ESTIMATES OF BREEDING VALUES AND GENETIC TRENDS FOR PRODUCTION AND REPRODUCTIVE TRAITS IN HOLSTEINS FRIESIAN HERD AT HOLETA BULLDAM FARM: A MULTIVARIATE ANIMAL MODEL ANALYSIS

M.Sc. THESIS

By

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APRIL, 2015

JIMMA, ETHIOPIA

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DEDICATION

This work is dedicated to God who is merciful onto me throughout my pursuit of my postgraduate study and to my Father and mother for their concern, support, prayer, patience and love. Without their decision that enabled me to pass different challenges through my education, I would have never been in my present position.

STATEMENT OF THE AUTHOR

I hereby declare that this thesis is my original 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 College of Agriculture and Veterinary Medicine and is submitted 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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BIOGRAPHY

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LISTS OF ABBREVIATIONS

305-dMY	Adjusted 305- days Milk Yield
AFC	Age at First Calving
AI	Artificial Insemination
BLUP	Best Linear Unbiased Prediction
CBPP	Contagious Bovine PleuroPneumonia
CI	Calving Interval
CV	Coefficient of Variation
DO	Days Open
DDE	Dairy Development Enterprise
h^2	Heritability
ILCA	International Livestock Centre for Africa
LL	Lactation Length
LMY	Lactation Milk Yield
NAIC	National Artificial Insemination Center
NSC	Number of Service per Conception
R	Repeatability
REML	Restricted Maximum Likelihood
SAS	Statistical Analysis Systems
USA	United States of America
VIF	Variance Inflation Factor
σ^2a	Additive Genetic Variance
σ^2e	Residual Variance
σ^2g	Genotypic Variance
σ^2p	Phenotypic Variance
σ^2pe	Permanent Environmental Variance
ONBS	open nucleus breeding scheme

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ABSTRACT

Animal evaluation and Genetic trend analysis was conducted in small exotic dairy cattle breeds of Holstein Friesian herd to evaluate the performance of the breed under Ethiopian condition, specifically at Holeta bull dam herd. A total number of 3733 lactation records from 1125 cows and 814 Dams sired by 137 bulls were used in this study. Performance records of animals from 1979 to 2014 archived for 35 years were analyzed for traits like. 305 day milk yield (305d MY), Total milk yield (TMY), lactation length (LL), Age at first calving (AFC), Calving interval (CI), days open (DO) and Number of service per conception(NSC) were studied by fitting GLM procedure of SAS (2010) for estimation of non-genetic factors on these traits. Genetic parameters and breeding value were estimated by multivariate BLUP procedures of multi-traits repeatability Animal Model. Estimated breeding values were used to regress the genetic and phenotypic trends for both production and reproduction traits against birth years of bulls and cows. Calving year and parity ($p<0.001$) and sire origin ($p<0.05$) had a significant effect on all milk production and reproductive traits. Season insignificantly affected all productive and reproductive traits except LL and NSC while Birth year and sire origin showed a significant ($p<0.001$) effect on AFC. The overall means of TLMY, 305d MY, LL, AFC, CI, DO and NSC were: 3732.3 ± 44.2kg, 3661 ± 37.4 kg, 314.3 ± 1.9 days, 40.6 ± 0.37 month, 461.1 ± 7.7 days, 173 ± 6.7 days and 1.98 ± 0.05, respectively. Estimates of heritability of milk production traits were 0.15±0.04 for TLMY and 305d MY, and 0.08±0.03for LL, whereas reproductive traits 0.38±0.025, 0.13±0.04, 0.10 ± 0.04 and 0.07±0.02 for AFC, CI, DO and NSC respectively. Genetic and phenotypic correlations between 305d MY, AFC and CI showed the existence of favorable correlation, implies that selection on 305d MY will results in early maturity which in turn helps to reduce the AFC and CI in the next generation. Estimates of all sire breeding values for 305d MY, AFC and CI ranged from (-538.4 to 946.7kg), (-13.7 to 9.4 m) and (-45.9 to 67.2 days), respectively. Aggregate genetic merit for all sires range from 119.2 to 66.3 *and female line ranges 125.9 to 64.2. The rate of phenotypic and genetic change over the study period for TLMY, 305d MY, AFC and CI were (4.5kg, 22.2 kg, -0.7 and -0.5 d) and (6.1, 9.5 kg 0.6 and -0.07d) per year, whereas 10.9 kg,-7.1and -1.1d for sires respectively. Positive genetic and phenotypic trends in production traits reflected the contribution of improved management after the bull dam farm was taken by NAIC plus the slight improvement observed as a result of pedigree based selection program of the center augmented with continued import of new sire lines from* *different country with better genetic merit overtimes. Low genetic progress of fertility traits as opposed to production trait were due to the there were not the main breeding goal traits and whatever small changes observed comes from the import of better genetics over the study period from different countries. The expected annual genetic change for 305d MY AFC and CI was 25-26kg,-5 and -3d per year if the three traits selection criteria and multi traits breeding goal is to be adopted.*

Key words: *Breeding Value, Genetic Trends, Production and Reproductive Traits*

1. INTRODUCTION

In Ethiopia, to meet the ever-increasing demand for milk, milk products and thus contribute to economic growth, genetic improvement of the indigenous cattle through crossbreeding has been practiced as one of the options. Commercial dairy production in Ethiopia had started with the upgrading of zebu cattle in the Central Highlands mainly using imported semen from temperate countries together with bulls imported from exotic dairy breeds had been the sources of germplasm to run the crossbreeding program. As the dairy population grew and the demand for semen concurrently increased, it was realized that relying on imports might not be sustainable (Aynalem Haile *et al* ,2011). Therefore, exotic dairy breed herds were established in Ethiopia as a source of dairy product supplying and young bull replacement stock for the national crossbreeding program based on the recommendation made by FAO (McDowell, 1983). As a result Holetta bull dam herd was selected by MOA as young bull replacement herd for over 30 years period. But, selections of young bull replacement and their dams were made based on the pedigree phenotypic performance and young bull growth performance only.

Genetic progress from the pedigree based selection and parallel imports of semen of different origin to boost the small herd available at the nucleus herd level were not evaluated for success or failure with appropriate methodology since then. It was believed that the importation in the last 30 years period was assumed to be resulting in an incremental improvement in production traits and other corelated traits since the exporting countries are already registering genetic improvement in every decade. Estimated breeding values (EBVs) are prediction breeding values from the performance values of an animal using Best Linear Unbiased Predictions (BLUP) which is one of the best methodologies for the prediction of breeding values of farm animals (Hill and Meyer, 1988). Accurate prediction of breeding value of animals is one of the prerequisite to maximize response ot selection program. Success of a breeding program can be assessed by actual change in breeding value expressed as a proportion of expected theoretical change in the mean for the trait under selection (Jurado*et al.*, 1994).

Ranking breeding animals according to their genetic merit for economically important traits adds value and efficiency to the success of a breeding programme. Therefore, an accurate identification and genetic evaluation of breeding animals is vital significance for genetic improvement program. Genetic trend evaluates the performance of every animal in the study population with estimates of real breeding value and genetic progress as the result of selection practiced over time and also explains the contribution of each selected animals to the next generation. The effectiveness of any dairy cattle genetic improvement program is measured by the genetic and phenotypic progress obtained (Hallowell *et al.,* 1998 and Bakir and Cilek (2009). A graphic historical perspective of a within-herd breeding program using phenotypic and genetic trend lines can convey a quick assessment of a breeder's selection success in previous generations. It is believed the exotic breed dairy cattle in Ethiopia had different genetic line sources with different selection criteria and index evaluation. Therefore trend analysis may be used to compare alternative methods of selection or pin point the management adjustment required (Wilson and Will ham, 1986). A standard way of measuring progresses in animal breeding is by regressing estimated breeding value on year of birth of the animals (FAO, 2007).

The National Artificial Insemination center had been importing semen and sometimes proven or pedigreed bulls in order to maintain the genetic variability of the nucleus herd over the last three decades. Therefore, the sire import from different country over the long period of time had been suggested to contribute best genetic mix over the same period. An Index of sires from exporting country had shown progress over the last two decades so that semen import from a given country had additional merit over time that would add possible change in the study herd. Accordingly NAIC imported semen from Israel for nearly fifteen years (1989 -2006). The progress in the productivity expected during this period (1989-192006) for milk production were 50Kg/year,15 days of cows longevity/year,0.1% fertility per year,0.08% persistency in the first lactation (www. sion-israel.com). Similar trends were also expected for worldwide sire genetics that currently supply the semen to the bull dam herd. The bull dam herd was selected as genetic improvement program started in the early 1980 and has never been subjected to any periodic evaluation for the genetic and phenotypic trends. Thus, the effectiveness of this selection program is not clearly known. Therefore, the impact of phenotypic selection by NAIC and its continuous sire semen import has not yet been evaluated in the current managementl situation in Holeta bull dam herd. However, the assumption in genetic trends is that improvement in the 305 days milk yield by NAIC of the MOA is assumed positive and genetic annualized mean of current generation greater than the former population. The single trait (milk yields) breeding goals of NAIC did not consider fertility merit of an animal to be evaluated. Therefore, the multivariate model seems better to evaluate a given dairy animals in Holeta situation where keeping variability among the small population by itself can be an objective with possible adaptive traits included in the selection criteria. The overall aims of this study is to investigate genetic and phenotypic trends of selection program run by NAIC in the current study herd and propose the future readjustment required to make best use of the exotic dairy lines in Ethiopia.

1.1.Objectives

The specific aims of this study are therefore the following

1. To estimate breeding values for production and reproduction performance trait.
2. To assess the phenotypic and genetic trends and genetic progress to suggest on the future breeding strategies at the Holeta bull dam farm.

2. LITERATURE REVIEW

2.1 Traits of Economic Importance in Dairy cattle genetic Improvement

Genetic improvement program on cattle performance is generally expressed by the change in phenotypic and genetic trends of traits of reproduction such as age at first calving (AFC), calving interval (CI), days open (DO), number of serves preconceptions (NSPC) and traits of production which include 305 days lactation, total lactation milk yield traits. The economic impact of these traits on a genetic improvement is examined by considering their effects on profitability of the enterprise contributed per given animal. These traits are related and therefore breeding program that incorporating most economic importance would be more effective than those considering a particular trait category. Selection for improvement of these traits in a production and reproduction system is influenced by the production environment influencing the ease of genetic expression (Indetie *et al.*, 2000).

2.2. Non Genetic Factors Influencing Performance of Dairy Animals

The knowledge of non-genetic factors and their influence on performance of dairy cattle is important in formulation of management and selection decisions (Goyache *et al.,* 2003). Fixed effects are sources of variation with defined classes comprising of all the possible levels of interest (Mrode, 2005). Examples of fixed effects include herd, year, season, sex, breed and parity are effect need to be to account for anticipated differences in management between herds when an analysis involves animals from various herds (Van Bebber *et al.*, 1997). Many investigations showed that season of calving constituted a significant source of variation in 305-day milk yield in dairy cattle (Ray *et a l.,* 1992, Conceicao *et al.,* 1993, Mokhtar *et al.,* 1993 , Salem and Omar, 1994, Afifi *et al.,* 1995, Aly , 1995, Mokhtar, 1995, El-Arian and Shalaby, 200, Nadia Fahim, 2004). In this respect, Sadek *et al.,* (1994) observed that season of calving exerted significant effect on 305-day milk yield in both the first and second lactations but it was not so in either the third or the fourth lactation. Contrarily, season of calving effect showed insignificant effect in this respect by other authors (Afifi *et al.,* 1992a, Badawy, 1994, El-Barbary *et al.,* 1999). The influence of season of calving on length of lactation period was evidenced to be significant in the cited literature by many research work like Abdel-Bary *et al.*, 1992, Mokhtar *et al.*, 1993, Khalil *et al.*, 1994, Kassab , 1995) . In this respect, and Nigm *et al.* (1994) noted that season of calving affected length of lactation period in the first lactation. On the other hand , insignificant differences in lactation period due to season of calving were reported by El-Khashab (1993), Salem and Omar (1994), Sadek *et al.* (1994) in different herds of dairy cattle. Season of birth effect on age at first calving was found to contribute significantly to the variance in age at first calving by different investigators (Safaa Ibrahim , 2002). Contrary, Soliman and El-Sheikh (1995), and Alnajjar (1997) found that the effect of season of birth on age at first calving was in-significant. Different studies revealed that season of calving contributed significantly to the variance of calving intervals Hammoud *et al.* (2010) and Million *et al.* (2010) days open and number of serves preconceptions (Hammoud *et al.*, 2010 and Million *et al.*, 2010, Mokhtar *et al.*, 1993, Soliman *et al.*,1994, Kassab, 1995). Cows calving in spring had longer CI compared with those calved in summer and winter because the environmental temperature is nearly optimal and green fodder is available for good fertility Contradicting results were obtained by other investigators Afifi *et al.*, 1992a, El-Menoufy *et al.*, 1994, Alnajjar, 1997). They found that season of calving did not contribute significantly to the variance of calving interval, DO NSC. The significant effect of season of calving on some reproductive traits could be attributed to the changes in climatic conditions and feeding regimes during different seasons. Parity of the dam shows varying levels of influence on both production and reproduction traits. Parity had significant ($P<0.01$) effect on DO and CI and non significant effect on NSC (Hammoud *et al.*, 2010). However, Chagunda *et al.* (2004) found that NSC was affected by parity of the dam in Malawi. Million *et al.* (2010) reported that parity of the dam had significant effect on, NSC, DO and CI of Holstein Friesian cattle in Ethiopia.

The potential effect of utilising imported semen alongside locally proven semen was evaluated in order to identify source countries with similar breeding objectives with the target population. However, the use of sires from heterogeneous sources without any clear strategy other than increased milk production is negatively impacting on early survival and fertility traits of Holstein Friesian cattle (Menjo *et al.,* 2009). Therefore, when selecting sires for breeding, breeders should look at information related to fertility of bulls in addition to their milk production. Sire of the cow effect was found to be a significant source of variation in 305-day milk yield by several investigators (Khattab and Sultan, 1990, Abdel-Glil, 1991, Mokhtar *et al.* , 1993, Khalil *et al.*, 1994 , Hamed and Soliman, 1994, Afifi *et al.*, 1995. The literature cited indicated that different studies proved that the effect of sire of the cow on length of lactation period was shown to be significant in different herds of dairy cattle (Soliman and Khalil, 1991, Afifi *et al.*, 1992b, Khalil *et al.*, 1994, Soliman and Hamed, 1994, Hamed and Soliman,1994. On the other hand, Bhatnagar *et al.*, 1983, Mokhtar *et al.*, 1993) proved that the effect of sire on length of lactation period was insignificant. Calving interval length and days open was found to be influenced significantly by the effect of sire of the cow by different investigators Afifi *et al.*, 1992 b. Sire of the cow was proved to have significant effect on age at first calving in dairy cattle by different research workers Mokhtar *et al.*, 1993 ; Safaa Ibrahim, 2002).

Milk yield is the most important economic trait that determines productivity and profitability in dairy cattle herds. Milk yield produced during the first 305 days of lactation is used as a standard measure for milk yield per lactation. Significant year of calving effect on 305-day milk yield was reported by different investigators (Mansour, 1992b, Mokhtar *et al.*, 1993, Ahmed, 1996, Abdel-Salam, 2000; Kassab *et al.*, 2001, El-Arian *et al.*, 200, Nadia Fahim, 2004). In this respect, Abdel-Glil (1991) found a significant effect of year of calving on the first and / or second lactation. Afifi *et al.*, (1992 b) indicated that year of calving effect was significant on 305-day milk yield. However, Sadek *et al.* (1994) found that year of calving contributed significantly to the variance in 305 day milk yield in the first , second and third lactations but not so in the fourth one. On the contrary, year of calving exerted non-significant effect on 305 day milk yield (Hamed and Soliman, 1994).

Year of calving effect was evidenced in many studies to be an important source of variation in milk production traits (305-day milk yield; length of lactation period, age at first calving, calving interval and days open) in dairy cattle herds and enterprises. This effect was attributed by different investigators to fluctuations in environmental conditions particularly those associated with managerial procedures, weather conditions, nutritional level and feeding practices which would change over years (e.g. Ahmed, (1996), Khattab and Sultan, 1990 b; Farrag *et al.* (2000) and Kassab *et al.,* (2001) noted that year of calving effect on milk production traits may possibly be due to differences in herd size, age of animals, variation in environmental conditions, availability of high quality roughage and improvement of managerial procedures used across years of calving of the study. Length of lactation period has a major impact on milk yield (Alhammad, 2005). It was evidenced that there was a clear close positive association between length of lactation period and milk yield by different investigators in dairy cattle (e.g. Agyemang and Nikhonjera (1990), Khattab and Sultan (1990a), Salem (1992) , El-Khashab (1993), Mokhtar et al (1993) ,Khalil *et al.,* (1994), Nigm *et al.,* (1994), Salem and Omar(1994), Rege *et al.,* (1994), and Alnajjar (1997) found significant effect for year of calving on length of lactation period. In this respect, Afifi *et al*. (1992a) showed that year of calving exerted significant effect on length of lactation period in the first lactation. On the contrary, Khattab and Sultan (1990a), Mostageer *et al.* (1990) reported insignificant effect for year of calving on length of lactation period.

Age at first calving of the dairy cow is of great economic importance in the efficiency of dairy cattle production as it affects productive life of the cow and its lifetime milk production (Bhagi and Epen, 1988). Afifi *et al*. (1992a) showed that reduction of age at first calving for the dairy cow would minimize the costs of raising and caring for the heifers, shorten generation interval and maximize the number of lactations given per cow during its productive life. El- Sheikh (1995) noted that reducing age at first calving of the dairy cow is of importance in attaining maximum of its lifetime milk production. Safaa Ibrahim (2002) reported that, under normal conditions, as age of the cow at first calving becomes earlier, number of calves delivered, number of lactations given and total milk yield produced during its productive life would be increased. This means that as age at first calving becomes earlier, its economic efficiency would be increased.

Year of birth effect constituted an important source of variation in age at first calving of the dairy cow by many investigators, i.e. Year of birth was found to have significant effect on age at first calving (e.g.; Mokhter *et al.,* 1993; El-Sheikh, 1995). On the other hand, Gad (1995) showed that year of birth of the cow had no significant effect on age at first calving.

All these findings might indicate the importance of year of birth as a factor influencing age at first calving. Afifi *et al.* (1992a,b), Mansour (1992a), Huba *et al.* (1993), Mokhtar *et al.* (1993) , Rege *et al.* (1994) and Kassab (1995) evidenced that year of calving effect exerted significant effect on calving interval and days open. On the contrary, year of calving effect was observed to have insignificant effect on length of calving interval Agyemang and Nkhonjera, 1990)**.**

2.3. Phenotypic Performance for Reproductive traits of Holstein Friesian cattle.

Female reproductive traits of lactating cows is a very complex trait, it can be defined as the cows ability to resume ovary function after calving, show a detectable estrus, become pregnant and or maintain pregnancy and succeed at calving. Therefore, many traits have been used as indicators of female reproductive performance, e.g. days open Gonzalez-Recio *et al.*, 2006; Huang *et al.*, 2007), Number of services, Calving Intervals, age at first calving (Chang et al., 2006). Male fertility traits are rarely included in genetic evaluations despite their influence on the female reproductive performance. These traits include semen quality and quantity traits and scrotal size. Most interval traits, such as days to first service (DFS), calving interval (CI), and days open (DO) are likely to be influenced by management decisions regarding the potential yield or season of calving of individual cows (Stott *et al.*, 1999; Butler & Smith, 1989; Darwash *et al.*, 1997). Reviewed means of some reproductive traits like age at first calving, calving interval, days open and number of service per conception in Holstein cattle raised in Egypt , countries of North America, Europe and in different tropical countries are presented below.

Means of length of calving interval for Holstein cows listed in that differed from 372 (Ahmed *et al.*, 2002) to 470 days (Salem *et al.*, 2006) in Egypt, from 378 (Schaeffer and Henderson, 1972) to 421 days, Chagunda *et al*., (2004) in Malawi 14.6 Ojango and Pollott (2001) in Kenya 14.5 months. This might be due to poor oestrous detection, silent heats, poor feed quality and health care and poor management. Abuzaid (1999) reported that the mean CI of imported and locally born Friesian cows in Sudan was 16.0 and 15.9 months, respectively. Many researchers reported results about CI of Friesian cattle in tropical countries; there is general agreement that the CI is not less than 14 months table1.

Table 1: CI of Holstein Friesian in some tropical countries

Country Mean CI (months) Authors	Country Mean CI (months) Authors	Authors
Cameroon	16.3	Gwaza *et al.* (2007)
Ghana	16.0	Osei *et al.* (2001)
India	16.3	Bhat *et al.* (1998)
Iraq	14.5	Tahir (2002)
Kenya	14.3	Ojango and Pollott (2001)
Libya	14.2	Salhab *et al.* (1999)
Mexico	15.9	Abubakar *et al.* (2003)
Nigeria	14.7	Mbap and Ngere (200)
Ethiopia	15.1	Mohammed, 2004
Egypt	14.1	Ibrahim (2006)

Also, other findings gave evidence that the average age at first calving varied from 23.7 (Afifi *et al.*, 2004) to 32.0 (Ashmawy, 2002) months for Holstein cows in Egypt, from 22.5 (Kulak *et al.*, 2005) to 33.6 months (Fonseca *et al.*, 2003) in countries of North America and Europe and from 26.18 (Oldenbroek, 2008) to 42 months (Florez *et al.*, 1989), Chagunda *et al.* (2000) Malawi 30.34 m. Percent of variation in calving interval ranged from 5.7 to 19.9 % in Egypt, from 29.0 to 57.3% in countries of North America and Europe, while, from 9.1 to 21.0% in different other countries. Percent of variation in age at first calving in Holstein cattle ranged from 6.3 to 11.0% in Egypt, from 8.8 to 17.3% in countries of North America and Europe and from 5.7 to 29.5 % in other tropical like Kenya 12.3 Malawi 20.2 countries. According to Oldenbroek, 2008 these percentages show the possibility of improving calving interval and age at first calving could be achieved through phenotypic selection in addition to improving managerial procedures and feeding systems conditions. The low age at first calving in a particular dairy cattle herd is a reflection of the good managerial strategy adopted in that herd. 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. According to Misztal and Rekaya (2004), an interval trait like DO is a composite trait largely affected by management factors, including reproductive protocols (estrous synchronization and timed AI), use of lactation promotants such as BST, intentional delay in re-breeding, seasonal effects, etc. DO for Holstein Friesian cattle in Ethiopia were 178.52 days, 174 ± 11 and 148 ± 1.72 day Mohammed (2004), Yosef (2006) and Million *et al.* (2010), respectively. Similarly Gader *et al.* (2007) reported DO of 167.79 ± 7.08 days in Pakistan, while lower estimate of 130.7 ± 1.9 days reported in Egypt for the same breed (Hammoud *et al.,* 2010). This variation may be due to difference management protocol and herds (Sandhu *et al.,* 2011).

