

Ethiopia's dairy production is predominantly traditional, dominated by indigenous breeds with low genetic potential for milk production (Alebachew *et al.,* 2017). However, population growth, urbanization, and consumer preference are main driving demands for dairy products in the country (Shiferaw *et al.*, 2017). As a result, genetic improvement of indigenous cattle is proposed as a quick solution to meet these demands, as indigenous cattle alone may not be suitable to fill this gaps (Haile *et al*., 2009).

Genetic improvement of indigenous cattle was initiated through crossbreeding with exotic dairy cattle to increase  milk production (Tadesse *et al*., 2021). The program uses Friesian, Jersey, and Simmental sires crossed with indigenous dams to test different exotic blood levels (Gojjam *et al.*, 2017). The ultimate goal of the program is to develop a new breed that is well-adapted to the local environment, has high milk production potential, and is disease-resistant (Effa *et al.*, 2016).

Genetic improvement of indigenous dairy cattle through crossbreeding is crucial way to increase productivity, as it exploits both additive and non-additive genetic effect (Mekonnen *et al*., 2020). Additive genetic effect is an important factor to consider when selecting parental lines for crossbreeding programs, as it directly influences the genetic potential of the offspring (Alebachew *et al.*, 2017). Apart from the additive contribution of each breed to overall performance, there are also large non- additive (heterosis) effects in milk production and reproduction traits, which combine to give a large advantage in total production to first filial generation (Tadesse *et al., 2019*).

It is commonly observed in animal breeding, where the offspring of two different purebreds' exhibit traits such as higher growth rates, increased resistance to diseases, or improved fertility compared to their parents, and results from the combination of different genetic backgrounds, leading to increased genetic diversity and the expression of favorable traits (Bunning *et al.*, 2019). By understanding the average merit of the parental breeds and their level of gene representation in the crossbred genotype, breeders can make informed decisions to optimize the performance and characteristics of the resulting progeny (Clasen, 2021).

Despite the promising performance of crossbred dairy cattle and high demands for milk in Ethiopia, the crossbreeding programs have not been able to produce a significant number of improved dairy cattle (Getahun *et al*., 2020). It has been one implication that out of 70 million head only 3% are crossbred dairy cattle with over 6 decades of crossbreeding activities in the country (CSA, 2020/2021). Therefore, enhancing dairy cattle can be accomplished by carefully evaluating the production system, cattle performance, identifying production constraints and designing of suitable breeding strategies (Mezgebe *et al*., 2017).

Milk production performance of dairy cattle is typically assessed through milk yield per lactation, average daily milk yield, lactation length, lactation persistency, and lifetime production (Wondifraw *et al*., 2013). Genetic enhancement of economically significant traits is associated with reproduction rate (Gizaw *et al*., 2013). Reproductive performance is commonly assessed through the analysis of female fertility, age at first calving, calving interval, and conception rate (Haile *et al.*, 2011). Besides milk yield, the composition of milk such as fat, protein, solid not fat (SNF), total solid, and lactose percentages have become more important due to the rise in the price of butter and cheese from year to year (Mesfin and Getachew, 2007).

The genetic makeup of a population can be analyzed by examining the significance of heredity and environmental influences on an individual's performance within that population (Goshu *et al.,* 2014). Environmental factors (non-genetic) like birth year, calving year, cow parity, and cattle birth season impact the performance of dairy cattle and should be taken into account when selecting for improved production efficiency of dairy cattle (Olawumi and Salako, 2010). Taking into account these non-genetic factors can help dairy farmers make more informed decisions when selecting breeding stock and managing their herds for optimal performance and efficiency (Beneberu, 2020).

It was through crossbreeding technique that the formation of different genetic group between indigenous Borana and exotic Holstein-Friesian which used us a reference breed for this study. Therefore, performance evaluation of Borana and Borana-Friesian crossbred genetic group is quite important for further expansion of the genotype or changing to the appropriate crossbreeding scheme or breeding system for the future. Differences among breed effects relative to magnitudes of heterosis and recombination effects are the major determinants of the efficiency of various crossbreeding systems. Hence, understanding the relative performances of different breeds and their crosses is essential for developing a successful crossbreeding program.

Indeed, performance evaluation of Borana and Borana-Friesian crossbred dairy cattle at Holetta Agricultural Research Center have been reported by several authors (Haile *et al*., 2009; Birhanu *et al.*, 2015; Getahun, 2018) However, recent data is needed for timely recommendations, as earlier estimations may not reflect current performance due to biological mechanism and environment. On the other hand, the performance of crossbred dairy cattle is judged not only by productive and reproductive performance but also by milk composition, which gets less focus from the breeder's point of view in Ethiopia, despite its paramount importance for dairy producers, processors and consumers at large. Therefore this study was designed with the following objectives:

## 1.2. Objective

### 1.2.1. General Objective

❖ To evaluate non-genetic and crossbreeding parameters on the performance of Borana and Borana-Frisian crossbred dairy cattle at Holetta Agricultural Research Center Dairy Farm

### 1.2.2. Specific objectives

- To evaluate non-genetic factors affecting productive, reproductive and milk composition performance of study herd
- To evaluate crossbreeding parameters of productive and reproductive performance of study herd

# 2. LITERATURE REVIEW

## 2.1 Genetic Improvement Program in Ethiopia

Genetic improvement program in Ethiopia has been started with dairy cattle genetic improvement to enhance milk production of indigenous breeds through crossbreeding. The program aims to introduce superior dairy cattle breeds crossbred with the local indigenous breeds in order to improve milk yield, enhance disease resistance, and increase overall productivity (Tadesse *et al.,* 2021). Crossbreeding of dairy cattle was introduced in the country either by introducing germ plasma or direct importation of exotic dairy cattle from temperate countries (Habtamu *et al.,* 2010).

Motivation for popularizing crossbreeding between high-yielding European dairy breeds and cattle breeds adapted to local environments was initiated in the national agricultural research system (NARS) of Ethiopia in the early 1970s (Effa *et al.*, 2011). Moreover, the establishment of NAIC in 1982, have accelerated crossbreeding in the form of artificial insemination (AI) in the country for many years; despite the efficiency and impact of the operation has not been well documented (Chebo and Alemayehu, 2012).

As compared to other dairy cattle genetic improvement strategies, crossbreeding approach is believed to be the only feasible and quick way of increasing milk production in Ethiopia (Effa *et al.,* 2011). The outcome of the crossbreeding programs have been amply reported in several literatures with various outcomes (Demeke *et al*., 2004; Effa *et al.*, 2006; Haile *et al.*, 2009; Effa *et al.*, 2011).

The breed composition of Ethiopian cattle has been largely influenced by Holstein Friesian and to a lesser extent Jersey and Simmental breeds, which have long been imported into the country as live animals or through artificial insemination (AI) to improve the native cow breed (Chebo and Alemayehu, 2012). These two novel breeds (Friesian and jersey) were crossed with indigenous Boran, Horro, Fogera and Bereca at on station level to test combined genotype performance with different blood levels. Consequently, as a result of several years of improvements, on station performances of crossbred (50% and 75%) animals improved for daily milk yield, lactation milk yield, and lactation length (Effa *et al*., 2016). When designing breed improvement program, the level of exotic inheritance to be used in the crossbreds also needs to be decided. Milk production, reproduction performance and milk composition traits were all in favor of the 50% exotic cross (Haile *et al*., 2011).

### 2.2. Milk Production Performance of Dairy Cattle

The primary breeding goal in dairy cattle is to achieve higher milk production, which is an indication of dairy cattle's productive performance Milk production traits are economically crucial, contributing to the profitability of dairy production (Lobago *et al.*, 2007). Dairy cattle's ability to produce milk is typically assessed using the following metrics: average daily milk yield, length of lactation, persistence of lactation, milk composition, and lifetime milk production (Wondifraw *et al*., 2013).

Even if a dairy animal's lactation milk production varies, the animal's performance is determined by the amount of milk it produces throughout the designated lactation time (Wondifraw *et al*., 2013). The primary cause of this variance is the animal's unique collection of genes and how they interact with non-genetic factors. In addition to genetic factors, environmental conditions such as nutrition, management practices, and overall animal health play crucial roles in determining a dairy cow's milk production potential (Tadesse and Dessie, 2003).

Non-genetic factors, such as the year of birth or calving, the parity of the cow, or the season of birth or calving of the cow, will affect the milk production performance of dairy cows. These factors must be considered when choosing to improve the production and reproductive efficiency of dairy cows (Olawumi and Salako 2010). Understanding non-genetic factors, such as the year of birth or calving, the parity of the cow, and the season of birth or calving of the cow, will affect the milk production performance of dairy cows.

#### 2.2.1. Lactation milk yield (LMY)

Lactation milk yield (LMY) is the total milk obtained per lactation. It is a very important production efficiency trait, which is a combination of daily milk yield and lactation length. Cows with high milk yield per lactation are economic producers and have more lactation milk yield (Wondifraw *et al*., 2013). The range of lactation milk yield for crossbred dairy cows in Ethiopia varies from 1293 to 2957 kg, this range was observed in on-station conditions, and it indicates the variability in milk production performance among different crossbreeding genotypes in Ethiopia (Haile *et al*., 2009).

The lactation milk yield reported for on-farm evaluation of crossbred dairy cows was higher than on-station performance as cited by (Dessalegn *et al.*, 2016).This could be attributed to the differences in management practices, environmental conditions, and feeding regimes between on-farm and on-station settings. Additionally, genetic variability and individual differences among cows may also play a role in the observed discrepancy in milk yield.

Beyond the level of feeding and management, non-genetic factors such as season, year, and parity influence milk production performances of dairy cows. Several authors have reported that lactation milk yield is significantly influenced by season and parity (Mohamed *et al*., 2007; Duguma *et al.*, 2012; Niraj *et al.*, 2014). Variation in lactation milk yield may be observed from one lactation to lactation for the same animal. The main reason for such variation can be attributed to the physiology of lactation is the given set of genes and their reaction with non-genetic factors (Wondifraw *et al*., 2013). Therefore, understanding and managing these non-genetic factors are crucial for optimizing milk production in dairy cows. Farmers can implement strategies such as adjusting feeding regimes, providing appropriate shelter, and monitoring healthy closely to mitigate the impact of seasonal variations and parity on lactation milk yield.

### 2.2.2 Lactation length (LL)

Lactation length refers to the time of period from when a cow starts to secrete milk after parturition to the time of drying off. Lactation length of cows depends mostly on the management objective of the herder, the herder may prolong the lactation length for the sake of continues milk production or dry off the dam at early stage for the purpose of breeding the cows (Msangi *et al*., 2005). In most modern dairy farms, a lactation length of 305 days commonly accepted as a standard. An extended lactation period has practical implications to the dairy farmer as it provides compensation for the extended calving interval (Lobago *et al.*, 2007). Nevertheless, the profitability of short or extended lactation length depends on lactation persistency.

Different authors have reported different values of lactation length, which might be related to breed/genetic composition, production system, herd management related to feeding, diseases, and other environmental differences (Getahun, 2018; Kassa, 2018). Accordingly, Janssens *et al*. (2012) reported an average lactation length of 9.13±1.99 months in crossbred cows in selected dairy farms in Jimma town. On the other hand, the lactation length of crossbreds in North Showa was 333.9 days (Ayalew and Asefa, 2016). The different values of lactation length reported by different authors elsewhere could be associated with breed/genetic makeup, production system, and herd management concerning feed, disease, and other environmental differences (Getahun *et al.*, 2020).

In addition to breed/genetic makeup, production system, and herd management practices, factors such as climate, availability of resources and overall animal health can also significantly influence the variability in reported lactation lengths across different regions and studies. These discrepancies underscore the complexity of dairy farming and the multitude of variables that can impact the duration of lactation in cows. Further research and comprehensive data collection are essential to better understand and address the diverse factors contributing to variations in lactation length among different breeds and locations.

### 2.2.3 Daily milk yield (DMY)

Daily milk yield is a very important production efficiency trait, which is a combination of milk yield and lactation length. Daily milk yield is the most economically important parameters in dairy production since it is the parameters which can judge the production ability of dairy cows from day to day. The daily milk yield of a crossbred cow at the on-farm level was in the range of 6.2-11.8L ( Kumar *et al.*, 2014; Abera, 2016), which is better than the daily milk yield reported for dairy cows at on-station level (Demeke *et al*., 2000; Effa *et al.*, 2016). The difference in the result might be associated with the weather condition change, decline of pasture productivity, production system, breed, and parity (Haile *et al*., 2009).

**Table 1:** Mean daily milk yield (DMY), lactation length (LL), and lactation milk yield (LMY) of dairy cows with different genetic groups

| | Production trait | | | |
|---|---|---|---|---|
| Genotype | DMY(kg) | LL(days) | LMY(kg) | Reference |
| 50%HFxBoran | 6.4±0.06 | 337.2±3.6 | 2031±20.9 | Gebreyohannes *et al*., 2013 |
| 75%HFxBoran | 7.0±0.11 | 343.2±6.3 | 2240±35.9 | Gebreyohannes *et* al., 2013 |
| 50%JxBoran | 5.6±0.08 | 315.3±0.6 | 1788±26.5 | Gebreyohannes *et* al., 2013 |
| 75%JxBoran | 5.7±0.17 | 302.8±9.8 | 1832±56.0 | Gebreyohannes *et* al., 2013 |
| 50%HFxBoran(F1) | 6.36±0.30 | 343.6±4 | 2203.2±38 | Getahun *et al*., 2020 |
| 75%HFxBoran (f1) | 8.7±0.17 | 374±7 | 2957.5±73 | Getahun *et al*., 2020 |
| 50%JxBoran (F1) | 6.2±0.17 | 343±6 | 2092±75 | Demeke *et al*., 2004 |
| 50%JxBoran (F2) | 4.5±0.24 | 304±9 | 1613±107 | Demeke *et al*., 2004 |
| 50% HF | 6.0±0.1 | 337±3 | 2019±26 | Haile *et al*., 2009 |
| 75% HF | 6.3±0.1 | 351±6 | 2182±4 | Haile *et al*., 2009 |
| 50%Jerseyx Horro | 4.9±0.10 | 303.8 ± 5 | 1621± 33.1 | Gebreyohannes *et* al., 2013 |
| 75%Jerseyx Horro | 5.5±0.23 | 329 ± 12 | 1724± 73.9 | Gebreyohannes *et* al., 2013 |

LMY: lactation milk yield, LL: lactation length, DMY: daily milk yield, HF: Holstein Friesian, F1: 1 $^{st}$ filial generation, F2: 2 $^{and}$ filial generation & J: Jerseys breed.

### 2.3 Reproductive Performance of Dairy Cattle

Genetic improvement of all traits of economic importance is related to the reproductive performance of dairy cattle. Reproductive performance of dairy cattle is one of the most crucial factors that influence the profitability of the dairy sector, since it is expressed by the extent of reduction of reproductive waste and, on top of that, affects life time milk and meat production (Ibrahim and Seid, 2017). The reproductive performance of Ethiopian indigenous and exotic breeds in various locations in Ethiopia is poor, mainly due to various environmental factors and management or husbandry practices (Tesfa and Garikipati, 2014). Additionally, poor reproductive performance is caused by the failure of cows to become pregnant due to anestrus (per-pubertal or postpartum) and calf losses (Janssens *et al*., 2012). The reproductive performance of dairy cattle is commonly evaluated by analyzing female reproductive traits (Haile *et al*., 2011). The main indicators that would be considered in assessing the reproductive performance of dairy cattle are age at first service, age at first calving, calving interval, and number of services per conception (Haile *et al.*, 2011).These traits can provide valuable insights into the efficiency and profitability of a dairy operation.

