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Estimation of Genetic Parameters for Crossbred Dairy Cattle in the Central Ethiopia

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አህፅሮት

የዚህ ጥናት ዓላማ በመካከለኛው ኢትዮጵያ ምርታማና አካባቢን የሚላመዱ ዲቃላ የወተት ከብቶች ዝርያዎችን በቀጣይነት ለማፍራት በተሻለ የማሻሻያ ስልት ለመደገፍ የዝርያዎች ንጽጽር እና የዘረ-ውርስ ሂደት ጥናት ለማካሄድ ነበር፡፡ ጥናቱ የቦረና እና 11 አይነት የዲቃላ የወተት ከብቶች ዝርያዎችን (የፍሬዥያን ከቦረና እና የጀርሲ ከቦረና ድቅሎች) የ38 ዓመት የወተት ምርት፣ የስነተዋልዶ እና አከባቢን የመላመድ ብቃት መረጃዎችን በመጠቀም ተከናውኗል፡፡ ውጤቱ እንደሚያሳየው የተለያዩ የዲቃላ ዝርያዎች ከቦረና ላሞች ጋር ሲነጻጸሩ ከ 3 አስከ 7 እጥፍ የወተት ምርት ይሰጣሉ፡፡ የዲቃላ ላሞች ቀጣይ ትውልዶች የደም መጠን በ50 በመቶ ላይ ከመጠበቅ ይልቅ ወደ 75 በመቶ የውጭ ደም መጠን ማሳደጉ የወተት ምርትን በ34 በመቶ ያሳድጋል፡፡ ነገር ግን የስነተዋልዶ ብቃታቸው በጥቂቱ ስለሚቀንስ የከብቶች መረጣ ላይ ትኩረት ሊደረግ ይገባል፡፡ የፍሬዥያን እና የጀርሲ ዝርያዎችን ለማዳቀል መጠቀማችን የዲቃላ ከብቶች የመጀመሪያ ትውልድ የወተት ምርትና የስነተዋልዶ ብቃታቸውን በከፍተኛ ደረጃ ቢያሻሽልም (additive and heterosis) በቀጣይ ትውልድ ላይ ግን በ recombination loss ምክንያት ምርታማነታቸው በከፍተኛ ደረጃ ቀንሷል፡፡ የወተት ምርት፣ የሚታለቡበት የቀን ብዛት (lactation length)፣ የመጀመሪያ ጥጃ የመውለጃ ዕድሜ፣ በወሊድ መካከል የቆይታ ጊዜ እና በእርባታ የሚቆዩበት ጊዜ (herd life) የዘረ-ውርስ (የመተላለፍ አቅም፤ heritability) መጠን በቅደም ተከተል 0.30±0.00፣ 0.18±0.02፣ 0.19±0.06፣ 0.09±0.03 እና 0.28±0.06 ናቸው፡፡ የዝርያ ባህሪያት ተዛምዶ (genetic correlation of traits) በተመለከተ በወተት ምርት እና በሚታለቡበት የቀን ብዛት (0.84±0.04)፣ በሚታለቡበት የቀን ብዛት እና በወሊድ መካከል የቆይታ ጊዜ (0.86±0.10) እንዲሁም በሚታለቡበት የቀን ብዛት እና በእርባታ የሚቆዩበት ጊዜ (0.94±0.07) መካከል ከፍተኛ ተዛምዶ ታይቷል:: በአጠቃላይ ውጤቱ በዲቃላ ከብቶች መካከል የታየው የምርት ልዩነት፣ ዘረ-ውርስ መጠን፣ የዝርያ ባህሪያት ተዛምዶ እና በትውልዶች መካከል ያለው የምርት መዋዥቅ የዲቃላ ከብቶችን በመረጣ ለማሻሻል እንደሚቻል የሚያመለክትና ለዚሁም ተስማሚ የማሻሻያ ስልት (breeding program) መንደፍ እንደሚያስፈልግ አመልክቷል፡፡

Abstract

The aim of this study was to estimate the additive, heterosis, recombination loss, heritabilities and correlations between milk yield (MY), lactation length (LL), calving interval (CI), age at first calving (AFC) and herd life (HL) for crossbred of Friesian (F) and Jersey (J) with Boran (B). Analysis of fixed effects and crossbreeding parameter were undertaken using general linear procedure. Genetic parameters were estimated by multivariate analysis procedure with wombat software. Crossbred cows significantly outperform the B cows by 3 to 7 folds of MY per lactation. Even though performance of CI and AFC are slightly compromised, upgrading from 1/2F:1/2B (F1) to 3/4F:1/4B (F1) had better advantage as average MY improved by about 34% following this approach. The additive effects of F and J breed were 3985.2±150 and 1195.6±257 kg for MY, 166.3±16 and 18.5±27 days for LL, 52.9±25 and -40.3±44 days for CI, -0.23±2 and -9.8±4 months for AFC, and 548.7±431 and -569.9±784 days for HL, respectively. The estimated heterosis effects were 1054.8±145 and -150.6±76 kg for MY, 62.4±15 and -7.3±8 days for LL, -58.1±24 and -88.7±13 days for CI, -1.9±3 and -4.7±1 months for AFC and -215.0±446 and -890.1±226 days for HL for J and F with B breed crosses, respectively. The loss due to recombination of F and B was significant ($p < 0.005$) and undesirable for MY, LL, AFC which reflect the need *of appropriate breeding program. The heritability (h^2) estimates were 0.30±0.00 for MY, 0.18±0.02 for LL, 0.09±0.03 for CI, 0.19±0.06 for AFC and 0.28±0.06 for HL. Strong genetic correlations were obtained between MY and LL (0.84±0.04), LL and CI (0.86±0.10) and LL and HL (0.94±0.07). The estimated genetic variance, heritabilities and correlations between traits and decline in performance of inter-se generations reveal the available potential of improvement through selection and the need of designing appropriate breeding program.*

Keywords: Heritability; Correlation; Additive; Heterosis; Boran

Introduction

The per capita milk consumption in Ethiopia was low (less than 20 kg) compared to neighboring tropical countries such as Kenya (90 lt) and Uganda (50 lt) (Land O'Lakes, 2010). The country foreign currency paid out for milk import was also increased from 3.1 to 9.3 million USD during 2001-2008 years (Haile, 2009) and then to 15 million USD in 2013 (FAO, 2017).