Number of Services per Conception which is one of parameters for measuring cow reproductive efficiency basically depends on the breeding system followed and it is higher under uncontrolled natural mating and low where hand mating or artificial insemination is used (Melaku *et al.,* 2011b). Earlier works revealed that the overall mean of NSC for Holstein Friesian cow in Ethiopia were 2.01 ± 0.07 Yosef (2006) and 1.8 by Million *et al.* (2010). Reported estimates for NSC of Holstein Friesian cattle in tropics were 2.1 ± 0.1 (Hammoud *et al.,* 2010), 1.5 ± 0.5466 (Chagunda *et al.,* 2004) and 2.80 ± 0.10 (Sandhu *et al.,* 2011). However, Eid *et al.* (2012) reported 3.92 ± 2.77 and 2.3 ± 1.70 for imported and homebred Friesian cattle in Sudan, respectively.

2.4. Phenotypic performance for productive traits of Holstein Friesian cattle.

The milk production traits are traits that include total milk yield, 305d Milk yield and lactation length etc. performance of an animal at various stages of the production directly influence profitability in production systems. The expression of these Production traits is dependent on the animal's inherent ability and production environment (Mackinnon *et al.,* 1991; Davis, 1993). And also influence various aspects of production ranging from maintenance requirements to cull cow value thus directly affecting revenue in production. These traits directly influence reproductive traits (Burrow, 2001) although they are affected by the adaptability of the animal to the production environment (Gaughan *et al.,* 1999; Burrow, 2001). They form the basis of selection in many of the genetic improvement programmes due to their early expression and ease of measurement. Mean of milk production traits (Total lactation milk yield, 305-day milk yield and length of lactation period) for Holstein cattle raised in different tropical and Europe countries are presented below.

Lactation milk yield (LMY) is the total milk produced during a given lactation. LMY of dairy cattle may show variations from lactation to lactation in the same animal. The main reason of variation attributed to the physiology of lactation in the given set of genes and their reaction with non-genetic factors (Zewdu *et al.,* 2013). According to Sendros *et al.* (2000) the mean

LMY of Holstein Friesian cattle in Ethiopia was 3311±76 kg/cow. However, Million *et al.* (2010) reported higher estimate (3710 kg/cow). Lateef *et al.* (2008) and Sandhu *et al.* (2011) reported LMY of Holstein Friesian 3019.81 ± 93.57 and 3977.75 ± 37.2 in Pakistan, respectively. but less than 5905 kg reported by Ajili *et al.* (2007) in Tunis and 4489 kg/cow in southern Malawi (Wollny *et al.,* 1998) for the same breed. According to Edi *et al.* (2012) the mean LMY for imported and homebred Friesian cows in Sudan were 5533.14 ± 1546.03 and 3784.20 ± 1095.2 kg, respectively. This shows that there are great variations in milk yield for Friesian cattle in different places. This could be attributed to variation in managerial practices such as nutrition, disease control in addition to the effect of climatic conditions. The mean of average performance 305-day milk yield for Holstein cows changed from 4571 (Moharram, 1988) to 10847 kg (Alhammad, 2005) in Egypt, from 4295 (Ashmawy and Khalil , 1990) to 10130 kg Meyer and Burnside (1987) in Mexico, from 3573 Avandano *et al.* (1992) to 7266 Ojango and Pollott (2001) in Kenya 4557 (Van Tassel et al ;1999) in countries of north America and Europe and from 3144 (Parmar and Gill , 1988) to 8086 (Choi *et al*, 2001) in different other countries. The percent of variation in 305 milk yield of Holstein cows varied from14.8 to 27.4 % in Egypt, from 19.7 to 32.8 in countries of north America and Europe and from 15 to 36% in different other countries.In most modern dairy farms, a lactation length of 305 days commonly accepted as a standard. This standard allows for calving every 12 months with a 60-day dry period (Zewdu *et al.,* 2013). The mean LL of Holstein Friesian cattle in Ethiopia was 335 ± 9 (Sendros *et al.,* 2000). Ibrahim (2006) reported that the mean lactation length for Holstein Friesian cattle in Egypt was 371 days, while Sandhu *et al.* (2011) have reported 314.19 ± 0.91 days for the same breed in Pakistan. The averages LL for imported and locally bred Friesian in Sudan were 376.74 ± 150.89 and 349.00±86.19 days, respectively (Edi et al., 2012). In contrary, Ahmad *et al.* (2003) reported lower estimates of 297.73 ± 3.47 and 315.46 ± 3.62 days LL for imported and locally bred Friesian cattle, respectively in Pakistan. In order to increase the yield level, it is necessary to optimize the environmental conditions and to improve the genetic structure of the animals. Therefore; adjusting records for known source of variation is important for accurate evaluation of individual animal. The average 305-DMY for Holstein Friesian cows were 4571 kg in Egypt (Moharram, 1988). Similarly, Ojango and pallot (2001) reported 4557 kg in Kenya for the same breed.

However, Zewdu *et al.* (2013) found lower estimate (1707.25 ± 13.25kg) for Holstein Friesian and Deoni crossbred cows. Katok and Yanar (2012) reported 3408.17 ± 48.54kg for Holstein Friesian cow in Turkey. The means and percentages of variation for milk production traits (305-day milk yield, Total milk yield and length of lactation) in Holstein cattle as cited from studies, high or moderate percent of variation in a given trait permits the possibility of its improvement through phenotypic selection. Difference among means of either 305-day milk yield, total milk yield and length of lactation shown one might be due to differences in any, some or all of (a) source these of animals which is thought to affect the genetic structure in the herd used (b) system of mating followed, (c) level of inbreeding if any, (d) intensity of selection if any, (e) number of animals whose records were used, (f) number of lactations used (g) data structure (h) climatic conditions prevailing in the location of the study and (i) managerial procedures practiced.

2.5. Heritability estimates for selected traits in dairy cattle

Heritability which is one of the main population parameters is the ratio of genotypic variance to phenotypic variance. Heritability can be divided in two ways; in brood sense and in narrow sense. Heritability in the brood sense, which can also be referred to as the degree of genetic determination, is the ratio of genetic variance to phenotypic variance that expresses the extent to which individuals phenotypes are determined by the genotype. Heritability in narrow sense or simply the Heritability (h^2) is the ratio of additive genetic variance (σ_A^2) to phenotypic variance (σ_y^2) and it expresses the extent to which phenotypes are determined by the genes transmitted from parent (the additive component). Since it is a fraction, its value can be varied by changes in the additive genetic variance (the numerator) or by changes in any one or all of the components which comprise phenotypic variance which are the additive genetic variance σ_A^2, dominance variance σ_D^2 epistatic variance σ_I^2 and the random environmental variance σ_e^2. The additive genetic variance is closely associated with the gene frequency of the gene influencing the trait. For most situations σ_A^2 is largest when the frequency of the genes influencing the trait is near 0.5. The heritability determines the degree of resemblance between relatives and is therefore of greatest importance in breeding programs (Falconer, 1989).

Since heritability is σ_A^2 / σ_y^2, the methods used to estimate σ_A^2 can also be used to estimate heritability (Weller, 1994). However, particular heritability value is descriptive of a trait in a particular population under particular conditions (Falconer, 1989). In general, fertility trait (age at first calving days open, calving interval) tend to have lower heritability values than production traits like milk yield. Age at first calving has a relatively medium heritability although some reports indicate heritability's as low as 0.04 (Seykora and McDaniel, 1983; Baco *et al.*, 1998) while other report values as high as 0.47 (Rege, 1991). Calving interval on the other hand has low heritability. The heritability for calving interval ranges from0.04 to 0.13.Days open, just like calving interval has low heritability values ranges from 0.01 to 0.13 this reproductive traits are normally categorized as a traits with low heritability, and that little change would be expected from selection for such traits (Makuza and McDaniel,1996), there is quite a variation between them. Heritability values for milk yield tend to vary more in tropics (rages from 0.17 in India to 0.35 in Zimbabwe) than in the temperate region (rages between 0.25 for Canada and 0.38 for Sweden). This indicates the differences that may exist in the additive genetic and the random residual (error) variance components between the two ecological regions. Apart from these differences in additive genetic variance component and the function of the error variance in different environments, heritability may also be different due to the difference in the estimation procedure (Ndlovu, 1993).

2.6. Breeding value and genetic variability

Each individual receives a random sample half of its sires genes and another random sample half of its dam`s genes. Johanson and Rendel (1968) showed that the assessment of the breeding value of an individual for a given trait is based on an estimate of the average effect of genes which that individual passes on to its offspring in random mating populations. Accordingly, the breeding value of an animal for a certain trait could be defined as the estimate that represents the average effect of genes which that animal is expected to pass on to its offspring under random matings in the population. In other words, the breeding value of an animal for a given trait is the average effect of its genes that determine the mean of the genetic value of its offspring for the considered trait. The range of the breeding values refers to the genetic variability. As the range of the breeding value of a certain trait increases the genetic variability of that trait becomes more wide and this gives the chance for improving such a trait through selection according the superiority of the breeding value of the animal for that trait.

2.6.1. Estimated Breeding values for both production and reproduction traits.

Reviewed estimates of minimum, maximum and range values of sire. breeding values for reproductive traits (calving interval; age at first calving) in Holstein cattle as cited from the literature are presented as follows. According to Hatem Ismail (2006), using the animal model , found that sire breeding values ranged from -9.12 to 13.57 days (the range -22.69 days) for calving interval and from -2.40 to1.61months (the range -4.01 months) for age at first calving. The same author (2006) observed that sire breeding values obtained using animal model ranged from -5.38 to 6.77days (the range was 12.15 days) for calving interval while from -1.2 to 1.95 months (the range - 2.15 months) for age at first calving. The latter range is lower than 30.0 months given by Abdel-Glil (1996) for age at first calving. In this respect, Hatem Ismail (2006) showed that sire breeding values ranged from -5.29 to 6.79 days for calving interval and from -1.20 to 0.93 months for age at first calving. Estimates reveal that the ranges of sire breeding values ranged from -66.0 to 266.0 kg for 305-day milk yield (Rozzi *et al.* 1990) in USA. Also Arian *et al.* (2003) reported that the range of estimated sire breeding values ranged from -628.0 to 1289.0, Zahed *et al*. (2003) in Egypt -45.0 to 2332 kg for 305-day milk yield.

2.7. Selection Index

The selection index is a useful method of selection to bring simultaneous genetic improvement in two or more traits selected at a time. The basic and widely recommended idea of the total score or Selection Index which was prepared by (Philipsso *et al.,* 1994; Hazel *et al.,* 1994; Visscher *et al.*, 1994; Gibson and Wilton, 1998) aims at combining traits according to their economic importance. Selection for total score or index of net desirability is much more efficient than selection for one trait at a time, and the selection on independent culling levels is less efficient then selection on total score. Selection Index combines information from several sources, be it in the same trait from different types of relatives or different traits measured on the same animal. Selection indexes based on total merit combine the estimated breeding values (EBV) for individual traits into a single number that can be used for selection (Dekkers and Gibson, 1998). The basic purpose of selection index is to maximize economic response from multi-trait selection (Hazel *et al.,* 1994). In developing breeding goals and selection indices, it is important to make clear distinction between economic trait that are included in breeding goal and indicator trait are undiluted in selection index (Dekkers and Gibson, 1998). The economic value of a trait is defined as the change in the overall (e.g. profit), expressed per animal, of one unit change in the trait while all other traits in the breeding goal are kept constant, or as the absolute practical benefit from improvement in an individual trait.

According to Wollny (1995), several theoretical and applied breeding programs in southern Africa are still focusing solely on output such as milk yield and ignoring the antagonistic relationships of yield with other important traits such as reproductive performance. He further indicated that in a harsh environment the realized response in improvement schemes may be well below expectations if important traits are not included in the aggregate genotype. This view is also expressed by Hansen et al. (1993) who noted that if single-trait selection of dairy cattle for milk production is continued, adverse effect such as reproductive failure or increased incidence of health disorders may result. For a given definition of the breeding objective, there will likely be several or many traits that contribute to the objective. The aggregate genotype is then defined as a function of the additive genetic values of the traits of interest of an individual, which if selected upon would achieve the breeding objective. In these cases, the main interest is to predict the individual's breeding value for the aggregate genotype. In practice, however, the sources of information that are available to develop the economic index are EBV for individual traits, rather than phenotypic records:

$$I= b1X_1 +b_2\,X_2+b3\,X_3,\ \ldots..\ b_m\,X_m$$

where, X1,X2,X3,…Xm are the breeding values of an individual or a group of relatives and the b's are the factors by which each measurement is weighed Falconer (1989). In practice, however, the sources of information that are available to develop the economic index are EBV for individual traits, rather than phenotypic records: This leads to a step-wise procedure for development of economic selection indexes, in which the first step consists of predicting BV for individual traits and the second step of combining the EBV into an economic index. An advantage of this step-wise approach is that it allows different breeders to put different emphasis on traits in the aggregate genotype, while utilizing the most accurate EBV for the component traits. The best animals may be described as those that have the highest overall economic value or aggregate genotype. Selection on aggregate economic value will balance all the good and poor characteristics of each individual available for selection, thereby maximizing improvement in overall economic merit. Development of the selection objective is a prerequisite to the determination of aggregate economic value of individual animals. A selection objective is a list of all the traits that are desirable to improve and their relative importance (Holmes *et al.,* 2000).

2.7.1 Current emphasis in selection indices

According to Miglior *et al.,* (2005) the level of dairy traits emphasis was reviewed for production traits, within the production component, in the 15 countries national selection indices studied. Milk mostly has negative emphasis as it is a cost to the system in a predominantly product manufacturing market. It increases energy requirements for lactation and transport and processing costs (Holmes *et al.,* 2000). Many studies (Van Arendonk *et al.,* 1989; Bagnato and Oltenacu, 1994; Boichard *et al.,* 1997; Esslemont and Kossaibati, 1997; Lucy, 2001; Olori *et al.,* 2002) have stressed the importance of including female fertility in breeding objectives for dairy cattle. In the past, female fertility was left out of most selection programmes, mainly due to its low heritability (Grosshans *et al.,* 1997; Pryce *et al.,* 1998; Kadarmideen, 2004). The relatively high additive genetic variation of fertility (Philipsson *et al.,* 1981; Hermas *et al.,* 1987; Raheja *et al.,* 1989; Oltenacu *et al.,* 1991; Grosshans *et al.,* 1997; Jong, 1998) however indicates scope for genetic improvement through selection. The increasingly evident antagonistic association between fertility and milk yield (Bagnato and Oltenacu, 1994; De Jong, 1997; Pryce *et al.,* 1997; Ojango and Pollot, 2001; Kadarmideen, 2004; Nilfrorooshan and Edriss, 2004; Pryce *et al.,* 2004; VanRaden, 2004) is of major concern. The continual genetic improvement in yield traits taking place in most dairy cattle populations around the world is therefore expected to cause deterioration in fertility.

The importance of female fertility in selection indices around the world has increased significantly in recent years. In 1994, only the Scandinavian countries included fertility in their selection indices (Leitch, 1994; Philipsson *et al.*, 1994). Recently, Wesseldijk (2004) reported that fertility contributed 13% to the “world index” in 2004. Ireland had increased emphasis on fertility considerably, from 8% to 23%, while the trait was first introduced in the US Net Merit index in 2003. The Irish EBI had the highest emphasis on female fertility (22%), followed by the French ISU (12.5%) and the New Zealand BW, Swedish TMI, Canada, Germany USA TPI Irland all are (10%). Although 4 of the 17 indices studied recently (Wesseldijk, 2004; Miglior *et al.*, 2005) did not have a fertility component, Italy, South Africa, Ireland and Spain were working towards introducing the trait in their indices.

Table 2. Weights (%) applied in selection indexes used worldwide in 2009 ordered by emphasis on production traits

Country	Protein	Fat	Milk	Conformation	Productive	Udder health	Fertility	Other health traits
Japan	54.7	20.3		25			8	
Australia	36.8	14	-18.5		8.2	7.1	5.1	10.3
New Zealand	40	12	-14		6	-7	10	-13
Italy	45	14		23	8	10		
Spain	35	12	12	35	3	3		
Israel	42	14.6			8.2	12.8	15.5	6.9
Hungary	40	15		35		10		
Switzerland	38.7	14.3		24	7	10	10	
South Africa	26	26		45		3		
Canada	30.6	20.4		27.2	6.8	3	10	
France	37	13		12.5	12.5	12.5	12.5	
Czech Republic	33.6	15.4		25	7	7	12	
USA, Net Merit	16	19		17	22	10	11	5
UK	21.9	12.4	-10.9	5.6	21.1	5.5	18.5	4.1
Germany	36	9		15	20	7	10	3
USA, TPI	26	16		25	14	5	10	4
Ireland	25	5	-12	11			23	24
The Nether lands	21.7	4.8	-6.5	22	20	6	19	
Scandinavia	20	5	-5	13	4	14	13	26

Schneider (2009)

2.8 Genetic and Phenotypic Trends of Reproductive and Productive Traits

Genetic, phenotypic and environmental trends are measures of changes that take place in herds (Falconer and Mackay, 1996). They are indicators of genetic and management progresses made and thus are important in evaluation of the effectiveness of breeding programmes and determining the success of a selection programme (Musani and Mayer, 1997; Hofgren and Schinckel, 1998; Ebangi *et al.*, 2000).

Positive genetic and phenotypic trends are expected in any breed improvement programme where selection has been taking place as they reflect the level of genetic progress while negative genetic and phenotypic trends on the other hand are undesirable and indicate failure of the selection programme in place (Khan *et al.*, 1999; Ebangi *et al.*, 2000; Ojango and Pollot, 2001). Positive environmental trends are favorable as they indicate the level of herd management in feeding and disease control while negative environmental trends point to poor management within a herd (Rege and Wakhungu, 1992; Khan *et al.*, 1999; Ebangi *et al.*, 2000).

Genetic trends are estimated by regressing the animals' breeding values in that trait on the year while environmental trend are derived by regressing the solutions for year-season effects on each seasons of the year. In a study conducted by Makgahlela *et al.* (2008), they stated that decreasing genetic trends for AFC and CI over the years. In general, there was decreasing genetic trends for AFC. On the other hand, the genetic means of CI was sharply decrease fore same year and increasing in other year. The decreasing trend observed for AFC, CI indicated an improvement in the genetic merit of these traits. (Gunawan *et al.,* 2011), was report a part of correlated response to selection for increase daily gain. However, the decreasing trend for PR more fluctuation compared to AFC and CI. The fluctuation of values observed for pregnancy rate indicated that environment may play a great role in the ability of cow to become pregnant in the breeding centre. Annual genetic trends were -3.384 days, -8.00 kg and -5.96 kg, -0.29 months and -0.88 days, for lactation length (LL), lactation milk yield (LMY), adjusted 305 milk yield (305-days MY), age at first calving (AFC) and calving interval (CI), respectively. Also, El-shalmani (2011) in Egypt reported regression coefficients of estimated breeding values of Friesian sires on time of -7.030 ± 1.830 kg/year, 0.001± 0.041 day/year and -0.096 ± 0.078 day/year for TMY, LL and DO, respectively with no apparent specific genetic trend which reflected no genetic progress achieved over time. According to (Gunawan *et al.*, 2012), also for all traits where close to zero or slightly above zero. In general there was an annual genetic decline of 0.4 kg and 0.03 day in LMY and LL, respectively, while CI increased by 0.01 day. Hammoud *et al.,* (2013) stated that the genetic trends estimated as the regression coefficients of estimated breeding values of sires on time were generally low and non significant for all traits. These estimated trends were negative for

TMY, 305-DMY, LL, but were positive for DO without any specific genetic trends observed for all traits. Norman *et al.* (1991) working on Holstein, cows, found that annual genetic trend in the breeding value for milk yield was 106 kg/year, Also, Powell (1990) indicated that genetic trend in breeding value for milk yield for Holstein by using the animal model evaluation was approximately 120 kg/year. On the other hand, negative genetic trends have been reported for milk yield by Sharaby and Elkimary (1982) on Friesian cattle in Egypt. Also, Rege (1991) working on Friesian cows in Kenya from 1978 to 1988, found that the genetic trends per year for 305-dMY and lactation milk yield were negative and not significant, being -2.5 and -5.2 kg, respectively. In addition, Powell *et al.* (1977) with Friesian cows, found strong negative genetic trends in two regions in the United States from 1961 to 1970 with average sire breeding values for milk (kg) dropping from 100 to -220 kg from 1961 to 1964 in the West region and from 25 to -150 kg during the same period of the time in the Midwest region.

Mohsen *et al.* (2000) used original data of 774 lactation records of daughters of 124 sires of Friesian herds in Egypt and 9219 lactation records of daughters of 679 sires of Friesian herds in Germany to estimate genetic and phenotypic trends of 305-day milk yield (305-dMY), lactation period (LL) and calving interval (CI). Annual genetic change was 112.99 kg, -0.92 day and 1.78 day for 305-dMY, LL and CI, respectively for Friesian cows in Egypt and was 200.38 kg, 0.12 day and -1.05 day for 305-dMY, LL and CI, respectively for Friesian cows in Germany. Abdel Glil (1985) working on Friesian cows in Egypt, found a positive annual phenotypic change for 305-dMY, being 33.29 ±13.50 kg. In addition, Weller *et al.* (1984) working on Israeli Holstein Friesian cows, reported that the phenotypic trend for a 305-day milk yield was 173 kg/year. On the other hand, a negative annual phenotypic change for milk yield has been reported by Canon and Munoz (1991) working on Spanish Holstein in Kenya, being -78 ± 8 kg and Rege (1991), being -5.5 kg, with Friesian cows in Kenya. Similarly, Mohamed *et al.,* (2000), Study on Friesian Herds Raised in Egypt and Germany; The annual phenotypic change for 305-dMY, LL and CI was 48.00 ± 7.05 kg, 56.83 ± 5.64 kg, -1.66 ± 0.39 d and -1.82 ± 0.48 d, respectively for Friesian cows in Egypt. These estimates were significantly varied (P<0.05 or P<0.01) except for LL and CI. This results in indicate that the differences in Performance between years were mainly due to different nutritional, climatic and management practices prevalent over different times. In Germany, The annual phenotypic change was 104.00 ± 2.56 kg for 305-dMY, 0.17 ± 0.02 d for LL and 0.78 ± 0.14 d for CI.

2.10. Univarate Models

Univarate models analyses one trait at time without considering the relationship between them (Meyer, 1993; Meyer and Hill, 1997). Analyses of growth traits using UM trait models are preferred for their ease of manipulation and reduced computational time (Meyer, 1993; Lynch and Walsh, 1998). These models have been utilized to analyses growth traits in most tropical dairy cattle. However, evaluation of growth parameters using UM gives estimates with lower accuracy due to their inefficiency in data utilisation and inability to account for trait correlation (Lynch and Walsh, 1998). Since use of these inaccurate parameters estimates creates selection bias which results in slow genetic progress and reduced expected genetic gain, MTM that account for trait correlation have therefore been employed.