The reproductive performance of Ethiopian indigenous and exotic breed in various location of Ethiopia is poor, mainly due to various environmental factors and management or husbandry practice (Tesfa and Garikipati, 2014). Additionally, low reproductive performance is caused by the failure of cow to become pregnant due to an-estrus (per-pubertal or postpartum), feeding and all other husbandry practice, and calf losses (Janssens *et al*., 2012).

### 2.3.1 Age at first calving (AFC)

Age at first calving, the period that heifers need to reach puberty and reproduce for the first time, is an important factor in the cost of rearing replacements in dairy herds. A reduction in AFC will minimize the raising costs, shorten the generation interval, and consequently take full advantage of the number of lactations per head (Ayeneshet *et al.*, 2018). On the other hand, prolonged AFC will have high production in the first lactation due to growth performance, and life time production will decrease due to a smaller number of calving's (Kumar *et al*., 2014).

The average value of AFC for dairy cattle was different based on differences in breed, production system, and agro-ecology, and even though there are differences not only between breeds but also within breeds, this might be related to environmental conditions, husbandry practices, which may have an effect on the growth of cattle and management fluctuation among years, as well as lower energy intake below the recommended amount (Dessalegn *et al.*, 2016). The values of age at first calving obtained by different workers in Ethiopia for different genetic groups were summarized in Table 2.

### 2.3.2 Calving interval (CI)

Calving interval is the interval between consecutive calving which is ideal from 12 to 13 months assuming an average of gestation period of 280 days and nearly 85 days would remain for post-calving conception to occur. Long calving interval would indicate the prevalence of reproductive problems or poor management of the herd that could affect the return to estrus, heat detections, serving and conception (Dessalegn *et al*., 2016).

Different authors reported different value of calving interval Table 3. For instance, (Tadesse and Dessie, 2003a) conducted a study on 50% HF x Barca, 50% HF x Borena, 75% HF x Barca, 75% HF x Borena, 87.5% HF x Barca and 87.5 HF x Borena, and reported mean calving interval of 400±14,400±14, 448±16,436±15,498±30 and 464±24 days respectively. Apart from the level of exotic gene other non-genetic factors (year, season, and parity) have been considered a great influence on calving interval traits. However, reports on the extent of the effect year and parity were variable. For instance, on station Studies by (Haile *et al*., 2009; Wassie *et al*., 2015; Mengistu *et al.*, 2016), reported that calving interval had been influenced by year of calving and parity. However, Belay and Janssens, (2014) reported the non-significant effect of year and parity on calving interval.

### 2.3.3 Number of service per conception (NSC)

Number of service per conception is one of parameters considered in determining the reproductive efficiency of the cow, it is defined as the number of services (natural or artificial) required for a successful conception, depends largely on the breeding system used, the reproductive health status of the animal, the management and feeding practices in a farm and the semen quality of AI or natural service bulls (Alemneh *et al.*, 2015); it shows that how many service are required for a successful conception of breeding animals and its calculated by dividing the number of conception with number of insemination and is considered poor if it is greater than 2 while it is recommended for the profitability of dairy cows if it ranges from 1 to 1.7 (Garwe, 2001). Number of service per conception depends largely on breeding system used; it is higher under natural breeding than artificial insemination (Alemayehu and Moges, 2014). The overall mean of NSC obtained at Holetta dairy center using AI was between 1.2 to 2.3 services (Gojjam *et al*., 2017).

**Table 2:** Mean age at first calving, calving interval and number of service per conception of different dairy cattle breed in Ethiopia

| Breed | AFC | CI | NSC | Reference |
|---|---|---|---|---|
| 50% HF x Bo (F1) | 38.70 ± 0.53 | 461.17±6.06 | 1.64 ± 0.04 | Getahun *et al*., 2020 |
| 50% HF x Bo (F2) | 46.13 ± 0.91 | 500.8±13.7 | 1.79 ± 0.09 | Getahun *et al*., 2020 |
| HF x Borana | 41.08 ± 0.44 | 405.50±3.32 | 1.36 ± 0.03 | Mengistu *et al*., 2016 |
| HFxBor | 37.42±0.35 | 476.35±3.91 | 1.75±0.03 | Getahun *et al*., 2020 |
| HFxBor & Arsi | 41.16±0.56 | 475.92±3.44 | 1.35±0.03 | Negussie *et al* (1998 |
| HFxBor | 39.49±0.83 | 476.36±4.73 | 1.39±0.05 | Wassie *et al.,* 2015 |
| Jersey | 29.92±0.17 | 497.08±3.69 | 2.02±0.02 | Direba *et al.*, 2012 |
| Jersey | 34.51±0.42 | 450.09±6.60 | 1.79±0.06 | Habtamu *et al*., 2011 |

### 2.4 Milk Composition

Milk composition refers to the chemical and nutritional makeup of milk. Smallholder dairy farmers in Ethiopia often face difficulties in managing the nutrition and feeding of their dairy animals, which can impact the milk composition (Aynalem and Getie, 2020). As a result, there is a need for improved breeding programs and better access to nutritional resources to enhance the milk composition of dairy animals. Additionally, there is a growing interest in promoting dairy cooperatives and value-added processing facilities to help smallholder farmers improve milk quality and composition (Senbeta, 2018).

Important characteristics of dairy and cheese industries include content of fat, protein, and casein, due to; amount of milk used to make cheese is increasing globally (Aynalem and Getie, 2020). Compositional regulation may be possible through selective breeding (Bovenhuis *et al.,* 2013). The main criterion for assessing milk quality is its composition, which varies between dairy animals and is influenced by a number of variables, including, Species, parity, breed, and body condition score (Sarkar *et al.,* 2006).

In order to satisfy consumer preferences, changes are frequently made to the chemical make-up of cow’s milk as well as the protein-to-fat ratio (Arnould *et al.,* 2013). Chemically raw milk is composed of 87.7% water, 3.4% fat, 3.3% protein, 4.9% lactose, and 0.7 mineral (Poulsen *et al.,* 2012). The greater the amount of fat and protein in milk the greater the yield of cheese and milk with a high fat content gives more butter than milk with a lower fat content (O'Connor, 1995).

Milk compositions vary between breeds of cattle indigenous, crossbreed, and exotic; this may be due to the influences of breed differences in feed conversion efficiency to specific feed type (Mesfin and Getachew, 2007). Milk from different cattle breeds holds distinct composition profiles because of genetic background (Poulsen *et al.*, 2012). The natural composition and Physico-chemical properties of raw milk may change by adulteration of milk by intentional addition of water or other substances are a common problem in many developing countries (Aynalem and Getie, 2020).

Fat is the main source of energy in milk and is most valuable constituent which is present in the form of an emulsion of fat cells suspended in the milk. The minimum fat percent for whole cow milk which is recommended by the Ethiopian standard agency (ESA) should not be less than 3.5% (ESA, 2009). The Food and Drug Administration requires not less than 3.25% milk fat for fluid whole milk similarly to the U.S. Public Health Service, milk ordinance and code also recommended of 3.25% butterfat in farm milk (Raff, 2011).Variations in fat content between breeds of cow is an inherited character; which implies that breeds with higher fat content produce less milk quantity than those with low fat content; accordingly, local and crossbreed genotype have significant effect on milk fat, lactose, and protein, respectively (Duguma, 2022).

Total protein content of bovine milk is approximately 3.5% by weight (36 g/L), providing almost 38% of the solid not-fat content of milk, and about 21% of whole milk energy (Ghafoori *et al.,* 2022). Bovine milk protein is considered a high-quality, or complete protein, because it contains all essential amino acid in proportion resembling amino acid requirements; due to, the high quality of bovine milk protein, it is regarded as a standard reference protein to evaluate the nutritive value of other food protein (Ghafoori *et al.,* 2022). There is recommended percent set for protein content scientifically, according to the Ethiopian Standard Agency, the minimum percent protein content of whole milk should be 3.20 percent (ESA, 2009). According to Food and Drug Administration, a minimum protein content of whole milk is 2.73% (Raff, 2011).

Similar to the previously mentioned parameters, lactose and solid not fat (SNF) are crucial chemical characteristic that affects the chemical quality of milk. Lactose is the main determinant of milk volume. A close relationship between lactose synthesis and the amount of water drawn into milk makes lactose a stable milk component. The minimum standard set by European quality standards for lactose and solid not fat in unprocessed whole milk is 4.2% and 8.5% respectively (Tamime, 2009).

Milk composition parameters ( fat, protein, solid-not-fat, and lactose) can be affected by many confounding factors, genetics, species, parity, lactation stage, feeding status, season, pregnancy and so on (Pratap *et al*., 2014).

**Table 3:** Mean of milk constituents for different cattle breed in Ethiopia

| | | Milk composition traits | | | |
|---|---|---|---|---|---|
| Breed/Genotype | Fat | Protein | Lactose | SNF | Reference |
| Boran | 6.01±0.05 | 4.05±0.05 | 4.00±0.05 | 16.02±0.05 | Mesfin and Getachew, 2007 |
| BXF | 5.48±0.02 | 3.80±0.03 | 4.18±0.05 | 15.32±0.03 | Mesfin and Getachew, 2007 |
| HF | 3.7+0.03 | 3.14+0.06 | 4.64+0.04 | 8.48+0.10 | Senbeta, 2018 |
| JR50*HO50 | 3.98+0.40 | 3.8+0.18a | 4.67+0.023 | 9.29+0.23 | Senbeta, 2018 |
| HF50*JR25*HR25 | 4.70+0.08 | 3.54+0.09 | 4.71+0.04 | 8.98+0.09 | Senbeta, 2018 |
| Ogaden | 4.69+0.01 | 3.9+0.14 | 4.57+0.19 | 9.28+0.50 | Senbeta, 2018 |
| Boran | 5.01±0.03 | 3.60±0.02 | | 8.66±0.05 | Haile *et al.*, 2009 |
| 50% HF | 4.77±0.03 | 3.40±0.02 | | 8.49±0.05 | Haile *et al., 2009* |
| 62.5% HF | 4.85±0.04 | 3.43±0.03 | | 8.43±0.05 | Haile *et al.*, 2009 |
| 75% HF | 4.21±0.05 | 3.07±0.03 | | 8.09±0.06 | Haile *et al.*, 2009 |

HF -Holstein Frisian, JR50-Jerry 50%,Ho50-Horro 50%, HF50- Holstein Frisian 50%, JR25-Jerrsey-25%,HR25-Horro 25%,SNF:solid not fat.

### 2.4 Non-genetic factors affecting production, reproduction and compositional traits

Non-genetic factors such as birth or calving year, parity of cow and birth or calving season of cattle influence the reproductive and productive performance of dairy cattle, which should be considered in the selection for increased production and reproductive efficiency of dairy cattle (Olawumi and Salako, 2010). Taking into account these non-genetic factors can help dairy farmers make more informed decisions when selecting breeding stock and managing their herds for optimal performance and efficiency. By understanding how factors such as birth year, parity, and calving season can impact productivity and reproductive success, farmers can tailor their breeding programs and management practices to maximize the potential of their dairy cattle.

Different authors have reported that lactation milk yield and lactation length were significantly influenced by season and parity (Duguma *et al.*, 2012; Kumar *et al*., 2014). Knowledge of these non-genetic factors and their influence on cattle productive, reproductive and compositional performance is important in the formulation of management and selection decisions.

**Table 4:**Non-genetic factors influencing productive performance traits of dairy cattle

| Factors | Breed | DMY | LL | LMY | Reference |
|---|---|---|---|---|---|
| Period | HFxBor | **** | **** | **** | Getahun *et al*., 2020 |
| | HFxBor | ** | ** | ** | Birhanu *et al*., 2015 |
| | HFxBor | ** | ** | ** | Haile *et al.*, 2009 |
| | Jersey | | **** | **** | Hunde *et al.*, 2015 |
| Season | JBxBor | **** | | **** | Gebreyohannes *et al.*, 2014 |
| | HFxBor | NS | NS | NS | Haile *et al.*, 2009 |
| | HFxBor | * | * | * | Birhanu *et al.*, 2015 |
| Parity | HFxBor | ** | ** | ** | Haile *et al.*, 2009 |
| | HFxBor | ** | ** | ** | Birhanu *et al.*, 2015 |

*****= (p< 0.0001), ***= (P< 0.001), **= (P< 0.01) *= (P< 0.05), NS= not significant, DMY= (Daily Milk Yield), LL= (Lactation Length), LMY= (Lactation Milk Yield), HF= Holstein Frisian, Bor= Borana, JB= Jersey Breed*

**Table 5:** Non-genetic factors influencing reproductive performance traits of dairy cattle

| | | Reproductive trait | | | |
|---|---|---|---|---|---|
| Factors | Breed | AFC(months) | CI(days) | NSC | Reference |
| | HFxBor | **** | **** | * | Getahun, 2018 |
| Period | HFxBor | ** | ** | ** | Tadesse, 2014 |
| | Jersey | **** | **** | **** | Hunde et al., 2015 |
| Season | HFxBor | **NS** | ** | **NS** | Getahun, 2018 |
| | HFxBor | * | * | * | Tadesse, 2014 |
| | Jersey | **** | **NS** | *** | Hunde et al., 2015 |
| Parity | HFxBor | | **** | NS | Getahun, 2018 |
| | Jersey | | **** | **** | Hunde et al., 2015 |
| | Jersey & HF | | ** | ** | Yosef, 2006 |

**** (p< 0.0001), *** (P< 0.001), ** (P< 0.01) * (P< 0.05) and NS= not significant, AFC (Age at First Calving), CI (Calving Interval), and NSPC (Number of Service per Conception)

**Table 6:**Non-genetic factors influencing milk compositional performance traits of dairy cattle

| *Factors* | | *Milk constituents* | | | |
|---|---|---|---|---|---|
| | *Fat* | *Protein* | *SNF* | *Lactose* | *Source* |
| *Lactation stage* | ** | *NS* | *NS* | *NS* | Gurmessa and Melaku, 2012 |
| *Parity* | *NS* | *NS* | *NS* | *NS* | Gurmessa and Melaku, 2012 |
| *Season* | *NS* | ** | ** | ** | Haile *et al.*, 2009 |
| | ** | *NS* | ** | ** | Haile *et al.*, 2009 |
| *Parity* | *NS* | *NS* | *NS* | *NS* | Mohamed *et al.*, 2023 |
| *Stage of lactation* | * | * | * | * | Ghafoori *et al.*, 2022 |

** (P<0.01), *(P<0.05), NS: not significant

### 2.5 Crossbreeding Parameters

Crossbreeding parameters refer to the specific traits or characteristics that are considered when breeding two different species or varieties together to create a new hybrid. These parameters can include genetic compatibility, desired traits, and overall breeding goals. The genetic basis for crossbreeding is broadly classified into two components; additive and non-additive. Estimates of crossbreeding parameters of reproductive and productive traits have been reported by ( Demeke *et al*., 2004; Haile *et al*., 2009; Effa *et al.,* 2011; Gebreyohannes *et al*., 2013; Getahun, 2018; Hunde *et al*., 2022).

### 2.6.1 Additive genetic effect

Additive genetic effect is the average merit of the parental lines or breeds, with simple weighting according to level of gene representation of each parental breed in the crossbred genotype (Swan and Kinghorn, 1992). This additive component can be divided into the individual and maternal additive genetic effect. The individual additive genetic effect is the contribution to offspring phenotype attributable to its own set of genes. Maternal additive genetic effects are defined as any contribution or influence on the offspring's phenotype attributable to its own dam (Vieira *et al*., 2022). Maternal effects can be classified into prenatal (e.g. cytoplasm of the egg and uterine environment) and postnatal (for example milk production, method of rearing and/or mothering ability). Previous work in Ethiopia revealed that the individual additive genetic breed difference for milk production traits were significant (Demeke *et al*., 2004). Furthermore, Demeke *et al.,* (2004) evaluated the additive genetic difference of Friesian against indigenous Borana and reported 2774 ± 81 kg, 7.1 ± 0.2 kg and 152 ± 7 days for LMY, DMY and LL, respectively. However, Haile *et al*., (2009) found slightly lower additive effect of Friesian breed that compared to the above author.