The low per capita consumption and increase in milk import overtime in Ethiopia could be attributed to low productivity of indigenous dairy cattle which accounts 98.2% of national cattle population (61.5 million heads) (CSA, 2019). Hence, the genetic improvement of dairy cattle was geared towards crossbreeding of indigenous cows with improved specialized breeds. Several researches indicated that performance of crossbred dairy cattle is encouraging as milk production can be enhanced by about 3-5 folds using crossbred dairy cattle breeds as compared to indigenous cattle (Sendros *et al*., 2004; Zelalem *et al*., 2006; Aynalem *et al*., 2011; Kefena *et al*., 2013). Agajie *et al*. (2016), has also noted that adopter of crossbred dairy cows generated 44% more income in Ethiopia.

There are two major problems which make the sustainability of crossbreeding in Ethiopia questionable. The first is drastic fluctuation in performance of crossbred from generation to generations and among exotic inheritances. The second challenge is, despite subsequent efforts that have been made by government and non- governmental institution and huge investment used up in the last 40 to 50 years, the proportion of crossbred dairy cattle in the country is less than 2% of the national cattle population. This could be associated with lack of appropriate breeding programs that sustain genetic improvement. A breeding program is an organized structure designed to genetically improve livestock populations and benefit livestock keepers and respective stakeholders (FAO, 2010; Philipsson *et al*., 2010). Hence, designing and implementing appropriate breeding program is prioritized as a key intervention area in the strategic documents of dairy development and research for the next 15 years in Ethiopia (EIAR, 2017; MOA, 2019). According to FAO Guideline (FAO, 2010) genetic parameters and other variance components of important traits are among essential inputs to design alternative breeding program. However, there is limited information reported on these regard in recent years in Ethiopia. The aim of this study was, therefore, to estimate crossbreeding parameters, variance components and genetic parameters for breeding goal traits of crossbred dairy cattle with different exotic sire breed and proportion using nucleus herd long-term data set.

Materials and Methods

Study area

The study was conducted at Holetta Agricultural Research Center (HARC). Holetta is sited in the central highlands of Ethiopia, 40 km west of Addis Ababa on the main road to Ambo. It is positioned at 38.5^0 E longitude and 9.8^0 N latitude with an altitude of 2500 meters above sea level. Average annual rainfall was about 1,200 mm. The mean annual temperature and relative monthly humidity were 18°C and 60%, respectively (Aynalem *et al*., 2011).

Data source and Herd management

The data for this study was obtained from data base of HARC. This center is the largest and oldest dairy research center conducting studies on crossbreeding in Ethiopia. In addition, the center serves as a source of crossbred bulls for crossbreeding carried out on smallholder farmers dairy cattle. The initial objective of the farm was to evaluate crossbred cattle with different exotic inheritance (Friesian and Jersey breed with indigenous breeds). Then it was intended to stabilize crossbred inheritance at 50%. This breeding program was interrupted after 10 years and shifted to stabilize the crossbred inheritance at 75% Friesian inheritance since 2009.

Almost similar amount of hay and concentrate supplement were provided for animals in similar age and physiological status. The amount of concentrate supplement provided to milking cows, dry cows and heifers per day were about 3-4 kg, 2-3 kg and 1-2.5 kg, respectively. However, it was influenced by availability of fund and feeds in stock. Calves were offered fresh milk twice a day for about 98 days. Calves less than 6 months, bulls and late pregnant cows were managed indoor and exercise outdoor for one to two hours per day. Cows and heifers were allowed to graze natural pasture for about 8 hours per day during dry and short rainy season. However, they were restricted from grazing during main rainy season as the pasture lands were reserved for hay production. The farm had regular vaccination and de-warming schedule against major disease and parasites. Milking was carried out twice a day at equal interval. Individual data were recorded on prepared format and transferred to farm data base for pedigree, growth, production, reproduction and survival information.

Mating was practiced throughout the year using mainly Artificial insemination (AI). Natural mating was also considered for replacement of Boran and for crossbred cows which did not conceive by AI. The main source of semen for crossbreeding research was National Artificial Insemination Center and the farm has also been using Friesian semen from worldwide sire for F1 and ¾ crossbred productions since 2009.

Data analysis

Recorded data in the last 38 years (1979-2019) on production, reproduction and survival were used for this study. The traits studied were milk yield (MY), lactation length (LL), calving interval (CI), age at first calving (AFC) and herd life (HL). Boran (B) has been serving as a dam line representing indigenous breed and Friesian (F) and Jersey (J) were the sire breeds. The following genotypes were considered for this study: B, ½F: ½B and ½J: ½B from 1st to 3rd generations, ¾F: ¼B (2 generations), ¾J: ¼B, 5/8F: 3/8B and 5/8J:3/8B inheritance. Data of genotypes with similar sire breed and proportion but different generation were pooled together for variance and genetic parameter analysis. Total number of records used across different genotype and pedigree structure are presented in Table 1 and Table 2.