2.11. Multivariate Trait Models

Multivariate trait models are preferred over Univarate models since they analyses several traits simultaneously and consider the relationships among them (Lynch and Walsh, 1998; Nobre *et al.*, 2003). Since it accounts for trait correlation, it is able to utilise the covariance structure by fully adjusting for the residual covariance between traits and thereby reducing the error variance (Mrode, 2005). One of the main advantages of mulivariatrait analysis in the selecion programs is to obtain some useful information for indirect selecion and increases the accuracy of evaluations. The efficiency of indirect selecion is related to the heritability of the trait and to the genetic correlaion between traits. If geneic correlaions betweenthe traits are high enough, selecion of the stock can be made easily and early measured trait using indirect selecion. Therefore, both generaion interval and financial cost in the herd can be reduced (Unalan and Cebeci, 2004). For example, overestimated results for correlation between direct and maternal genetic effects were reported using UM instead of MTM (Rumph *et al.*, 2002).

Better reliabilities have also been achieved when predicting genetic merit using MTM than UM due to their ability to use extra information from correlated traits (Strabel *et al.,* 2001). The MTM therefore have improved accuracy of parameter estimates and have thus become the ideal model where selection is based on multiple traits (Khan *et al.,* 1999; Maiwashe *et al.,* 2002). The increased accuracy of estimates derived from the use of MTM has resulted to improved genetic progress in selection programmers. For this reason, use of MTM in evaluation has replaced the UM.

3. MATERIAL AND METHODS

3.1. Description of the Study Area

The Holeta bull dam is located approximately 45 km west of Addis Ababa at 38.5°E longitude and 9.8° N latitude. It is situated at about 2400 m above sea level and is delineated as one of the areas known as “the Addis Ababa milk shed”. The average annual rainfall is about 1200 mm and the average monthly relative humidity is 60.6% (Haile *et al.,* 2009). The dry season lasts from October to February followed by light showers between March and May and the main rainy season between June to September. The Holeta Bull dam is situated in the central highlands of Ethiopia.

3.2. The Holeta Bull Dam Farm and Its National Role

The farm was established in 1954 due the high demand for milk and other dairy products in and around Addis Ababa as human population increased necessitated the establishment the farm. The National Artificial Insemination Center was mandated to produce and distribute semen from elite bulls and use the bull dam farm for young bull replacement and co-ordinate cross breeding program Nationwide since 1981. NAIC has been making use of the farms under then DDE as bull dam herds from which recruitment of best cows based on the phenotypic performance of their milk yield would enable it to be the potential dam line that upon which imported pedigree selected or proven sire semen from different countries had been used to get the young replacement bulls for the semen production and then its distribution supplying crossbreeding program nationwide. Procurement from different countries at different times was intended to avoiding inbreeding. The evaluations of the bull calves for replacement were based on birth weight, weaning weight, body condition and breeding soundness or conformity of the young bull.

3.3 Herd Management

Holeta bull dam nucleus herd of National Artificial Insemination Center (NAIC) has so far been engaged in maintenance of elite Holstein Friesian cattle population in Ethiopia to produce replacement dairy bull for the production of high quality semen at reasonable cost and bring genetic improvement throughout the country by cross breeding of indigenous cattle with exotic semen. Animals were housed free in shaded open yards, grouped and managed according to their age into three basic classes: calves, weaned, and mature stock. Groups of 50 cows were housed together in a single barn. Generally, the management practice is that calves are removed from their dams at birth, weighed and ear tagged. They are bucket fed, receiving colostrums for the first 5 days, and whole milk for about 120 days, during which period they are gradually weaned onto concentrates and roughage feeds. The concentrate mix offered to animals is basically based on their age; it is composed of the following ingredients: Nuge – cake 28%, maize 10%, wheat milling 18%, wheat bran 40%, Lime stone 2%, and salt 2%. For heifers & bulls 30%, 10%, 30%, 25%, 4%, 1% and for Calf 40, 15, 25, 15, 4, 1%, respectively.

In pre weaning period they are bucket fed by milk and supplement rate showed descending trend as 5 liters, 4 liters, 3 liters, and 1 liter milk per day for 55, 30, 20 and 15 days respectively. Calves are supplied with milk for 120 days by the time they are weaned at four months of age. During this period they also fed on concentrate calf starter after 15 days at rate of 0.75 kg a day till their six month of age. Hay is also made available, during the process of transferring them from milk to a grass based diet. Cows are fed according to their production potentials. Lactating cows are provided with a concentrate feed for their yield at a rate of 0.5 kg/liters of milk they produces. While pregnant, in the last two months of pregnancy, were supplemented with extra concentrate ration of 2 Kg. Bulls and heifers are separated and managed in different herds after weaned. In the bull dam herd young bulls to be recruited are selected at one years of age for AI bull replacement and natural service from the herds on the basis of pedigree performance against average milk yield, physical appraisal of growth performance and conformation of the young bulls, before production and dissemination of semen for AI service. All heifers calves born are retained in farms for the next replacement.

Sires were systematically assigned to dams assumed to be remotely related to cows that were artificially inseminated by frozen semen. Voluntary culling based only on low production was not regularly practiced in the study herd. Culling was based mainly on cumulative effects of reproductive failure, low daily milk production; feed shortage in the farm, serious mastitis infection and old age and TB test results.

Improved grass and legume species commonly used as a green fodder are Cocks foot (Dactylic glomerata), Oat (Avena sativa), Rhodes (Chlorisgayana), vetch (Vicia sativa) and was supplemented through a cut and carry system (Nega and Sendros, 2000). It is done more intensively during the wet season when the animals are mainly stall-fed. Priority is given to milking cows. In addition to concentrate and green feed lactating cows and heifers aged above six months were allowed to graze on natural pasture for about 3- 8 hr during the time throughout the year except June, July and August and milked twice daily manually. Water is provided to all groups adlibitum. Routine vaccinations per six month were carried out for endemic diseases such as Foot and Mouth Disease, Lumpy Skin Disease, Anthrax, Contagious Bovine Pleura-Pneumonia (CBPP) and Bovine Pasteurelosis. However, specific treatment was given when any disease occurrence was reported.

3.4 Data source and Its Edition

Data used in this study were obtained from performance recording of Holstein Friesian herd maintained at Holeta bull dam farm from 1979-2012for nearly 35 years. On the farm, records for individual animals were kept on animal cards arranged in order according to the year in which the animal was born. All information about the animal, including whether it had been sold or had died, was written on the card. Daily milk yield were recorded in the milk record format. This are summarized in to monthly milk yield, which are later summed up when the cow ceased lactating. Total yield and dry off date were then recorded on the individual animal card. The data were collected from individual animal card recorded in to excel sheet and records with irregularity in pedigree information and birth or calving dates were discarded. Three seasons were classified based on weather and climatic conditions of the area; June to September as long rain season, March to May as short rainy season and October to February as dry season. Further, data from first second and third lactation consider with the third lactation containing all parities above 3 pooled together (3+).

Prior to analyses, abnormal records affected by diseases or lactations initiated as a result of abortions, Records with unknown birth and calving dates and other irregularity were deleted. For lactation milk yield greater than 1000 kg were included and lactation lengths less than 220 and greater than 450 days were excluded based on the method adopted from (Ayied *et al.*, 2011). A lactation record was considered normal if a cow had produced milk for at least 21 days were standardized to 305-dMY by following the projection procedures of (Rege, 1991) for 305 days milk yield and lactation greater than 321 days were adjusted by developing a regression model considering R-square and Variance Inflation Factor (VIF) for each independent variable in multiple linear regression model (Khan *et al.,* 2011).

Reproduction traits (CI and DO) were obtained from calving records, first calving date and second and third calving data. Age at first calving was calculated as difference between first calving date and birth date of an animals. Age at first calving between 18 month to 60 month and records greater than 60 month were considered as 60 month, calving interval between 300 and 900 days, days open between 21 and 500 days (Ajili *et al.,* 2007). Records on the number of service per conceptions that are greater than seven were considered as seven. Details of traits considered in this study are given in table 3.

Table 3: Summary data statistics for the traits under the study

Variables	N	Mean	SD	Minimum	Maximum
LL d	2938	314.3	48.5	220	450
LMY kg	3552	3732.3	1288.7	1001	9000
305-dMY	3733	3661	1222.6	1004	9301
AFC m	1125	40.1	9.8	18	60
NSC	3914	1.9	1.4	1	7
CI d	2764	461.1	124.3	301	897
DO d	2773	173	107.6	25	500

3.5 Data Analysis

3.5.1 Adjustment of Milk Yields to 305 days

The data consisted of total milk yields from lactations of varying lengths of days in lactation. Due to various reasons, some animals had been sold before completing lactation, or died in the middle of lactation, and, some animals left the herd while lactation was still in progress. Unless a standard reference point is taken in to account, the terms complete and incomplete are also subjective. A standard lactation is considered for dairy cattle on the basis of 10-month (305-days). However, animals may terminate milk yielding prior to the standard lactation days or may continue to produce beyond this point. In this study, the standardization procedure of incomplete lactation developed by Rege (1991a) and adoptable for tropical Africa was applied for projecting incomplete lactation records of cow that die or leave that herd prior to 305 day in milk. While, the model developed by Khan *et al.,* (2011) was used for lactations longer than 305 days converted by linear regression expressed as;

SLMY = a + b1*CLMY+ b2 *LL+ e

Where,

a: intercept

b1: regression of standard lactation milk yield (SLMY) on complete lactation milk yield (CLMY)

b2: regression of SLMY on Lactation length (LL), and

e: random error term.

Records of animals still being milked when data for the study were prepared were adjusted to a 305-d length, if the lactation had been in progress for a minimum of 21 days.

3.5.1. Analysis of Non- Genetic Factors

To evaluate the effects of non-genetic factors (year, season, parity and origin of sire) preliminary analysis were performed by the General Linear Models Procedure of SAS (SAS, 2010). The two statistical models were used to assess the effect of non-genetic factors on productive and reproductive performance are as follows;

Model 1: $Y_{ijkl} = \mu + S_i + Yr_j + B_k + e_{ijkl}$

Where:

Y_{ijkl}= AFC of l^{th} cow in K^{th} sire origin, j^{th} year of birth, i^{th} season of birth

μ = overall mean

S_i = the effect of i^{th} season of birth

Yr_j = the effect of j^{th} year of birth

B_k = the effect of k^{th} sire origin

e_{ijkl} = random residual error term

Model 2: $Y_{ijklm} = \mu + S_i + Yr_j + P_k + B_l + e_{ijklm}$

Where:

Y_{ijklm} = LMY, 305-dMY and LL, CI, DO and NSC of m^{th} cow in l^{th} sire origin, k^{th} parity, j^{th} year of calving, i^{th} season of calving

μ = overall mean

S_i = the effect of i^{th} season of calving

Yr_j = the effect of j^{th} year of calving

P_k = the effect of k^{th} parity

B_l = the effect of l^{th} sire origin

e_{ijklm} = random residual error term

3.5. 2 Estimation of variance and (co)variance components and Breeding value

3.5. 2 .1 Estimation of variance and (co)variance components

Estimation of (co)variance components and resulting parameters; heritability, repeatability, (co)variances and correlations were made using the mixed model restricted maximum likelihood procedure of the ASRML (Gilmour *et al.,* 2009) package, fitting multiple trait repeatability animal model were used for the traits studied (TMLY, 305 d MY, LL, AFC,CI,DO and NSC). Two different models, model 1, and 2, were used for estimation of genetic and phenotypic parameters. In general the effects included in these models were season of calving, calving or birth year, sire origin and parity as fixed effects and permanent environmental effect, animal genetic effect and random residuals as random effects. Model 1 was used for parameters estimation of both productive and reproductive traits like 305 day milk yield, CI, DO and NSC fitting permanent environmental effect due to repeated records per cow whilst model 2 was used for the analysis of AFC. The general descriptions of the models in matrix form are given below:

Model 1

$$Y = Xb + Zp + Wu + \varepsilon$$

Model 2

$$Y = Xb + Wu + \varepsilon$$

$$\begin{bmatrix} y1 \\ y2 \\ y3 \end{bmatrix} = \begin{bmatrix} X1 & 0 & 0 \\ 0 & X2 & 0 \\ 0 & 0 & X3 \end{bmatrix} \begin{bmatrix} b1 \\ b2 \\ b3 \end{bmatrix} + \begin{bmatrix} Z1 & 0 & 0 \\ 0 & Z2 & 0 \\ 0 & 0 & Z3 \end{bmatrix} \begin{bmatrix} p1 \\ p2 \\ p3 \end{bmatrix} + \begin{bmatrix} W1 & 0 & 0 \\ 0 & W2 & 0 \\ 0 & 0 & W3 \end{bmatrix} \begin{bmatrix} u1 \\ u2 \\ u3 \end{bmatrix} + \begin{bmatrix} \varepsilon1 \\ \varepsilon2 \\ \varepsilon3 \end{bmatrix}$$

Where Y represents one of the traits studied, X, Z and W represent incidence matrices of the fixed factors, permanent environment and random animal effects, respectively. b, p and u stand for vector of fixed, permanent environmental and additive effects, respectively whereas ε= vector of random residual effect

The estimated variance and covariance components were summarized and used for the corresponding genetic and phenotypic parameters. Heritability was estimated as the ratio of the additive genetic variance to total phenotypic variance; and repeatability, as the ratio of the sum of the additive genetic variance plus permanent environmental variance to phenotypic variance, as described by Falconer and Mackay (1996):

$$h^2 = \frac{\sigma^2 a}{(\sigma^2 a + \sigma^2 pe + \sigma^2 e)} \qquad r = \frac{(\sigma^2 a + \sigma^2 pe)}{(\sigma^2 a + \sigma^2 pe + \sigma^2 e)}$$

Where

h^2 = heritability

r = repeatability

$\sigma^2 a$ = direct additive genetic variance

$\sigma^2 pe$ = permanent environmental variance related to repeated records

$\sigma^2 e$ = residual variance

The genetic correlations were estimated as the ratio of additive covariance of the two traits to the products of additive genetic standard deviations of the two traits whilst phenotypic correlations were estimated as ratio of the sum of the genetic and environmental covariance (phenotypic covariance) to the products of phenotypic standard deviations of the two traits.

$$r_g = \frac{\sigma_{aij}}{\sqrt{\delta^2{}_{ai} . \delta^2{}_{aj}}} \qquad r_P = \frac{\sigma_{pij}}{\sqrt{\delta^2{}_{pi} . \delta^2{}_{pj}}}$$

Where:

r_g = genetic correlation

r_P = phenotypic correlation

$\delta^2{}_{ai}$ = additive genetic variance for trait i

$\delta^2{}_{aj}$ = additive genetic variance for trait

$\delta^2{}_{pi}$ = phenotypic variance for trait i

$\delta^2{}_{pj}$ = phenotypic variance for trait j

$\delta^2{}_{aj} =$ additive genetic covariance between trait i and j

σpij = phenotypic covariance between trait i and j

3.5.2.2. Estimates of breeding values

Estimates of breeding value were made using complete data set without restriction in progeny number per family with all records of a trait to estimate its breeding value. Estimates of breeding values of animals were estimated by DMU package Best Linear Unbiased Prediction (BLUP) procedure fitting an animal model (Madsen and Jensen, 2013). Accuracy of breeding values were calculated from standard error estimates based on the standard error conversion formula of Gilmour *et al. (*2009).

The phenotypic and genetic trends for the selection program were calculated by regressing the annualized mean phenotypic and breeding values of animals in the data set against birth years of animals. This showed the direct annual genetic and phenotypic trends (linear regressions) on both productive and reproductive traits. The trend analysis had been made by taking the current generation found in the bull dam farms as a reference or as base group. Accordingly, in this study, the base is set to the average of a group of animals born in 2008, usually called the base population for the sake of comparing the current generation with that of the former generation. The average breeding values for these base populations were set to zero for all traits to form a reference point for comparison. sire trend analysis was done by classifying the years in to six periods (1979 to 1985) period 1; (1986 to 1990) period 2; (1991 to 1995) period 3; (1996 to 2000) period 4; (2001 to 2005) period 5 and (2006 to 2012) period 6.

The total genetic merit indices of animal in the evaluation were developed for each breeding goal (305d MY, AFC and CI) traits being set to be the selection criteria to achieve the most efficient population replacement. Accordingly, in order to allow selection of sires and dams for simultaneous improvement for both production and reproduction traits by standardize breeding values for bulls and cows were obtained using the index set up by Scandinavian country. A total of 145 dairy farmers and 122 customers of the dairy products to substantiate the index model to be adopted for Addis milk shade of Ethiopian context were selected by purposive random sampling technique for identification of traits preferences as the reflection of economic benefit of dairy cattle traits. Preliminary survey was conducted on the level of traits preferences of dairy cattle in and around Addis Abba, (Bishoftu and Holeta), in order to identify prioritized breeding goal traits for implementation of appropriate indigenous breeding program by developing relevant selection index with the participation of the Dairy farmers and customers. Traits like milk yield, fat and longevity were grouped as milk production traits while traits like age at fires calving; calving intervals and NSC were considered as fertility traits. Index = sum of (8 for rank 1+7for rank 2 +…1fo rank 8) given for an individual reason divided by the sum of (8 for rank 1+7for rank 2 +…1fo rank 8) for over all reasons.

Accordingly:

H= 0.60*305d MY Index BV +0.25* Age at first calving Index BV +0.15* calving interval Index BV.

Where, 0.60, 0.25 and 0.15 are the Weights given for 305d milk yield, Age at first calving and calving interval, respectively.

Simulation of response to selection through assumption for best ranking sires and dams use in the bull dam herd were made to assess the overall genetic response within certain breeding plan set up using Anders & Jan Philipsson, for two traits breeding program and Julius. Vander werf for three traits breeding program implementation model.

$$RHtu = [\sum_{i=1}^{2} i_n \ c_n] \frac{b_{u'} G a_t}{\sqrt{b_{u'} p b_u}}$$

Where:

I_n = selection intensity in path n;

c= cumulative discounted expression for path n;

b_u= vector of selection index weights corresponding with the used set of economic weights;

at = vector of economic weights used,

G =matrix of covariances between traits in aggregate genotype and index,

P= matrix of covariances between traits in the selection index.

The subscript n which stands for path n and follows what Anders and Jan Philipsson. Anders and Jan Philipsson pointed out that in any breeding program there are four basic pathways of genetic improvement, corresponding to the total of four sources of parental genes of male and female progeny. These four pathways are: male parents of male progeny (sires of sons); female parents of male progeny (dams of sons); male parents of female progeny (sires of daughters); and female parents of female progeny (dams of daughters). The subscripts u and t refers to economic weights used at the time of selection.

4. RESULT AND DISCUSSION

4.1 Phenotypic performance of production traits

4.1.1 Total lactation milk yield.

The overall mean of total lactation milk yield was 3732.25 ± 44.2 kg with a coefficient of variation of 24.6%. This is higher than the reported values of 3175.7±41.0 kg and 3311±76 kg/cow by Mohamed, (2004) and Sendros *et al.*, (2000), respectively, for the same herd. The analysis of variance (Table 4) indicated that calving year, parity number, sire origin had significant effects (P<0.001) on TLMY trait. The variation in milk yield from one year to other could be attributed to changes in the performance of herd due to fluctuating of management condition over years. The lowest total lactation milk yield (2320.3) was observed in 1991 and the highest milk yield (4826.3kg) in 2010.

Sire origin had significant effect on TLMY (P<0.001). The best ranking sire origin like sires from Israel, Italy and Ethiopian origin are among the best performing sire origin. The inferior performance observed by sire origin like unknown group and Cuba origin. But in the contrary, Bhat (1980), Garcha and Dev (1985) reported no significant effect of sire on milk yield. Therefore, the results obtained in this study show the possibility of using locally born sires which had shown the comparable mean performance with, sire origins like Israel, USA, and Italy indicated the possibility of running the genetic improvement using locally adapted sire line small bull dam herd.

4.1.2 305 day milk yield performance

The overall mean performance adjusted for 305 days milk yield was 3661 ± 37.4kg (Table 4). The current result was higher than 3096.0±26.9 reported by Mohamed (2004) and 3333± 65kg reported by Mureja (1994) on the same farm. However, this performance is lower than reports from other tropical countries. For instance the 305 days milk yield of Holstein cows in Tunisia was 5905 kg, 5353 kg in Morocco and between 4597 and 6464 kg in Turkey. The factors included in the model i.e., calving year, parity and sire origin had a significant effect on 305 d milk yield with the exception of calving season (Table 4). The effects of parity on 305 day milk yields followed the expected pattern that first parity was significantly different from the following parities. This result is consistent with Chagunda *et al.* (2004). who found significant (P<0.05) effect of parity on milk yield. Nevertheless, the result differed from that of Habib *et al*. who found non-significant (P>0.05) effect of parity on 305 days milk yield. The significant effect of parity on productive performance is due to the changes associated with the physiological maturation of the cows' as her age progress. The effects of calving year on 305 day lactation yield was significant (p<0.001).The least square mean 305 day milk yield of the herd was 4786.5±136.1 kg in 2010 and 2178.8±66 in the year 1992. This could be due to improving management conditions, like general improvement in feeding and husbandry practice over the last 5 years. Sire origin was found to be a significant (p<0.001) as source of variation in 305-day milk yield. This might be due to difference in breeding objective and selection criterion between those exporting and importing countries and adaptability to Ethiopian management situation. Our results are in line with Mokhtar *et al.,* (1993) and Shereen Genena (1998) Muasya *et al.,* 2014) who also found out that sire origin had a significant effect on 305-day milk yield (Table 4).

