

Genetic and Environmental Influences on Growth Performance of Jersey and Friesian Crossbred Dairy Cattle in Central Ethiopia

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Abstract: This study was undertaken to evaluate the growth performance and estimate their genetic parameters for the crossbred of Jersey and Friesian with Boran breeds. Traits analyzed included birth weight (BW), weaning weight (WW), six-month weight (SMW), yearling weight (YW), pre-weaning weight gain (PRWWG), and post-weaning weight gain (PTWWG). Correlations of growth traits with age at first calving (AFC) were also computed to identify a better indicator of growth traits for AFC. Data collected from Boran (B) and crosses of Friesian (F) and Jersey (J) with Boran during 1978 to 2020 were used. A general linear model procedure (Models 1 and 2) was used for analysis. The first model was used to estimate the effect of fixed factors, while the second model calculated the crossbreeding parameters by fitting the coefficients of breed additive, heterosis, and recombination as covariates. In addition, multivariate analysis with fixed and random effects (model 3) was performed using WOMBAT to estimate genetic parameters. The overall least squares means of B and crosses of F and J with B were 27.09 ± 0.1 kg for BW, 64.42 ± 0.2 kg for WW, and 385.35 ± 2 g for PRWWG. The corresponding estimates for post-weaning traits were 88.87 ± 0.4 kg for SMW, 142.10 ± 0.8 kg for YW, and 284.75 ± 2 g for PTWWG. Genotype, birth year, birth season, and sex of calves significantly ($p < 0.05$) influenced all studied traits except for the effect of sex on WW. For instance, 1/2F:1/2B (F1) crossed calves gain approximately 80-100 g more weight per day than B and other F x B crosses. Furthermore, 1/2F:1/2B (F1) attained 131 g and 119 g more PRWWG and PTWWG per day than their J counterparts, respectively. The contribution of the additive effect of the F breed was positive and significant ($p < 0.001$) for BW (11.99 ± 0.7 kg) and WW (12.64 ± 2). Likewise, heterosis from the F x B cross resulted in substantial improvement for all traits ($p < 0.01$). However, the weight gain obtained through heterosis was not sustained in subsequent generations of F x B crosses because of recombination loss in all traits. Estimates of recombination loss varied from -19.92 ± 2 kg for WW to -68.49 ± 7 kg for YW. Heritability estimates varied across traits and were reduced by approximately 26% to 56% for all traits expressed after BW. Strong genetic correlations were obtained between WW and SMW (0.86 ± 0.03), WW and PRWWG (0.84 ± 0.03), PRWWG and SMW (0.80 ± 0.04), and YW and PTWWG (0.94 ± 0.10). The results also showed desirably higher negative genetic correlations between YW and AFC (-0.77 ± 0.09) and PTWWG and AFC (-0.80 ± 0.09). The moderate to high estimated variances and h^2 indicate sufficient genetic variation within the population and the potential for genetic response to selection if an appropriate breeding program is implemented in the farm. The significant effect of year and season of calving and reduction in h^2 for growth traits expressed at later ages suggest these traits are highly influenced by environmental factors, highlighting the need for appropriate management and environmental interventions to optimize performance and complement genetic strategies.

Keywords: Additive; Correlation; Heritability; Heterosis; Weight gain

Introduction

In central Ethiopia, dairy farming is a crucial source of family nutrition and income generation for smallholder farmers (Agajie *et al.*, 2016; FAO, 2019; Direba *et al.*, 2020). Over the last four to five decades, crossbreeding has been a primary strategy employed by governmental and non-governmental organizations to enhance the genetic potential of dairy cattle (MOA, 2014; MOA, 2019). Consequently, a larger population of crossbred cattle exists in this area compared to other parts of the

country. According to CSA (2017), the central part of Ethiopia (the Arsi and West Shewa Zones, the North Shewa of the Amhara region, and the North Shewa of the Oromia region) is home to roughly 35% of the country's crossbred cattle population. Crossbred cattle play multiple roles for smallholder farmers. A study by Direba *et al.* (2020) showed that farmers in the central part of Ethiopia keep crossbred cattle mainly for milk production, draught power, and beef, with an index of 0.5, 0.26, and 0.24, respectively.