Earlier works in Ethiopia also reported that crossbreeding had significant additive genetic effect on some reproductive traits. For instance, the report on AFC by Demeke *et a*l., (2004) had described the additive genetic effects. On the contrary, Birhanu *et al.*, (2015) presented non-significant additive genetic effect on CI, and AFC for Ethiopian Borana and Holstein Friesian. Haile *et al*., (2009), studied the crossbreeding effects between Ethiopian Borana and Holstein Friesian and found non-significant additive effect for calving interval.

### 2.6.2 Non additive (heterosis) genetic effect

Heterosis is a measure of the superior performance of the crossbred relative to the average of the purebreds involved in the cross. Significant Heterosis values are usually obtained under optimum conditions by combining indigenous and exotic breeds (Galukande *et al*., 2013). It is widely used in the world in order to enhance production of milk and meat, particularly under commercial farms (Cunningham and Syrstad, 1987). The genetic basis of Heterosis requires expression of non-additive action including dominance (interactions between allele's within-locus) and epistasis (interaction among allele's between-loci) (Galukande *et al*., 2013).

Heterosis is a bonus that dairy producers can expect in addition to the positive effects of individual additive gene. However, Heterosis alone will not guarantee success in a crossbreeding program. The effect of Heterosis is known to be generally higher for traits with low heritability such as reproductive traits (Bunning *et al.,* 2019). From a genetic point of view, Heterosis quantifies the amount of non-additive genetic effects that deviates from the additive component. Heterosis in crossbred animals may contain a dominance effect and negative component caused by the breakdown of favorable interactions between loci that have been built up on through both natural and artificial selections(Galukande *et al*., 2013). (Bunning *et al.,* 2019) found gains in heterosis of 35.15% for milk yield in crossbred cows (Bos Taurus x Bos indicus), while Lembeye *et al.,* (2016) found a heterosis variation of 3.3-5.9% for crossbreed animals (Holstein-Friesian cross Jersey) and concluded that lactation and production level of cows affect the expression of heterosis.

# 3. MATERIALS AND METHODS

## 3.1. Description of the Study Area

This study was conducted at Holetta Agricultural Research Center, which is found in West Shewa Zone of Oromia regional state of Ethiopia. It is located at 40 kilometers west of Addis Ababa, in the central highlands of Ethiopia at 38°50'E longitude and 9°80'N latitude, and at an altitude of 2400 meters above sea level. The average annual temperature is 15$^{o}$C with a minimum temperature of 6$^{o}$C and a maximum temperature of 24$^{0}$c and an average monthly relative humidity is 60% (Haile *et al.*, 2011).

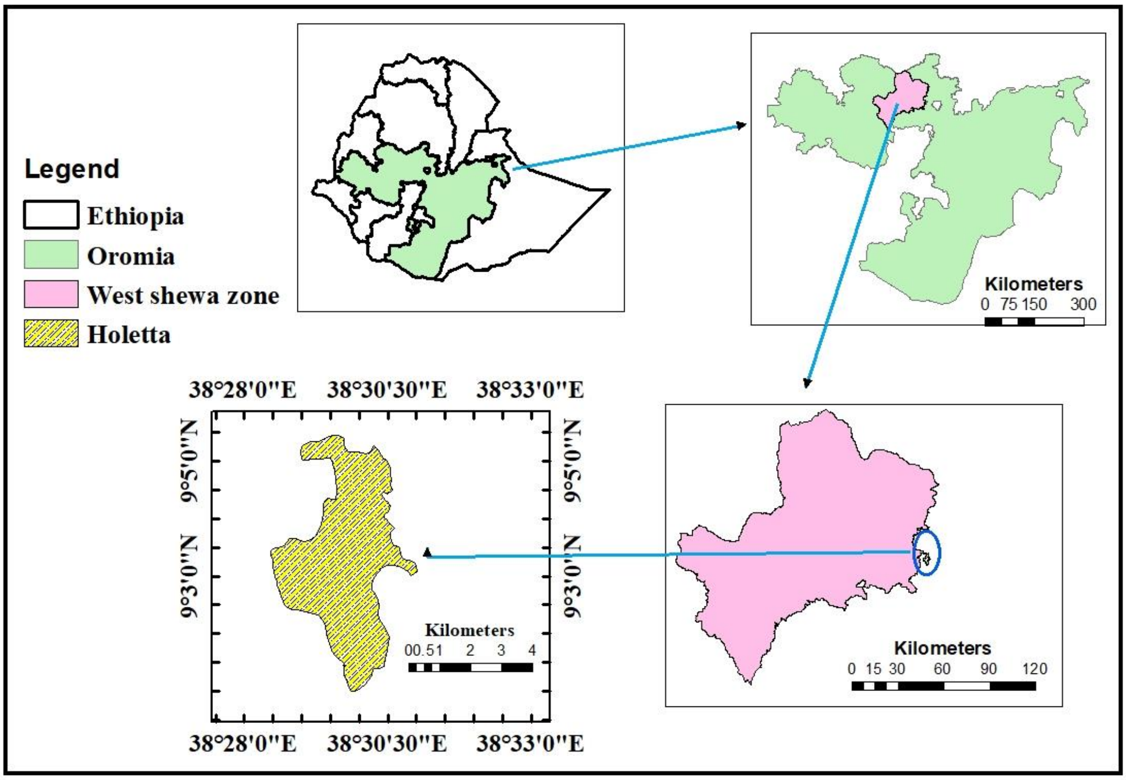


**Fig 1:** Map of the study area

Source; ArcGIS

## 3.2. Description of the farm

Holetta Agricultural Research Center is the largest dairy cattle research in Ethiopia, which agro-ecologically, found in the central highlands of the country. The farm has long term data collected on growth, reproduction, production and survival traits. The farm has been working on evaluation and selection of crossbred dairy cattle in the last 50 years.

Furthermore, the center has demonstrated crossbred dairy cows and heifers with associated feeding, health and other husbandry packages for smallholder farmers mainly in the central Ethiopia (Direba *et al*., 2022).

### 3.3. Animal Management

Herds were managed separately depending on sex, age, pregnancy and lactation (dry or milking cow). Female calves were allowed to suckle their dam immediately after birth for about five days to receive colostrum and then separated from their dams and offered fresh milk twice a day for about 6 months. However, male calves were weaned within 98 days. Weighting and ear tagging were also engaged within 24 hours after birth. Cows and heifers were allowed to graze natural pasture for about 4 hours a day and supplemented with hay and concentrate feeds up on return to the barn during the dry and small rainy seasons. The animal has free access to clean water all the time. All animals were restricted from grazing and managed indoor during main rainy season. Calves less than 6 months, bulls and late pregnant cows and heifers were usually isolated and managed indoor. All animals were supplemented with hay and concentrate feeds constituting 60 % wheat bran (sometimes with wheat middling), 38% noug seed cake (Guizotia abyssinica) and 2% salt. The amount consumed is not exactly known, since it depends up on the amount of feed available in the stock.

### 3.4. Breeding Program

Breeding program was undertaken between indigenous (Borana) and Friesian semen. The Borana cattle, used as a dam line for crossbreeding, were purchased from Borana pastoralists in southern Ethiopia (their center of origin) and reared on the station, then inseminated randomly to produce required generations. Seasonal breeding was undertaken until 2000. However, after 2000, the mating practice was changed and undertaken throughout the year using natural mating with locally recruited crossbred bulls or inseminated with Friesian semen from Livestock development institution (LDI) and Worldwide sire (WWS). Natural mating was also practiced when animals became repeat breeders by teaser bulls. Cows detected in heat were inseminated. Cows not seen in heat within 45-60 days of service were considered pregnant. Borana dams were mated with Friesian semen to produce F1; then backcrossed with 75% Borana x Friesian or Friesian semen to produce 62.5% and the 75% generation, respectively. The later generations F2

(50% F1 dam x 50% F1 sire), F3 (F2 dam x F2 sire), and 75% second generations were produced by inter se mating using 50% and 75% Friesian genotypes (Getahun, 2018).

### 3.5. Data Source and Data Collection

Retrospective types of data on productive and reproductive trait were obtained from the long-term (1982-2020) crossbreeding activity done on Ethiopian Borana and their crosses with Holstein Friesian dairy cattle maintained at the Holetta research station. The recorded data on Borana and on different genetic group ranging from 50% to 75% was used for this study.

Milk production traits include lactation milk yield (LMY), daily milk yield (DMY) and lactation length (LL). While, reproductive trait includes; age at first calving (AFC), calving interval (CI), and number of service per conception (NSC). Age at first calving of each cow was determined from the difference between the date of birth and the date of first calving. Calving interval of each cow was determined from the difference between two consecutive calving. Service required for fruitful conception recorded for each cow was used as number of services per.

### 3.6. Milk Data Collection and Quality Analysis

Laboratory based investigation was done for milk composition. Lactating cows was purposively selected based on their parity and lactation stage. Accordingly, four (4) genotypes were selected 50%F1, 75%F1, 75%F2 and Borana. Milking was done by milking machine twice a day at an equal milking interval at 5:00 AM and 5:00 PM. Morning and evening milk yields for each cow were separately weighed by using a sensitive balance and recorded for 120 days. Milk samples (100 ml each) were collected separately for the morning and evening at monthly interval from each cow and mixed together and thoroughly homogenized by hand and analyzed in duplicate for mixed sample. A sample was taken four (4) times per cow per month for each milking time, i.e. morning and evening time. A mixed analysis was done for the morning and afternoon milk for fat, protein, lactose and solid-not fat (SNF) by using a milk analyzer (Milko-scan) machine at Holetta research center dairy laboratory.

### 3.7. Data Management and Description of Fixed Effects

Data screening was made to avoid manmade errors during data entrance on individual animal card or in the computer writing. During data editing, lactation length below 100 days and above 665 were removed from the data set which regarded as incomplete lactation for analysis of lactation milk yield, daily milk yield and lactation length. The same clearing of data was applied on age at first calving (AFC) below 20 month and above 60 months. Cows have on average 285 days gestation length and 45 days voluntary waiting period after calving (330 days CI). Based on this assumption, cows that recorded below 330 days calving interval (CI) and above 850 were removed from the analysis. Repeat breeder cows more than 5 times were very few compared from the rest of the population and were removed. The animals that have abnormal calving, i.e., abortion and stillbirths were not included in the analysis of breeding data.

The fixed effect included was genetic group, year, season, parity and lactation stage. Genetic group includes seven groups (Borana, 50%F1, 50%F2, 50%F3, 62.5%, 75%F1 and 75%F2).

Due to the erratic nature of crossbred development in the station, the years of calving ranged from 1982 to 2020 were grouped into 7 periods and birth year ranged from 1982 to 2017 were grouped into 6 periods and each grouped year period consists 5 years for convenient analysis of fixed effect.

For season of birth, calving and service, months of the years were classified into 3 seasons based on distribution of rainfall. Dry season: from October to February, short rain season: from March to May and main rain season: from June to September.

For the parity effect lactation records of above eighth parities were pooled together in parity eight because of few records.

Lastly, lactation stage for milk composition were classified into three early (7-90 days), mid (91-180 days) and late above 181.

### 3.8. Statistical Analysis of Fixed Effect

Preliminary data analysis like normality test was employed before conducting the main data analysis. Two models were applied to determine fixed effects and crossbreeding parameters.

Model for fixed effects of genetic group, year, season, parity and lactation stage for milk constituents were conducted using General Linear Model (GLM) procedure of the Statistical Analysis System (SAS, version 9; 2003).

Least square means were estimated for different genotype and other fixed effects (model 1). Differences between least squares means of a trait were tested using the Tukey-Kramer test. Summary of Statistical description on the data set were described under Table 7.

For analysis of crossbreeding parameter (model 2), all fixed effect fitted were similar with model one except genotypes class which was replaced by coefficients of expected breed additive, heterosis and recombination loss were fitted as covariates Table 8.

The multiple regression approach developed by Robison *et al.*, (1981) was used to estimate the contribution of breed additive, heterosis and recombination effects. The breed additive effect for Frisian was estimated as deviations from the Borana breed. The coefficient of breed additive ($g_i$), heterosis ($h_{ij}$) and recombination ($r_{ij}$) effects were calculated according to Wolf *et al.,* (1995)

The equation used to calculate breed additive ($g_i$), heterosis ($h_{ij}$) and recombination loss ($r_{ij}$) effects were as follows:

$$\text{Breed additive}(gi) = 1 \,/\, 2\,(\alpha i^{s} + \alpha_i d)$$

$$Heterosis\left(h_{ij}\right) = \alpha i^{s} \alpha j^{d} + \alpha j^{s} \alpha i^{d}$$

$$Recombination\ loss\left(r_{ij}\right) = 4 g_i g_j - h_{ij}$$

Where:

α = additive, s = sire and d = dam.

Effects of maternal heterosis and recombination were assumed to be negligible in this analysis.

Model used for estimation of different effects

**1.** Statistical model for analysis of lactation milk yield (LMY), daily milk yield (DMY), lactation length (LL) and calving interval (CI) were represented as a follow:

$$Y_{ijkl} = \mu + G_i + P_j + S_k + T_d + \varepsilon_{ijkl}$$

Where: $Y_{ijkl}$ represent performances of LMY, DMY, LL and CI; $\mu$ is overall mean; $G_i$ is fixed effect of $i^{th}$ genotype; $P_j$ is fixed effect of $j^{th}$ period of calving; $S_k$ is fixed effect of $k^{th}$ season of calving; $T_l$ is fixed effect $d^{th}$ parity; $\varepsilon_{ijkl}$ is random residual term.

**2.** Statistical model for analysis of number of service (NSC)

$$Y_{ijkl} = \mu + G_i + P_j + S_k + T_d + \varepsilon_{ijkl}$$

Where: $Y_{ijkl}$ represent performances of NSC; $\mu$ is overall mean; $G_i$ is fixed effect of $i^{th}$ genotype; $P_j$ is fixed effect of $j^{th}$ period of service; $S_k$ is fixed effect of $k^{th}$ season of service; $T_l$ is fixed effect $d^{th}$ parity; $\varepsilon_{ijkl}$ is random residual term.

**3**. Statistical model for analysis of age at first calving (AFC)

$$y_{ijk} = \mu + G_i + P_j + S_k + \varepsilon_{ijk}$$

Where: $y_{ijk}$ represent performance of AFC; $\mu$ is overall mean; $G_i$ is fixed effect of $i^{th}$ genotype; $P_j$ is fixed effect of $j^{th}$ period of birth; $S_k$ is fixed effect of $k^{th}$ season of birth; $\varepsilon_{ijk}$ is random residual term.

**4.** Statistical model for analysis of milk composition trait;

$$Y_{ijkl} = \mu + G_i + L_j + S_k + T_d + \varepsilon_{ijkl}$$

Where; $Y_{ijkl}$ represent individual sample measurement of fat%, protein%, and lactose%, SNF%; $\mu$ is overall mean; $G_i$ is fixed effect of $i^{th}$ genotype; $L_j$ is fixed effect of $j^{th}$ lactation stage; $S_k$ is fixed effect of $k^{th}$ season of calving; $T_l$ is fixed effect $d^{th}$ parity; $\varepsilon_{ijkl}$ is random residual term.