Table 4: Least squares means and standard error (LSM ± SE) of LMY, LL and 305d MY

Sours of variation	Trait					
	N	TLMY (kg)	N	LL days	N	305d MY (kg)
Overall	3552	3732.3 ± 44.2	2938	314.32 ± 1.9	3733	3661.0 ± 37.4
CV (%)	32			14.43		29
Season		NS		*		NS
Short rainy	849	3671.8 ± 56.7^{a}	720	311.7 ± 2.5^{b}	943	3632.4 ± 48.4^{a}
Long rainy	1070	3752.9 ± 52.9^{a}	869	318.4 ± 2.3^{a}	1134	3668.8 ± 44.8^{a}
Dry	1588	3771.9 ± 47.7^{a}	1349	312.8 ± 2.1^{b}	1656	3681.8 ±40.7^{a}
Parity		***		***		***
1	1014	3317.36 ± 48.29^{c}	836	323.1 ±2.1^{a}	1077	3173.7 ± 40.8^{c}
2	803	3700.14 ± 55.72^{b}	664	316.6 ± 2.4^{ba}	826	3621.5 ± 47.7^{b}
3	1735	3941.22 ± 61.67^{a}	1439	315.9 ± 2.7^{bc}	1830	3870.3 ± 52.9^{a}
Sire origin		***	***	***		***
Cuba	1054	3461.3 ±48.0^{b}	837	314.8 ± 2.1^{a}	1127	3379.5 ± 41.2^{b}
Finland	152	3615.8 ± 114.8^{ba}	118	316.2 ± 5.1^{a}	164	3556.8 ± 98.4^{ba}
Ethiopia	292	3809.6 ± 72.5^{a}	245	312.9 ±3.1^{a}	302	3813.6 ± 62.7^{a}
Israel	776	3988.6 ± 61.5^{a}	679	313.7 ± 2.6^{a}	811	3923.3 ± 53.9^{a}
Italy	91	3976.5 ± 127.4^{a}	77	323.7 ± 5.4^{a}	94	3832.9 ± 110.6^{a}
Kenya	410	3587.9 ± 66.9^{ba}	355	322.5 ± 2.8^{a}	420	3878.7 ± 58.2^{a}
Unknown	746	3441.2 ± 48.5^{b}	602	317.0 ± 2.1^{a}	778	3435.9 ± 41.9^{b}
USA	31	3579.1 ± 238.4^{ba}	25	293.5 ± 10.5^{a}	37	3467.4 ± 196.8^{ba}
Year	33	***	33	***	33	***

***P<0.001; **P< 0.01; *P<0.05; NS= Not Significant. Means with the same letter are not significantly different.

4.1.3 Lactation length

The overall least square mean of lactation length (LL) of Holstein Friesian cows in the study herd was 314.3 ± 1.9 days and the coefficient of variation of 14.46%.This performance of 314 days was longer than the ideal 305 days generally accepted period. This length of lactation was longer than results reported by Sattar *et al.,* (2005) and Alin (1988) who reported a lactation length of 293 ± 3 and 291.86 ± 6.55 days in Friesian cows in Libya and Pakistan, respectively. The possible reason for the higher mean of LL in this study can be due to the nature of data edition being employed, that all lactation below 220 days were omitted in the analysis.

The analysis of variance in (Table 4) indicates that, sire, parity and year of calving and season of calving had a significant effect on lactation length. The significant effect of parity on lactation length showed a definite reduction from the first lactation (323.1 days) to the third (315 days) lactation. Year effects indicated that lactations in 1992 and 1998 were longer (342.3and 340), respectively and shorter in 2006 and 2001(299 and 301).Sire origin significantly affected the lactation length. These results are in agreement with those of Afifi *et al.,* (1992b) and Hamed and Soliman (1994).

4.2 Phenotypic performance of reproduction traits

4.2.1 Age at first caving

The overall mean of AFC in the present study was 40.1 ± 0.4 months (Table 5). Our estimate is slightly higher than the reported by Makgahlela *et al.*, 2008 (28 month), Chagunda *et al.*, (2004), 32 ±0.14, Gader *et al.* (2007) 29.76 ± 0.40, Hammoud *et al,* (2010) 30.70 ±2.10 and Sandhu *et al.,* (2011) 29.82 ± 0.44. for Holstein Friesian in other African countries.

The analysis of variance showed that season of birth had no significant ($P > 0.05$) effect on AFC (table Table 5). This is in line with the results by Sattar *et al.,* (2005). On the other hand birth year had significant ($P < 0.001$) effect on AFC. Heifers born in the year 2011 attained1st calving at younger age of 23.64 months, whilst those born during 1989 give birth relatively at late age of 58.62 months. Age at first calving was significantly ($P<0.001$) affected by sire origin indicating that differences between sires origin in the rate of maturity of their daughters were important that may be due to different in the genetic basis of semen imported from different country. Similar finding was reported by Mokhtar *et al.*, 1993 and Safaa Ibrahim, 2002).

4.2.2 Calving interval

The overall mean calving interval was 461.1 ± 7.7 days (Table 5). This estimate is comparable with earlier reports of Mohammed, 2004 (454.8±4.6 days). But it is significantly higher than that report by Ibrahim (2006), 394±0.3days. Results of presented on table 5 showed that sire of the cow, year of calving, parity, had significant effect on calving interval.

Whereas season of calving was not a significant source of variation for the interval days between consecutive calving. The effect of parity number on calving interval clearly showed a decline in calving interval from first to third parity, the mean intervals being 510, 454, and 396 days respectively. The causes of these age-related differences in calving interval of cows might be due to nutrient requirement discrepancy for milk production, physiologically growing stages and maintenance (Negussie *et al.*, 1998). The effect of year of calving indicated significant increases in calving intervals between 1970 and 1978. This is due to the changes in general management; feeding and climatic factors were the most likely reasons causing this difference. The sire of the origin showed significant effect on calving interval and this is in agreement with the findings of, Afifi *et al.*, (1992b), Shereen Genena (1998) who also reported the calving interval was significantly influenced by the sire origin.

4.2.3. Days opens

The overall means of DO in the current study was 173 ± 6.7 days. This finding was similar to the reported by of Mohammed (2004), 178.52 days but it was higher than 124±83.7 days open for Holstein Friesian in Egypt (Tail, 2000). The days open was significantly affected by calving year. This is in agreement with reports of Gebeyehu *et al.,* (2007) and Hammoud *et al.,* (2010). The least square mean days open for the year 1986 (132.8) was the minimum while the maximum days open obtained from year 1992 (293.8). The number of days open was not affected by seasons of calving and this observation was in agreement with Amani *et al., (*2007) who reported that the number of days open was not affected by seasons of calving.

Number of days open decreased significantly with the increase in parity number from 215.89 ± 6.96 in the first parity to 158.9±15.1 in the third parity. This might be due to negative energy balance during early lactation in high producing cows that affected the onset of estrus and hence result in longer days open and calving interval. Origin of the sire had a significant ($P < 0.05$) effect on days open of cows and this is in incongruity with Moussavi and Mesgaran, (2009).

4.2.4 Number of service per conception

The overall means of NSC was 1.98 ± 0.1.This is comparable with NSC of 1.8 which is reported by of Million *et al.* (2010) for Holstein Friesian cow. But it was higher than NSC of 1.5 ± 0.5 estimated by Gebeyehu *et al.* (2007). However the present results were lower than the earlier estimates of 2.80 ± 0.10 Sandhu *et al.*, (2011) and 3.92 ± 2.77 and 2.3 ± 1.7 for Holstein Friesian in Sudan (Enid *et al.*, 2012). Variations in the management, improper heat detection and fertility status of the breeding cows can lead to differences in number of services per conception. The analysis of variance results (Table 5) showed that season of calving had significant ($P < 0.05$) effect on NSC. This significant effect of the season of calving was in agreement with results of Asimwe and Kifaro (2007). Year of calving had significant ($p<0.001$) effect on NSC. The significant effect of the year of calving was in agreement with results of Chagunda *et al.*, (2004) and Hammoud *et al.*, (2010). However, Million *et al.*, (2010) reported that year of calving had no significant effect on NSC. The present result showed that cows inseminated during 1988 had lower NSC (1.55 ± 0.15) whereas those inseminated in 1999 had higher NSC (2.45 ± 0.12). Parity had a significant effect on number of service per conception. The number of service per conception was lower in first parity compared to second and the third parity cows in the study herd. Similar findings were reported by Nega and Sendrose (2000) for the same herd. The significant effect of parity is in agreement with results of Chagunda *et al.*, (2004).Origin of sire had also a significant influence on number of service per conception. The study showed that higher NSC with semen used from unknown group and recruited in the bull dam compared to other sire origins. This might be due to variations in fertility status of the breeding bull.

Table 5: Least squares means and standard error (LSM ± SE) of AFC, CI, DO and NSC

Factor	Traits							
	N	AFC (m)	N	CI days	N	DO days	N	NSC
Overall	1125	40.1 ± 0.4	2764	461.1 ± 7.7	2773	173 ± 6.7		1.9 ± 0.6
CV (%)		17.5		25		55.0		67.4
Season		NS		NS		NS		*
Short rainy	256	40.6 ± 0.5^{a}	685	458.1 ± 8.8^{a}	687	173.6 ± 7.6^{a}	974	1.9 ± 0.7^{b}
Long rainy	510	39.6 ± 0.5^{a}	832	459.8 ± 8.4^{a}	845	171.8 ± 7.3^{a}	1201	2.8 ± 0.7^{a}
Dry	359	39.9 ± 0.4^{a}	1247	465.4 ± 7.9^{a}	1241	175.6 ± 6.9^{a}	1736	1.9 ± 0.6^{b}
Parity				***		***		***
1			855	503.2 ± 8.0^{a}	847	215.8 ± 6.9^{a}	1099	1.6 ± 0.6^{b}
2			654	473.2 ± 8.6^{b}	654	181.2 ± 7.5^{b}	876	2.8 ± 0.6^{a}
3			1197	455.8 ± 9.2^{cb}	1272	171.3 ± 7.9^{b}	1936	1.9 ± 0.6^{a}
Sire origin		***		*		*		*
Cuba	277	35.4 ± 0.7^{c}	884	473.9 ± 5.5^{a}	870	185.7 ± 4.8^{a}	1168	2.2 ± 0.05^{ba}
Finland	88	45.5 ± 1.5^{a}	94	445.1 ± 14.8^{a}	100	152.6 ± 12.5^{a}	184	1.7 ± 0.1^{b}
Holeta	91	38.3 ± 0.8^{bc}	228	455.1 ± 8.2^{a}	228	163.9 ± 7.1^{a}	323	2.6 ± 0.8^{ba}
Israel	303	39.7 ± 0.6^{b}	550	461.8 ± 7.4^{a}	571	176.6 ± 6.3^{a}	869	1.9 ± 0.7^{ba}
Italy	38	41.6 ± 1.4$_{ba}$	57	482.2 ± 15.8^{a}	56	190.5 ± 13.9^{a}	94	1.9 ± 0.2^{ba}
Kenya	97	39.1 ± 1.0$_{bc}$	333	484.3 ± 7.7 ^{a}	333	195.7 ± 6.6^{a}	424	1.9 ± 0.8^{ba}
Unknown	97	37.4 ± 0.7^{bc}	613	462.2 ± 5.5^{a}	610	176.2 ± 4.8^{a}	810	2.3 ± 0.6^{a}
USA	34	43.4 ± 2.2^{ba}	5	424.3 ± 54.5^{a}	5	146.4 ± 47 .3^{a}	39	1.7 ± 0.3^{ba}
Year		***		***		***		***

***P<0.001; **P< 0.01; *P<0.05; NS= Not Significant. Means with the same letter are not significantly different.

4.3 Estimates of variance components and genetic parameters

Designing of effective selection and breeding programs for genetic improvement requires quantitative information concerning nature and scale of genetic and environmental sources of variation and correlation among the components of performance. The information on genetic parameters, i.e. heritability and repeatability of different production and reproduction traits and genetic correlations among them is prerequisite for making efficient selection strategies as well as for the formulation of effective breeding plans. Heritability which is one of the main population parameters is the ratio of genotypic variance to phenotypic variance; and the greater the heritability, the greater would be the response to selection. This is because the additive genetic variation, which is passed from parent to offspring have a relatively greater role in determining a phenotypic performance (Bourdon, 2000).

Furthermore, estimation of heritability is the key tool for indications of determining genetic variability for selective improvement among individuals and herds either through selection or improving the management condition. Repeatability is another derivative of genetic determination and defined as the proportion of phenotypic variance due to additive genetic, non additive genetic and permanent environmental effects (Hohenboken, 1985). It is an indicator of individual's superiority or inferiority for a particular trait that is expected to be expressed next time. According to Hammoud *et al.,* (2010), genetic improvement of any trait depends, in part, on the heritability of that trait. Therefore, if estimating heritability is high there is considerable amount of genetic variation of individual in a population and this helps to recommend selection. But, if the heritability is low, the amount of genetic gain will be very small and also the progress will be slow. Therefore, the low heritability traits much more and faster progress could be achieved through improved environmental and management conditions. Hence, improvements in nutrition, productive and reproductive management should considerably improve the trait than genetic selection (Vergara *et al.*, 2009).

The heritability estimates for the traits included in this study is presented in table 6. The result showed that the heritability for days open, number of service per conception and Lactation length (0.10± 0.035, 0.07 ± 0.02 and 0.08 ± 0.025 respectively) were small, and indicates that the genetic variation in those traits are relatively lower. This may possibly be due to small data size or lack of information concerning the management sources of variation that should be accounted for in the model. However, the heritability estimates for traits like 305d milk yield (0.15), total lactation milk yield (0.15), age at first calving (0.38) and Calving intervals (0.13) were of medium magnitude indicating that proper selection strategy followed by proper breeding plan will improve the performance of these traits.

Our results indicated the possibility of undertaking a multi trait selection at Holeta bull dam herd with the breeding goal traits being 305 days milk yield, and fertility traits such as AFC and CI as a breeding objective appeared worthwhile to set up a breeding program to be applied on Holeta bull dam farm.

Table 6: Heritability and repeatability estimates of fertility and production traits from multivariate model analyses

Trait	Heritability	Repeatability
Total lactation	0.15 ± 0.04	0.45 ± 0.02
305-d Milk Yield	0.15 ± 0.04	0.41 ± 0.02
Lactation length	0.08 ± 0.03	0.12 ± 0.02
Age at first calving	0.38 ± 0.25	-
Calving intervals	0.13 ± 0.04	0.23 ± 0.02
Days open	0.10 ± 0.04	0.20 ± 0.02
Number of services per conception	0.07 ± 0.02	0.11 ± 0.04

In most dairy cattle breeding program more emphasis had been placed on production or yield traits than reproductive performance traits (Lucy, 2001). Increased emphases to those production traits have caused a lower reproductive efficiency and hence replacement of herds was impaired even in Holeta bull dam farm. As a result today in Holeta a single cow replacement was possible only after 5 to 6 calvings of a given average cow that costs much more than its return on production (NAIC report, 2009). Longer reproductive performance at Holeta farm can be seen in the longer age at first calving of on average 40 months and the extremes of 60 to 80 months for certain animals in the herd. Similarly with the current estimates of heritability (0.13) for CI and (0.38) for AFC would also indicate that there are cows having better calving interval and AFC respectively. This indicated that those cows can be selected to be the parent of next generation. Therefore, selection for AFC and CI as representative traits for fertility and 305 days milk yield for production trait can be the best combination of breeding goals traits that Holeta bull dams can make use of in its future breeding and selection programs.

4.3.1 Phenotypic and genetic correlation among the production and reproductive traits

Livestock are usually bred for multiple rather than single traits, these traits of farm animals are always bound to have a relationship among each other. This relationship can be shown through the correlation of traits as positive or negative values in an individual (falconer, 1989). The phenotypic and genetic correlation estimated by fitting a multitrait repeated records model confirmed the presence of favorable genetic and Phenotypic correlations between traits 305-dMY, AFC and CI (Table 7). The magnitude and direction of genetic and phenotypic correlation of these traits shows favorable associations, that means selecting for high 305d MY animal will favor selecting for early maturing and shorter calving intervals. This was in line with the conclusions by Salman (1985) and Evans (1996) who indicated that the correlations between 305d milk yield and reproduction trait that raged from 0.04 to -0.39 and -0.4 to -0.81 for phenotypic and genetic respectively is considered antagonistic relationship. Rege (1991) reported phenotypic correlation of 0.08 between milk yield and age at first calving and 0.108 between milk yield and calving interval is considered antagonistic relationship. Therefore, the traits being observed on the same animal would mean that if selection on such combination trait is carried out, it will build a framework for sound breeding program for Holstein dairy cattle in Ethiopia.

Table 7: Correlation between production and fertility traits from three trait analysis

Traits	305-dMY	CI	AFC
305-dMY		-0.12 ± 0.024	-0.01 ± 0.02
CI	-0.13 ± 0.14		0.10 ± 0.04
AFC	-0.24 ±0.12	0.04 ± 0.01	

Phenotypic correlations above diagonal and Genetic below diagonal

4.4 Estimated Sire Breeding Values

4.4.1 Estimated Sire Breeding Values for 305 days milk yield

The sires of Holstein Friesian herd in Holeta originated from eight (8) different countries origin and they are said to be one of the heterogeneous mixture of a sire genetic pool existing in Ethiopia (Table 9). One of the objectives of this study was to investigate the existing adaptive and performance variation observed among the sire progenies based on the average breeding values for 305-day milk production, calving interval and age to first calving.

The estimates of breeding values of 137 sires having 1476 half sibs and full sib progenies being born in the bull dam within nearly 35 years were evaluated by fitting the multi-traits repeated record animal model have shown that significant ranges of variability exited among the sire families. Estimates of sire breeding values for 305 day milk yield ranges from -631.2 to 965 with SD 236.3 kg (Table 9). This result was comparable in having higher level of variation in estimated breeding values with the study by Rozzi *et al.*, (1990) among sires used in USA which have shown estimated breeding value rages from -276.0 to 812.0 kg. The current study slightly lower range of variation than those reported by Arian *et al.*, (2003) on Holstein cattle in Egypt -628.0 to 1289.0 by using multi-trait animal model. The standard deviation (SD) of 236.3kg and the heritability of 0.15 for this trait indicate high variability implying a possibility for selection based on their genetic merit that can bring the improvement in the next generation if these high ranking groups are used as the parent in new breeding plan. Sires with positive values for 305 day milk yield were among the preferable sire categories. Accordingly, sires with ID No. 10-091, Lichy, Hoiken, Koivalan, Lappalan, Bavel, (Table 8), were the best sire which have higher mean than the mean value of the population. Selecting the daughter of those sires for breeding purposes may lead to a relatively faster genetic improvement in 305 d milk yield.

There was a notable difference in the mean of estimated breeding values of the sire based on origins category over the study period. The mean of estimated breeding values for 305 day milk yield obtained from Ethiopian, (237.8 kg) and worldwide sire of United States daughter

(114.2 kg) had the highest mean breeding value for milk yield followed by bulls from Italy (50.7 kg), Israel (47.6 kg) and Cuba (38.5 kg) (Table 9). Differences between estimated breeding values for these traits might due to differences in breeding objective of the countries of origin, and possible genetic environment interaction effect due to the change in environmental factors relation to the countries of origin. This result of EBV for adjusted 305 d milk yield on sire origin was lower than similar study reported by (Ojango and Pollott 2001) where bulls from the United States had the mean (231 kg) and Israel (409 kg) for 305 day milk yield of breeding value higher than the mean of all bulls used. Muasya et al, (2014) also reported sires originated from USA were better performing in Kenya environment than Canada and Kenya sires on 305 d MY. On the other hand the bulls origin named as unknown (26.2 kg) and Kenya (-11.4 kg) had the lowest mean breeding values for 305 day milk yield as compared to the sires imported from other origins (Table 9). This result is in agreement with Ojango and Pollot (2001) which said that Kenyan bull on Holstein Friesian cattle on large-scale Kenyan farms was below the mean value of (-17 kg) in 305 day milk yield.

Table 8: Rank of sires based on estimated breeding value for 305d MY and estimates of its reliability for Holstein Friesian in Holeta bull dam herd

Rank	Sire ID	The best ranking sires		
		EBV	No daughters	r_A
1	Lichy	376.2	46	0.64
2	Bavel	366.3	56	0.67
3	Balon	325.8	19	0.60
4	Loten	315.4	21	0.64
5	10-091	132.5	124	0.72
6	Hoiken	242.3	27	0.67
7	Lappalan	238.2	26	0.65
8	Sumelian	211.5	89	0.78
9	Ginoser	205.9	56	0.76
10	Goliat	205.9	87	0.75

Table 9: Mean of estimated breeding value with its SD, daughter groups of diverse sires group defining numbers of progeny (N) for fertility and milk traits

Origin		AFC			CI			305d MY		
	N	Mean ±SD	Max	Min	Mean ±SD	Max	Min	Mean±SD	Max	Min
Cuba	258	-1.5±5.1	10.2	-15.21	2.8±21.6	71.8	-52.5	38.5±226.4	650.2	-465.6
Finland	86	-0.5±2.3	5.6	-6.6	-0.2±16.3	47.1	-46.64	67.6±222.7	965	-631.2
Ethiopian	120	-0.1±3.2	9.2	-11.84	0.02±21.8	62.1	-48.54	237.9±371.7	945.8	-518.1
Israel	450	-0.1±2.4	8.5	-10.26	0.7±6.2	69.5	-50.9	47.6±207.6	948.6	-522.5
Italy	126	-0.1±1.6	3.7	-3.09	-6.9±16.9	39.5	-46.9	50.7±309.8	1039	-508.7
Kenya	153	0.1±2.8	9.1	-4.76	3.2±29.6	70.2	-56.1	-11.4±204.7	469.8	-519.3
Unknown	163	-0.5+3.6	8.4	-11.34	-0.9+18.8	52.5	-53.3	26.2±201.9	495.5	-475.8
USA	131	0.2±1.5	2.7	-2.441	-1.8±8.7	20.7	-18.3	114.2±356.2	892.5	-473.8
Total sire	137	-0.1±3.3			0.7±18.8			22.2±236.3		

4.4.2. Estimated Sire breeding value for age at first calving

Estimated breeding value of AFC in this study ranged from -15.2 to 10.1 months, indicating the presence of high genetic variability between sires used in this study. This result showed highly strong level of variation compared with some of the studies by Hatem Ismail (2006) who reported estimated breeding value ranges from of -1.2 to 1.95 months among their study herd in Egypt and Abdel-Glil (1996) reported a range of -1.20 to 0.93 months. The genetic standard deviation of AFC was 3.21 month (Table 9) indicating the genetic difference among the sire families in the herd, which determines the rate of genetic improvement that can be achieved through selections. Therefore, using this variability is an important opportunity to improve the traits in the bull dam farm. Generally, the results in the current study have shown that estimated sire breeding values with negative value are among the best performing groups in shortening AFC as a breeding goals targets (Table 10). Sires which have ear tag numbers of 1624, 1545, 1700, 85, 20 and 50 were among the best selectable sire in terms of age at puberty.

The genetic variances for AFC in the current study showed difference in ranking of sires from that of production traits among the sire origins. The mean of estimated breeding values obtained from all daughters of sire origin for age at first caving was negative except United States and Kenya origin which have 0.2 and 0.1 months respectively. According to table 9 bulls from Cuba have -1.5 month comparatively is the lowest mean EBV for age at first caving followed by bulls from the Finland with -0.5 month, unknown group had -0.5 month, Italian -0.1, Ethiopian -0.1 month, and Israel -0.1 month subsequently.

Table 10: Rank of sires based on estimated breeding value for AFC and estimates of its reliability for Holstein Friesian in Holeta bull dam herd

Rank	Sire ID	The best ranking sire		
		EBV days	No daughters	r_A
1	1624	-13.7	27	0.90
2	1545	-9.6	52	0.78
3	1700	-8.6	11	0.83
4	85	-6.7	18	0.82
5	50	-5.9	18	0.80
6	20	-5.5	28	0.87
7	19	-4.9	30	0.88
8	310.	-4.7	59	0.71.
9	244	-4.6	22	0.79
10	179-84	-4.2	61	0.72

4.4.3 Estimated Sire breeding value for calving interval

The range of estimated sire breeding values obtained for calving interval was -56.1 to71.8 days with genetic standard deviation of 18.77days (Table 9). This result is higher than the ranges obtained by Abdel-Glil (1996) using the same model which ranged from -5.38 to 6.77 days for calving interval in Egypt. The range of breeding values of the study herd for calving interval indicated the existence of sire genetic variability in the herd. This will help to boost the reproductive performance and breeding efficiency of the existing herd by selecting sires with minimum calving days interval. Accordingly the EBVs, showed that sires like 329, 155-91, 37,155-91,134, 296-84,105, (Table 11) were among the better performing for calving interval in the herd.