Table 1. Number of records used for analysis of genetic and crossbreeding parameters for different traits

Genotype	Traits				
	MY	LL	CI	AFC	HL
F x B crosses	2564	2564	1901	808	613
J x B crosses	584	584	450	110	120
1/2F:1/2B inter-se crosses	2026	2026	1547	590	495
3/4F:1/4B inter-se crosses	462	462	298	200	97
B	480	480	983	29	223

B, Boran (used as a dam breed); F, Friesian; J, Jersey; MY, lactation milk yield; LL, lactation length; CI, calving interval; AFC, age at first calving; HL, herd life. The fraction values are the proportion of respective breeds to the genotypes.

Table 2. Summary of pedigree structure used for analysis of variance component and genetic parameters

Genotypes	Animals without offspring	Animals with offspring	Sire	Dam	Animals with maternal grandsire	Animals with maternal grand dam
F x B crosses	664	549	97	452	388	337
J x B crosses	91	99	23	76	83	46
½ F:1/2B	577	394	84	310	174	143
3/4F:1/3B	578	427	72	355	252	229

B, Boran (used as a dam breed); F, Friesian; J, Jersey. The fraction values are the proportion of respective breeds to the genotypes.

Three models were applied to determine fixed effects, crossbreeding parameters, variance components and genetic parameters. The analyses for the first two models were conducted using General Linear Model (GLM) procedure of the Statistical Analysis System (SAS, version 9; 2002). Least square means were estimated for different genotype and other fixed effects (model 1). Genotype (12 classes with different breed proportion), calving year: 38 years grouped in to 8 classes (1982-1986, 1987-1991, 1992-1996, 1997-2001, 2002-2006, 2007-2011, 2012-2016 and 2017-2019) and parity: eight classes (1, 2, 3, 4, 5, 6, 7, 8+) were fitted as fixed effect for analysis of MY, LL and CI. For analysis of HL, genotypes (12 classes) and calving years: 30 years grouped in to 6 classes (1982-1986, 1987-1991, 1992-1996, 1997-2001, 2002-2006 and 2007-2011) were accounted. Genotypes (12 classes) and birth years: 38 years grouped in to 8 classes (1979-1983, 1984-1988, 1989-1993, 1994-1998, 1999-2003, 2004-2008, 2009-2013 and 2014-2016) were fitted for estimation of AFC. For analysis of crossbreeding parameter (model 2), all fixed effect fitted were similar with model one except genotypes class which was replaced by coefficients of expected breed additive, heterosis and recombination loss fitted as covariates (Table 3). The Multiple Regression approach developed by Robison *et al.* (1981) was used to estimate the contribution of breed additive, heterosis and recombination effects. The breed additive effects for F and J were estimated as deviations from the B breed. The coefficient of breed additive (g_i), heterosis (h_{ij}) and recombination (r_{ij}) effects were calculated according to Wolf *et al* (1995) where: $g_i = ½(\alpha^s_i + \alpha^d_i)$, $h_{ij} = \alpha^s_i\alpha^d_j + \alpha^s_i\alpha^d_j$ and $r_{ij} = 4g_i\, g_j – h_{ij,}$ α = additive, s = sire and d = dam. Result of preliminary analysis showed that season (birth and calving) had no significant influence on all studied traits and so removed from final analysis. Furthermore, effects of maternal heterosis and recombination were assumed to be negligible in this analysis. The overall structure of the model 1 and 2 used to analyze most of the trait was presented as follow;

$$Y_{ijk} = \mu + G_i + C_j + P_k + e_{ijk}$$

Where, Y_{ijk} represent performances of MY, LL, CI, AFC and HL; μ is the overall mean; G_i is the fixed effect of i^th genotype; C_j is the fixed effect of j^th year of birth or calving; P_k is the effect of k^th cow parity; e_{ijk} is random residual term.

Table 3. Genetic coefficient used for estimation of crossbreeding parameter

	Genetic coefficients					
Genotype	gF	gJ	hFB	hJB	rFB	rJB
B	0	0	0	0	0	0
1/2F:1/2B (F1)	0.5	0	1	0	0	0
1/2F:1/2B (F2)	0.5	0	0.5	0	0.5	0
1/2F:1/2B (F3)	0.5	0	0.5	0	0.5	0
3/4F:1/4B (F1)	0.75	0	0.5	0	0.25	0
3/4F:1/4B (F2)	0.75	0	0.375	0	0.375	0
5/8F:3/8B	0.625	0	0.5	0	0.438	0
1/2J:1/2B (F1)	0	0.5	0	1	0	0
1/2J:1/2B (F2)	0	0.5	0	0.5	0	0.5
1/2J:1/2B (F3)	0	0.5	0	0.5	0	0.5
3/4J:1/4B (F1)	0	0.75	0	0.5	0	0.25
5/8F:3/8B	0	0.625	0	0.5	0	0.438

B, Boran used as dam breed; F, Friesian; J, Jersey; g, breed additive; h, heterosis and r, recombination loss. The fraction values are the proportion of respective breeds to the genotypes

Multivariate analysis of mixed animal model (Model 3) with repeated and single records was used to estimate variance components (phenotypic, genetic and permanent environmental variances), genetic and phenotypic correlations, and genetic parameters (heritability and repeatability) for MY, LL, CI and AFC traits. Wombat software program (Meyer, 2007) was used for this computation. For comparison of heritability, records of different genotypes were analyzed in 5 approaches. These are (1) records of all genotype, (2) records of F x B crosses of different genotype (B, ½F: ½B from 1st to 3rd generation, ¾F: ¼B (2 generations) and 5/8 F: 3/8 B), (3) record of Jersey x Boran crosses of different genotype (B, ½J: ½B from 1st to 3rd generation, ¾ J: ¼ B and 5/8 J: 3/8 B), (4) records of 1/2F: ½ B inter-se mated crosses (B, ½F: ½B from 1st to 3rd generation), and finally records 3/4F:1/4B inter-se mated crosses (B, ½F: ½B (F1) and ¾F: ¼B (F2) generations). The overall matrix of repeatability animal model was the following:

$$Y = \mathbf{X}b + \mathbf{Z}u + \mathbf{W}c + e$$

Where Y represents a vector of observations for one of studied traits and b, u and c represent vectors of fixed, random individual additive and permanent environmental effects respectively. X, Z and W denote matrices relating records to fixed, random individual additive and permanent environmental effects, respectively. Finally e is vector of random residual effect. The fixed effects (genotype, years and parity) considered in the third model for the respective traits are similar with effects fitted in model one. Permanent environmental effect was removed from analysis of traits with single record per individual (AFC and HL).