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Calf growth is crucial in dairy farming because it lowers the heifer's unproductive age, ensures adequate animal availability for herd replacement or farm expansion, and enhances the market value of calves and heifers (Boulton *et al.*, 2017; Machado *et al.*, 2020; Busanello *et al.*, 2022). The growth performance and other traits of crossbred cattle depend on additive and heterosis effects (Schiermiester *et al.*, 2015; Lembeye *et al.*, 2016; Bunning *et al.*, 2019) and environmental factors such as climatic conditions and husbandry practices across years and seasons (Kefena *et al.*, 2013; Robinson *et al.*, 2014). Furthermore, understanding the genetic variation, heritability (h^2) of target traits, and correlations among traits is essential to design or optimize the breeding program (select better animal, estimate the genetic gain, and measure response of correlated traits for selection) for future profitability and sustainability of crossbred population (FAO, 2010; Philipsson *et al.*, 2010). Earlier at HARC, some research reports on the growth performance of calves were produced by using limited data. Today, analyzing data spanning over four decades presents a unique challenge, as continuous selection pressure and significant fluctuations in management and climate are expected to have caused non-constant growth performance and genetic parameters over time. Therefore, this study aims to evaluate the growth performance and estimate genetic parameters of Jersey and Friesian crossbreds with Boran cattle in the central Ethiopian highlands by exploiting big data.

Materials and Methods

Study Area

This study was carried out at the dairy cattle research station of Holetta Agricultural Research Center (HARC). Holetta is located at 38.5° E longitude and 9.8° N latitude with an altitude of 2400 meters above sea level. It is located 30 km west of Addis Ababa (the capital city of Ethiopia) on the main road to Ambo. The area has received about 1,200 mm of annual rainfall with 60% average monthly humidity. The mean annual temperature was 18 °C (Aynalem *et al.*, 2011).

Data Source and Herd Management

Long-term data collected from 1978 to 2020 at HARC were used for this study. The center has been engaged in crossbred dairy cattle research and has established a well-organized database to store data on growth, reproduction, production, and longevity traits. The center has served as Ethiopia's national coordinator for dairy cattle research. In addition, this herd serves as a source of crossbred bulls required by the LDI (Livestock Development Institute, the then National Artificial Insemination Center) for semen collection used in crossbreeding of farmers' cattle.

Boran (B) cows from the indigenous breed serve as the dam breed, while Friesian (F) and Jersey (J) represent the sire breeds for crossbreeding. The center has conducted three main research phases. The first was a targeted evaluation of crossbred cattle with different exotic inheritances. The second phase of the study was aimed

at stabilizing crossbred inheritance at 50%, and in the third phase, the center has been working to develop a synthetic breed with 75% Friesian inheritance since 2009. However, the second phase program was interrupted after 10 years due to the low productivity of *inter se* matings. Artificial insemination (AI) was the primary mating tool. Natural mating was also practiced to serve crossbred cows that failed to conceive by repeated AI service, and for the replacement of Boran. Mating occurs throughout the year. The center primarily used semen from LDI. Additionally, since 2009, they have purchased internationally sourced Friesian semen for F1 and $\frac{3}{4}$ crossbred productions.

The feeding and housing system was based on physiological status (milking cows, dry cows, and late pregnant cows) and age category (calves and heifers). Cows with similar physiological status and calves and heifers in the same age category received similar amounts of hay and concentrate supplements. The daily concentrate supplement provided was approximately 3-4 kg for milking cows, 2-3 kg for dry and late pregnant cows, 1-2 kg for heifers, and 0.3 to 1kg for calves (Direba *et al.*, 2022). The availability of supplemental feed was not consistent across the year and season, as it depends on the availability of funds. During the dry and short rainy season, some groups of animals (cows and heifers) were allowed to graze on natural pasture for about 8 hours per day. Other groups of animals (calves younger than six months, bulls, and late-pregnant cows) were kept indoors and given a few hours of exercise outdoors. During the main rainy season, all animals were prohibited from grazing because the pasture lands were protected for hay production. Milking was undertaken twice a day, early in the morning and late in the evening. Calves were offered fresh milk twice a day until weaning (98 days). To prevent major transmissible diseases and control parasite infection, vaccines, acaricides, and anthelmintics were administered on a regular schedule.

Statistical Analysis

Records on growth performance were obtained from the HARC dairy research farm database. The growth traits considered in this study included birth weight (BW), weaning weight (WW), six-month weight (SMW), yearling weight (YW), pre-weaning weight gain (PRWWG), and post-weaning weight gain (PTWWG). Furthermore, genetic and phenotypic correlations of growth traits with age at first calving (AFC) were estimated to identify the traits that could serve as better indicators for AFC. Data from B and crosses of F and J with B were used for analysis. The total number of records used across different traits and the pedigree structure are summarized in Tables 1 and 2, respectively.