The mean of estimated breeding values based on their origin indicated that bulls from Italian have -6.98 days, USA-1.8 days and unknown origin with -0.9days had comparatively the lowest mean EBV for calving interval followed by sires from the Finland with -0.2, days. According to Ojango and Pollot (2001) who reported from Kenya, sire from Italy had -0.2 days, USA -0.8 days which is in line with the current result. Therefore, the current result of the sire performance with the sire originated from Italia, USA had showed their better fertility performance of the Holsteins Frisian lines in both Ethiopian and Kenyan condition. On the other hand, Bulls from Ethiopia with 0.1 days, Israel 0.7 days, Kenya 3.2 days and Cuba 2.8 days, had the highest wastage days for calving interval which indicate poor performances (Table 9).This result of Kenyan sires (3.2 d) was different in performance reported in their home land by Ojango and Pollot (2001) that showed -0.63 days mean of calving interval.

Table 11: Rank of sires based on estimated breeding value for CI and estimates of its reliability for Holstein Friesian in Holeta bull dam herd

Rank	Sire ID	The best ranking sire		
		EBV	No daughter	r_A
1	329	-45.9	23	0.75
2	296-84	-32.1	18	0.65
3	105	-31.2	5	0.27
4	155-91	-29.5	6	0.54
5	134	-26.6	34	0.80
6	10-013	-20.4	43	0.79
7	37	-19.2	7	0.54
8	10-091	-15.4	124	0.65
9	loten	-18.2	94	0.53
10	10-024	-18.1	7	0.51

4.5 Accuracy of breeding value.

The ranges of reliability i.e. the correlation between estimated and true breeding value as the measure of accuracy in this study were found between 23-86%, 54-93% and 15-76% for 305d MY, AFC and CI, respectively. The accuracy of breeding value observed for the age at first calving was found to be high, indicating the existence higher genetic bases in variability that have positive correlation with heritability estimates. van der Werf (2006), who stated that when selection is on the animals own phenotype, the accuracy of selection is equal to the correlation between phenotype and breeding value, which is equal to the square root of heritability. Similarly, if animals in relationship among the study increase the accuracy of estimated for breeding value increase, as Kejal (2013), justified that the accuracy is higher when more information is used which is the rationale behind the accuracy of 305d MY was greater than CI. In the current evaluation the ranking of animals with lower estimates of precision had been avoiding for the reason that its selection on estimated breeding value would not be reliable at all (Muasya *e t.*, 2014)

4.6. Trait preference and its Economic index Interpretation

The trait preference survey had confirmed that nearly 101 (70%) of the respondent had given the first rank to milk production traits, followed by Fertility traits of 43 (30%) and 116 (81%) for AFC and CI (2nd and 3rd) respectively. The ranking indices of trait preference indicated farmers rated milk production traits as first and fertility traits as second (Table 12). The Preference expressed as index value on dairy traits by the respondent had indicated that (0.54) for milk production traits and 0.43 for fertility traits (Table 12). The economic weightage for dairy traits across the developed and developing countries reviewed and indicated that the weightage for production traits surmount >56% (Schneider, 2009), which support the index value we have used in the current study. Therefore the current ranking index of traits and previous literatures on economic traits of importance were used as a base for developing economic weightage for the three prioritized traits in this study as (0.60 for MY, 0.25 and 0.15 AFC and CI, respectively).

Table 12. Index of traits perceived by farmers and consumers as of economic importance

Trait	farmers ranking index									consumers ranking index			
	R1	R2	R3	R4	R5	R6	R7	R8	Index	R1	R2	R3	Index
MY	101	24	20	-	-	-	-	-	0.25	93	20	9	0.45
AFC	3	43	74	4	11	10	-	-	0.18	-	-	-	-
CI	1	8	116	-	-	16	-	-	0.17	-	-	-	-
Longevity	-	5	9	112	18	2	-	-	0.17	-	-	-	-
Growth rate	-	-	-	6	8	34	68	25	0.07	-	-	-	-
NSC	-	-	-	7	36	30	37	27	0.08				
Fat	-	8	15	67	21	22	13		0.12	7	64	51	0.27
Yoghrt	-	-	-	-	-	-	-	-	-	8	61	53	0.27
Adder health	-	-	-	-	19	28	27	67	0.06	-	-	-	-

**R= rank I= index;index sum of (8 for 1+7for 2+….1 for rank 8) given for an individual reason divided by the sum of (8 for 1+7for 2+….1 for rank 8) for over all reasons*

4.7. Aggregate Genetic merit index for sires

An animal evaluation with total aggregate genetic merit takes care of both productive and reproductive traits and helps to select an animal with efficient performance. This is possible through linear summation index of the breeding values standardized by the methods of Hazel and Lush (1943). The aggregate genetic merit index shows the biological efficiency of the given animal by combining the production and fertility traits. This view is also expressed by Hansen *et al*. (1993) who noted that if single-trait selection of dairy cattle for milk production is continued, adverse effect such as reproductive inefficiency would be encountered.

The breeding objectives of the Holeta bull dam farm as per the current study need to be modified to include traits like AFC and CI in addition to 305 d MY so that animals selected as parent of the next generation have the best combination of genes for production and fertility traits. Therefore, selection criteria base on all 305 days lactation, Age at first calving and calving interval after standardization of the merits of the estimated breeding value would identify sires and dams with higher aggregate genetic merit. In this herd, the aggregate genetic merit from multivariate model evaluation showed that aggregate breeding value for sires line ranged from (119.2 to 66.3) of the total genetic merit for the breed maintained under the period of study. The genetic variability expressed by genetic standard deviation (43.5 indexes) for total merit indicated that larger proportion of genetic variance might be due to the use of different source semen imported by NAIC at different time period. But, the current estimate is not as good as expected, this could be due to the absence of all rounded selection goal trait and mismanagement of the imported gene pool by NAIC that had shown preference for certain sire origin than other semen sources and even bulls of certain trade mark. This had caused more homogeneity of the herd that triggered lower estimated heritability, besides small herd size contributing to possibly lower h^2 estimate. Certain sires like 1624, Marlin, 1700 and 1545 (Table 12) had a best performance in combined total merit index for both production and reproduction trait.

Table 12: Rank of sire based on estimated breeding value and total genetic merit and estimates of reliability for Holstein sires in Holeta bull dam herd

Sire ID	No Dou	EBV AFC	I_{Ar}	Index AFC	EBV CI	I_{Ar}	Index CI	EBV 305	I_{Ar}	Index 305	weighted Agg
1624	27	-13.7	0.93	233.2	0.9	0.79	98.1	-538.4	0.80	77	119.2
Marlin	12	-1.2	0.54	100.6	-3.7	0.77	101.4	946.7	0.19	128.1	117.2
Dalta	27	-2.2	0.69	110.5	-18	0.75	111.9	623.4	0.34	117	114.6
1700	29	-8.6	0.83	178.4	-5.1	0.66	102.4	-201.1	0.68	88.6	113.1
1545	7	-9.6	0.78	189.1	4.9	0.58	95.1	-372.1	0.60	82.7	111.2
85	18	-6.7	0.82	158.8	0.7	0.62	98.2	-71.3	0.65	93.1	110.3
50	18	-5.9	0.8	150.5	-0.3	0.6	98.9	4.6	0.62	95.7	109.9
Bavel	21	-2	0.84	108.8	-3.2	0.57	101	366.3	0.67	108.1	107.3

No = number of daughter EBV = estimated breeding value weighted Agg = weighted aggregate I_{Ar} = reliability

4.7.1. Ranking of sires' index based on the country of origin

The implication of sires ranking in the first 1-50 ranks based on the total merit index for production and reproductive performance as sire summaries was ranked to develop possible conclusion on the use of locally selection program in relation to direct import based improvement strategies. In this study the best sires ranking from 1st to 50 th in total merit index indicated that locally selected sire groups from Holeta and Unknown origin took the 30% of the sires samples (15 sire families) in the lists of best ranking aggregate merit index, this could be due to the reason that NAIC had been selecting these sires from locally adapted population, that might helps it to excel in overall performance in Ethiopian management scenario. The sires from Israel had nearly contributed 22% of sire samples i.e. (11 sires) families with the best ranking aggregate merit index ,followed by again sires from USA contributing 20% sire lines (10) sire families in the ranking which are being proven to show best fertility parameters especially for CI (-1.8 days) and optimum 305 days milk yield (114.2 kg).The Finish sire line even if the samples of sire used over the study period were small for fair comparison, it had best fertility index (-0.5 month, -0.2 days) for AFC and CI respectively and 305 d MY (67.6 kg), we can see the 9% of the sire in the ranking are from

Finland. Similarly the Cuban are best in the rank of Fertility traits specifically the Age at first calving contributing 6.5% of the sire lines in the rank, Italian also good in fertility traits in both AFC and CI, contributes 6.5% the Kenyan even if they are from tropical origin it contributed 4.4% of the ranking sire samples with 3 sires families only in the list of best ranking summaries.

The current study confirmed that the bull dam and follower herd based genetic improvement program through selection on locally adapted Holstein Friesian in Ethiopian environment had proved success to adapt and yet give more overall performance, which presuppose that relying on mere import of semen from abroad would be not the right strategy alone. As Smith (1988) pointed out, if genetic and environment interactions are important across countries, then an independent domestic genetic improvement programme would be needed and would be justified. He however cautioned that what developing countries should avoid is the unnecessary duplication of expensive breeding efforts being carried out in other countries, and from which they could benefit at little cost. Therefore, NAIC have to continue with selection on multiple traits goals of two or more traits with possible import of semen or germplasm intermittently. The import of semen by MoA or NAIC have to follow the total merit index of sires to be imported to avoid, the possible genotype by environment interaction that may arise due to selection criteria difference between the country of origin and the Ethiopian management situation.

4.8 Aggregate genetic merit index for Cows

The estimated values of cow’s aggregate genetic merit for 305d milk yield, age at first calving, calving interval from multi trait animal model evaluations ranged from (125.9 to 64.2). The genetic variability expressed by genetic standard deviation of (40.3 index) estimated for cows total genetic merit indicated that larger proportion of genetic variance might be due to the use of different source semen imported by NAIC at different time period. The genetic standard deviation for sire lines were better than the deviation for cow index indicating the base of diversity comes from sire sources. Certain dams like h1-1514, h1-1511, h1-1506 and h1-1505 (Table 14) had a best performance in combined total merit index for both production and reproduction traits. This could be used for bull dam selection for young bull replacement scheme at NAIC and the remaining female line herds are to be used as test herd group for young bull progeny testing scheme.

Table 13: Ranking of cows based on estimated breeding value for total genetic merit and its accuracy estimate for Holstein sires in Holeta bull dam herd

Cow ID	EBV AFC	Index AFC	I_{Ar}	EBV CI	Index CI	I_{Ar}	EBV 305	Index 305	I_{Ar}	weighted Agg
h1-1514	-0.8	101.3	0.82	-32.9	116.2	0.54	965	122.1	0.63	113.4
h1-1511	-0.4	98.8	0.81	-3.9	97.2	0.55	945.8	121.4	0.61	114.1
h1-1506	-1.9	108.4	0.81	29.4	75.4	0.46	766.9	115.3	0.58	89.1
h1-1505	0.9	91.5	0.82	-2	96	0.52	748.2	114.7	0.61	93.3
h1-1501	0.4	94.2	0.82	-24.5	110.7	0.53	711.1	113.4	0.61	99.3
h1-1498	-1.8	107.4	0.82	-12.5	102.9	0.52	691.9	112.8	0.61	92.8
h2-1493	-1.6	106.4	0.83	-34.3	117.1	0.59	649.1	111.3	0.64	107.4
h1-1488	-2.11	109.2	0.81	-5.5	98.3	0.31	639.1	111	0.51	86.9

No = number of daughter EBV = estimated breeding value weighted Agg = weighted aggregate I_{Ar} *= reliability*

4.9. Phenotypic and genetic trends for production and reproduction traits for cow in Holeta bull dam

4.9.1 Phenotypic and genetic trends of total lactation Milk yield for cow

The annual phenotypic trend in the Holeta bull dam herd over the study period in total lactation milk yields was 4.5 kg increment in milk yield per year (Table14). The present findings were lower than Mohsen *et al.,* (2000) who reported an annual phenotypic change of 200.38 kg, per year. The trend for total milk yield showed slight decline in phenotypic performance from 1982 to 1985 and 2000 to 2002 but high deterioration in 1991 to1994. Even though, the phenotypic trend for total lactation milk yields showed a negative trend (Fig.1), the genetic milk production potential of these animals were good. The decreasing performance could not be due to genotype of animal, it might be due to lack of better feeding as well as improvement in management practices. The waving line from 1979 to 1994 may largely be attributable to environmental factors, lack of well designed selection criteria in the herd. The other possible reason for this deterioration of phenotypic trend in 2010-2012 may be due to the fact that different diseases occurred during different years and high performances cows were culling due to TB cases especially in 2012. The graph showed from 2000 to 2007 milk yields has increased irregularly. However, from 2003 to 2010 total lactation milk yield were bounced up after the NAIC has started supporting the bull dam farm.

Table 14: Phenotypic and genetic trends for both production and reproduction traits

Dam Phenotypic trend/y	Traits	Regression equation	R^2
	TLMY	4.5x+166.12	0.44
	305 Day milk yield	22.2x-63.29	0.47
	AFC	-0.7x+23.53	0.69
	CI	-0.5x+36.67	0.41
Dam Genetic trend /y	TLMY	6.1x-41.60	0.29
	305 d MY	9.5x-87.72	0.35
	AFC	0.6x+27	0.40
	CI	-0.07x+2.24	0.48
Sire genetic trend/p	305d MY	10.9x+102	0.63
	AFC	-7.1+18.9	0.58
	CI	-1.1x+4.12	0.53

The genetic trend for total lactation milk yield over the study period showed positive trend compared to the base population of 2008 indicating a genetic improvement in averaged total milk yield presenting the bull dam performance (Table 14).The result was signifying the genetic increases of 6.1 kg per year. This result is significantly higher than Gunawan *et al.*, (2012), which reported the annual genetic increment of 0.4 kg per year for total lactation milk yield. This increment might be due to the use of frequently imported semen at different time from sires having some better breeding values for milk yield. The genetic trend in total lactation milk yield (Figure 1) showed a gentle trend compared to phenotypic changes over the years. Though the general trend showed improvement but a decrease in trends were observed during 1986, 1990, and 1996- 1999. This might be due to the use of semen from inferior quality sires Cuban and Kenyan origin and over utilized of certain semen sources on those years. Similar findings have been reported by Javed *et al*., (2003) in Pakistan which was mainly due to high use of semen from sires recruited from the same herd. The present results

(Fig 1) showed continuous improvement in the genetic trend from 1999 onwards to 2012. This may possibly be duo to the selection based on production traits conducted by NAIC.

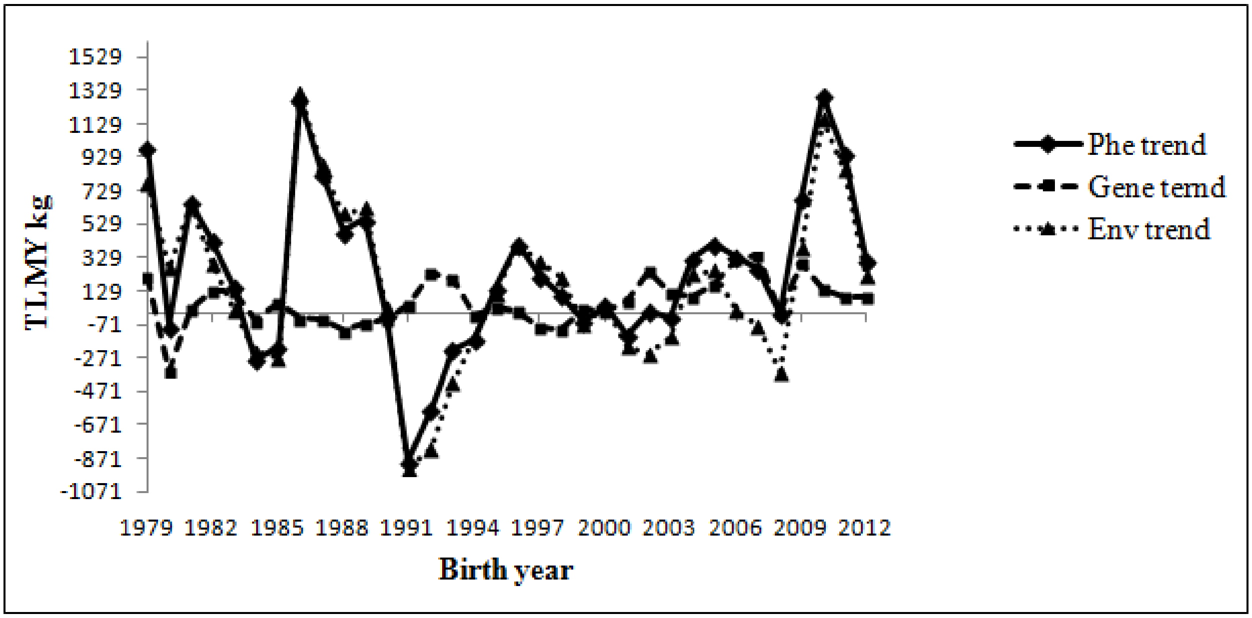

Figure 1: Genetic and phenotypic trends of TLMY for cows at Holeta bull dam farm

4.9.2 Phenotypic and genetic trends of 305 day milk yield for cow

The overall phenotypic trend for 305 days milk yield in the current study was positive with estimates of 22.2 kg per year (Table 14).The present results were lower than the reports of earlier studies (Mohammed *et al.*, 2000; Glil, 1985 and Weller *et al.*, 1984) for the same breed of cattle. Mohammed *et al.* *(*2000) reported an estimate of 48.00 ± 7.05 kg/ year in Egypt and Germany, Glil (1985) reported a positive annual phenotypic change of 33.29 ±13.50 kg in Egypt and Weller *et al.*, (1984) computed a change of 177 kg/ year in Israel. However Canon and Munoz (1991) and Rege (1991) reported negative annual phenotypic change of -78 ± 8 kg and -5.5 kg in Friesian cows from Spain and Kenya, respectively.

The graphical representation of the trends for the 305 days milk yield (Figure 2), this trend has the followed the same pattern as the trend for total lactation milk yield. The graph shows that, the decline in the phenotypic performance has also been seen in 1982-1985 and 1990-1993. The declining trend in the phenotypic performance might be attributed to poor management as the consequence of government transition and political instability from (1991-1993). Since deterioration has been consistent during those years, it may also be an indication of the fact that the selection procedure practiced in the herd during that time was not effective. The slight improvement observed in trend line from the year 2000 to 2009, which has became markedly high after it up to 2012. This might be due to the effects of environmental influence and the management change extend used in the period. Especially, from 2009 the NAIC was producing concentrate by its own formulation and this could be one of the reasons for the improvement of milk yield. Therefore, it had concluded that phenotypic trend for 305 day milk yield of the studied bull dam herd can be increased with introduction of good management application.

The genetic trend for 305-days milk yields from the linear regression on birth year of dams and sire was 9.5kg per year (Table 14), this result was significantly higher than Yaeghoobi *et al.*, (2011) who reported positive genetic trends for milk yield as 0.171 kg/year. On the other hand, a negative annual phenotypic change has been reported by Rege (1991) working on Friesian cows in Kenya who found that the genetic trend for 305-dMY was -2.5kg /year. The genetic trend for the 305 day milk yield in Holeta bull dam farm was in general positive (Fig. 2) indicating a slight genetic improvement in the Holstein Friesian herd. The population of the first generations of 1979 to 1993and 1997 had show decreasing genetic trend and a worst fall trend observed between 1984 to1992. The average genetic performance trend fluctuation as positive and the decreasing trend probably might be due to repeated use of small number of sires, use of semen for certain sire for long time (Cuban Kenya and Israelis origin) or lack of systematic mating and selection which can cause waving in the EBVs. However, positive trend was observed after 1993 in the study period. This could be due to the use of imported semen of the sires and bulls selected locally having better breeding values for milk yields from different source during the last period of the study. The current study indicates that there was apparent change in the herd composition through attempted selection or mating strategy in addition to the germplasm which was imported. The slight recovery after 1999 compared to the other previous years might be the result of newly imported germ line from Finland, USA, and those recruited in Holeta farm plus selection procedure practiced by the NAIC in addition to environmental improvement during this time period.

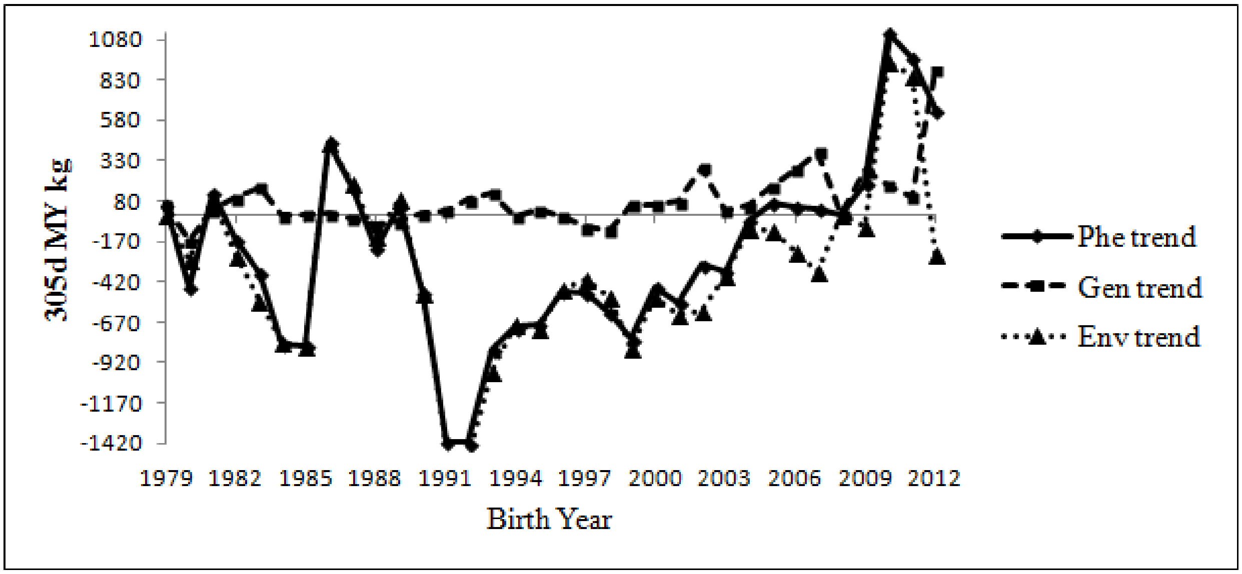

Figure 2: Genetic and phenotypic trends of 305d MY for cows at Holeta bull dam farm

4.9.3 Genetic and phenotypic trends of age at first calving for cow

The phenotypic trend for age at first calving in the study period was negative -0.7 month per year (Table 14). This negative trend indicates that the quality of sire and dam entering the herd was improving over time. This would imply that sires used in the herd, which were supposed to inject new superior genes into the population, were actually meeting the targeted goal. The result was better than that of Gunawan *et al*. (2011) who reported positive (1.7 months) per year. The phenotypic trend for AFC is in figure 3. The figure shows that phenotypic trend from 1979 to 1993 was increasing in AFC. This was due to management problem such as poor heat detection, the skill of technician and nutrition which can affect the AFC. But, the improvement was seen after 1994 to 2012. This trend might be due to the effect of environmental factors and management situation during this period. It was then shows improvement from 2008 to 2012 and that reached to 26.66 month on average (which is less than 30 month in each year). The continued decreasing trend from 2006 up to 2012 was due to the emphasis given to all components of the breeding program, including management improvement in feeding and breeding (Fig.3) that lead to a decrease in the AFC. The genetic progress in AFC was calculated by regressing EBV for AFC on birth year of animals and this showed that the trend in Holeta bull dam farm was nearly zero 0.02 days per year. This finding is in contrary to (Gunawan*et, al.*, 2012), who stated that the annual genetic trends were -0.29 months for age at first calving. But this result was in line with the estimation of South African Holstein 0.07 month per year. According to Van vleck, (1986) the failure in annual genetic gain of AFC could be attributed to long generation interval, lack of emphasis on the traits, and weaknesses in genetic evaluations of bulls and cows.