The random individual additive, permanent environmental and residual effects were assumed to be normally distributed and uncorrelated with means of zeros and variances $\sigma^2 a$, $\sigma^2 c$ and $\sigma^2 e$, respectively, where var (a) = $A\sigma^2 a$, var (c) = $I\sigma^2 c$ and var (e) = $I\sigma^2 e$ where A is additive numerator relationship matrix among animals in the population and I is the identity matrix. Heritabilities ($h2 = \frac{\sigma 2a}{\sigma 2p}$) and Repeatability ($r2 = \frac{\sigma 2a + \sigma 2c}{\sigma 2p}$) of traits with repeated records were defined based on additive, permanent environmental and phenotypic variances estimated by the program, where p represent phenotype. The genetic correlations (r_g) between traits were calculated as follow: ($rg = \frac{\sigma a12}{(\sqrt{\sigma 2a1} \text{ x } \sqrt{\sigma 2a2})}$), where σal2 represent genetic covariance of trait 1and 2, $\sigma^2 a1$ and $\sigma^2 a2$ are genetic variance of trait 1 and 2 respectively. The phenotypic correlations (r_p) between traits were also estimated as follow: ($rp = \frac{\sigma p12}{(\sqrt{\sigma 2p1} \text{ x } \sqrt{\sigma 2p2})}$), where σpl2 represent phenotypic covariance of trait 1and 2, $\sigma^2 p1$ and $\sigma^2 p2$ are phenotypic variance of trait 1 and 2, respectively.

Results and Discussion

Genotype and fixed effects analysis

The estimates of least square means and standard error for MY, LL, CI, AFC and HL traits of B and crosses of F and J with B are presented in Table 4. Genotype, calving year and parity had significant ($p < 0.001$) effect on MY, LL and CI. Similarly genotype and birth year were among the main factors that influence ($p < 0.001$) AFC and HL (Table 4 and Table 5). The significant effect of years on performance of crossbred cattle indicates the inconsistent husbandry practices and change in culling practices of the farm across study periods. All crossbred genotypes perform much better than B breed (indigenous) in MY and LL. Crossbred cows outperform the B cows by 833 kg to 2600 kg (3 to 7 folds) milk yield per lactation. Further comparison among crossbred genotype revealed that significantly higher average milk yield was recorded in 3/4F:1/4B (F1) followed by 3/4F:1/4B (F2) and 1/2F:1/2B (F1) than other studied contemporaries. However, drastic reduction in performance of milk yield was detected across different generations. Milk yield radically reduced in inter-se generations by about 26% from 1/2F:1/2B (F1) to 1/2F:1/2B (F2) and 30% to 1/2F:1/2B (F3). Furthermore, these figures escalate to 30% and 39% deterioration for Jersey crosses of the same genotypes, respectively. Upgrading from 1/2F:1/2B (F1) to 3/4F:1/4B (F1) had better advantage as average lactation milk yield improve by about 34% and effect of segregation on 1/2F:1/2B (F2) inter-se mating reduced. In addition, The F1 1/2F:1/2B (2257.9±29 kg) and F2 3/4F:1/4B (2357.2±107 kg) provided comparable MY.

First generations of F and J with B crosses showed significantly ($p < 0.05$) lower estimate for CI and AFC compared to that of other contemporaries. B (523.8±6) and F1 3/4F:1/4B (520.5±9) cows exhibited significantly prolonged CI which could reduce the lifetime milk yield and calves crop. First generation J crosses calved about 6 months earlier than B breed and F inter-se and upgraded crossbred generations. Most of inter-se mated generations did not have significant difference ($p > 0.05$) with B breed in CI and AFC.

Herd life (stayability) is described as the time span between first calving and disposal from the herd either by death or culling. The B breed cows significantly ($p < 0.001$) stay longer in the herd than all F and J with B crossbred cows. Almost similar HL ($p > 0.05$) was estimated for F1 and crossbred cows with three quarter inheritances of both sire breeds (F and J). However, stayability of inter-se mated F2 and F3 50% crossbred inheritance was significantly reduced by 35% and 52%, respectively as compared to F1 F x B crosses. This might be associated with lower milk yield performance of these genotypes as the likelihood of inferior cows to be culled from herd is higher than others in dairy business.

In general, the variation observed due to year, parity and among different genotypes for most of the traits were in agreement with several studies conducted elsewhere in the tropics (Fadlelmoula *et al*., 2007; Aynalem *et al*., 2011; Kefena *et al*., 2013; Galukande *et al*., 2013; Gebregziabher *et al*., 2013). The MY value estimated for 1/2J:1/2B (2070.45) and 5/8F:3/8B (2047.1) in the current study were close to the report of Amasaib *et al*. (2011) and Zambrano *et al* (2006) who found 2026 kg for F1 crossbred dairy cattle in Sudan and 2093 kg for ½ Criollo Limonero: ½ Friesian crossbred in topical area of Venezuela, respectively. The MY performance of 3/4F:1/4B (3043.8) backcrossed inheritance observed in this study is close to 3174 kg obtained for 62.5 exotic improved breed inheritance (Fadlelmoula *et al*., 2007) and 2579-3320 kg for crossbred in Sudan (Amasaib *et al*., 2011). However, it is different from previous studies reported by Million and Tadelle (2003) and Aynalem *et al*. (2011) who found 2373 kg and 2182 kg for backcrosses of F x Barka breed and F x B breed in Ethiopia, respectively.