**Model 2.**Genetic model used for estimation of crossbreeding parameters

$$Y_{ijkd} = \mu + P_j + S_k + T_d + G_F^I b1 + H_{FB}^I b2 + R_{fB}^I b3 + \varepsilon_{jkd}$$

Where; $Y_{ijkd}$ is LMY, LL, DMY, CI and NSC; $\mu$ is overall mean; $P_j$ is fixed effect of $j^{th}$ period of calving; $S_k$ is fixed effect of $k^{th}$ season of calving; $T_l$ is fixed effect $d^{th}$ parity;

$G_F^I$ = breed additive genetic effect of Holstein Friesian breed relative to Borana

$H_{FB}^I$ = the expected individual heterosis in the crossbred cow

$R_{fB}^I$ = The expected recombination effect in the individual cow

$b1$= breed additive coefficient of the trait

$b2$= heterosis coefficients of the trait

$b3$= recombination coefficient of the trait

Genetic model used for estimation of age at first calving (AFC)

$$Y_{ijkd} = \mu + P_j + S_k + G_F^I b1 + H_{FB}^I b2 + R_{fB}^I b3 + \varepsilon_{jkd}$$

Where; $Y_{ijkd}$ is AFC; $\mu$ is overall mean; $P_j$ is fixed effect of $j^{th}$ period of birth; $S_k$ is fixed effect of $k^{th}$ season of birth; $G_F^I$ = breed additive genetic effect of Holstein Friesian breed relative to Borana

$H_{FB}^I$ = the expected individual heterosis in the crossbred cow

$R_{fB}^I$ = The expected recombination effect in the individual cow

$b1$= breed additive coefficient of the trait

$b2$= heterosis coefficients of the trait

$b3$= recombination coefficient of the trait

**Table 7:** Summary of Statistical description on the data set

| Variable | N | Mean | Std Dev | Minimum | Maximum |
|---|---|---|---|---|---|
| LMY | 2953 | 2034.76 | 1076.45 | 204.20 | 7352.30 |
| LL | 2953 | 317.72 | 84.28 | 100 | 665 |
| DMY | 2953 | 6.34 | 2.82 | 0.32 | 20.36 |
| CI | 3047 | 474.82 | 121.77 | 330 | 848 |
| NSC | 3037 | 1.68 | 1 | 1 | 5 |
| AFC | 858 | 36.5 | 8.62 | 20.64 | 59.7 |

AFC: age at first calving; CI: calving interval; NSC: number of service per conception LMY: lactation milk yield; LL: lactation length; DMY: daily milk yield; Std Dev: standard deviation.

**Table 8**: Proportion of additive, heterosis and individual recombination effect

| Genetic coefficient | Breed and genetic group | | | | | | |
|---|---|---|---|---|---|---|---|
| | Borana | 50%F1 | 50%F2 | 50%F3 | 62.5% | 75%F1 | 75%F2 |
| $g_i$ | 0 | 0.5 | 0.5 | 0.5 | 0.625 | 0.75 | 0.75 |
| $h_{ij}$ | 0 | 1 | 0.5 | 0.5 | 0.5 | 0.5 | 0.375 |
| $r_i$ | 0 | 0 | 0.5 | 0.5 | 0.438 | 0.25 | 0.375 |

$g_I$; individual additive genetic effect, $h_I$; individual heterosis effect, $r_I$ *individual recombination effect*

# 4. RESULTS AND DISCUSSION

## 4.1 Productive Performance and Effects of Non-genetic Factors

Productive performance of dairy cattle is the most economically interested traits in genetic improvement program for dairy producer worldwide; the productive performance of dairy cattle is judged by milk it produces for specified period of time with daily milk yield over lactation period (Miglior *et al.,* 2017; Wondifraw *et al*., 2013).

### 4.1.1 Lactation milk yield (LMY)

Lactation milk yield is the amount of milk that a cow can deliver during her lactation period. Performance of dairy cows could be judged from the milk it produces during a specified period of lactation (Wondifraw *et al*., 2013).

The analysis of variance of LMY for fixed effects of genetic group, year period of calving, season of calving, and parity were summarized in Table 9. The overall least squares mean and standard error of LMY for the Borana and Borana-Frisian crossbred genetic groups in the present study was 1841.80±34.02 kg, as significantly ($p < 0.0001$) affected by genetic group, year period of calving, season of calving, and parity.  In biological sense the obtained result is low, as the center uses intensive management of production system. This indicates that the inconsistent husbandry practices and lack of culling practices of the farm across the study periods.

Genetic group comparisons revealed that 75%F1 could produce significantly (p <. 0.0001) highest (2989.25±53.47 kg) milk yield per lactation compared with other genetic groups, and the difference was about 27.4%, 46.2%, 51.1%, 34.3%, and 26% more milk than 50%F1, 50%F2, 50%F3, 62.5%, and 75%F2, respectively. This might be due to an upgrading of the level of exotic inheritance from 50%F1 to 75%F1, which consequently increased the milk gene. Furthermore, this result indicates that the level of management (feeding, health, and other husbandry) provided by the farm was good enough to support the crossbred cows in expressing their genetic potential. However, there is no significant difference ($p > 0.05$) between 75%F2 and 50%F1. Furthermore, our findings indicated a decrease in milk yield from 50%F1 to 50%F2 and 50%F3 and from 75%F1 to 75%F2. This might be because of the significant recombination losses (lack of selection of elite sires for inter-Se mating and segregation effect), which causes a decrease in heterosis in inter-se mated generation.

The Calving period had a highly significant ($p < 0.0001$) effect on LMY. The result showed that there were inconsistent trends in LMY from period to period. Comparably, the highest average lactation milk yield was observed during a period from 1994–1999 (2081.47 kg), while the lowest lactation milk yield was recorded during a period from 1988–1993 (1512.89 kg). However, the two periods 2000–2005 and 2006–2011 have no statistical difference from the period 1994–1999. The variation in milk yield from one period to another could be attributed to changes in herd size, composition of the genetic group, and inconsistent management practices from year to year at the center.

The least squares analysis indicated that lactation milk yield was significantly ($p < 0.0001$) affected by the season of calving. Our findings showed that during the two seasons (the dry and main rainy seasons) a higher lactation milk yield was observed compared to the short rainy season. Cows calved during the dry and main rainy seasons likely experienced more favorable environmental conditions and better farm management, leading to significantly ($p < 0.001$) higher milk yields (1878.93±37.54 and 1880.59±43.61 kg), respectively, compared to those calving during the short rainy season. However, there is no significant difference between the dry and main rainy seasons.

The result of the present study showed that parity had a highly significant ($p < 0.0001$) effect on LMY. This suggests that the number of times a cow has calved has a strong effect on her lactation milk yield. According to the present findings, lactation milk yield appears to increase linearly from the 1$^{st}$ (1618.29±38.91) to the 5$^{th}$ (1965.46±60.23) parity, followed by a subsequent decline then after. The gradual increase in lactations milk yield from 1$^{st}$ to 5$^{th}$ parities might be attributed to the growth with respect to body size and increase in the active secretory tissues of udder due to, recurring pregnancies and the decrease, then after might be due to, physiological change as cows age go through multiple lactation cycle, their mammary gland undergo changes and growth of secreting tissue become less pronounced.

Comparatively, the overall obtained result for Borana and Borana-Frisian crossbred genetic groups in the present study is in line with a previous study by Gebreyohannes *et al.,* (2013), who found values of 1836 ± 31.6 kg and 1832 ± 56.0 kg for 50% HF x Horro and 75% Jersey cross Borana, respectively. However, the current result is lower than the study by Kumar *et al.*, (2014) who found a value of 2123.43 ± 65.67 kg for crossbred in Gondar, Ethiopia, and Gebreyohannes *et al.*, (2014) who found a value of 2111.91 ± 16.88 kg for Borana cross Holstein-Friesian in central Ethiopia. Furthermore, this result is higher than the report by Haile *et al*., (2009) who found a value of 1798 ± 25 kg for Borana cross Holstein-Friesian, and Effa *et al.,* (2006) who found a value of 1788 ± 26.5 kg for 50% Jersey x Borana.

In line with the current findings, the superiority of the 75%F1 genotype over 50%F1 was also reported by some other studies (Million and Tadelle, 2003; Haile *et al.,* 2009; Getahun *et al.,* 2020). However, studies by Demeke *et al.,* (2004), Effa *et al.* (2006), and Gebregziabhere *et al*., (2013) could not detect a significant difference between 50% F1 and 75%F1. These contradicting results suggest that further investigation is needed to fully understand the potential advantages of the 75%F1 genotype over the 50% F1 generation. Factors such as environmental conditions, management practices, and genetic variability within the populations studied may have influence on the reported results.

The inconsistent trends of period of calving over LMY was in agreement with the result reported by (Million and Tadelle 2003; Demeke *et al.,* 2004; Getahun, 2018). The fluctuations in milk yield across different periods could be attributed to factors such as feed quality, disease outbreaks, and overall herd health can also play a significant role in the fluctuations of milk yield over time.

Our results suggest that optimizing calving times to coincide with the dry or main rainy seasons could potentially enhance lactation milk yield in dairy cows. Consistent with this study, many scholars have also noted the significant effect of the calving season on lactation milk yield (Demeke *et al.,* 2004; Mohammed, 2007; Getahun *et al*., 2020).

The incremental trends of parity as the age of the cow increased up to 5th parity were in agreement with Gojjam *et al*., (2017), Getahun *et al.,* (2018), and Getahun *et al., (2020)*, and the decrease thereafter was also in agreement with the report by Tadesse *et al.* (2010). In contrast to this result, Janssens *et al*., (2012) reported a decrease in lactation milk yield as parity increased.

### 4.1.2 Lactation length (LL)

Lactation length is an important production trait as it influences the total milk yield. Cows with high milk yield per day of lactation length are cost-effective producers and have extra lactation milk yield (Ayeneshet *et al.,* 2018).

The analysis of variance of LL for fixed effects of genetic groups, year period of calving, season of calving, and parity were summarized in Table 9. The overall least squares mean and standard error of LL for the Borana and Borana-Frisian crossbred genetic groups in the present study was 317.15±3.10 days. The possible reason for this mean of LL in this study might be due to the nature of the data edition being employed, that all lactation below 100 and 665 days were omitted in the analysis, and also other confounding factors such as genotype and all management procedures followed in the farm.

The analysis of variance showed that lactation length was significantly ($p<0.0001$) affected by genetic group. This suggests that genetic factors play a crucial role in determining LL in dairy cattle populations. Accordingly, comparison of genetic groups revealed that among all genetic groups evaluated, 75%F1 has longer LL (364.21±4.89 days), followed by 50%F1 (329.38±2.56 days), whereas indigenous Borana has shorter (270.09±4.69) LL. In another way, the 50%F2 and 50%F3 backcrossed genetic groups showed shorter lactation lengths than other contemporary groups, but their lactation length is comparable with an ideal lactation length of 305 days. In all, there is no significant difference between 50%F2, 50%F3, 62.5%, and 75%F2. This might be due to the breakdown of a favorable gene during gene recombination.

Analysis of variance showed that calving period significantly ($p<0.0001$) affects lactation length. From the current result the longest lactation length (375.76±9.35 days) was occurred during a period from 1982-1987, whereas, the shortest (248.77±5.94 days) was occurred during a period from 2018-2020, this can figure out that there is consistent improvement in management at the farm from period to period to bring standard lactation length (305) for the cow.

Analysis of variance showed that parity significantly ($p < 0.0001$) affects lactation length. The longest lactation length (333.17±3.54 days) was observed in the 1st parity, and the lowest lactation length (284.97±7.76) was recorded in the 8th parity. Statistically, lactation length was decreasing from 1st parity to 8th parity. This means that as the age of the cow increases, LL decreases. Therefore, it is evident from the data that there is a clear trend of decreasing lactation length as parity increases in cows.

Lactation length was not significantly affected ($p > 0.05$) by season of calving. This result is in line with the finding of (Demeke *et al.*, 2004; Effa *et al*., 2006; Haile *et al.,* 2009; Hunde *et al.*, 2015; Getahun, 2018).

The overall least squares mean and standard error of LL obtained in the current study is in line with the findings of Gebreyohannes *et al.*, (2013) 315 ± 0.6 and Gedefa *et al.*, (2019), 314 ±1 days for 50% Jersey x Borana and Arsi-Holstein-Friesian crossbred dairy cattle, respectively. A slightly higher estimation from the present result was reported by Effa *et al.* (2006) 360.76 ± 6.11 days and Hunde *et al.*, (2015) 336±2.3 days. In another way, Belay and Janssens (2014) reported a slightly lower value of 9.13±1.99 months for crossbred dairy cows in Jimma town, Ethiopia. The variation in the length of the lactation period among different studies can be attributed to a multitude of factors such as genetic differences in the breeds studied, management practices, environmental conditions, and nutritional factors.

The significant ($p < 0.0001$) effect of genetic group on LL in the current study is in agreement with the report of Kassa *et al.*, (2020) for Holstein Friesian dairy herd at Elfora Cheffa dairy farm and contradicts with Gedefa *et al*., (2019) for Arsi-Holstein-Frisian crossbred dairy cattle. This variation might be due to variations in the management of the animals, breeds, and models used.

The significance effect of calving period on lactation length in the present study agrees with the report of Heyredin, (2014). Contrarily, Worku *et al*., (2016) and Haile *et al*., (2009a) reported the insignificance of the calving period on lactation length.

The significance effect of parity on lactation length in the current study is supported by many scholars, Haile *et al*., (2009a), Birhanu *et al.*, (2015) and Getahun, (2018). However, Worku *et a*l., (2016) reported non significance effect of parity on lactation length.

### 4.1.3 Daily milk yield

Daily milk yield is a very important production efficiency trait, which is a combination of milk yield and lactation length (Ayeneshet *et al.,* 2018). It is crucial for dairy farmers to monitor and improve daily milk yield in order to maximize their profits and ensure the overall well-being of their cows.

The least square mean and standard error for effects of genetic group, period of calving, season and parity on DMY were summarized in Table 9. The overall least square mean and standard error of DMY for Borana and Borana Frisian crossbred genetic groups in the present study was 5.79±0.08 kg. This is due to different genetic group included in data analyzing including indigenous Borana, number of records, and management under taken.

Genetic group comparison revealed that among all genetic groups evaluated 75%F1 perform the highest (8.34±0.12 kg) daily milk yield. This might be due to an upgrading of the level of exotic gene. There is decreasing trends of daily milk yield from 50%F1 to 50%F2, 50%F3 & 62.5% but, there is no significance difference between 50%F1 and 75%F2. This might be due to reduction of heterosis and increase of recombination loss during breed combination.

Analysis of variance showed that calving period significantly ($p < 0.0001$) affects daily milk yield. There is significant variation in daily milk yield from period to period for the overall study period; this might be due to a gradual change in the genetic group structure of the herd in the farm, as well as management practices and climate change from time to time. Significantly ($p <0.001$) the highest (6.89±0.11 kg) and the lowest (3.93±0.14 kg) of DMY was recorded during the 2012-2017 and 1988-1993 period of calving respectively. The observed increase in DMY from 2000 to 2020 demonstrated the success of implementing improved genetic selection strategies and optimizing management practices to enhance productivity.

Analysis of variance showed that parity significantly ($p < 0.0001$) affects DMY. As observed from the least squares mean, the highest (6.42±0.19 kg) DMY occurred in parity $8^{th}$ and the lowest (4.77±0.09 kg) occurred in parity 1. Comparably, there were increasing trends in DMY from parity one to parity five, but there was no statistical difference between parity $4^{th}$, $5^{th}$, $6^{th}$ and $7^{th.}$ Therefore, DMY increased as parity increased. The present result indicated that cows were produced more milk as they became matured enough associated with secretory tissues of udder and adaptation to lactation stress.

Calving season significantly ($p < 0.0001$) affects DMY. Cows calved during the dry and main rain seasons produced better DMY than during the short rain season. This might be the variation in availability of supplemental feed and access to pasture during the calving period and season, and the variability of weather across years and seasons could be the determinate factors that affect the DMY of the study population.