The genetic trends for AFC in this study have shown improvement in performance from 1979 to 1985. This may be due to the use of sires from Cuban origin which is better in breeding value at early maturation. In contrast, the trend after 1999 linear trend line which might signal the absence of selection done toward AFC.

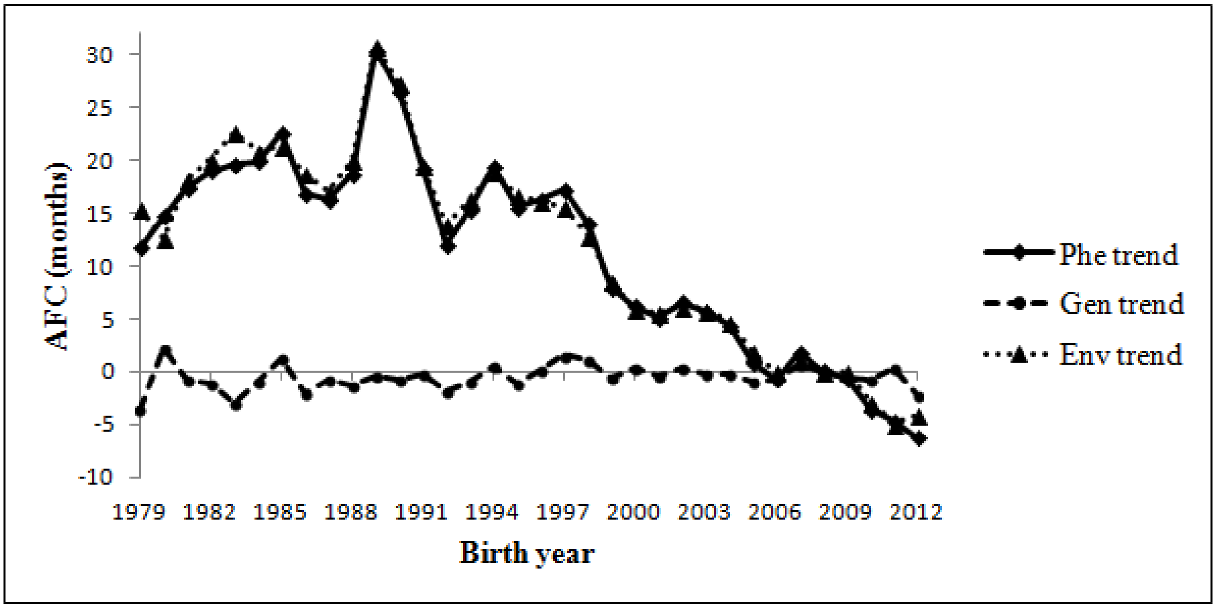

Figure 3: Genetic and phenotypic trends of AFC for cow at Holeta bull farm dam

4.9.4 Genetic and phenotypic trends of calving interval for cow

The change in phenotypic trend for calving intervals traits in the current study was -0.5 day per year (Table 14), which showed improvement in performance which might attributed to improved feeding, heat detection, the skill of technician and breeding management through the time period under the study. The result was nearly similar with that of Mohamed *et al.*, *(*2000), who stated the annual phenotypic change is -0.51. Concurrently, Hare *et al.* (2006) reported that regression of phenotypic trend for CI that was 1.07 year coinciding with Mohsen *et al.*, (2000) who reported 1.78 day for CI in Egypt.

The graph (Fig 4) depicted that phenotypic values of CI was increasing in around the year 1982 to 1985 and similar worse situation occurred during the time of change of the government and management deterioration in Holeta bull dam in 1996 and 2009. However, the graph had depicted those phenotypic values of CI from 1994 to 2005 in the bull dam herd shows irregular trends with some improvement through time (Fig. 4). This waving changes along the years in the mean phenotypic values observed in herd can be a reflection of applying management system improvement by NAIC even if there was no systematic selection and non-stability in the management system geared to improve calving intervals. Generally, the graph showed that there was no selection procedure performed for the improvement of calving interval in the bull dam herds. This could be due to the fact that selection was only focused on production traits and attention was not given to fertility traits in breeding program of the farm for replacement heifers.

The annual genetic changes in calving interval were not significantly different from zero but changes had occurred in the same direction as phenotypic trend. The rate of genetic change for Calving interval represented a genetic progress of -0.07 day per year (Table 14). This negative sign indicate that the genetic quality of heifers' replacement entering the herd was minimizing the length of calving interval. This would imply that sire importation, which is supposed to inject new superior genes into the population, was actually having a favorable positive effect. This finding is nearly similar to (Gunawan *et al.*, 2011), who reported the annual genetic trends were -0.88 days of calving interval.

However, the increment of the genetic trend were also seen in 1986, 1999 and 2000 showed favorable trend which have been decreasing performance in calving intervals. This positive trend may be due to the fertility problems such as silent heat and ovarian cysts, which were as the result of increasing milk production (Harman, 1994). These kinds of fertility problems obviously make an early conception more difficult.

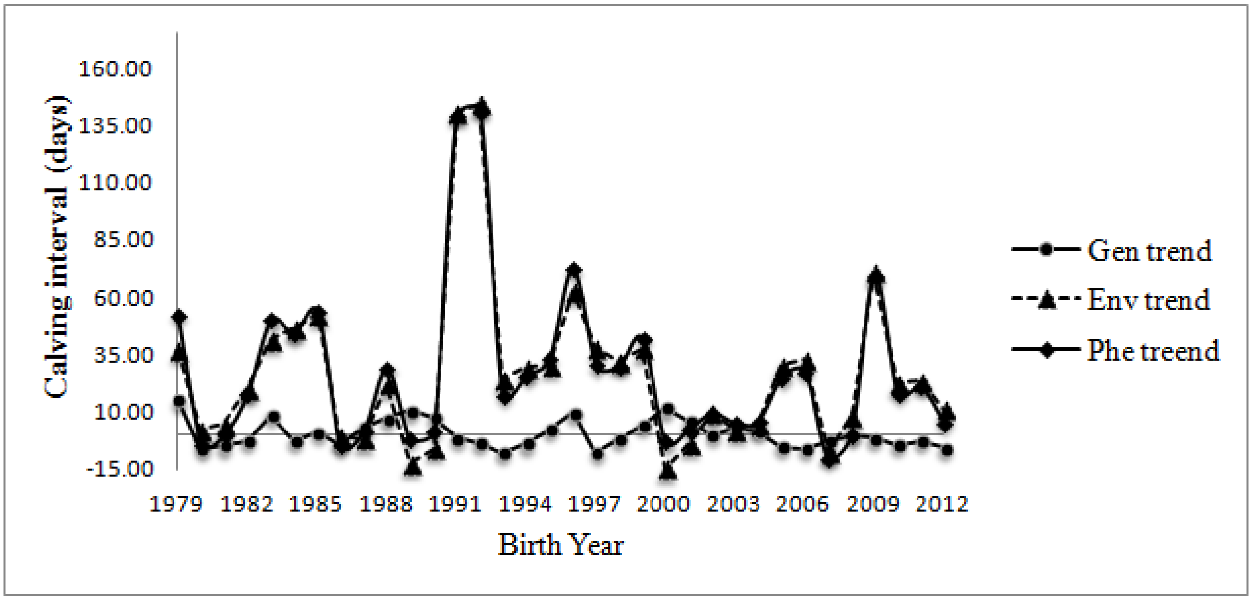

Figure 4: Genetic and phenotypic trends of CI for cow at Holeta bull dam farm

4.10. Sire genetic trends for production and reproduction traits.

4.10.1 Genetic trends for the Fertility traits

The annual genetic trend in the Holeta bull dam based on sire trend analysis over the study period in age at first calving and caving interval was -7.1 and –1.1 days/year in AFC and CI, respectively (Table14). This annual genetic progress indicated that most of the genetic gain to the bull dam farm comes from sire line import over the years and selection done local by the NAIC. However relatively high increment of trend line for CI and flat linear trend for AFC for the 1st and 2nd period of the years between (1979 to 1990) indicted the use of sires being originated from Cuban that had best performance in AFC and poorly performing Kenya sires in both traits, that makes the near linear mean performance of the population under the study. Similarly, both sire origin used in during this period were poor in CI that is why graphs shows increment in CI trait at these particular periods. However, the 3rd period which comprise the year from 1991-1995 within which some improvement have been observed in fertility traits where later on in period 4th (1996-2000) the trend indicated slight prolonged duration in performance of AFC and CI , which might be due to the absence of selection objectives by NAIC confounded with management situation. The period 5th and 6th which includes the birth year (2001 to 2012) indicated the improvement in both traits which have something to do in the attempted to import sires from different origin like Italy, USA and Israelis which had better overall breeding efficiency and performance that contributed in shorting age at first calving and calving interval.

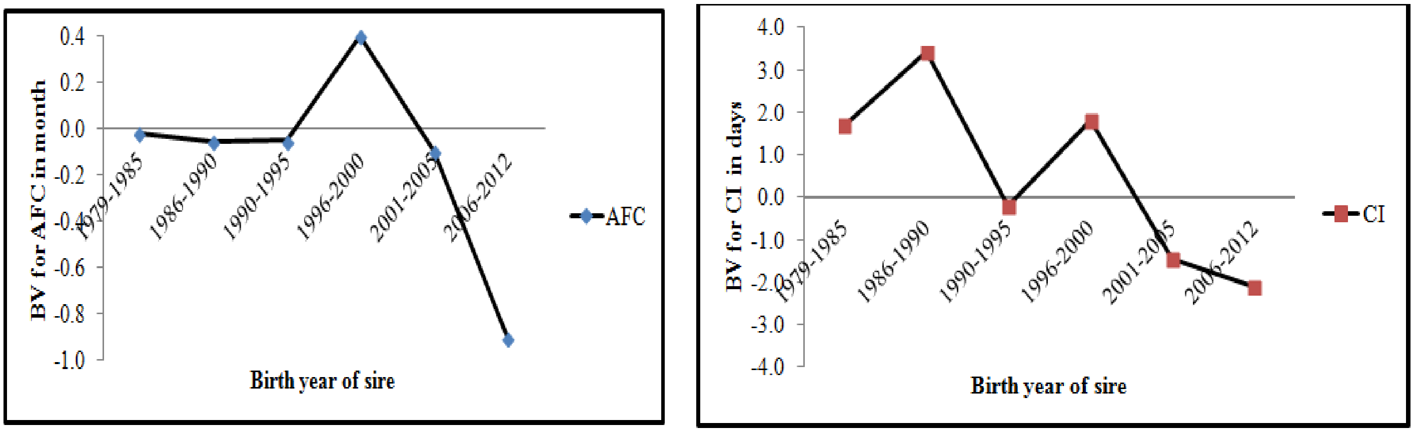

Figure 5: Genetic trend of AFC and CI for bulls in the Holeta bull dam farm.

4.10.1 Sire Genetic trends for 305 days Milk yield trend

The annual genetic change of sire over the study period in 305 days milk yield was 10.9 kg/year increment in milk (Table14). This annual genetic progress indicated that there is significant change on milk yield over the study period. The same is true with that of fertility traits, sire trend line shows more annual genetic change than females line trends(6.12 kg/year). The genetic trend line for 305 days milk yield in period 1st, 2nd and 3rd which comprise the years from 1979 to 1995 indicated the improvement of 305 days milk yield, indicating that the sire used from Cubans, Kenyans and locally selected bulls were used with nearly annual progress of 2kg/year. It was the time when farms was run by DDE and the role NAIC had been annual recruitment replacement only. But, starting from the end of period 4th which was (2000-2005) is the time period the NAIC had taken the responsibility of running the bull dam farm with the shift in the main objectives. In this period the annual genetic change (12kg/year) observed seems good enough to justify the Indigenous selection program on sire replacement and overall change it had been mandated to. But, the progress being made in period 6th were somewhat shown to slow (4kg/year) down relative to 5th period until the end of the study period. The overall progress by the sire trend analysis made to evaluate the indigenous selection program appears that the local selection program by NAIC had ascertain some improvement that would justify its very existence special after the change from phenotypic and pedigree based animal evaluation system to genetic merit (by Univarate animal evaluation) and the use of other better performing sires import from different countries (Italian, Israel and USA).

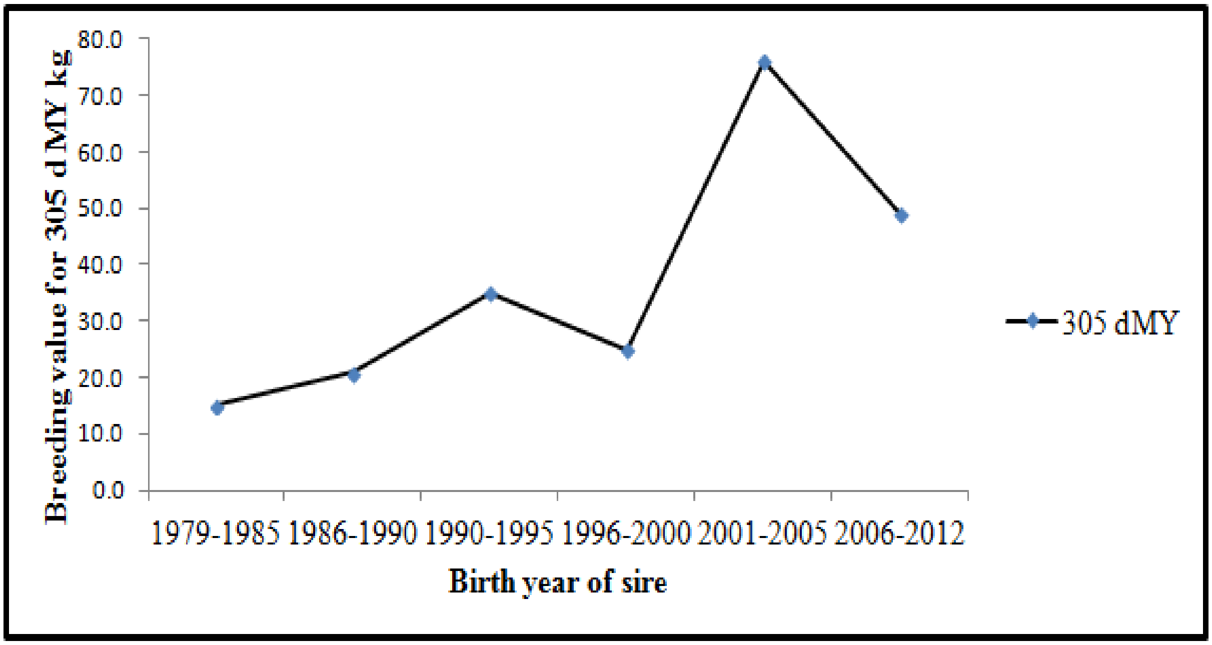

Figure 6: Genetic trend of 305d MY for bulls in the Holeta bull dam farm.

4.11 Prediction of genetic gain with revised breeding plan of Holeta bull dam open nucleus breeding (ONBS)

The simulation model on response to selection if selection for female line that have highest ranking among the bull dam herd and bull dam with best indices are to be selected to produce the next generation, the response to selection per current breeding objective of (305d milk yield, age at first calving and calving intervals) by multivariate models had indicated response projection of 23.85 kg milk yield increment, -5.41 and -3.83 days decrement per year for AFC and CI respectively, with the precision of 96. Relatively the greater improvement of 305d M than CI and AFC is mainly because of high weightage value (0.60%) that was applied. This response to selection was lower than the report of (chagunda, 2000) in Malawi , who reported 213.1kg,-8.02 days and -12.31day for 305d milk yield age at first calving and calving intervals, respectively for first and second scenarios. There was a relatively more expected genetic gain for all traits in bi-variate breeding program model after introduction of both reproduction (CI and AFC) and production trait (305d MY) than multivariate model prediction which was 25.4 and 26.4 kg of milk yield in both first and second scenarios respectively, whereas -6, -11 day for CI and AFC respectively. This is the rationale behind the idea of lower genetic progress when wore traits are in breeding program (Julius van der Werf, 2006). The reduction in the genetic gain for milk yield by multivariate model with the optimum genetic gain by reducing the calving intervals and age at first calving is beneficial to the farmers in log run in order to optimizing the number of traits in breeding goal. The reducing calving interval and age at first calving means within a given productive life time, a cow would produce more replacement calves . This would result in more replacing in the herd as well as more lactation per productive life time of a cow which is a good opportunity to solve the problem of replacement rate and fertility problem existing in Holeta bull dam farm. This would off-set the loss that is envisaged in the reduction in milk yield per lactation which comes as a result of including CI and AFC in the selection criteria.

Response to selection based on the phenotypic and genetic parameters obtained in this study, were made using the two trait goals of 305 days milk yield and one of the reproductive traits (AFC) or (CI) as breeding objectives scenarios, to observe the possible genetic change using the best bull dam cows group being selected with (25%) selection intensity among the currently exiting cows and heifer in the evaluation and importation of proven sires used (75%) and young bulls (25%) from the selectable dam line. The two alternatives scenario being considered were selection for 305d milk yield versus calving interval, and 305 d MY versus age at firs calving as the target traits in the objectives were used to evaluate the response to selection with the assumption being taken in table 15.

Table 15: The assumption taken to predict genetic change

Functional value from the study	Scenarios				assumption	
	Scenarios 1		Scenarios 2		Proportion of young bull semen	0.25
	305 d	CI	305 d	AFC		
Overall mean	3661 kg	461d	3661 kg	1200d	No. of proven AI-bulls selected/year	2
Additive genetic variance (s_{A1}^2)	165900	1841	165900	19	No. of proven bull-sires selected/year	6
Phenotypic variance (s_{P1}^2)	1106000	14160	1106000	49	Proportion of young bulls with proven sires	0.75
Heritability (h_1^2)	0.15	0.13	0.15	0.38	Recorded population size, cows	400
Repeatability	0.41	0.23	0.41	-	No. of cows calving/year	317
Covariance					No. of services/cow calving	2.0
Additive genetic covariance(s_{A1A2})	-2272		-422		Proportion of cows used as dams	0.74
Phenotypic covariance (s_{P1P2})	-15017		-74		No. of candidate bull dams/young bull calf	10
Correlation					Period a young bull is used (months)	24
Genetic correlation (r_g)	-0.13		-0.24		Period a proven bull is used as bull-sire	60
Phenotypic correlation(r_p)	-0.12		-0.01		Replacement rate, proportion	0.30
					Culling rate, proportion	0.10

Table 16: Expected predicted genetic change for305 d MY, AFC and CI

Selection criteria	S	SD	Response to selection for traits in different S					
			MYkg	CI d	AFC d	ΔG	GI	I_{Ar}
305d MY +CI	1	249	25.4	-6	-	21	6.4	59
305d MY +AFC	2	65	26.4	-	-11	19.7	6.4	62
305d MY + CI +AFC	3	72	23.3	-3	-5 d	15.1	6.5	95

Number of sire per daughter =10 G= genetic gain GI=generation interval I_{Ar} *= accuracy of selection SI (i) =selection intensity ΔG =Aggregate Index Gen. Var = Genetic variation S1,S2= scenario SD = standardivation*

The current result of the response to selection by fitting 305 days milk yield and calving interval (first scenarios) as the target traits with 400 herd size had shown the change of nearly 25.4 kg milk/year increase in milk yield and reduction in -6 days of the calving interval decrement in a year period. with the total genetic changes of 21.6 Index value of combination (Table 16).

The second scenario of 305 days milk yield with Age at first calving, expected annual genetic change was 26.4 kg increment of milk yield and decrement of -11 days of Age at calving days, with the total genetic merit index changes of 19.9 for the two traits. The four paths of the gene flow for Sire to son/daughter shows (Table 18) the generation interval were 6.35 years for both scenarios indicating the worst performance for the replacement of the herd under this study indicting the need to shorten the interval to have the better response to selection.

Table 17: Expected predicted genetic change by path in both scenario

Genetic change by path	**Response to selection in both scenario by path**							
	Gen. Var		G.305d MY		G. CI	G.AFC	GI	SI(i)
	S1	S2	S1	S2				
Sire-son	241.9	246.9	124.6	122.1	-1.4	-0.6	7.7	1.4
Sire-daughter	241.8	246.9	124.6	122.1	-1.4	-0.6	8.6	1.4
Dam-son	191.7	200.6	329.5	314.9	-3.1	-2.2	4.6	0.2
Dam-daughter	197.4	207.7	91.1	86.5	-0.7	-0.7	5	0.2

GI=generation interval I_{Ar} *= accuracy of selection SI (i) =selection intensity ΔG =Aggregate Index Gen. Var = Genetic variation*

4.11.1 Sire to son genetic path

The four paths of the gene flow showed the sire to son genetic path is one of the four paths to bring change on the new replacement population in breeding value of the traits in breeding goal. The estimation of expected genetic change for this path of selection was 124.60, 122.06 kg milk yield increment with -1.41 and -0.63day of CI and age at first calving decrement per year for fertility traits in both scenarios, respectively (Table 18). The generation interval was considerably longer (7.66 yr) for first and second scenario, shows the longer time taken to make progeny testing, if we adopt selection based on the sires line evaluation; expected improvement would be weak, due to prolonged generation interval.