The report of Swai *et al*. (2007) for CI (476 days) in crossbred dairy cattle in Tanzania is comparable with value obtained for 1/2F:1/2B (F3) and 1/2J:1/2B (F2), but higher than that of 1/2F:1/2B (F1) and other J x B crossbred inheritance estimated here. Zambrano *et al* (2006) found higher CI (577) for crossbred dairy cattle in Sudan than the value computed for all genotype in our study. The AFC value obtained for 1/2J:1/2B (F1) and 3/4J:1/4B is consistent with the report of Rokonuzzaman *et al*. (2009) and Galukande *et al*.(2013) who found 34 to 36 months AFC for crosses of F, Sahiwal and Sindhi with indigenous breed in Bangladesh and Red Poll x Zebu crosses in Brazil, respectively. However, their estimate of AFC is lower than the figures of all other contemporary groups in the present study. For B breed comparison Sendros *et al*. (2004) and Aynalem *et al*. (2011) reported higher MY (507-529 kg) and shorter CI (439-473 days) and LL (193-240 days), but closer AFC (42.5-43.5 months) to the results estimated here.

The value estimated for HL of B cows (2715.9±93 days) is significantly higher than crossbred genotypes (839.5-2242.3 days), but comparable to the report of Kefena *et al*. (2013) who found 2435 to 3107 days for F x B and J x B crosses with different breed proportions. Similarly, Direba *et al*. (2015) obtained close (1813 days) value, for pure J cattle in Ethiopia, to our estimates for some of crossbred genotype (1/2F:1/2B (F1), 3/4F:1/4B (F2) and 3/4J:1/4B (F1)).

It can be point out from our results that though adaptation is slightly compromised, production and reproduction performance is significantly enhanced through crossbreeding. Friesian crosses outshine the J counterpart in production performances while the J crosses were superior in reproduction performances. The practical challenge detected by this study, which is supported by literatures, is drastic reduction of performances in inter-se generations. This could be attributed to loss of heterosis due to gene segregation and lack of breeding value based selection on sire used for inter-se mating. Even though CI and AFC is slightly compromised, instead of maintaining at 50% upgrading from 50% to 75% had better advantage as average lactation MY substantially improved and effect of segregation on F2 (50%) inter-se mating reduced following this approach.

Table 4. Least square means and standard error estimated for production, reproduction and herd life traits

Breed group	MY (kg)	LL (days)	CI (days)	AFC (months)	HL (days)
Boran (B)	410.3±46^{h}	264.7±5^{e}	523.8±6^{a}	42.8±1^{abc}	2715.9±93^{a}
Friesian crosses (F)					
1/2F:1/2B (F1)	2257.9±29^{b}	340.8±3^{b}	461.3±5^{c}	37.8±0.4^{de}	2104.8±69^{b}
1/2F:1/2B (F2)	1680.4±58de	316.2±6^{c}	503.0±11^{ab}	44.1±0.7^{a}	1367.5±125^{cd}
1/2F:1/2B (F3)	1510.6±74^{efg}	312.1±8^{cd}	476.2±14^{bc}	43.3±0.9^{ab}	1007.4±143de
3/4F:1/4B (F1)	3043.8±54^{a}	376.0±6^{a}	520.5±9^{a}	42.2±0.7^{abc}	2058.4±148^{b}
3/4F:1/4B (F2)	2357.2±107^{b}	333.9±11^{bc}	461.5±20^{c}	42.2±1^{abc}	1779.9±288^{bc}
5/8F:3/8B	2047.1±101^{c}	327.5±11^{bc}	520.2±18^{a}	42.5±2^{abc}	1274.4±264^{cde}
Jersey Crosses					
1/2J:1/2B (F1)	2070.5±58^{c}	336.7±6^{b}	447.9±10^{c}	35.8±1^{e}	2242.3±204^{b}
1/2J:1/2B (F2)	1435.3±67^{fg}	314.8±7^{cd}	475.9±12^{bc}	39.7±1^{cd}	1416.1±173^{cd}
1/2J:1/2B (F3)	1244.1±122^{g}	288.2±13^{d}	444.5±24^{c}	40.3±1^{bcd}	839.5±209^{e}
3/4J:1/4B (F1)	1764.4±93^{d}	310.2±10^{cd}	466.4±16^{c}	36.3±2de	1638.7±298^{bcd}
5/8J:3/8B	1655.0±134^{def}	326.7±14^{bc}	445.5±23^{c}	37.0±2de	1320.8±332^{cde}

B, Boran (used as a dam breed); F, Friesian; J, Jersey; MY, lactation milk yield; LL, lactation length; CI, calving interval; AFC, age at first calving; HL, herd life. The fraction values are the proportion of respective breeds to the genotypes. Least squares means with same superscript indicate non significance ($p > 0.05$).