The overall least squares mean and standard error of DMY obtained in this study is in line with the result of Gebreyohannes *et al.,* (2014) 5.88±0.05 kg for Holstein-Frisian cross Borana and 5.21±0.05 kg for Jersey x Borana. Additionally, it is also comparable with the findings of Haile *et al.,* (2009), 5.3±0.1 for Holstein-Frisian cross Borana. Comparatively, Getahun, (2018), found a higher value of 6.88±0.05 for Holstein-Frisian cross Borana, than the current result. Effa *et al*., (2019) also found a higher value of 12.57±0.08 kg than the current result for Holstein-Frisian and crossbred dairy cattle at large, medium, and small-scale dairy farms in Ethiopia. It is important to note that variations in results across studies can be influenced by factors such as genetic differences in the cattle breeds, management practices, and environmental conditions.

The significance ($p < 0.0001$) effect of genetic group in the present study is comparable with the results of previous studies by Haile *et al.,* (2009), Getahun *et al*.,(2018) and Getahun *et al*., (2020). However, Gebreyohannes *et al*., (2013) reported that upgrading from 50% to higher Friesian fractions for Holstein-Frisian cross indigenous breed have shown no significant differences for daily milk yields.

The significant ($p < 0.0001$) effect of calving period on DMY obtained in the current study is in line with the report of Getahun *et al*., (2020).

These incremental trends of DMY as parity increase were supported by Haile *et al*., (2009) and Getahun *et al*., (2020). This might be related with body growth as cow body increase feeding appetite will increase which increase yield.

The significant ($p < 0.0001$) effect of season of calving obtained in this study is in agreement with the result of Getahun (2018) and contradicts the result of Haile *et al*., (2009), who found the insignificance effect of season of calving on daily milk yield.

Generally, all crossbred genotypes perform much better than indigenous Borana breeds in LMY, LL, and DMY. Crossbred cows outperform Boran cows by 3–6 folds in milk yield per lactation. Further comparison among crossbred genotypes revealed that significantly higher average milk yield was recorded in 75% F1, followed by 75% F2, 50% F1, and 62.5%, than other studied contemporaries. However, there is no significant difference between 75% F2, 50% F1, and 62.5%. On the other hand, there is a reduction in milk yield observed in backcrossed genotypes. The investigated variation in lactation milk yield, lactation length, and daily milk in the current result might be due to the exotic gene effect; this means that as the exotic gene increases, there is an increase in milk yield and a heterosis effect between the crossing of indigenous breeds and high-yielding exotic breeds.

**Table 8:** Least squares means and standard error of lactation milk yield (LMY), lactation length (LL) and daily milk yield (DMY)

| Effect | | Production trait | | |
|---|---|---|---|---|
| | N | LMY(kg) | LL(days) | DMY(kg) |
| Overall | 2953 | 1841.80±34.02 | 317.15±3.10 | 5.79±0.08 |
| CV (%) | | 41.63 | 24.28 | 30.47 |
| Genetic group | | **** | **** | **** |
| Boran | 393 | 487.39±51.53$^{d}$ | 270.09±4.69$^{d}$ | 2.16±0.12$^{e}$ |
| 50%F1 | 1671 | 2170.79±27.74$^{b}$ | 329.38±2.56$^{b}$ | 6.75±0.06$^{b}$ |
| 50%F2 | 224 | 1607.12±61.67$^{c}$ | 305.26±5.62$^{c}$ | 5.45±0.14$^{cd}$ |
| 50%F3 | 134 | 1461.94±78.84$^{c}$ | 304.50±7.18$^{c}$ | 4.91±0.18$^{d}$ |
| 62.5% | 73 | 1963.33±107.27$^{b}$ | 324.32±9.77b$^{c}$ | 6.09±0.24$^{bc}$ |
| 75%F1 | 391 | 2989.25±53.47$^{a}$ | 364.21±4.89$^{a}$ | 8.34±0.12$^{a}$ |
| 75%F2 | 67 | 2212.76±108.51$^{b}$ | 322.32±9.89b$^{c}$ | 6.76±0.25$^{b}$ |
| Period of calving | | **** | **** | **** |
| 1982-1987 | 77 | 1704.28±102.70$^{bc}$ | 375.76±9.35$^{a}$ | 4.72±0.23$^{d}$ |
| 1988-1993 | 218 | 1512.89±62.54$^{c}$ | 362.62±5.69$^{ab}$ | 3.93±0.14$^{e}$ |
| 1994-1999 | 360 | 2081.47±51.31$^{a}$ | 343.88±4.67$^{b}$ | 5.90±0.12$^{c}$ |
| 2000-2005 | 663 | 2047.61±44.79$^{a}$ | 317.80±4.08$^{c}$ | 6.27±0.10$^{b}$ |
| 2006-2011 | 609 | 2062.93±47.65$^{a}$ | 298.26±4.34$^{d}$ | 6.59±0.11$^{ab}$ |
| 2012-2017 | 801 | 1942.43±46.70$^{ab}$ | 272.98±4.25$^{e}$ | 6.89±0.11$^{a}$ |
| 2018-2020 | 225 | 1540.97±65.28$^{c}$ | 248.77±5.94$^{f}$ | 6.20±0.15$^{bc}$ |
| Season of calving | | **** | NS | **** |
| Dry season | 1411 | 1878.93±37.54$^{a}$ | 319.28±3.42 | 5.90±0.09$^{a}$ |
| Short rainy season | 819 | 1765.87±42.34$^{b}$ | 313.95±3.86 | 5.60±0.10$^{b}$ |
| Main rainy season | 723 | 1880.59±43.61$^{a}$ | 318.23±3.97 | 5.86±0.10$^{a}$ |
| Parity | | **** | **** | **** |
| 1 | 826 | 1618.29±38.91$^{a}$ | 333.17±3.54$^{a}$ | 4.77±0.09$^{d}$ |
| 2 | 632 | 1806.38±42.84$^{b}$ | 333.06±3.90$^{a}$ | 5.35±0.10$^{c}$ |
| 3 | 480 | 1860.14±46.68$^{ab}$ | 317.08±4.25$^{b}$ | 5.80±0.11$^{b}$ |
| 4 | 356 | 1919.34±52.21$^{c}$ | 322.08±4.75$^{ab}$ | 5.92±0.12$^{ab}$ |
| 5 | 248 | 1965.46±60.23$^{bc}$ | 320.59±5.48$^{ab}$ | 6.04±0.14$^{ab}$ |
| 6 | 181 | 1886.45±69.06$^{d}$ | 322.45±6.29$^{ab}$ | 5.92±0.16$^{ab}$ |
| 7 | 109 | 1873.10±87.17$^{cd}$ | 303.83±7.94$^{bc}$ | 6.08±0.20$^{ab}$ |
| $8^{+}$ | 121 | 1805.20±85.26$^{e}$ | 284.97±7.76$^{c}$ | 6.42±0.19$^{a}$ |

N: number of observation, LMY: lactation milk yield, LL: lactation length, DMY: daily milk yield, CV: coefficient of variation, F1, 2 &3: first, second & third filial generation, ****= (P<0.0001), NS: not significant (P>0.05), Least squares means with same superscript in the same fixed effect indicate non significance.

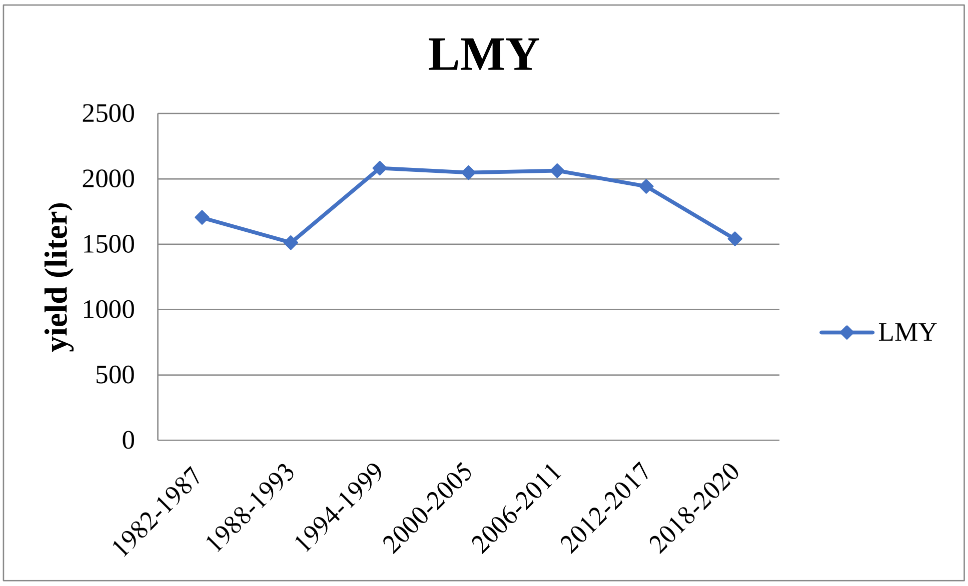


**Figure 2**: Trends of lactation milk yield over study period

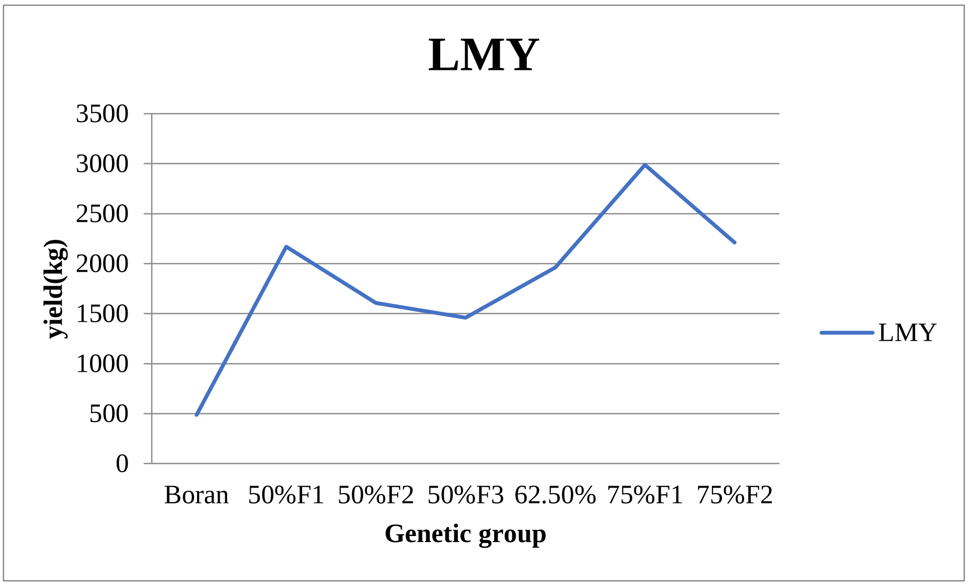


**Figure 3:** Genetic group comparison of lactation milk yield over study period

### 4.2 Reproductive performance and effect of non-genetic factors

Reproductive performance of the cow and heifer is one of the most important factors that influence the profitability of the dairy sector (Haile *et al.*, 2011).

#### 4.2.1 Age at first calving (AFC)

The least squares means and standard errors for the effects of genetic group, period of birth, and season of birth on AFC were summarized in Table 10. The overall least squares mean and standard error of AFC for the Borana and Borana Frisian crossbred genetic groups in the present study were 41.40±0.48 months. The prolonged AFC of Borana and Borana Frisian crossbred genetic groups in the present study could be attributed to factors such as poor nutrition and management practices including poor heat detection at the time of mating the heifers. Additionally, the lack of closely monitored early management given to the heifers at the center makes the heifers delay from an early calving. Excellent level of management allows the growing heifers to reach the suitable body weight for breeding earlier and this in turn leads to lower age at first calving.

List square analysis had shown that among genetic groups, 50%F1 significantly ($p < 0.0001$) had lower (33.93 ±0.44 months) early calving than other contemporary groups, while 62.5% significantly ($p< 0.0001$) had higher (54.09 ±1.85 months) delayed AFC than other contemporary groups. In this study, 50% of the first generation could have significantly ($p < 0.0001$) earlier calving compared with other genetic groups, and the difference was about 6.6%, 7.5%, 25.7%, 26.5%, 28.4%, and 59% earlier calving than 75%F2, 75%F1, Borana, 50%F3, 50%F2, and 62.5%, respectively. This might be due to the accumulation of heterosis effects on 50%F1, and the management given at the center is more favorable for the 50%F1 genetic group than the high-grade genetic group. On the other hand, there is no significance difference between 50%F2 and 50%F3, 75%F1 and 75%F2. This might be due to recombination loss and reduction in heterosis between backcrossed generations.

Analysis of variance revealed that period of birth had highly significant ($p < 0.0001$) effect on AFC. The AFC ranged from (38.98±0.89-46.53±1.37 months) in this study for different period. The heifers which were born in the period from 1994-1999 and 2012-2017 had early calving, whereas the heifers which were born in the period 1982-1987 and 2006-

2011 showed a delay AFC. Significance ($p < 0.05$) reduction of AFC from 46.53±1.37 months in period 1982-1987 to 39.17±0.54 in period 2012-2017 is an implication of progressive improvement in management, replacement of heifers and also adaptation of Frisian gen to the prevailing environment.

Birth season has no significant ($p > 0.05$) effect on AFC in the present study. This is in agreement with other literature reports by Haile *et al.,* (2009), Heyredin, (2014), and Getahun, (2018).

The result obtained in this study is comparable with the results of Haile *et al.*, (2009b) 41 ± 0.7 months for Borana cross Holstein-Friesian. However, this result is lower than the study by Zeleke *et al*., (2016) 52.3 ± 1.77 months for Fogera x Holstein-Friesian. On the other hand, this result is higher than the study by Getahun, (2018) 37.42 ± 0.35 months for Borana cross Holstein-Friesian. Additionally, Haile, (2018) reported lower value of AFC 37 month for Holstein Friesian dairy cows at Alage Dairy Farm. The variation in the result reported by different authors is not only due to breed differences, but there is also a difference for some breeds under the same management due to many factors like feed conversion ability, interaction within the environment, and disease resistance.

The early calving of 50%F1 genotype over upgraded genotype was reported by some other studies conducted in the tropics (Demeke *et al.*, 2004; Haile *et al.*, 2009, Birhanu *et al*., 2015). The main factors for this difference were level of management, genetic composition and other confounding factors such as climate, adaptability to environmental condition and ability to diseases resistance.

The significance ($p < 0.0001$) effect of period of birth on AFC in the present study is in agreement with other literature report in the tropics (Demeke *et al.*, 2004; Haile *et al*., 2009, Birhanu *et al*., 2015; Getahun, 2018; Kassa *et al*., 2020). This effect might be due to the different in breed management, health care, environmental conditions like; temperature, rainfall and humidity, feeding management, and type and availability of basal feed resources at different locations and farms.

**Table 9:** Least square mean and standard error of age at first calving (AFC)

| Effect | N | AFC(months) (LSM ± SE) |
|---|---|---|
| Overall | 858 | 41.40±0.48 |
| CV% | | 20.07 |
| Genetic group | | **** |
| Boran | 29 | 42.65 ±1.41[b] |
| 50%F1 | 446 | 33.93 ±0.44[c] |
| 50%F2 | 83 | 43.56 ±0.84[b] |
| 50%F3 | 60 | 42.92 ±1.01[b] |
| 62.5% | 18 | 54.09 ±1.85[a] |
| 75%F1 | 170 | 36.48 ±0.66[c] |
| 75%F2 | 52 | 36.19 ±1.08[c] |
| Birth period | | **** |
| 1982-1987 | 32 | 46.53±1.37[a] |
| 1988-1993 | 50 | 39.70±1.10[b] |
| 1994-1999 | 98 | 38.98±0.89[b] |
| 2000-2005 | 211 | 40.42±0.67[b] |
| 2006-2011 | 243 | 43.57±0.60[a] |
| 2012-2017 | 224 | 39.17±0.54[b] |
| Birth season | | NS |
| 1 | 407 | 41.45±0.59 |
| 2 | 244 | 41.69±0.62 |
| 3 | 207 | 41.05±0.63 |

AFC: age at first calving, N: number of observation, CV: coefficient of variation, LSM: least square mean, F 1, 2 & 3: first, second & third filial generation. ****= P<0.0001, NS: not significant (P>0.05). Least squares means with same superscript in the same fixed effect indicate non significance.