4.11.2 Sire-daughter

The expected genetic change for sire to daughter pathway shows relatively the same trend with that of sire to son gene flow path. The expected annual change was 124.6, 122.1 kg for milk yield, -1.41 and -0.63 decrement months for AFC and CI in both scenarios respectively. Similarly, the generation interval from both sire paths showed longer, even if sire to daughter (8.15yr) is greater than sire to son (7.66 yr).

4.11.3 Dam to son

The predicted expected annual genetic change from dam to son path of selection indicated a substantial improvement 314.9, 329.45 kg of milk yield whereas -3.03 of calving interval and – 2.2 days per year decrement for AFC in both first and second scenario, respectively. Better genetic improvement was observed in this path selection (Table 18). This could be due to generation interval (4.6 year) was showed shorter time space for replacement than all the rest paths, in both scenarios.

4.11.4. Dam-daughter

The predicted expected annual genetic change from dam to daughter path of selection was 86.5, 91kg of 305 day milk yield and -0.75 d and -0.7 d per year for AFC and CI in both scenarios, respectively (Table 18). This indicated that expected annual genetic change in both scenarios were very minimal performance increment as compared to other gene flow paths. However, selection of dam of daughter could become much more important in the minimizing of generation intervals in the heard (5) years.

4.11.5. **The effect of herd size on the predicted genetic change**

In the current study, the small herd size in Holeta bull dam had contributed to the existence of lower variability which has contributed to high homogeneity, even if the sire import from different country had been made by NAIC. The predicted response to selection simulated with the higher herd size using the follower herds and contractual breeding scheme in the breeding program simulated had shown better response to selection. The estimates of response based upon different herd size in recording scheme to selection per year and selection accuracy are given in (Table 19).

Table 178: Expected predicted genetic change by herd size

Size of herd	Response to selection for both scenario CI and AFC with 305 days MY							
	305 d MY with Calving intervals				305 d MY with age at first calving			
	MY kg	CI	ΔG	I_{Ar}	MY kg	AFC	ΔG	I_{Ar}
400	25.4	-6	21.6	0.59	26.4	-11.0	19.7	0.62
1000	30.2	-8.4	25.7	0.61	31.3	-13.1	23.4	0.67
1500	32.2	-9.2	27.7	0.64	33.7	-15.5	25.3	0.71
2000	35.2	-12.2	29.7	0.68	36.2	-17.3	27.1	0.70

I_{Ar} = *accuracy of selection* ΔG = *Aggregate Index*

The annual change predicted for different herd size under the open nucleus herd and follower herds being in the data base of National Artificial insemination Center had been taken to assumptions to come up with possible alternative strategies of the open nucleus breeding schemes (ONBS) that were recommended by wolly, (1995) and other pioneer of animal breeding and genetic (Lohuis, 1998). Therefore, per the prediction from the current model we recommend the NAIC to adopt open nucleus breeding schemes using the exotic Holstein

Frisian herds being owned by different stakeholder private, Government institutions that can get engaged by contractual agreement to participate in recording and allowing the test of young bulls and participate in progeny testing scheme in the country.

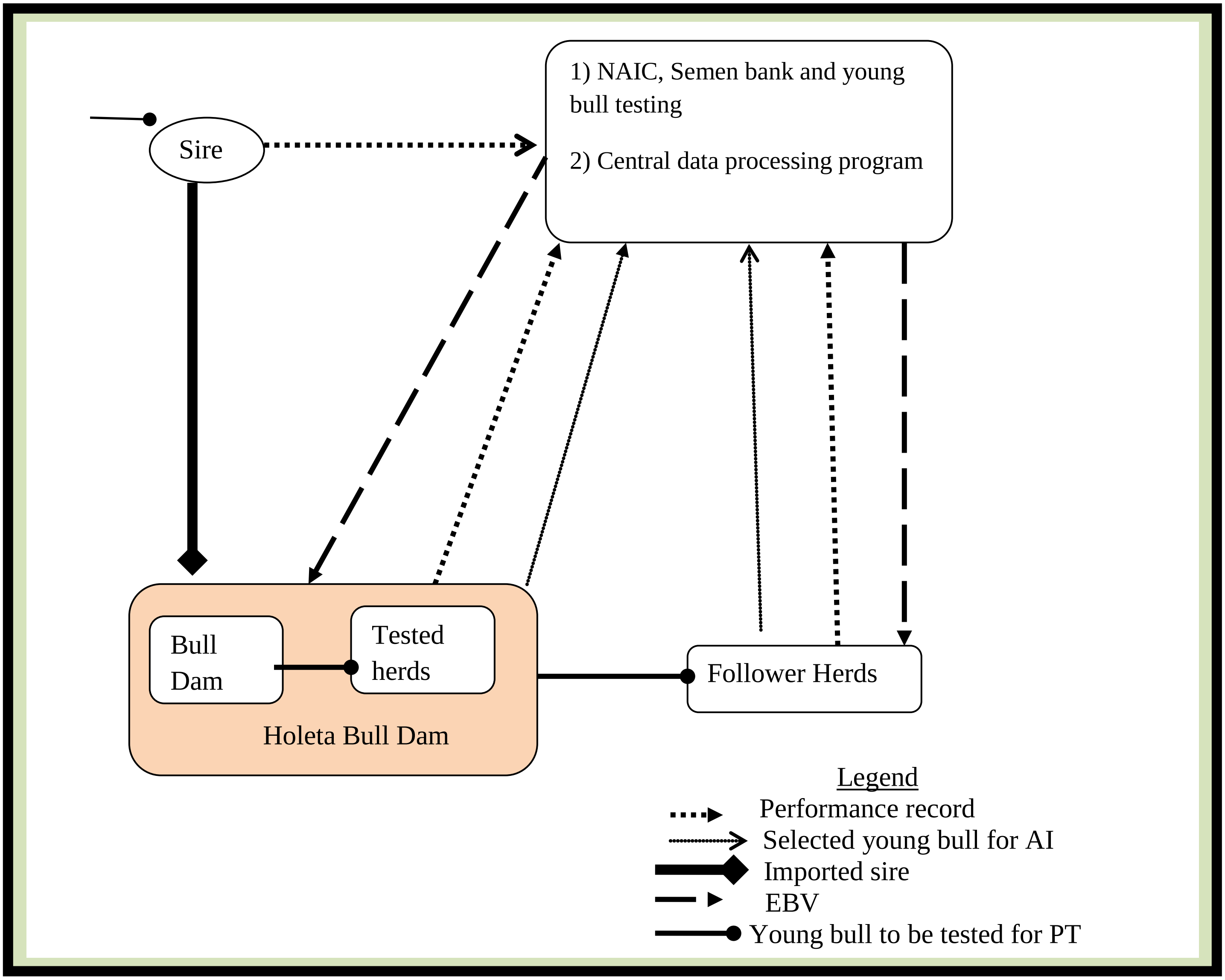

Figure 7: Proposed diagrammatic open nucleus breeding scheme

Since importation of foreign genetic material involves the use of foreign exchange which is extremely scarce and existence of genotype environment interaction slows down the rate of genetic progress (Mpofu *et al.*, 1993). This calls for revising the existed breeding strategy in order to assure the sustainable utilization and conservation of well adapted superior genotypes for achieving sustainable genetic improvement of dairy cattle. This is achieved by designing appropriate breeding strategies to find the best suitable and adapted bull(s) for different production systems in Ethiopia. The appropriate breeding programme for the large scale dairy farms like Holeta bull dam would be the dispersed open nucleus scheme as represented in Fig.5 by definition, in dispersed open nucleus scheme, the animals are not found in one place and this is allowance of inflow of foreign germplasm in to the system (Lohuis, 1998). As compared to the centralized closed nucleus scheme, the dispersed open nucleus scheme has more advantages.

In the proposed nucleus breeding programme, as schematically presented in fig.7, sires would be imported from abroad and their semen is utilizing in the nucleus herd (selected bull dam) then the young bull born from those sires can be disseminated to the follower herds and systematically mated with tested herds for progeny testing to prove young bulls. The performance records from the nucleus and follower herds can be transferred to the central data system. Feedback based on their performance in central data base analysis (EBVs), the young bull are selected for semen production from the nucleus and follower herds and then physically taken to NAIC. Accordingly the owner of the follower herds can select best replacement heifers for their farms based up on the feedback from NAIC and similarly heifers would have to be selected in the nucleus herds to be the parents of the next bull dam in the nucleus. All the effective breeding and selection activities would be confined within the nucleus scheme, which would be the source of male stock in the system.

5. SUMMARY AND CONCLUSION

The present investigation of animal evaluation and genetic trend analysis was undertaken to evaluate the performance of exotic dairy cattle of Holstein Friesian in Ethiopian situated specifically on Holeta bull dam farms over the study period of 35 years to come up with estimate of breeding values using multivariate animal model and regressed the genetic and phenotypic trend of the productive (TLMY and 305days MY) and reproductive traits (CI and AFC) against the birth years. The data on 1125 cows and 814 Dams sired by 137 bulls were used in this study. Holstein Friesian cows maintained during 1979 to 2012 at Holeta bull dam nucleus herd were utilized. The breeding value of animal is one of the best parameters available to evaluate the genetic performance of an animal in relatives to its contemporaries. This study had shown year of calving, year birth for AFC, parity and origin of sire were important factors affecting both productive and reproductive traits under this study. However, season was not significantly influence both productive and reproductive traits except LL and NSC.

The phenotypic performance evaluation of production traits like TLMY, 305d MY and LL was 3732.3 ± 44.2, 3661 ± 37.19, 314.3 ± 1.9, respectively and reproductive traits such as, AFC, CI, DO, and NSC was 40.1 ± 0.37, 461.1 ± 7.7, 173 ± 6.7 and 1.9 ± 0.5, respectively. The diversity in productive and reproductive traits detected during different years reflected the level of feeding and management different over the 35 years period. The performance of Holstein Friesian cattle in the present study were higher than previous study in the same herd by Mohamed (2004) 3175.7±41kg, 3096±26.9 and 319.3± respectively for production and 43.6± 0.33,454.8± 4.57d, 178.52± 4.36 and 1.9 for reproduction trait. Concurrently, with the reports of other tropical countries like Morocco, Tunisia. The estimates for genetic parameters like heritability for LL, DO and NSC traits in the present study is relatively low (0.08 ± 0.03, 0.10 ± 0.04 and 0.07 ± 0.02), respectively in the present study. The low heritability estimates for those traits indicates that the major part of variation for those traits were due to non genetic factors, this could be due to the size of the data, lack of information concerning the managemntal sources of variation to be accounted for in the model. Therefore, these traits can only be improved by adequate environmental and managemental influences. However, estimates for traits like 305d milk yield, total lactation milk yield, age at first calving and Calving intervals had shown the existence of considerable genetic variability (0.15 ± 0.04 ,0.15 ± 0.04,0.38 ± 0.25 and 0.13 ± 0.04), respectively, in the herd. These result indicated that the possibility of undertaking multi trait selection goals by Holeta bull dam herd with selection goal objectives of the production traits (305 days milk yield, and fertility traits (AFC and CI) applied on Holeta bull dam farm. The estimate of phenotypic and genetic correlation between 305-dMY and AFC (-0.24), and 305-dMY and CI (-0.13) and fertility traits AFC and CI (0.04) was generally favorable in direction and to lesser extent in magnitude. The present results indicate that selection for 305d MY might result in shorter younger AFC and CI. Therefore, since these traits being observed on the same animal would mean that if selection up on this combination trait is carried out, it will build a framework for sound long term breeding programmes for Holstein dairy cattle in Ethiopian.

The sires of Holstein Friesian herd in Holeta are originated from several different countries and they are said to be heterogeneous mixture of the genetic pool exiting in Ethiopia. The estimates of breeding values of a total of 137 sires being used in the bull dam estimated by multi-traits animal model had shown the significant ranges of variability. Estimates of sire breeding values for 305 day milk yield AFC and CI ranges from (-538.40 to 946.70) with 236.3 kg SD, (-13.71to 9.37) with 3.31month SD and -45.90 to 67.22) with 18.77d SD, respectively. The mean of estimated breeding values for CI fertility traits obtained from all daughters of sire origin indicated that bulls from Italian, and USA, origin had comparatively better performance mean for calving interval. On the other hand, bulls from Ethiopia, Israel, Kenya and Cuba Showed positive breeding value which indicate more wastage days of inter calving for fertility traits.

The mean of estimated breeding values obtained from all daughters of sire origin for Age at first calving was negative except United States and Kenya origin (0.164 and 0.13 month) respectively. However, bulls from Cuba (-1.51 month) had comparatively the lowest mean EBV for Age at first caving followed by bulls from the Finland, (-0.49 month). In terms of 305 days milk yield Ethiopian or bulls whose origin was from Holeta had (237.86 kg) and worldwide sire of United States daughter had (114.2 kg) had the highest mean breeding value for milk yield followed by bulls from Italy but the unknown had (26.15 kg) and Kenya (-11.44 kg) had the lowest mean breeding value for 305 day milk yield. Mismanagements of the imported gene pool and breeding practices, and difference in breeding objectives of selection from exporting countries might leads to GXE interaction that showed some progenies are better performing than expected and others are not. This is manly important to provide base line information regarding where to importing sires for breeding.

The aggregate genetic merit for all sires in the study range (119.2 to 66.34) and female line ranges (125.9 to 64.2) from the total genetic merit for the breed maintained under the period of study. The genetic variability expressed by genetic standard deviation (40.46) for total merit indicated that larger proportion of genetic variance might be due to the use of different source semen imported by NAIC at different time period. The implication of sires ranking in the first 1-50 based on the total merit index for production and reproductive performance as sire summaries had been observed to develop possible conclusion on the use of locally selection program versus direct import based improvement strategies. In this study the best sires ranking from 1st to 50 th in total merit index indicated that locally selected sire groups from Ethiopian origin took the 30% of the sires samples (15 sire families), Israel had nearly contributed 22% of sire samples i.e. (11 sires) ,followed by USA contributing 20% sire (10), and Finish 9% Similarly the Cuban are best in the rank of Fertility traits specifically the Age at first calving contributing 6.52% in the rank followed by Italian 6.52% and Kenyan 4.35%.

The rate of phenotypic changes in the Holeta bull dam herd over the study period in total lactation milk yields, 305d milk yield, Age at first calving and calving intervals was 4.45, 22.2 kg, -0.66 month and -0.51 day per year, respectively. The genetic trend for milk yield over the study period depicted positive trend. Indicating genetic improvement in production traits (TLMY and 305d MY) presenting the bull dam performance overtime 6.12 and 9.98 kg per year, respectively where as fertility trait (AFC and CI) was 0.6 days and -0.07 day. Whereas 10.87kg,-7.14 and -1.1 days for sire trend. The negative direction for genetic trend indicated in reproduction traits was slightly improvement in the genetic merit for calving intervals. Low genetic progress of fertility traits as opposed to production trait were due to the there were not the main breeding goal traits and whatever small changes observed comes from the import of better genetics over the study period from different countries. Generally this trend line indicates the significant change for milk yield but AFC and CI is not significant different from zero. Response to selection based on the phenotypic and genetic parameters obtained in this study, were made using the two trait goals of 305 days milk yield and one of the reproductive traits (AFC) or (CI) as breeding objectives scenarios, to observe the possible genetic change using the best bull dam cows group being selected. The expected genetic gain bi-variate model for two trait breeding goal of 305d MY 26 and 25kg, CI -0.24 and (-0.16) of AFC days per month for first and second scenarios respectively. However, the expected annual genetic change for 305d MY AFC and CI was 25-26kg,-5 and -3d per year if the three traits selection criteria and if multi traits breeding goal is to be adopted.

6. RECOMMENDATION

The national breeding program of selection by the NAIC in the bull dam should accommodate production and fertility traits.,
Importation of semen and animals have to consider the merit of sires imported are proven for here in the Ethiopian mangement situation, therefore, semen import from Israel, USA, and Finland is advisable etc. In addition, During importation of semen/live animal breeders should look at information related to selection indexes of exporting country to match with the Ethiopian selection goals.

Transformation on animal Evaluation from phenotypic value of traits has to be replaced by estimated breeding value of animal using BLUP procedures of animal model. This BLUP procedure helps in correct identification of superior dams for contract mating programme that will helps to get replacement young bulls form which selection of AI sires for nationwide use can be attained

The number of animals in the follower herd has be larger enough to get more accurate breeding values in selection of the parent of upcoming generation

Economic valuation of the traits in the selection index need to be undertaken for more precise quantification of the merit of traits on individual animals under evaluation.

Further research needed on the GXE effects of sire semen exporting and importing country level performance

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8. APPENDIX

Appendix table 1: Prediction of Standard lactation Milk Yield (305-dMY) from completed lactations of longer duration in Holstein Friesian (>320 days)

Predictor	Estimate	Standard error	R^2 (%)	VIF
Constant	2243.4	51.14	96.31	
LMY	0.85084	0.00881		1.127
LL	-5.6978	0.1268		1.127
Prediction Equation	305-dMY = 2243 + 0.851 LMY - 5.70 LL			

Appendix table 2: variance component from three trait analysis

Trait	Additive	Permanent	Residual
LMY	229781	294639	830914
DO	1035.07	791.589	8761.03
AFC	6.04579		59.5979
LMY	226813	298001	830615
CI	1713.72	1075.82	11219.7
AFC	31.2901		58.3825
305-dMY	170290	288361	647238
CI	1767.71	1436.88	10954.7
AFC	32.5955		52.3549
305-dMY	169065	289024	647356
DO	1080.28	1017.23	8579.24
AFC	10.2619		57.1034

Appendix table 3: Summary of all sire used in the bull dam farm for 35 years

Sire ID	No	BV AFC	accu	Inde AFC	BV CI	accu	Index CI	BV 305	accu	Index 305	weighted index
1624	27	-13.7	0.90	233.2	0.9	0.79	98.1	-538.4	0.80	77.0	119.2
Marlin	27	-1.2	0.54	100.6	-3.7	0.03	101.4	946.7	0.19	128.1	117.2
Dalta	27	-2.2	0.69	110.5	-18.0	0.09	111.9	623.4	0.34	117.0	114.6
1700	11	-8.6	0.83	178.4	-5.1	0.66	102.4	-201.1	0.68	88.6	113.1
1545	7	-9.6	0.78	189.1	4.9	0.58	95.1	-372.1	0.60	82.7	111.2
85	18	-6.7	0.82	158.8	0.7	0.62	98.2	-71.3	0.65	93.1	110.3
50	18	-5.9	0.80	150.5	-0.3	0.60	98.9	4.612	0.62	95.7	109.9
02-052	9	-3.3	0.65	122.4	-8.8	0.08	105.2	253.1	0.29	104.2	108.9
Ready paker	25	0.1	75	86.1	6.3	0.06	94.1	760.5	0.22	121.7	108.7
Regis	21	-0.9	0.76	97.3	-26.3	0.19	118.0	410.7	0.44	109.7	107.8
Bavel	56	-2.0	0.84	108.8	-3.2	0.57	101.0	366.3	0.67	108.1	107.3
Lichy	46	-1.8	0.83	106.6	-4.9	0.54	102.3	376.2	0.64	108.5	107.1
310	7	-4.7	0.71	137.7	1.4	0.48	97.7	22.37	0.48	96.3	106.9
244	22	-4.6	0.79	136.0	16.0	0.56	87.0	92.55	0.59	98.7	106.3
Hoiken	40	-2.2	0.84	110.7	-10.4	0.58	106.3	242.3	0.67	103.9	106.0
Romany	21	-1.8	0.76	106.6	-4.5	0.31	102.0	276.2	0.49	105.0	105.0
Loten	94	-0.8	0.84	96.2	-18.2	0.53	112.1	315.4	0.64	106.4	104.7
294	15	-3.0	0.67	119.2	-3.5	0.33	101.3	111.6	0.37	99.4	104.6
Balon	32	-0.4	0.80	91.7	-20.5	0.44	113.7	325.8	0.60	106.8	104.0
Boliver	17	0.1	0.61	86.0	-15.1	0.15	109.8	410.5	0.24	109.7	103.8
19	36	-4.9	0.88	139.3	-0.3	0.72	98.9	-157.8	0.75	90.1	103.7
105	1	-0.7	0.61	94.9	-31.2	0.27	121.6	209.2	0.28	102.7	103.6
20	60	-5.5	0.87	145.9	12.2	0.68	89.7	-182.7	0.71	89.2	103.5
266	4	-3.5	0.66	124.7	3.7	0.34	96.0	24.89	0.37	96.4	103.4
10	3	-5.8	0.71	149.1	26.5	0.41	79.3	-154	0.44	90.2	103.3
Koivalan	46	-2.1	0.86	110.0	17.2	0.59	86.1	267.9	0.69	104.8	103.3
155-91	5	-2.0	0.73	108.8	-29.5	0.54	120.3	5.211	0.54	95.7	102.7
179-84	5	-4.2	0.72	131.8	18.9	0.50	84.9	-18.36	0.49	94.9	102.6
10-003	15	-0.4	0.70	92.0	-4.2	55	101.8	332.7	0.41	107.0	102.5
11-036	9	-2.0	0.67	108.2	6.2	0.30	94.1	184.7	0.36	101.9	102.3

No = number of daughter EBV = estimated breeding value weighted   accu = accuracy of Estimated breeding value