Table 5. Estimates of effect of years and parities on dairy traits for crossbred cattle

Effect	MY (kg)	LL (days)	CI* (days)	HL (days)	AFC (months)	
Year group					Year group	Value
1982-1986	1696.94±98de	396.37±10^{a}	540.83±17^{a}	2963.35±182^{a}	1979-1983	48.66±1^{a}
1987-1991	1752.72±60^{d}	356.11±6^{c}	495.32±10^{b}	2332.74±166^{b}	1984-1988	42.27±1^{b}
1992-1996	1800.13±48^{cd}	372.59±5^{b}	489.34±8^{b}	2138.02±144^{b}	1989-1993	48.87±1^{a}
1997-2001	2150.68±48^{a}	333.39±5^{d}	437.98±8^{c}	1544.12±123^{c}	1994-1998	38.61±0.8^{c}
2002-2006	1912.52±51^{c}	308.80±5^{e}	501.81±10^{b}	867.01±125^{d}	1999-2003	37.65±0.7^{c}
2007-2011	2081.83±54^{ab}	291.81±6^{f}	431.98±10^{c}	770.24±135^{d}	2004-2008	43.89±0.8^{b}
2012-2016	1987.18±53^{bc}	273.82±5^{g}	436.94±9^{c}		2009-2013	34.12±0.8^{d}
2017-2019	1549.91±57^{e}	247.17±6^{h}			2014-2016	33.88±1^{d}
Parity						
1	1705.21±38^{c}	335.82±4^{ab}	525.52±7^{a}			
2	1898.07±42^{b}	337.00±4^{a}	495.48±7^{b}			
3	1971.60±47^{ab}	326.68±5^{bcd}	472.63±8^{c}			
4	2031.86±54^{a}	331.05±5^{abc}	469.03±9^{c}			
5	2048.87±62^{a}	323.86±6^{bcd}	462.92±10^{c}			
6	1962.96±69^{ab}	317.64±7^{cd}	464.86±12^{c}			
7	1939.55±83^{ab}	312.27±8de	467.52±15^{bc}			
8+	1909.73±80^{ab}	295.75±8^{e}	452.58±15^{c}			

MY, lactation milk yield; LL, lactation length; CI, calving interval; HL, herd life; AFC, age at first calving; *CI, last year group contain years from 2012 to 2018 for calving interval (7 year groups); 8+, Parities greater than 8 merged to parity 8; Least squares means with same superscript indicate non significance ($p > 0.05$).

Crossbreeding parameters

Estimates of crossbreeding parameters for MY, LL, CI, AFC and HL are shown in Table 6. The effects of calving years and parities were significant ($p < 0.0001$) on MY, LL and CI. Similarly birth year had significant ($p < 0.0001$) influence on AFC and HL. The individual breed additive of F and J breeds was significant ($p < 0.0001$) for improvement of MY. Furthermore, the individual additive effect of F breed on LL and CI and J breed on AFC were substantial ($p < 0.05$). However, the direct additive contribution of F breed on AFC and HL and J breed on LL, CI and HL did not show significant effect ($p > 0.05$). The additive effects of F and J breed were 3985.2±150 and 1195.6±257 kg for MY, 166.3±16 and 18.5±27 days for LL, 52.9±25 and -40.3±44 days for CI, -0.23±2 and -9.8±4 months for AFC, and 548.7±431 and -569.9±784 days for HL, respectively.

Crossing of F with B breed brought significant heterosis ($p < 0.05$) effect on MY, CI, AFC and HL. Whereas, heterosis due to J and B breeds combination had significantly ($p < 0.01$) influenced MY, LL and CI. The heterosis effects expressed as deviation from mid parent estimated here were 1054.8±145 and -150.6±76 kg for MY, 62.4±15 and -7.3±8 days for LL, -58.1±24 and -88.7±13 days for CI, -1.9±3 and -4.7±1 months for AFC and -215.0±446 and -890.1±226 days for HL for J and F with B breed crosses, respectively. The loss due to recombination of F and B gene was significant ($p < 0.005$) and undesirable for MY, LL, AFC. However, the significant effect of recombination loss ($p < 0.0001$) for J x B crosses was observed only on HL. Our estimate revealed that higher individual additive and recombination loss was detected for most of the traits in the F x B crosses than J x B crosses. The contribution of F breed on MY improvement was mainly due to additive but that of the J breed was through both additive and heterosis. Likewise the additive effect of J breed significantly reduce AFC (by -9.8 months) with low recombination loss compared to F breed (-0.23 AFC) and the contribution F breed on CI was significant and undesirable.

Our results on effects of additive, heterosis and recombination loss is generally in agreement with findings in the literatures (Kahi *et al*., 2000; Magaña and Correa, 2001; Gradiz *et al*., 2009; Aynalem *et al*., 2009; Hatungumukama and Detilleux, 2009). For instance, Sendros *et al*. (2004) found close estimates of additive for MY (1473 kg) and LL (146 days) of J breed and LL (152 days) of F breed, but lower estimates for MY (2774 kg) and CI (-13 days) of F breed. The value obtained by Kahi *et al*. (2000) in Kenya (296 to 426 kg) and Gradiz *et al*. (2009) in subtropical lowland of Honduras (194 to 668 kg) for heterosis of MY are low compared to our estimates for J x B crosses but higher than that of F x B crosses. Similar to the result of the present study, Gradiz *et al* (2009) estimated high (-1142 kg) recombination loss for MY in crosses of Brown Swiss with Brahman. Our estimate of recombination loss for MY of J x B breed (-261.8±201 kg) is higher than -132 kg reported for J x B breed in Ethiopia (Sendros *et al*., 2004). Some of the variation detected between our studies and literatures could be attributed to the difference on genetic potential of the breeds and gene combining ability, data size used and model considered for analysis. It can be noted from analysis of crossbreeding parameter that the substantial improvement obtained through additive and heterosis is considerably lost by effect of recombination in inter-se generations.

Table 6. Estimate of contribution of additive, heterosis and recombination loss for production, reproduction and herd life traits

Breed group	MY(kg)	LL (days)	CI (days)	AFC (months)	HL (days)
B	410.3±46	264.7±5	523.8±6	42.8±1	2715.9±93
gF	3985.2±150***	166.3±16***	52.9±25*	-0.2±2	548.7±431
gJ	1195.6±257***	18.5±27	-40.3±44	-9.8±4*	-569.9±784
hFB	-150.6±76*	-7.3±8	-88.7±13***	-4.7±1***	-890.1±226***
hJB	1054.8±145***	62.4±15***	-58.1±24**	-1.9±3	-215.0±446
RFB	-1496.6±143***	-64.2±15***	-26.5±26	7.1±2***	-2696.4±336***
RJB	-261.8±201	11.3±21	-16.1±35	6.4±4	-2245.3±566***

F, Friesian; J, Jersey. B, Boran, gF and gJ are F and J breed additive contributions relative to B; hFB, hJB are heterosis effect for crossing F and J with B, respectively. RFB and RJB are recombination loss when crossing F and J with B breeds, respectively. MY, lactation milk yield; LL, lactation length; CI, calving interval; AFC, age at first calving; HL, herd life *p < 0.05, **p < 0.01, ***p < 0.0001.