### 4.2.2 Calving interval (CI)

The least squares mean and standard errors of CI for fixed effects of genetic group, calving period, calving season, and parity were summarized in Table 11. The overall least squares mean and standard error of CI for the Borana and Borana-Frisian genetic groups in this study were 487.71±5.20 days. This longer CI is the result of longer lactation length which could be related to poor management of the existing farm including poor breeding management and lack of closely monitoring the herd, like estrus detection, estrus synchronization, and overall fertility management.

Analysis of variance revealed that genetic group had highly significant ($p < 0.0001$) effect on CI. List square analysis had shown that among genetic group, 50%F1 had shorter

(445.74±4.21) CI than other genetic groups, whereas, 62.5% had longer (530.29±16.53) CI, even longer CI than indigenous Borana. 50%F1 perform shorter calving interval than other contemporary groups and the difference was about 13.95%, 2.62%, 19%, 6.14%, 11% and 12.25% shorter calving interval than 75%F1, 75%F2, 62.5%, 50%F3, 50%F2 & Boran respectively. This is due to accumulation of heterosis effect on 50%F1.

Least squares mean displayed that calving period had highly significant ($p < 0.0001$) effect on CI. There were fluctuations from period to period which indicate that there is inconsistence husbandry practice given to herd at farm from year to year.

Least squares mean displayed that no significant ($p > 0.05$) difference was observed between calving seasons. This is in agreement with the findings of (Haile *et al*., 2009b; Tadesse and Dessie, 2003; Habtamu *et al.* 2009).

The other effect is parity effect which showed highly significant ($p < 0.0001$) effect on CI as observed from least square mean Table 11. The trend of CI was a gradually declined from parity one to parity three and has some fluctuation after parity three fig 5. The decrease in CI as parity increase was due to the ability of the animal to recover the uterine environment within shorter periods as age increases and adaptation to parturition and lactation stress.

The result obtained in this study is comparable with the report by Effa *et al.*, (2006) 481.30 ± 25.73 days for Jersey and Borana-Frisian crosses, and Getahun, (2018) 476.35 ± 3.91days for Borana-Frisian crosses. Additionally, it also close to the study by Wassie *et al.*, (2015) 475.92 ± 3.44 days for Arsi and Boran crossed with Holstein-Frisian and Effa *et al.*, (2011) 472.8 ± 8 days for Borana cross Holstein-Frisian and Jersey. However, *Haile et al*., (2009) reported lower value of 435 ± 11 days for Holstein-Frisian Crosses. On the other hand, the current result is lower than the findings of Ayalew *et al.*, (2018) who found a value of 20.19±1.62 months for crossbred in tropical highland . The variation of the present finding from other literatures might be due to, herd composition, management practice, climate, and geographical differences across the study area.

The significance ($p < 0.0001$) effect of genetic group on CI in the present study is in line with the findings of (Haile *et al*., 2011; Getahun, 2018; Hunde *et al.*, 2022). Furthermore, the superiority of 50%F1 in calving interval than other contemporary groups in the current study were supported by (Tadesse and Dessie, 2003; Haile *et al*., 2011; Hunde *et al*., 2022). This is due to genetic composition and management effect which effects overall fertility trait.

Least squares mean displayed that calving period had highly significant ($p < 0.0001$) effect on CI. This significance effect is in line with findings of (Tadesse *et al*., 2010; Mengistu *et al.* 2016; Kassa, 2018; Getahun, 2018). However the current result was contradicted with the findings of Zeleke *et al.*, (2016) for Fogera cross Holstein-Friesian. This difference might be due to breed (genotype), management and other confounding effects.

The significance ($p < 0.0001$) effect of parity on CI is parallel with the studies by (Tadesse *et al.*, 2010; Wassie *et al.* 2015; Mengistu *et al*. 2016; Kassa *et al*., 2020). However this result contradict with the findings of Haile *et al*., (2009).

Generally, the CI in the present study is longer than the generally accepted calving interval of 365 days expected on a commercial dairy farm. In fact, the extended calving interval observed in this study may have significant implications for overall herd productivity and reproductive efficiency. A longer CI could result in decreased milk production per cow over time, as well as potentially impacting the overall profitability of the dairy operation. This longer CI is the result of longer lactation length which could be related to poor management of the existing farm including poor breeding management. In addition, the extended calving interval may also be influenced by factors such as suboptimal nutrition, health issues among the herd, or environmental stressors.

**Table 10:** Least square mean and standard error of calving interval trait (CI)

| Effect | N | CI(days) (LSM ± SE) |
|---|---|---|
| Overall | 3047 | 487.71±5.20 |
| CV% | | 24.25 |
| Genetic group | | **** |
| Boran | 1094 | 500.35±4.69$^{ab}$ |
| 50%F1 | 1352 | 445.74±4.21$^{c}$ |
| 50%F2 | 152 | 499.13±9.93$^{ab}$ |
| 50%F3 | 86 | 473.11±13.04$^{abc}$ |
| 62.5% | 54 | 530.29±16.53$^{a}$ |
| 75%F1 | 267 | 507.92±8.27$^{ab}$ |
| 75%F2 | 42 | 457.42±18.33$^{bc}$ |
| Calving period | | **** |
| 1982-1987 | 44 | 540.47±18.13$^{a}$ |
| 1988-1993 | 182 | 486.99±9.32$^{bc}$ |
| 1994-1999 | 279 | 463.13±7.65$^{d}$ |
| 2000-2005 | 639 | 486.21±6.47$^{c}$ |
| 2006-2011 | 743 | 504.96±6.36$^{b}$ |
| 2012-2017 | 810 | 447.13±6.36$^{e}$ |
| 2018-2020 | 350 | 485.08±7.56$^{c}$ |
| Calving season | | NS |
| Dry season | 1395 | 486.65±5.65 |
| Short rainy season | 885 | 486.82±6.17 |
| Main rainy season | 767 | 489.66±6.29 |
| Parity | | **** |
| 1 | 783 | 524.58±5.96$^{a}$ |
| 2 | 645 | 502.55±6.30$^{b}$ |
| 3 | 507 | 480.26±6.78$^{c}$ |
| 4 | 395 | 486.20±7.45$^{bc}$ |
| 5 | 302 | 476.31±8.11$^{c}$ |
| 6 | 206 | 482.42±9.44$^{bc}$ |
| $7^{+}$ | 209 | 461.65±9.66$^{c}$ |

CI: calving interval, N: number of observation, CV: coefficient of variation, LSM: least square mean, F 1, 2 & 3: first, second & third filial generation. ****= P<0.0001, NS: not significant (P>0.05). Least squares means with same superscript in the same fixed effect indicate non significance.

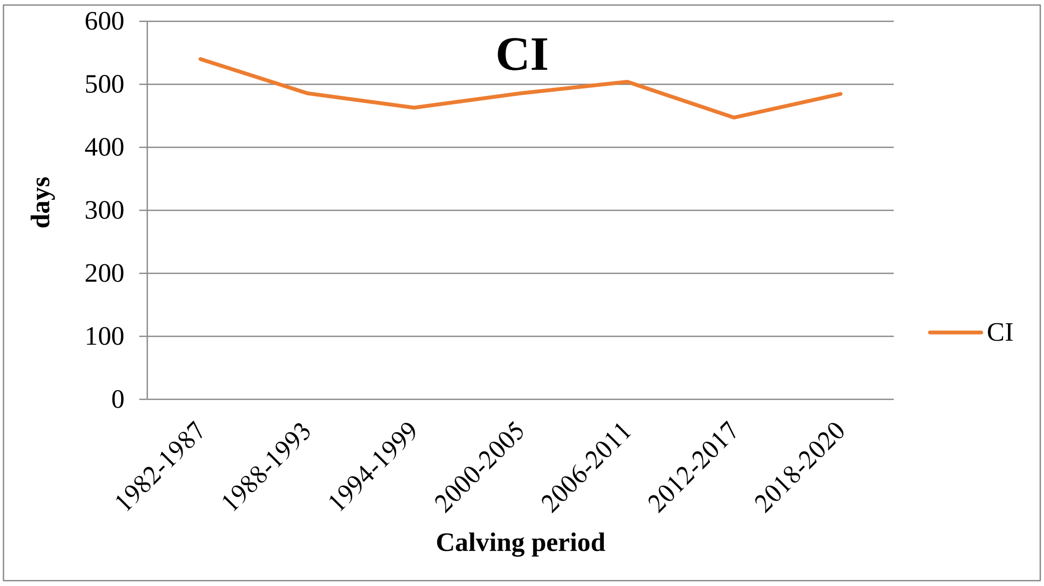


**Figure 4:** Trends of calving interval over the study period

### 4.2.3 Number of Service per Conception (NSC)

The least square means and standard errors of NSC for fixed effects of genetic group, service period, service season and parity were summarized in Table 12. The overall least square means and standard errors of NSC obtained for Boran and Borana- Friesian genetic group in the current study was 1.69±0.04. The obtained result is somewhat good as it is below the two services per conception. The main factors for this is monitored culling practice at the center of highly repeat breed and using different breeding system (natural mating and artificial insemination) and what else like ability of AI technician.

Analysis of variance revealed that Number of services per conception is not significantly ($p > 0.05$) affected by genetic group and parity. The insignificance ($p > 0.05$) effect of parity on NSC in the present study is in line with study by Getahun, (2018) and Tesfa *et al.,* (2016).

Analysis of variance demonstrated highly significant ($p < 0.0001$) effect of service period and Service season on NSC. The significant difference in period of service and season of service on NSC in the present study might be due to variation of heat detection, skill of inseminator, time of insemination, semen quality, silent ovulation of cows, inconsistent management (feeding) and environmental variability. The lowest NSC was recorded during a period from 1982-1987 (1.32±0.10) and the highest one was recorded during a period from 2018-2019 (1.99±0.07). Trend analysis has shown that there is increasing trends of number of service per conception from initial period to the current period fig 6.

Animal served during dry (1.60±0.04) and main (1.68±0.04) rainy season had less service for conception than those served during short (1.80±0.05) rainy season. However, there was no significance ($p > 0.05$) difference between the herd which were inseminated during dry and main rainy season.

The current result is comparable with the study by Ayeneshet *et al.*, (2018) 1.68 ± 0.60 for indigenous dairy cows under smallholder farmers management system and Dabi and Kebede, (2015), 1.69±0.07 and 1.75 ± 0.11 for Holstein-Frisian cross Horro and Jersey cross Horro respectively at Bako research center, and Effa *et al.*, (2006) 1.68 ± 4 for 50% Jersey crosses (F2), and Alemneh *et al*., (2015) 1.67 ± 0.04 from the on-farm survey of Holstein-Frisian crosses around Adigrate area. However, the current result is lower from the study by Getahun, (2018) 1.97±0.09 for Borana cross Holstein-Frisian crossbred and Hunde *et al*., (2015) 2.02±0.02 for Jersey breed and Haile *et al*., (2009) 2.33±0.1 for Borana cross Holstein-Frisian. This result is slightly higher than the report by Worku *et al.*, (2016) 1.30±0.06 for Holstein-Frisian, and Wassie *et al*.,(2015) 1.32±0.06 for Holstein-Frisian cross Arsi.

The significant effect of service period ($p < 0.0001$) observed in the present study is in agreement with findings of (Haile *et al.*, 2009b; Mengistu *et al*., 2016; Getahun, 2018; Beneberu, 2020). The significance effect of season of service ($p < 0.0001$) on NSC in the present study is in line with findings of Wassie *et al*., (2015) for Holstein-Frisian cross Borana and Holstein-Frisian cross Arsi and Habtamu *et al*., (2010) for Jersey breed. However, this result contradict with the findings by Mengistu *et al*., (2016).

In conclusion, the result of NSC found in this study suggests comparatively better result from most of the previous study done at the center. This might be due to semen quality, use of reproductive technology, heat detection ability and individual skill difference of AI technicians. Furthermore, favorable environmental condition in the center makes more animals to have first service.

**Table 11:** Least square mean and standard error of number of service per conception trait

| Effect | N | NSC (LSM ± SE) |
|---|---|---|
| Overall | 3037 | 1.69±0.04 |
| CV% | | 58.10 |
| Genetic group | | NS |
| Boran | 83 | 1.86±0.11 |
| 50%F1 | 1926 | 1.67±0. 03 |
| 50% F2 | 249 | 1.65±0.07 |
| 50%F3 | 160 | 1.73±0. 08 |
| 62.5% | 76 | 1.58±0. 12 |
| 75%F1 | 456 | 1.80±0.06 |
| 75%F2 | 87 | 1.56±0.11 |
| Service period | | **** |
| 1982-1987 | 119 | $1.32{\pm}0.10^{d}$ |
| 1988-1993 | 244 | $1.59{\pm}0.07^{c}$ |
| 1994-1999 | 269 | $1.83{\pm}0.06^{ab}$ |
| 2000-2005 | 538 | $1.62{\pm}0.06^{c}$ |
| 2006-2011 | 695 | $1.69{\pm}0.06^{bc}$ |
| 2012-2017 | 901 | $1.78{\pm}0.05^{b}$ |
| 2018-2019 | 271 | $1.99{\pm}0.07^{a}$ |
| Service season | | **** |
| Dry season | 1300 | $1.60{\pm}0.04^{b}$ |
| Short rainy season | 667 | $1.80{\pm}0.05^{a}$ |
| Main rainy season | 1070 | $1.68{\pm}0.04^{b}$ |
| Parity | | NS |
| 1 | 743 | 1.70±0.05 |
| 2 | 684 | 1.65±0. 05 |
| 3 | 502 | 1.66±0. 05 |
| 4 | 363 | 1.59±0.06 |
| 5 | 268 | 1.60±0.07 |
| 6 | 186 | 1.70±0.08 |
| 7 | 133 | 1.82±0.09 |
| 8 | 158 | 1.80±0.09 |

NSC: number of service per conception, N: number of observation, CV: coefficient of variation, NS: not significant (P>0.05), ****= P<0.0001. Least squares means with same superscript in the same fixed effect indicate non significance.