Sire ID	No	BV AFC	accu	Index AFC	BV CI	accu	Index CI	BV 305	accu	Index 305	weighted index
22	6	-3.1	0.75	120.0	-18.1	0.41	112.0	-102.2	0.49	92.0	102.0
	21	-3.0	0.68	119.7	0.4	0.38	98.4	-28.99	0.40	94.5	101.4
31-013	64	-2.2	0.69	110.5	14.9	0.19	87.8	158	0.37	101.0	101.4
134	1	-2.6	0.62	114.9	-26.6	0.33	118.2	-119.8	0.32	91.4	101.3
Sumelian	85	-1.0	0.87	98.0	-2.4	0.68	100.5	211.5	0.78	102.8	101.3
Casmir	22	0.8	0.77	79.3	-5.7	0.19	102.9	418.8	0.47	110.0	101.2
11-134	2	-0.2	0.61	89.4	-6.9	0.06	103.8	289.3	0.10	105.5	101.2
Kapitein	7	0.2	0.73	85.3	-10.9	0.25	106.7	297.9	0.37	105.8	100.8
10-091	124	0.4	0.85	82.7	-15.4	0.65	110.0	302.5	0.72	106.0	100.7
Goliat	87	-2.0	0.83	109.0	28.0	0.68	78.2	205.6	0.75	102.6	100.5
10-245	6	-1.1	0.62	99.2	-10.8	0.33	106.6	110.8	0.31	99.3	100.4
Gan	16	1.3	0.71	73.2	13.1	0.10	89.1	548.7	0.37	114.4	100.3
10-014	118	-2.5	0.89	113.5	35.9	0.76	72.4	176.6	0.80	101.6	100.2
81-006	3	-1.9	0.70	107.2	-9.1	0.37	105.4	3.267	0.41	95.6	100.0
329	2	-1.5	0.62	103.8	-0.3	0.26	98.9	80.81	0.29	98.3	99.8
Menekki	35	-1.2	0.82	99.9	-1.9	0.49	100.1	101.7	0.61	99.0	99.4
055-91	37	-2.0	0.80	108.3	-5.6	0.66	102.8	-22.87	0.68	94.7	99.3
94-103	6	-0.5	0.63	92.8	-17.5	0.22	111.6	98.13	0.29	98.9	99.3
125	83	-3.2	0.93	121.7	8.5	0.84	92.5	-135.5	0.86	90.9	98.8
933	1	-1.5	0.62	102.9	-3.1	0.18	101.0	26.06	0.25	96.4	98.7
328	32	-0.8	0.83	96.4	-1.7	0.59	100.0	84.25	0.64	98.4	98.1
6	63	-2.9	0.92	118.5	8.4	0.80	92.6	-136.2	0.82	90.8	98.0
110	4	-2.5	0.74	114.2	2.0	0.52	97.2	-136.1	0.51	90.8	97.6
397	12	-0.3	0.69	90.1	11.6	0.33	90.2	203.2	0.40	102.5	97.6
1271		-3.4	0.61	123.4	15.8	0.25	87.2	-197.5	0.27	88.7	97.2
955	85	-0.6	0.89	93.9	-10.4	0.75	106.4	19.5	0.77	96.2	97.2
Alton	28	2.1	0.78	64.7	17.9	0.22	85.6	521.6	0.47	113.5	97.1
296-84	2	0.2	0.69	84.9	-32.1	0.44	122.2	-5.274	0.44	95.4	96.8
331Bull	2	-0.4	0.63	91.3	-3.2	0.29	101.0	63.54	0.32	97.7	96.6
20	2	-2.1	0.62	109.8	18.7	0.19	85.0	-86.61	0.27	92.6	95.7
10-024	7	1.7	0.71	68.9	-18.2	0.43	112.0	205.4	0.46	102.6	95.6
348-84	5	-1.5	0.61	102.8	10.7	0.30	90.9	-63.73	0.28	93.3	95.3
55-82	6	-0.8	0.63	95.8	2.9	0.29	96.6	-28.45	0.31	94.6	95.2
2	4	0.2	0.62	85.7	-9.4	0.26	105.6	-317	0.27	84.6	88.0
38	21	3.5	0.76	50.4	-0.7	0.37	99.2	152.2	0.50	100.8	88.0
25	87	1.6	0.80	70.5	-1.5	0.56	99.8	-103.3	0.59	92.0	87.8

No = number of daughter EBV = estimated breeding value weighted accu = accuracy of estimated breeding value

Sire ID	No dou	BV AFC	accu	Index AFC	BV CI	accu	Index CI	BV 305	accu	Index 305	weighted index
27	16	-1.1	0.81	99.2	-3.2	0.58	101.0	-103.4	0.61	92.0	95.2
10-117	2	-0.6	0.67	93.4	-8.6	0.33	105.0	-63.15	0.32	93.4	95.1
014-86	7	-0.6	0.67	93.6	5.1	0.39	94.9	2.962	0.40	95.6	95.0
341	17	-0.2	0.68	89.4	5.2	0.41	94.9	50.98	0.42	97.3	94.9
26	4	-0.7	0.71	94.7	-9.8	0.51	105.9	-96.1	0.51	92.2	94.9
088-85	13	-1.2	0.73	100.3	9.4	0.46	91.8	-65.11	0.49	93.3	94.8
10-013	227	1.5	0.91	71.5	-20.4	0.79	113.7	123.1	0.82	99.8	94.8
10-095	1	0.8	0.62	78.7	-2.3	0.25	100.4	125.4	0.29	99.9	94.7
34-95	2	0.4	0.67	83.2	1.4	0.28	97.7	71.35	0.34	98.0	94.3
91-78	1	0.2	0.61	85.1	-6.6	0.18	103.5	-5.584	0.22	95.3	94.0
279-84	8	-0.8	0.62	96.1	16.8	0.31	86.4	-19.84	0.30	94.9	93.9
298	1	0.2	0.62	85.6	9.0	0.28	92.1	61.19	0.28	97.6	93.8
10-087	8	0.7	0.68	80.2	30.8	0.34	76.1	234	0.38	103.6	93.6
1594		-1.1	0.61	99.2	-2.9	0.25	100.8	-194.3	0.26	88.8	93.2
93-341	15	-1.1	0.73	98.9	11.7	0.45	90.1	-113.5	0.49	91.6	93.2
34973	4	2.0	0.67	65.7	-15.0	0.39	109.7	130.9	0.40	100.0	92.9
10-011	67	1.4	0.85	72.8	0.9	0.64	98.1	114.9	0.70	99.5	92.6
030-86	9	0.1	0.61	85.9	10.0	0.06	91.4	1.44	0.22	95.6	92.5
96-010	1	1.5	0.63	71.7	2.1	0.24	97.2	126.6	0.29	99.9	92.5
273	11	1.8	0.68	67.7	-20.1	0.41	113.4	48.07	0.41	97.2	92.3
Anchile	1	1.1	0.62	76.0	-9.8	0.30	105.9	-31.29	0.30	94.5	91.6
184-85	38	0.6	0.81	81.2	-3.4	0.62	101.2	-61.64	0.64	93.4	91.5
Ginoser	56	2.5	0.87	60.3	2.6	0.70	96.8	205.9	0.76	102.6	91.2
10-010	189	2.4	0.91	61.7	-11.5	0.80	107.1	112	0.84	99.4	91.1
90-064	14	1.8	0.67	68.4	-5.1	0.33	102.4	39.16	0.37	96.9	90.6
1951		-2.4	0.61	112.9	25.2	0.28	80.3	-346.1	0.28	83.6	90.4
930	10	2.4	0.70	61.6	-19.1	0.37	112.7	34.14	0.42	96.7	90.3
338	10	2.0	0.70	65.9	-1.8	0.42	100.0	36.08	0.44	96.8	89.5
114		2.0	0.61	66.4	-20.2	0.06	113.5	-74.52	0.22	93.0	89.4
329	27	4.1	0.89	44.2	-45.9	0.75	132.4	45.94	0.78	97.1	89.2
Lappalan	40	3.2	0.84	53.3	13.3	0.54	88.9	238.2	0.65	103.7	88.9
498	6	0.3	0.60	84.2	1.7	0.32	97.4	-208	0.30	88.4	88.7
1701	9	0.6	0.80	81.3	-7.9	0.58	104.5	-230.7	0.61	87.6	88.5
54	6	1.7	0.61	69.0	7.0	0.60	93.6	-8.716	0.10	95.2	88.4
1717	8	1.1	0.81	75.9	-10.2	0.62	106.2	-185.4	0.64	89.2	88.4

No = number of daughter EBV = estimated breeding value weighted accu = accuracy of Estimated breeding value

Sire ID	No	BV AFC	accu	Inde AFC	BV CI	accu	Index CI	BV 305	accu	Inde 305	weighted index
1944		-2.2	0.61	110.2	42.8	0.27	67.4	-355.5	0.28	83.3	87.6
1909		0.5	0.61	82.1	-15.6	0.25	110.1	-350.8	0.27	83.5	87.1
86-36	34	1.9	0.82	67.4	4.4	0.64	95.5	-67.71	0.65	93.2	87.1
Malachy	4	-0.3	0.70	90.1	67.2	0.43	49.4	-17.66	0.46	94.9	86.9
954	35	2.3	0.83	62.5	1.0	0.65	98.0	-40.03	0.68	94.2	86.8
1496		-0.9	0.61	97.2	21.6	0.28	82.9	-352.2	0.28	83.4	86.8
1700		1.0	0.71	76.6	7.9	0.35	92.9	-187.5	0.41	89.1	86.5
83-85	1	2.4	0.61	62.2	2.7	0.25	96.7	-41.28	0.26	94.1	86.5
286	25	2.1	0.81	64.8	11.3	0.57	90.5	-30.18	0.61	94.5	86.5
142	7	1.8	0.61	68.3	10.1	0.28	91.3	-81.16	0.28	92.7	86.4
1738		-1.4	0.65	101.8	19.3	0.33	84.6	-446.9	0.36	80.1	86.2
96	10	2.2	0.61	63.8	10.0	0.13	91.4	-72.99	0.16	93.0	85.5
120	8	2.0	0.83	65.6	1.3	0.63	97.7	-150.5	0.65	90.4	85.3
10-017	11	4.5	0.66	39.8	-6.2	0.31	103.2	114.4	0.36	99.5	85.1
92	13	2.5	0.76	60.7	3.3	0.50	96.3	-88.81	0.54	92.5	85.1
219-85		2.6	0.71	59.2	20.3	0.45	83.9	-11.37	0.46	95.1	84.5
133	9	2.6	0.71	60.0	11.1	0.31	90.6	-71.37	0.39	93.1	84.4
8-245	17	4.4	0.62	40.8	-4.6	0.23	102.1	50.44	0.28	97.3	83.9
46-82	6	4.1	0.67	43.7	-23.5	0.24	115.9	-87.02	0.35	92.5	83.8
498		2.2	0.61	63.7	-20.5	0.29	113.7	-323.9	0.28	84.4	83.6
155		1.0	0.66	76.9	16.3	0.36	86.8	-310.8	0.38	84.8	83.2
129	6	3.2	0.78	53.5	1.3	0.54	97.7	-122.4	0.57	91.3	82.8
283-94	1	2.3	0.62	63.4	39.4	0.26	69.9	-43	0.28	94.1	82.8
Bootmar	6	4.2	0.72	42.2	-3.2	0.43	101.1	-27.32	0.47	94.6	82.5
29	3	4.0	0.71	44.7	-11.5	0.45	107.1	-120.8	0.46	91.4	82.1
1722	9	1.8	0.80	68.1	29.7	0.59	77.0	-190.8	0.62	89.0	81.9
1973		1.6	0.65	70.5	33.7	0.21	74.0	-274	0.33	86.1	80.4
24	4	3.7	0.71	48.2	6.2	0.47	94.1	-158.8	0.47	90.1	80.2
124	2	4.4	0.67	41.0	6.6	0.36	93.9	-109.5	0.37	91.8	79.4
95	10	5.2	0.83	32.2	-1.2	0.62	99.6	-129.6	0.65	91.1	77.6
287	4	6.6	0.73	16.7	-2.9	0.44	100.8	24.18	0.44	96.4	77.1
17	35	5.7	0.86	26.6	6.9	0.71	93.6	-147	0.72	90.5	75.0
37	7	8.5	0.78	-3.0	-19.2	0.54	112.8	-104.2	0.56	91.9	71.3
117	11	7.3	0.82	9.4	11.6	0.55	90.2	-107.7	0.61	91.8	71.0
1594	7	9.4	0.78	-12.4	-14.8	0.52	109.5	-209.2	0.58	88.3	66.3

No = number of daughter EBV = estimated breeding value weighted accu = accuracy of Estimated breeding value

Appendix table 4: Summary of dam selected based on the current breeding goal traits for bull dam

Cow ID	BV AFC	Inde AFC	accu	BV CI	Index CI	acc	BV 305	Index 305	acc	weighted index
h1-1353	5.6	63.1	0.82	-17.6	106.2	0.47	-37.2	87.9	0.55	84.4
h1-1423	2.4	82.4	0.81	7.8	89.6	0.45	128.4	93.6	0.55	90.2
k-1428	1.4	88.1	0.82	-10	101.2	0.46	-195	82.6	0.6	86.8
k-1364	0.6	93.4	0.81	-7.4	99.5	0.35	10.7	89.6	0.54	92.0
h1-1368	-0.4	99.1	0.78	17	83.5	0.41	50.3	90.9	0.54	91.8
k-1375	-0.9	101.8	0.82	-12.7	103	0.35	78.4	91.9	0.53	96.0
h1-1389	-0.2	97.7	0.81	16.3	84	0.54	102.8	92.7	0.6	92.6
h1-1392	-0.1	97.3	0.82	-25.8	111.6	0.53	102.4	92.7	0.6	96.7
h1-1419	-1.2	104.1	0.82	9.3	88.5	0.53	129.1	93.6	0.6	95.5
h1-1427	-1.7	106.6	0.82	-17.2	105.9	0.5	178.7	95.3	0.56	99.7
h1-1429	0.7	92.5	0.81	-7.2	99.4	0.56	203.2	96.1	0.61	95.7
h2-1424	-1.2	103.9	0.82	-9.5	100.9	0.48	227.1	96.9	0.55	99.3
h1-1433	-1.6	106.3	0.81	-17.3	106	0.4	248.7	97.7	0.46	101.1
h1-1440	-1	102.7	0.82	-19.8	107.6	0.53	280.8	98.8	0.6	101.1
h1-1441	-3.1	115	0.82	-3.6	97.1	0.53	289.5	99.1	0.6	102.8
k-1447	-2.7	113	0.82	-14.6	104.3	0.47	347.6	101	0.58	104.5
h2-1454	-2.6	112.3	0.81	-40.2	121.1	0.55	386.8	102.4	0.59	107.7
h1-1458	-0.2	97.7	0.82	-27.9	112.9	0.53	398.5	102.8	0.6	103.0
h1-1469	-2.2	109.7	0.81	-15.6	104.9	0.53	436.2	104.1	0.59	105.6
h1-1455	0.7	92.6	0.81	-18	106.4	0.5	448.7	104.5	0.59	101.8
h1-1472	1.7	86.5	0.82	-0.5	95	0.54	478.6	105.5	0.61	99.2
h1-1475	-2	108.6	0.82	-26.2	111.9	0.6	506.6	106.5	0.63	107.8
h1-1481	1.5	87.7	0.82	-3.1	96.7	0.56	565.1	108.4	0.61	101.5
h1-1490	1.2	89.5	0.82	-3.2	96.8	0.57	608.9	109.9	0.62	102.8
h1-1505	0.9	91.5	0.82	-2	96	0.52	748.2	114.7	0.61	106.1
h1-1511	-0.4	98.8	0.81	-3.9	97.2	0.55	945.8	121.4	0.61	112.1
h1-1514	-0.8	101.3	0.82	-32.9	116.2	0.54	965	122.1	0.6	116.0
h1-1394	0.9	91.2	0.8	20.7	81.1	0.31	-147.6	84.2	0.49	85.5
h1-1359	-0.6	100.5	0.91	6.3	90.5	0.36	-106.5	85.6	0.54	90.1
h1-1371	-0.6	100.4	0.8	-6.1	98.7	0.36	29.7	90.2	0.57	94.0
k-1380	-0.2	98	0.81	0.2	94.5	0.48	93.4	92.4	0.59	94.1
h1-1382	-2.3	110.3	0.81	0.5	94.3	0.54	90.1	92.3	0.61	97.1
h1-1467	-1.6	106.3	0.79	-13.7	103.6	0.34	423.3	103.6	0.52	104.3
h1-1473	0.4	94.5	0.83	13.2	86	0.55	572	108.7	0.6	101.7

CowID	BV AFC	Index AFC	acc	BV CI	Index CI	Acc	BV 305	index 305	acc	weighed index
h1-1411	-1.8	107.4	0.81	1	94	0.48	119.8	93.3	0.58	96.9
h1-1413	0.8	91.7	0.82	4.7	91.6	0.5	131	93.7	0.57	92.9
h1-1434	0.1	96.1	0.78	5.6	91	0.43	145.9	94.2	0.57	94.2
h1-1426	1.8	85.7	0.8	-2	96	0.35	184.2	95.5	0.52	93.1
h1-1430	-2.1	109	0.81	0.7	94.2	0.51	213.3	96.5	0.59	99.3
h1-1432	-1.3	104.3	0.82	4	92.1	0.5	246.5	97.6	0.59	98.5
h2-1435	-1.3	104.1	0.81	-18.5	106.8	0.36	251.9	97.8	0.46	100.7
h1-1442	-2.2	110	0.81	-5.4	98.2	0.48	268.5	98.3	0.58	101.2
h1-1438	-0.2	97.7	0.81	-18.3	106.6	0.55	279.8	98.7	0.61	99.6
h1-1445	-0.4	99.1	0.81	-6.4	98.9	0.47	337.7	100.7	0.58	100.0
h1-1471	-0.6	100.2	0.81	-8	99.9	0.46	462.6	105	0.57	103.0
h1-1470	-2.5	111.8	0.82	-13.9	103.8	0.54	488	105.8	0.6	107.0
k-1496	-0.9	102.1	0.81	-46.6	125.3	0.53	560.9	108.3	0.6	109.3
h1-1483	0.2	95.4	0.81	-11	101.9	0.37	571	108.6	0.54	104.3
k-1478	1.7	86.3	0.8	5.3	91.2	0.3	595.3	109.5	0.51	101.0
h1-1486	-1.2	103.9	0.81	1.3	93.8	0.48	635.4	110.8	0.58	106.5
h1-1498	-1.8	107.4	0.82	-12.5	102.9	0.52	691.9	112.8	0.61	110.0
h1-1506	-2	108.4	0.81	29.4	75.4	0.46	766.9	115.3	0.58	107.6
h1-1356	-0.6	100.2	0.8	22.2	80.1	0.47	-353	77.2	0.58	83.4
h1-1334	0.4	94.3	0.8	-6	98.6	0.31	-163.3	83.6	0.5	88.5
h1-1409	0.2	95.2	0.8	-18.3	106.6	0.42	-146.8	84.2	0.55	90.3
h1-1331	-1.1	103.3	0.81	-10.8	101.7	0.48	-83.6	86.4	0.58	92.9
s-1323	-1.4	105.1	0.8	-5.3	98.1	0.42	-62.7	87.1	0.56	93.3
k-1358	0.2	95.7	0.81	9.9	88.1	0.35	-42.8	87.7	0.54	89.8
k-1365	1.9	85.1	0.81	-4.1	97.4	0.32	62.8	91.3	0.52	90.7
h1-1390	0.3	94.8	0.8	9.2	88.7	0.45	109.1	92.9	0.57	92.7
h1-1417	-0.1	97.4	0.81	-0.9	95.3	0.46	157.1	94.6	0.57	95.4
k-1442	-1.7	106.7	0.8	1.7	93.6	0.44	175.8	95.2	0.57	97.8
h1-1425	-1.1	103.3	0.81	2.1	93.3	0.47	254.4	97.9	0.58	98.6
h1-1465	-3.1	115	0.81	-6.1	98.7	0.48	318	100	0.58	103.6
h1-1449	-0.5	99.9	0.81	3.2	92.6	0.31	363.9	101.6	0.51	99.8
h2-1452	-0.6	100.5	0.8	3.8	92.2	0.45	389.3	102.5	0.57	100.5
h1-1453	-1.2	103.7	0.81	0.4	94.4	0.41	388.9	102.4	0.55	101.5
h1-1457	-1.5	105.3	0.81	-10	101.2	0.48	391.1	102.5	0.58	103.0

EBV = estimated breeding value weighted   accu = accuracy of estimated breeding value

Cow ID	BV AFC	Index AFC	acc	BV CI	Idex CI	acc	BV 305	index 305	acc	weighed index
h1-1467	-1.6	106.3	0.79	-13.7	103.6	0.34	423.3	103.6	0.52	104.3
h1-1468	-2.3	110.4	0.81	7.4	89.8	0.49	458.8	104.8	0.59	104.0
k-1484	-1.1	103	0.81	-17.4	106.1	0.39	570.4	108.6	0.54	106.8
h2-1487	-1.9	107.8	0.81	4.3	91.9	0.28	637.4	110.9	0.51	107.3
h1-1373	-0.6	100.2	0.81	9.4	88.5	0.3	-473.8	73.1	0.51	82.2
h2-1324	2.1	84.4	0.8	8.5	89.1	0.18	-449.6	73.9	0.45	78.8
h2-1345	-0.6	100.3	0.81	-5.5	98.3	0.41	-428.5	74.6	0.55	84.6
h1-1327	0.9	91.1	0.79	-13.8	103.7	0.35	-298.4	79	0.52	85.7
h1-1355	2.2	83.4	0.81	1.3	93.8	0.3	-269.3	80	0.5	82.9
h1-1336	-0.2	97.8	0.8	-2.5	96.3	0.26	-164.8	83.6	0.49	89.1
h1-1415	-2.4	111.2	0.79	-1.9	95.9	0.12	-107.1	85.6	0.44	93.5
h1-1341	2.5	81.6	0.81	-1.1	95.4	0.32	-52	87.4	0.42	87.2
h1-1360	2.6	81	0.81	9.5	88.4	0.33	-8.6	88.9	0.51	86.9
h1-1342	1.8	86.2	0.79	1.1	93.9	0.14	60.1	91.3	0.45	90.4
h1-1400	1.2	89.7	0.81	-11.1	101.9	0.31	108.4	92.9	0.52	93.5
h1-1416	1.3	89.1	0.8	-2	96	0.41	149.7	94.3	0.55	93.3
h1-1421	0.7	92.4	0.81	-1.4	95.6	0.31	166.4	94.9	0.51	94.4
h2-1405	-0.6	100.1	0.8	-2.9	96.6	0.31	234.1	97.2	0.51	97.8
h1-1466	-0.3	98.7	0.81	-6	98.6	0.34	327.2	100.3	0.52	99.6
h1-1448	0.7	92.6	0.79	-11.1	102	0.22	360.4	101.5	0.48	99.4
h2-1450	-0.8	101.6	0.81	0.2	94.5	0.34	368.7	101.8	0.52	100.7
k-1456	-0.7	100.9	0.81	-6.2	98.7	0.31	390.6	102.5	0.4	101.5
h1-1488	-2.1	109.2	0.81	-5.5	98.3	0.31	639.1	111	0.51	108.6
h1-1500	-0.4	99.1	0.81	-6.4	98.9	0.33	696.7	112.9	0.52	107.4
h1-1507	-0.9	101.7	0.79	-28.7	113.5	0.37	850.2	118.1	0.54	113.3
h1-1509	-2.3	110.1	0.62	-5.8	98.5	0.21	892.5	119.6	0.45	114.1
h1-1329	0.8	92.2	0.79	4.4	91.7	0.12	-394.6	75.8	0.44	82.3
h2-1346	0.6	93.3	0.87	8.8	88.9	0.35	-47.5	87.6	0.54	89.2
h1-1384	1.1	90.1	0.81	-16.1	105.2	0.33	98.7	92.6	0.51	93.9
k-1420	4.4	70.6	0.82	-12.3	102.7	0.39	167.5	94.9	0.56	90.0
h1-1444	-3.2	115.9	0.83	18.7	82.4	0.5	293.3	99.2	0.6	100.9
h1-1476	-0.2	97.6	0.84	-7.5	99.6	0.58	509.4	106.5	0.63	103.2
h1-1479	-2	108.4	0.83	-7.6	99.6	0.56	528.1	107.2	0.61	106.4

Estimated breeding value weighted   accu = accuracy of estimated breeding value