Variance components and genetic parameters

Heritability and repeatability

Estimate of variance components, heritability and repeatability of all traits for pooled data set of all genotype are shown in Table 7. The overall heritability (h^2) estimates for studied traits were 0.30±004 for MY, 0.18±0.02 for LL, 0.09±0.03 for CI, 0.19±0.06 for AFC and 0.28 for HL. The corresponding estimates of repeatability were 0.52±0.65, 0.26±0.15 and 0.17±0.19 for MY, LL and CI, respectively. The h^2 computed for MY was moderate and within the range of 0.24-0.34 reported by several literatures (Gebregziabher *et al.*, 2013; Pritchard *et al.*, 2013; Chawala *et al.*, 2017; Cayo *et al.*, 2018; Wahinya *et al.*, 2020). However, it was higher than 0.1 reported for crossbred in Ethiopia (Aynalem *et al.*, 2009) , 0.23 for crossbred cattle in New Zealand (Sneddon *et al.*, 2016) and 0.19 for Jersey breed in South Africa (Opoola *et al.*, 2020). On the contrary Ali *et al.* (2019) found higher (0.46) value for crossbred cattle in Pakistan. The estimated h^2 of MY (0.3) may show that there is sufficient additive variance with in the population and effect of environment is relatively low as the management of this research herd is almost intensive (and uniform management was provided for cows).

Estimate of h^2 for CI in present study was low (0.09±0.03) and close to values obtained for crosses of F x B and J x B (0.08) in Ethiopia (Sendros *et al.*, 2004), crossbred and improved exotic breed (0.03-0.06) in Kenya (Wahinya *et al.*, 2020), F (0.04) in United Kingdom (Pritchard *et al.*, 2013), crossbred cattle (0.14) in Pakistan (Ali *et al.*, 2019) and J breed (0.1) in sub-tropical part of Pakistan (Suhail *et al.*, 2010). The low h^2 obtained for CI implies that the trait is highly influenced by environmental factors and indicates that improvement of this trait can be obtained more by enhancing management than selection. Moderate to low h^2 estimated here for AFC (0.19±0.06) is similar to 0.20 obtained for Girolando breed in Brazil and 0.19 for Holstein breed in Kenya (Opoola *et al.*, 2020) and crossbred in Pakistan (Ali *et al.*, 2019), but higher than 0.10 for crossbred of Holstein with local and Shahiwal breed in Bangladesh (Das *et al.*, 2013), 0.10 for Holstein breed in Zimbabwe (Opoola *et al.*, 2020) and 0.05 for different crossbred genotypes and exotic breeds in high production system in Kenya (Wahinya *et al.*, 2020). On the contrary Wahinya *et al.* (2020) and Dhal *et al.* (2016) found higher AFC (0.26 and 0.46) for crossbred and exotic dairy breed in medium production system in Kenya and for crosses of J with Deshi in Odisha, respectively. The value of h^2 could imply that AFC can be improved in this herd through selection and the difference observed with other literature could be associated with data size, breed and model fitted.

The h^2 presented here for LL (0.18±0.02) is close to 0.15 recorded for J crosses in India (Ratwan *et al.*, 2016). However, Aynalem *et al.* (2009) and Das *et al.* (2013)

found higher (0.63 and 0.27) value for crossbred cattle in Ethiopia and Bangladesh, respectively and Wahinya *et al.* (2020) reported lower figure (0.04-0.10) in Kenya than our estimate. On the other hand, the h^2 value of HL found here is high and similar to 0.28±0.06 reported for Holstein cattle in Egypt (Sadek *et al.*, 2009) and 0.24-0.30 for Angus in South Africa (Maiwashe *et al.*, 2009 as cited by Chikosi *et al.*, 2015). However, it is strongly deviated from 0.02 - 0.18 values obtained by some of the authors (Abou Bakr, 2009; Strapáková *et al.*, 2013; Pelt *et al.*, 2015; Vinothraj *et al.*, 2016; Clasen *et al.* 2017; Zefrehei *et al.*, 2017; Musingi *et al.*, 2018). The differences of estimates for some of the traits with other literature could be associated with breed difference, methods of analysis, data size used and culling practices of the farms.

Further comparison of h^2 results indicated that genotype was a source of variation mainly for MY and AFC (Table 8). The estimated h^2 of MY (0.22) for J x B crosses agree with 0.19 obtained for J breed in South Africa (Opoola *et al.*, 2020), 0.20 for B breed in Ethiopia (Aynalem *et al.*, 2009) and 0.21-0.25 for crossbred in Kenya (Wahinya *et al.*, 2020). However, h^2 of MY in J x B crosses was reduced by 26% compared to the value obtained from pooled data set and other F x B crosses with different proportions in present study. Even though h^2 estimate for AFC of J crosses (0.47±.25) is consistent to the findings of Sendros *et al.* (2004), Suhail *et al.* (2010), Dhal *et al.* (2016) and Osman *et al.* (2013) who found 0.44, 0.48, 0.46 and 0.43, respectively, it was much higher than estimate of 0.19±0.06 for pooled data of all genotype, 0.18±0.06 for F x B crosses, 0.16±0.08 for 1/2 F: 1/2B inter-se crosses and 0.1±0.07 for 3/4F: 1/4B inter-se crosses in our study. The implication of the results is that better estimates of h^2 can be used in the design of breeding program for breed and breed proportion selected. The result of genetic parameters estimated here for Jersey crosses and Boran breed could be influenced by low number of records used indicating the need of further study using sufficient data.