Three statistical models were used in this study. The first model was fitted to calculate growth performance (least square means and associated standard error). The second model was designed to analyze crossbreeding parameters (additive, heterosis, and recombination loss). The last model was used to estimate genetic parameters, including heritabilities, genetic and phenotypic

variances, covariances, and correlations among studied traits. Analyses for the first two models used the General Linear Model (GLM) in SAS version 9 (SAS, 2002).

Model 1: analysis of least square means: The GLM procedure of SAS (2002) was used to analyze the least squares means and associated standard errors of growth traits, as well as the effect of various factors. The fixed factors considered were:

1. Genotype: a total of 12 genotypes, including B, ½F: ½B (F₁, F₂, and F₃ generations), ½J: ½B (F₁, F₂, and F₃ generations), ¾F: ¼B (first and second generations), ¾J: ¼B, 5/8F: 3/8B, and 5/8J:3/8B inheritances.
2. Birth year: 42 years (1978-2020) grouped into 9 classes based on preliminary analysis (1978-1982, 1983-1987, 1988-1992, 1993-1997, 1998-2002, 2003-2007, 2008-2012, 2013-2017, and 2018-2020).
3. Season: divided into 3 categories considering rainfall conditions of the area: dry period (October to February), light rain (March to May), and main rain (June to September).
4. Sex (Male and Female).

The model structure was as follows;

$$Y_{ijkl} = \mu + G_i + C_j + S_k + P_l + e_{ijkl}$$

Where, Y_{ijkl} represent performances of BW, WW, SMW, YW, PRWWG and PTWWG; μ is the overall mean; G_i is the fixed effect of i^{th} genotype; C_j is the fixed effect of j^{th} calf year of birth; S_k is the fixed effect of k^{th} calves season of birth; P_l is the fixed effect of l^{th} calf sex; e_{ijkl} is random residual term.

Model 2: Analysis of crossbreeding parameter: A Multiple regression model was used to estimate crossbreeding parameters (additive, heterosis, and recombination loss). Similar to model 1, birth year, birth season, and sex were fitted as fixed factors. However, genotype class was replaced by coefficients of expected breed additive, heterosis, and recombination loss, and fitted as covariates. 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: $g_i = \frac{1}{2}(\alpha^s_i + \alpha^d_i)$, $h_{ij} = \alpha^s_i \alpha^d_j + \alpha^s_j \alpha^d_i$, and $r_{ij} = 4g_i g_j - h_{ij}$, α = additive, s = sire, and d = dam. Effects of maternal heterosis and recombination were assumed to be negligible in this analysis. Table 3

contains genetic coefficients used for this analysis. The statistical model is described as follows;

$$Y_{ijkl} = \mu + P_j + C_k + S_l + G^1 E b_1 + H^1 E b_2 + R^1 E b_3 + e_{ijkl}$$

Where, Y_{ijkl} = BW, WW, SMW, YW, PRWWG, and PTWWG; μ is the overall mean; P_j is the fixed effect of j^{th} calf birth year; C_k is the fixed effect of k^{th} calf season of birth; S_l is the effect of l^{th} calf's sex; e_{ijkl} is the random residual term; $G^1 E$ = Individual additive genetic effect of exotic breed (Friesian or Jersey) (deviation from Boran breed); $H^1 E$ = Expected individual heterosis effect in the crossbred cow (heterosis); $R^1 E$ = Expected individual recombination effect in the crossbred cow (recombination loss); b_1 = Individual breed additive coefficient of the trait (calculated as proportion of genes from Friesian or Jersey); b_2 = Individual heterosis coefficients of the trait (calculated as proportion of heterozygous loci); and b_3 = Individual recombination coefficient of the trait.

Model 3. Multivariate analysis of mixed animal model: This model estimated variance components, including phenotypic and genetic variances, genetic and phenotypic correlations among traits, and heritabilities for the six growth traits (BW, WW, SMW, YW, PRWWG, and PTWWG). Genetic and phenotypic correlations of growth traits with AFC were also estimated. Records from all genotypes indicated in Models 1 and 2 were used. The overall matrix of the mixed animal model is:

$$Y = Xb + Zu + e$$

Where, Y is a vector of observations for studied traits, and b and u are vectors of fixed and random individual additive effects, respectively. X and Z are matrices relating records to fixed and random individual additive effects, respectively. Finally, e is a vector of random residual effects. The fixed effects (genotype, birth years, birth season, sex) were grouped similarly to models 1 and 2. The random individual additive and residual effects were assumed to be normally distributed and uncorrelated with means of zeros and variances $\sigma^2 a$, and $\sigma^2 e$, respectively, where $\text{var}(a) = A\sigma^2 a$, and $\text{var}(e) = I\sigma^2 e$, where A is the additive numerator relationship matrix among animals in the population, and I is the identity matrix. Details of formulas for calculating heritabilities and correlations are described in Direba *et al.* (2022). The WOMBAT software program (Meyer, 2007) was employed for the analysis.