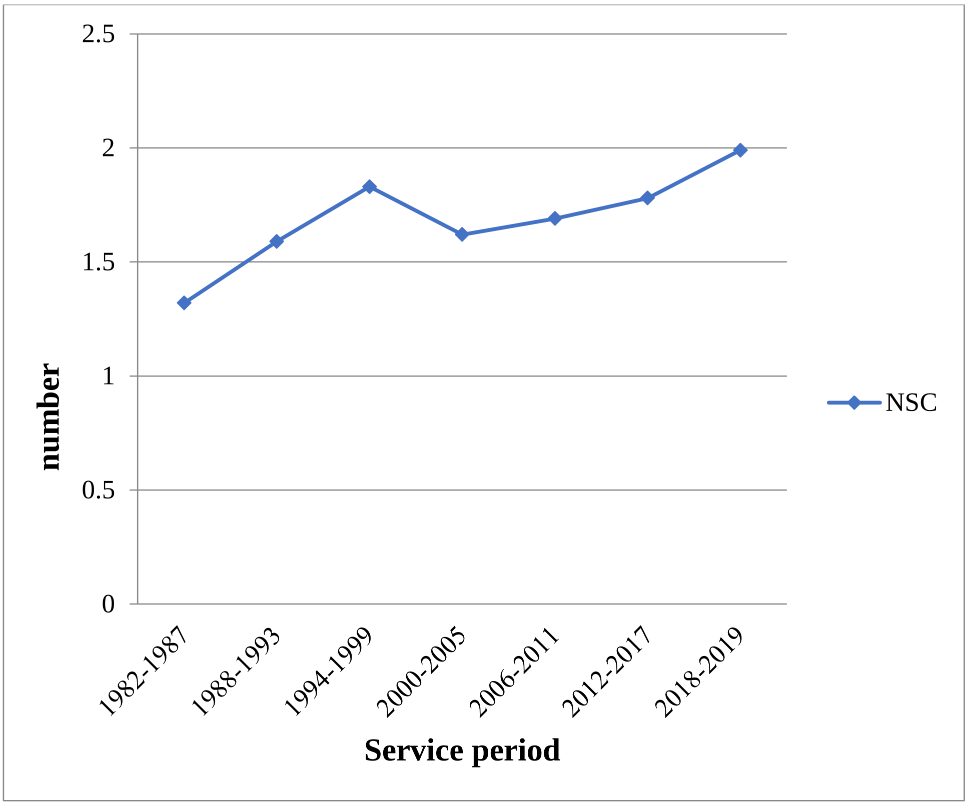


**Figure 5:** Trends of number of service per conception over service period

### 4.3 Milk composition

Knowledge of milk components is crucial for ensuring the health and safety of the consumer, as well as for the economic and innovative growth of the dairy industry (Lemma *et al*., 2018).

### 4.3. Effect of genotype, parity, season, and lactation stage on milk constituents.

The least squares mean and standard errors of fat, protein, lactose, and solid not fat (SNF) content for fixed effects of genetic group, parity, season, and lactation stage were summarized in Table 13. The overall least squares mean for milk fat, protein, lactose, and solid not-fat content in the current study were 3.85±0.14, 3.29±0.14, 4.73±0.06 and 8.63±0.14 respectively Table 13. The obtained result is low due to the genetic group included and the season of sampling. The genetic group included in the study had a significant impact on the milk fat content, with certain groups exhibiting consistently lower levels compared to others. Additionally, the season of sampling played a role in the results, as milk fat content can vary depending on factors such as diet, and weather conditions.

The overall result obtained for different constituents in the current study were meet with recommended level of whole raw cow milk composition set by Ethiopian standard agency ESA,(2009). The minimum fat percent and protein percent, for whole cow milk recommended by the Ethiopian Standards Agency (ESA) should not be less than 3.5% and 3.2% respectively ESA, (2009). The overall result for both fat content and protein content in the current study is higher than the minimum recommended level set by ESA. Additionally, the overall result for both lactose content and SNF content is higher than the minimum recommended level set by the European Union Quality standards for unprocessed whole milk. Accordingly, the lactose content should not be less than 4.2 percent and SNF is 8.5 percent Tamime, (2009). The overall least square mean in the current study is lower than the findings of Mohamed *et al*., (2023) for fat content 4.67±0.001 and lactose content 5.18±0.001, and similar result for both protein content 3.45±0.01 and SNF content 8.52±0.01. Mesfin and Getachew, (2007) also reported higher 6.01%, and 4.05% result than the current results for fat and protein content respectively. The result of fat content obtained in the current result is also lower than the report by Zelalem *et al*., (2004) who indicated a value of 5.43% and Alganesh *et al*., (2007), 6.05%.

Least square mean showed that fat content was significantly ($p < 0.001$) affected by genetic group. Among genotype evaluated Borana breed had significant ($p < 0.001$) higher percentage of fat content followed by 50%F1. The variations in fat content between breeds of cow is an inherited character which implies that breeds with higher fat content produce less milk quantity than those with low fat content. The significance effect of genetic group on fat content were in agreement with several studies conducted elsewhere in the tropics (Mesfin and Getachew, 2007; Bobbo *et al.*, 2014; Senbeta, 2018).

The variations in fat content between breeds of cow is an inherited character which implies that breeds with higher fat content produce less milk quantity than those with low fat content (Mesfin and Getachew, 2007). Accordingly, the indigenous Boran breed significantly produce higher percentage of fat, protein, lactose and SNF compare to the other contemporary groups; whereas, among crossbred genotype the 50%F1 produce higher percentage of fat than 75%, but there is no significance difference between crossbred genotype for protein percentage. There is significance difference between crossbreed genotype for lactose and SNF percentage. 75%F1 genetic group produce higher percentage of lactose and SNF than both 50%F1 and 75%F2, whereas, there is no significance difference between both 50%F1 and75%F2.

There is no significance ($p > 0.05$) effect of parity, season and lactation stage on fat, protein, lactose, and SNF this might be demonstrate that similar management of the farm across all the season.

In all the overall result obtained in the current study fulfills the recommended range, even though, it is below average for the high grade genetic groups. This might be due to, within breed difference, between breed difference, gene segregation, feeding, free access for water, pasture, and all management aspects given for the herd.

**Table 12**: Effect of genotype, parity, season, and lactation stage on milk composition

| Effect | N | Fat | Protein | Lactose | SNF |
|---|---|---|---|---|---|
| Overall | 40 | 3.85±0.14 | 3.29±0.14 | 4.73±0.06 | 8.63±0.14 |
| CV% | | 18.06 | 6.62 | 6.76 | 8.13 |
| Genotype | | *** | *** | * | * |
| Boran | 10 | 5.6±0.31[a] | 3.94±0.10[a] | 5.04±0.14[a] | 9.24±0.38[a] |
| 50%F1 | 10 | 4.15±0.36[b] | 3.05±0.11[b] | 4.63±0.16[b] | 8.46±0.36[ab] |
| 75%F1 | 10 | 2.81±0.35[c] | 3.15±0.11[b] | 4.80±0.16[ab] | 8.75±0.35[ab] |
| 75%F2 | 10 | 2.85±0.31[c] | 3.02±0.10[b] | 4.46±0.14[b] | 8.04±0.31[b] |
| Parity | | Ns | Ns | Ns | Ns |
| 1 | 6 | 3.5±0.35 | 3.37±0.11 | 4.92±0.16 | 9.01±0.35 |
| 2 | 4 | 5.08±0.47 | 3.62±0.15 | 5.23±0.21 | 9.79±0.48 |
| 3 | 6 | 4.37±0.26 | 3.20±0.08 | 4.74±0.12 | 8.63±0.26 |
| 4 | 6 | 3.61±0.30 | 3.41±0.09 | 4.75±0.13 | 8.58±0.30 |
| 5 | 4 | 4.57±0.58 | 3.12±0.15 | 4.34±0.22 | 7.90±0.48 |
| 6 | 5 | 3.14±0.59 | 3.13±0.18 | 4.39±0.27 | 7.87±0.59 |
| 7 | 4 | 3.55±0.68 | 3.20±0.21 | 4.68±0.31 | 8.5±0.68 |
| 8 | 5 | 2.97±0.51 | 3.29±0.16 | 4.81±0.23 | 8.73±0.5 |
| Season | | Ns | Ns | Ns | Ns |
| Dry season | 19 | 3.81±0.20 | 3.38±0.06 | 4.82±0.09 | 8.83±0.19 |
| Short rainy season | 12 | 4.03±0.28 | 3.26±0.09 | 4.52±0.13 | 8.20±0.28 |
| Main rainy season | 9 | 3.72±0.33 | 3.24±0.10 | 4.86±0.15 | 8.85±0.35 |
| Lactation stage | | NS | NS | NS | NS |
| Early | 13 | 3.10±0.28 | 3.35±0.09 | 4.66±0.13 | 8.46±0.28 |
| Mid | 10 | 3.95±0.21 | 3.20±0.06 | 4.68±0.09 | 8.52±0.21 |
| Late | 17 | 3.61±0.34 | 3.33±0.11 | 4.86±0.15 | 8.91±0.34 |

N: number of observation, CV: coefficient of variation, NS: not significant (P>0.05), ***= P<0.001, *=P<0.05. Least squares means with same superscript in the same fixed effect indicate non significance.

### 4.4 Crossbreeding parameters

Accurate estimation of crossbreeding parameters (breed additive and non-additive) effects and separation of their direction of effect is essential for development of breeding programs in the way that it sets the design to be implemented and fully exploit the value of crossbreeding (Schoeman and Jordaan 1999).

#### 4.4.1 Effect of additive, non-additive and recombination loss on milk Production trait

The effect of parity and period of calving were significant ($p < 0.0001$) on LMY, LL and DMY. Similarly season of calving were significant ($p < 0.0001$) on LMY and DMY. Estimates of crossbreeding parameters for breed additive, heterosis, and recombination effects on LMY, LL, and DMY were presented in Table 15. The breed additive effect of Holstein-Friesian breed compared to Borana was 3939.55±156.18 kg for LMY, 154.73±14.07 days longer for LL and 8.89±0.35 kg for DMY. These estimates indicate a substantial breed additive effect of the Holstein Friesian breed over Borana in terms of LMY, LL, and DMY. These values suggest a significant ($p < 0.0001$) advantage of the Holstein Friesian breed in terms of milk production compared to the Boran breed, due to gene effect.

Crossbreeding Holstein Frisian with Boran showed a significant ($p < 0.05$) heterosis effect on LMY and LL, while it had an insignificant effect ($p > 0.05$) on DMY. Heterosis effects, as deviations from mid-parent values in this study, were -241.36±80.34, -17.41±7.24, and 0.26±0.18 for LMY, LL, and DMY, respectively. The results suggest that crossbreeding Holstein Frisian with Borana has a notable effect on certain traits such as LMY and LL, indicating potential benefits in terms of milk yield and lactation length. These findings highlight the complexity of heterosis effects and the importance of considering specific traits when evaluating the outcomes of crossbreeding programs.

The loss resulting from the recombination of Holstein Friesian and Borana genes was highly significant ($p < 0.0001$), estimated at -1547.34±149.26, -76.01±13.45, and -2.65±0.33 for LMY, LL, and DMY, respectively. These results indicate a significant influence of genetic recombination on important production traits in the crossbreeding of Holstein Friesian with Borana breed in the current study. The loss due to recombination of gene might be attributed to the decline in performance from F1 to F2 or back cross generations.

Our findings regarding the effects of additive, heterosis, and recombination loss generally in agreement with previous literature (Kahi *et al*., 2000; Demeke *et al*., 2004; Birhanu *et al.,* 2015; Getahun, 2018; Hunde *et al.,* 2022). The main difference lies in the numerical values; for example, Getahun, (2018) estimated a lower breed additive value for LMY (2674 kg), LL (88 days), and a comparable value for DMY (7 liters) compared to our current findings. Similarly, Birhanu *et al.*,(2015) reported lower breed additive values for LMY (2040 kg), LL (85 days), and DMY (5 liters). Consistent with our results, Hunde *et al.*, (2022) found higher breed additive values for LMY (3985 kg) and LL (166 days) in Borana-Friesian crossbred. Additionally, this author also found lower breed additive value for LMY (1195 kg) and LL (18 days) for Borana-Jersey crossbred.

Our observation of a negative and significant heterotic effect on LMY and LL agrees with Hunde *et al*., (2022) who noted a negative and significant heterotic effect on Borana-Friesian crossbred on LMY (-150 kg) and LL (-7). Conversely, Birhanu *et al.,* (2015) reported a positive and significant heterotic effect of Borana-Friesian crossbred on LMY (899 kg), LL (43 days), and DMY (2.78). In contrast to our findings, Getahun (2018) reported a non-significant heterotic effect of Borana-Friesian crossbred on LL.

The highly significant ($p < 0.0001$) recombination loss of Borana-Friesian crossbred on LMY, LL, and DMY in the current study is lower compared to the findings of Getahun, (2018) -1902kg, -91 days, and -4 liters for LMY, LL, and DMY respectively. On the other hand, Birhanu *et al.*, (2015), reported a lower recombination loss of -586 kg, -25 days, and -0.61 liters for LMY, LL, and DMY on Borana-Friesian crossbred. These results suggest that the impact of recombination effect varies across different traits, with LMY, LL, and DMY showing substantial losses attributed to this effect.

The variation detected between the current findings and other findings obtained from literature could be attributed to the difference on genetic basis of the breed and gene combining ability. The reason for large breed additive and smaller heterosis effect obtained in the current study could be resulted from good production environment at the center. Furthermore, Cunningham and Syrstad, (1987) stated that when there is substantial difference between the F1 and indigenous breed, it is likely that there is genotype by environmental interaction, where production in poor environment is influenced heavily by heterosis. Those authors finally concluded that in crossbreeding between Bos Taurus and Bos Indicus breeds in the tropics additive effects could be more important than heterosis effects in suitable environments. To sum up, breed additive, heterosis and recombination effect obtained in the current study fulfilled the requirement for crossbreeding between Bos Taurus and Bos Indicus in tropics

**Table 13:** Estimate of contribution of additive, Heterosis and recombination loss for lactation milk yield (LMY), lactation length (LL) and daily milk yield (DMY)

| Breed | Production traits (Estimates ± SE) | | |
|---|---|---|---|
| | LMY(kg) | LL(days) | DMY(kg) |
| B | 487.39±51.53 | 270.09±4.69 | 2.16±0.12 |
| $G_F^E$ | 3939.55±156.18*** | 154.73±14.07*** | 8.89±0.35*** |
| $H_{FB}^E$ | -241.36±80.34** | -17.41±7.24* | 0.26±0.18$^{ns}$ |
| $R_{fB}^E$ | -1547.34±149.26*** | -76.01±13.45*** | -2.65±0.33*** |

B=Borana, F=Friesian, $G_F^E$=expected breed additive contributions of F relative to B, $H_{FB}^E$=expected heterosis effect of crossing F with B, $R_{fB}^E$= expected recombination loss when crossing F with B, LMY=lactation milk yield, LL= lactation length, DMY= daily milk yield, *p < 0.05, **p < 0.01, ***p < 0.0001, ns= not significant (p > 0.05).

### 4.4.2 Effect of additive, non-additive and recombination on reproductive traits

The effect of parity and period of calving were significant (p < 0.0001) on CI. Similarly season of service and period of service were significant (p < 0.0001) on NSC; and AFC was significantly (p < 0.0001) affected by period of birth. Estimates of breed additive, heterosis and recombination effect for calving interval (CI), number of service per conception (NSC) and age at first calving (AFC) in the present study were summarized in Table 16. The corresponding estimate values of breed additive on CI, NSC and AFC were 33.59±22.53 days, 0.15±0.18 and -6.57±2.25 months respectively. The breed additive contribution of Holstein Friesian on CI and NSC is not significant (p > 0.05), whereas, it was significant on AFC.

The breed additive contribution of Holstein Friesian on AFC is significant (p < 0.01). The significant effect of breed additive on AFC obtained in the current result is in agreement with findings of Hunde *et al.*, (2022). In contrast to the current findings Birhanu *et al.*, (2015) reported non-significant additive effect on AFC. This result indicated that the individual additive contribution of Friesian breed for the improvement of reproductive performance of the progeny was only negatively significant ($p < 0.001$) for AFC and positively non-significant for CI and NSC, which might be figure out that small additive effect of Holstein Friesian breed for these traits.