Table 7. Estimate of variance components, heritabilities and repeatabilities for production, reproduction and herd life traits of all studied genotypes.

Estimate	MY(kg)	LL(days)	CI(days)	AFC(months)	HL(days)
Va	206172±0.00	1456.6±204	1419.5±426	7.1±2.5	286406±0.00
Vc	155555±0.00	681.5±178	1204±426	-	-
Ve	313913±8630	5418.9±148	13070.8±377	31.2±2.5	747582±0.00
Vp	690359±8630	8175.6±183	15694.3±415	38.3±1.9	1033990±0.00
h^2	0.30±0.00	0.18±0.02	0.09±0.03	0.19±0.06	0.28±0.06
r^2	0.52±0.65	0.26±0.15	0.17±0.19	-	-

Va, additive genetic variance; Vc, permanent environmental variance; Ve, residual variance; Vp, phenotypic variance; h^2, heritability; r^2, repeatability; MY, lactation milk yield; LL, lactation length; CI, calving interval; AFC, age at first calving; HL, herd life.

Table 8. Estimates of heritabilities for production, reproduction and herd life traits across different genotype

Traits	Genotypes				
	All genotype	F x B crosses	J x B crosses	1/2 F:1/2B inter-se crosses	3/4F: 1/4B inter-se crosses
MY	0.30±0.00	0.30±0.00	0.22±0.02	0.30±0.01	0.30±0.01
LL	0.18±0.02	0.18±0.03	0.12±0.06	0.21±0.03	0.19±0.03
CI	0.09±0.03	0.08±0.03	0.06±0.09	0.09±0.03	0.09±0.03
AFC	0.19±0.06	0.18±0.06	0.47±0.25	0.16±0.08	0.1±0.07
HL	0.28±0.06	0.25±0.06	0.27±0.12	0.24±0.07	0.24±0.08

B=Boran used as dam breed; F=Friesian; J=Jersey; MY=lactation milk yield; LL=lactation length; CI=calving interval; AFC=age at first calving; HL=herd life; The fraction values are the proportion of respective breeds to the genotypes.

Genetic and phenotypic correlations

As shown in Table 9, the genetic correlations observed between all studied traits were positive and varying from 0.15 to 0.94. Similarly, the phenotypic correlations of all traits, except AFC with HL (-0.01±0.04), were positive. Strong genetic correlations were obtained between MY and LL (0.84±0.04), LL and CI (0.86±0.10), LL and HL (0.94±0.07) and CI and HL (0.78±0.14). Whereas, the genetic correlation between MY and AFC (0.37±0.13), AFC and LL (0.27±0.15) and AFC and HL (0.15±0.21) were moderate to low. Likewise the phenotypic correlations between most of the traits were moderate to low ranging from 0.55 to 0.02. In general, estimates of genetic and phenotypic correlations between most of the traits are within the range of literatures in the tropics (Gebregziabher *et al.*, 2013; Ratwan *et al.*, 2016; Cayo *et al.*, 2018; Ali *et al.*, 2019; Wahinya *et al.*, 2020). The negative phenotypic correlation estimated between AFC and HL might be attributed to the farm culling practice where cows that calve at later age had higher risk to be disposed from the herd than others. The positive genetic and phenotypic association of MY and CI is undesirable as selection to increase MY, would cause prolonged calving interval and should be appropriately addressed in the selection index of the breeding program. The higher genetic than phenotypic correlations detected here could reflect that traits react differently to change in environment. The low phenotypic correlations between most of the traits may indicate that the selection based on phenotype could have undesirable consequence on some of the other traits. The good genetic correlation observed between traits suggests that genetic improvement in one trait can result in improvement of other trait. In general the results of this analysis disclose that there are good genetic and phenotypic variations, moderate heritability and high to medium correlations for most of the traits which could create favorable condition for long term improvement of crossbred inheritance through selection.

Table 9. Genetic and phenotypic correlation of production, reproduction and herd life traits

Traits	Traits				
	MY	LL	CI	AFC	HL
MY		0.84±0.04	0.64±0.12	0.37±0.13	0.64±0.18
LL	0.55±0.01		0.86±0.10	0.27±0.15	0.94±0.07
CI	0.23±0.02	0.37±0.02		0.61±0.19	0.78±0.14
AFC	0.17±0.04	0.01±0.04	0.02±0.04		0.15±0.21
HL	0.07±0.00	0.15±0.02	0.14±0.03	-0.01±0.04	

MY, lactation milk yield; LL, lactation length; CI, calving interval; AFC, age at first calving; HL, herd life; Above diagonal genetic correlation; below diagonal phenotypic correlation.

Conclusions

Crossbred genotypes perform much better than the indigenous B breed in MY, LL and AFC, which is mainly due to additive and heterosis effects. The substantial improvement obtained through additive and hetersosis was considerably lost by effect of recombination in inter-se generations which reflect the necessity of appropriate breeding program. Friesian crosses outshine the J counterpart in production performances while the J crosses were superior in reproduction performances. Even though performance of CI and AFC are slightly compromised, upgrading from 50% to 75% exotic inheritance had better advantage on MY performance of crossbred cattle if supported by well-designed breeding program. It can be noted that crossbreeding for dairy cattle in selected niches can bring substantial change and the result of this analysis can be used as an input to develop breeding program. The estimated genetic variance, h^2 and correlations between traits and drastic decline in performance of inter-se generations reveal the available potential of improvement through selection and the need of designing appropriate breeding program.

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