The estimate for direct heterosis in the present study was negative and significant ($p < 0.0001$) for CI and also negative and significant ($p < 0.001$) for NSC. However, there is negative and non-significant direct heterosis effect on AFC. The corresponding estimate values of direct heterosis effect were -72.06±11.59 days, -0.31±0.11 and -1.32±1.36 months for CI, NSC and AFC respectively. The negative and significance effect of direct heterosis on calving interval in the present study is comparable with the findings of Birhanu *et al.*, (2015) -70.14±27.88 days and Hunde *et al.*, (2022) -88.7±13 days on Borana Frisian crosses. The negative and significant effect of direct heterosis on NSC in the present study is not in line with the findings of Getahun, (2018) who found negative and non-significance (-0.2 ± 0.2) effects.

The loss due to recombination of Frisian and Borana breed for CI is non-significant whereas, negative and significant ($p < 0.05$) for NSC, and it is positive and highly significant ($p < 0.0001$) for AFC. The non-significance recombination effects of Friesian cross Boran on CI and significant recombination effect of Friesian cross Boran on AFC in the present study is in line with the findings of Hunde *et al.*, (2022). On the other hand, Birhanu *et al.*, (2015) found that non-significant recombination effect on CI which is similar to our results; in addition to this he reported non-significance effect of recombination on AFC which is different from our results.

In all, the Contradictory results in literatures and the present findings for breed additives, heterosis and recombination loss might be due to, different reason such that, genetic potential of breeds, breaking up of epistatic, data size and breed composition of animal included in data analyzing procedure. It was estimated from our results that higher heterosis effect was obtained for calving interval and number of service per conception, whereas higher recombination loss was obtained for age at first calving. The contribution of Frisian breed to the improvement of reproduction trait (CI & NSC) was mainly due to, heterosis effect but it was due to breed additive for age at firs calving.

**Table 14:** Estimate of contribution of additive, Heterosis and recombination loss for calving interval (CI), number of service per conception (NSC) and age at first calving (AFC)

| Breed group | Reproduction traits (Estimates ± SE) | | |
|---|---|---|---|
| | CI | NSC | AFC |
| B | 550.98±25.32 | 2.58±0.72 | 28.65±2.18 |
| $G_F^E$ | 33.59±22.53 $^{ns}$ | 0.15±0.18 $^{ns}$ | -6.57±2.25** |
| $H_{FB}^E$ | -72.06±11.59*** | -0.31±0.11** | -1.32±1.36 $^{ns}$ |
| $R_{fB}^E$ | 23.01±23.23 $^{ns}$ | -0.34±0.18* | 19.32±2.23*** |

B=Borana, F= Friesian, $G_F^E$=expected breed additive contributions relative to B, $H_{FB}^E$= expected heterosis effect of crossing F with B, $R_{fB}^E$= expected recombination loss when crossing F with B, CI= calving interval, NSC= number of service per conception, AFC = age at first calving, *p < 0.05, **p < 0.01, ***p < 0.0001 ns= not significant (P>0.05).

# 5. SUMMARY AND CONCLUSION

The present study was designed to evaluate non-genetic and crossbreeding parameters on the performance of Borana and Borana-Frisian crossbred dairy cattle with different exotic inheritance at Holetta Agricultural Research Center. Methodologically, two types of data set were used for this study. For both productive and reproductive trait retrospective type of data was used from the long-term (1982-2020) recorded data kept at the center, whereas, laboratory based investigation was used for milk composition.

The fixed effect analyzed had shown significance ($p < 0.0001$) effects of genetic group, parity, period of calving and season of calving on lactation milk yield (LMY), lactation length (LL), daily milk yield (DMY) and calving interval (CI). Only LL and CI does not affected by season of calving. Age at first calving (AFC) was significantly ($p < 0.0001$) affected by genetic group and period of birth. Number of service per conception (NSC) was significantly ($p < 0.0001$) affected only by period of service and season of service. The overall least squares mean obtained were 1841.80±34.02kg, 317.15±3.1days, 5.79±0.08 liter, 487.71±5.20 days, 41.40±0.48 months and 1.69±0.04 for LMY, LL DMY CI, AFC, and NSC respectively.

Fixed effect analyzed had shown only genetic group has significant effect ($p < 0.05$) on fat, protein, lactose and SNF contents. The overall least squares mean for fat, protein lactose and SNF content were 3.85±0.14%, 3.29±0.14%, 4.73±0.06% and 8.63±0.14% respectively.

The extent of breed additive and heterotic contribution is varied among traits in this study. Accordingly, breed additive significantly ($p < 0.0001$) affect LMY, LL and DMY, with estimate value of 3939.55±156.18 kg, 154.73±14.07 days and 8.89±0.35 kg respectively. The contribution of breed additive on CI and NSC is not significant ($p > 0.05$) and estimated as 33.59±22.53 days and 0.15±18 respectively. However, it is significant ($p < 0.001$) on AFC with estimate of -6.57±2.25 months.

The heterosis effects expressed as deviation from mid parent estimated were -241.36±80.34 kg, -17.41±7.24 days, and 0.26±0.18 kg for LMY, LL, and DMY respectively, with a significant ($p < 0.05$) effect on LMY and LL and no significant ($p > 0.05$) effect on DMY. There was a significant ($p < 0.001$) heterotic effect on CI and NSC, but non-significant ($p > 0.05$) heterotic effect on AFC. The estimated heterotic deviations from mid parent were -72.06±11.59 days, -0.31±0.11, and -1.32±1.36 months for CI, NSC, and AFC respectively.

The loss due to recombination effect of the two breeds was significant ($p < 0.0001$) and estimated at -1547.34±149.26 kg, -76.01±13.45 days, and -2.65±0.33 kg for LMY, LL, and DMY, respectively. However, the loss due to recombination effect of the two breeds was not significant ($p > 0.05$) on CI but significant ($p < 0.05$) on both NSC and AFC, with estimated values of 23.01±23.23 days on CI, -0.34±0.18 on NSC, and 19.32±2.23 months on AFC.

Generally, the productive and reproductive traits evaluated showed significant variation among genetic groups, parity, year, and season. This suggests that notable improvements can be achieved through enhanced management and strategic crossbreeding. Comparing genetic groups, an increase in the percentage of exotic genes corresponded to higher yields. Specifically, in the current study, 75%F1 recorded a higher yield than all other groups. On the reproductive side, 50%F1 calved earlier than the other contemporary groups, indicating it's advantageous in reproductive performance. Additionally, 50%F1 produce more fat percentage than other crossbred genotypes in the current study. The success of the 75%F1 genetic group in LMY and the early calving of the 50%F1 cows serves as clear indicators of the benefits that can be brought through strategic crossbreeding

The findings from crossbreeding parameter estimates confirmed that improvement in production trait was brought both by breed additive and heterosis effects while, improvement in reproduction trait was brought due to, heterosis effect except for age at first calving which was due to, breed additive. The results suggest that a combination of breed additive and heterosis effects play a significant role in shaping the overall performance of the crossbred animals. However, the improvement brought through additive and heterosis effects were lost by effect of recombination loss in inter-se mated generation. This information can be valuable for making informed decisions regarding breeding strategies and selection criteria.

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# 6. RECOMMENDATION

Moving forward, these results emphasize the potential for significant advancements in livestock management practices. By carefully selecting breeding pairs and considering factors such as genetic makeup, parity, and environmental conditions, farmers can maximize both productivity and reproductive of their herd.

Before conducting crossbreeding, some considerations need to be made by the farmer. The most beneficial strategy depends on the herd conditions, production system, and the purpose of changing the herd by crossbreeding.

The scenarios achieving 75% F1 in higher yield and 50% F1 in early calving, as well as compositional performance, were not fully optimized for economic output; thus, additional economic factors need to be taken into account.

In the future, more economic emphasis may be put on the milk composition instead of the quantity and milk pricing system will be changed from ordinary quantity to its quality which is the current situation in some eastern African country like Kenya and Tanzania, therefore it is recommended to have wide range of data on milk composition.

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# 8. APPENDIXS

**Appendix table 1:** Analysis of variance of lactation milk yield (LMY)

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Genetic group | 6 | 946815844.7 | 157802640.8 | 219.97 | <.0001 |
| Parity | 7 | 39517493.8 | 5645356.3 | 7.87 | <.0001 |
| Calving period | 6 | 87146708.2 | 14524451.4 | 20.25 | <.0001 |
| Calving season | 2 | 7415796.5 | 3707898.2 | 5.17 | 0.0057 |

**Appendix table 2**: Analysis of variance of lactation length (LL)

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Genetic group | 6 | 1316792.041 | 219465.340 | 36.90 | <.0001 |
| Parity | 7 | 350535.703 | 50076.529 | 8.42 | <.0001 |
| Calving period | 6 | 2484144.820 | 414024.137 | 69.60 | <.0001 |
| Calving season | 2 | 14704.979 | 7352.490 | 1.24 | 0.2907 |

**Appendix table 3**: Analysis of variance of daily milk yield (DMY)

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Genetic group | 6 | 6232.599034 | 1038.766506 | 278.62 | <.0001 |
| Parity | 7 | 733.893732 | 104.841962 | 28.12 | <.0001 |
| Calving period | 6 | 1587.094978 | 264.515830 | 70.95 | <.0001 |
| Calving season | 2 | 48.799846 | 24.399923 | 6.54 | 0.0015 |

**Appendix table 4**: Analysis of variance of Age at first calving (AFC)

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Genetic group | 6 | 13311.46721 | 2218.57787 | 41.35 | <.0001 |
| Birth season | 2 | 43.38009 | 21.69004 | 0.40 | 0.6676 |
| Birth period | 5 | 3655.31829 | 731.06366 | 13.63 | <.0001 |

**Appendix table 5**: Analysis of variance of calving interval (CI)

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Genetic group | 6 | 2264617.296 | 377436.216 | 28.46 | <.0001 |
| Parity | 6 | 1144810.267 | 190801.711 | 14.39 | <.0001 |
| Calving period | 6 | 1555982.261 | 259330.377 | 19.55 | <.0001 |
| Calving season | 2 | 4899.176 | 2449.588 | 0.18 | 0.8314 |

**Appendix table 6**: Analysis of variance of (NSC)

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Genetic group | 6 | 11.15686627 | 1.85947771 | 1.89 | 0.0788 |
| Parity | 7 | 9.90891363 | 1.41555909 | 1.44 | 0.1850 |
| Service season | 2 | 17.66525030 | 8.83262515 | 8.98 | 0.0001 |
| Service period | 6 | 46.21902810 | 7.70317135 | 7.83 | <.0001 |

**Appendix table 7**: ANOVA of LMY for crossbreeding coefficient

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Gi | 1 | 453465030.3 | 453465030.3 | 636.31 | <.0001 |
| Hi | 1 | 6431508.1 | 6431508.1 | 9.02 | 0.0027 |
| Ri | 1 | 76586367.2 | 76586367.2 | 107.47 | <.0001 |
| PARITY | 7 | 23827728.5 | 3403961.2 | 4.78 | <.0001 |
| Calving year | 37 | 149351415.4 | 4036524.7 | 5.66 | <.0001 |
| Calving season | 2 | 5635417.2 | 2817708.6 | 3.95 | 0.0193 |

**Appendix table 8**: ANOVA of LL for crossbreeding coefficient

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Gi | 1 | 699476.946 | 699476.946 | 120.86 | <.0001 |
| Hi | 1 | 33452.666 | 33452.666 | 5.78 | 0.0163 |
| Ri | 1 | 184817.042 | 184817.042 | 31.93 | <.0001 |
| PARITY | 7 | 452315.918 | 64616.560 | 11.16 | <.0001 |
| Calving year | 37 | 3230052.240 | 87298.709 | 15.08 | <.0001 |
| Calving season | 2 | 23386.363 | 11693.181 | 2.02 | 0.1328 |

**Appendix table 9:** ANOVA of DMY for crossbreeding coefficient

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Gi | 1 | 2308.143244 | 2308.143244 | 654.55 | <.0001 |
| Hi | 1 | 7.600687 | 7.600687 | 2.16 | 0.1422 |
| Ri | 1 | 224.203668 | 224.203668 | 63.58 | <.0001 |
| PARITY | 7 | 642.171668 | 91.738810 | 26.02 | <.0001 |
| Calving year | 37 | 2410.251763 | 65.141940 | 18.47 | <.0001 |
| Calving season | 2 | 32.914522 | 16.457261 | 4.67 | 0.0095 |

**Appendix table 10**: ANOVA of CI for crossbreeding coefficient

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Gi | 1 | 27054.975 | 27054.975 | 2.22 | 0.1361 |
| Hi | 1 | 470813.553 | 470813.553 | 38.69 | <.0001 |
| Ri | 1 | 11943.432 | 11943.432 | 0.98 | 0.3219 |
| Parity | 6 | 1148285.381 | 191380.897 | 15.73 | <.0001 |
| Calving year | 37 | 5389287.273 | 145656.413 | 11.97 | <.0001 |
| Calving season | 2 | 16233.779 | 8116.889 | 0.67 | 0.5133 |

**Appendix table 11**: ANOVA of NSC for crossbreeding coefficient

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Gi | 1 | 0.64558030 | 0.64558030 | 0.66 | 0.4172 |
| Hi | 1 | 6.96948881 | 6.96948881 | 7.11 | 0.0077 |
| Ri | 1 | 3.49115972 | 3.49115972 | 3.56 | 0.0593 |
| Parity | 12 | 10.54208273 | 0.87850689 | 0.90 | 0.5507 |
| Service season | 2 | 15.18268812 | 7.59134406 | 7.74 | 0.0004 |
| Service year | 37 | 91.32318186 | 2.46819410 | 2.52 | <.0001 |

**Appendix table 12:** ANOVA of AFC for crossbreeding coefficient

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Gi | 1 | 362.21828 | 362.21828 | 8.54 | 0.0036 |
| Hi | 1 | 40.02830 | 40.02830 | 0.94 | 0.3316 |
| Ri | 1 | 3187.85241 | 3187.85241 | 75.16 | <.0001 |
| Birth season | 2 | 86.86829 | 43.43415 | 1.02 | 0.3596 |
| Birth year | 35 | 16655.20936 | 475.86312 | 11.22 | <.0001 |

**Appendix table 13**: ANOVA for Fat content

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Genotype | 3 | 27.18650877 | 9.06216959 | 17.93 | <.0001 |
| Parity | 7 | 9.02545195 | 1.28935028 | 2.55 | 0.0397 |
| season | 2 | 0.22506036 | 0.11253018 | 0.22 | 0.8020 |
| L stage | 2 | 0.34467954 | 0.17233977 | 0.34 | 0.7143 |

**Appendix table 14**: ANOVA for Protein content

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Genotype | 3 | 3.31130914 | 1.10376971 | 23.11 | <.0001 |
| Parity | 7 | 0.65597220 | 0.09371031 | 1.96 | 0.1015 |
| season | 2 | 0.13251206 | 0.06625603 | 1.39 | 0.2684 |
| L stage | 2 | 0.15668765 | 0.07834382 | 1.64 | 0.2141 |

**Appendix table 15**: ANOVA for SNF content

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Genotype | 3 | 5.85614985 | 1.95204995 | 3.95 | 0.0196 |
| Parity | 7 | 6.70757515 | 0.95822502 | 1.94 | 0.1054 |
| season | 2 | 1.47570095 | 0.73785047 | 1.49 | 0.2441 |
| L stage | 2 | 0.46837457 | 0.23418728 | 0.47 | 0.6281 |

**Appendix table 16:** ANOVA for Lactose content

| Source | DF | Type III SS | Mean Square | F Value | Pr > F |
|---|---|---|---|---|---|
| Genotype | 3 | 1.31875457 | 0.43958486 | 4.28 | 0.0144 |
| Parity | 7 | 1.47482326 | 0.21068904 | 2.05 | 0.0880 |
| season | 2 | 0.32431919 | 0.16215960 | 1.58 | 0.2262 |
| L stage | 2 | 0.10300292 | 0.05150146 | 0.50 | 0.6117 |