Table 1. Number of individuals/records for pairs of traits.

Traits	BW	WW	SMW	YW	PRWWG	PTWWG
BW	4035	3364	2849	1918	3302	1822
WW		3397	2753	1836	3302	1833
SMW			2874	1849	2688	1755
YW				1930	1808	1833
PRWWG					3302	1806
PTWWG						1833
AFC	960	960	960	960	960	960

BW, WW, SMW, YW, PRWWG, PTWWG, and AFC denote birth weight, weaning weight (birth to 98 days age), six-month weight, yearling weight, pre-weaning weight gain, post-weaning weight gain (99 to 365 days age), and age at first calving, respectively.

Table 2. Summary of pedigree structure for the random effect.

Type of animals	Number
Animals without offspring	3225
Animals with offspring	1230
Sire	136
Dam	1094
Animals with maternal grandsire	2530
Animals with maternal grand dam	2461
Animals with paternal grandsire	1087
Animals with paternal grand dam	1096

Table 3. Genetic coefficients used to estimate crossbreeding parameters.

Genotype	Genetic coefficients					
	g ^F	g ^J	h ^{FB}	h ^{JB}	r ^{FB}	r ^{JB}
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 denotes Friesian breed; J denotes Jersey breed; g denotes breed additive; h denotes heterosis; r denotes recombination loss. The fraction values represent the proportion of respective breeds in the genotypes.

Results and Discussion

Growth Performance

The least squares means and standard errors of growth traits across fitted fixed effects are presented in Table 4. The overall performance of B and crosses of F and J with B was 27.09±0.1 kg for BW, 64.42±0.2 kg for WW, and 385.35±2 g for PRWWG. The corresponding estimates of post-weaning traits were 88.87±0.4 kg for SMW, 142.10±0.8 kg for YW, and 284.75±2 g for PTWWG. The growth rate of calves before weaning was considerably higher (by about 100 g per day) than post weaning. This may result from better management, such as milk feeding and other husbandry practices provided for calves during the pre-weaning period. Furthermore, post-weaning stress when milk feeding ceases may also affect PTWWG.

The figures obtained in this study are close to estimates of 28.2 kg BW and 138 kg YW for crossbred calves in Ethiopia (Aynalem *et al.*, 2011), 27.6 kg BW for crossbreds in Rwanda (Manzi *et al.*, 2012), and 27.5 kg BW and 64 kg SMW for crossbred calves in Bangladesh (Rahman *et al.*, 2015; Mostari *et al.*, 2017). However, the values from the current study are lower than the 28.8 kg to 34.2 kg BW and 149.1 kg to 167.1 kg YW reported for crossbreds of Friesian, Ankole, and Sahiwal breed in Rwanda (Manzi *et al.*, 2012), and the 33.7 kg BW and 82.9 kg WW reported for Friesian x Kenana crosses in Sudan (El Nazeir *et al.*, 2015). Additionally, most results from the present study are lower than values calculated for beef and dual-purpose breeds (Neser *et al.*, 2012; Correa *et al.*, 2017; Brito *et al.*, 2020; Coleman *et al.*, 2021).

These differences may be due to breed differences, data size, and farm breeding programs.

This study showed that genotype, birth year, birth season, and calf sex significantly ($p < 0.05$) influenced all studied traits except for the effect of sex on WW. Birth weight varied from 20.50±1 kg to 30.42±0.4 kg across the compared genotypes. High-grade calves recorded the highest BW, followed by 1/2F:1/2B generations. The lowest BW was observed in crosses of J and B breeds. Similarly, F crosses were heavier than J crosses in all other traits. This could be attributed to the natural characteristics of sire breeds that F cattle are larger than J and B breeds. On the other hand, B calves had growth performance almost similar to high-grade F x B crosses for most traits. First-generation F x B crossbred calves outperformed all other genotypes in all growth traits except BW. For instance, 1/2F:1/2B (F1) crossbred calves gained about 80-100 g more weight per day than the B and other F x B crosses. Furthermore, 1/2F:1/2B (F1) attained 131 g and 119 g more PRWWG and PTWWG per day than the J counterparts, respectively. This might be due to the naturally higher physical characteristics of F and B, and their heterosis effect, than the J contemporaries (Table 5). The genotype differences observed are consistent with studies by Aynalem *et al.* (2011) and Molla (2021) in Ethiopia, Mulindwa *et al.* (2012) in Uganda, and Leal *et al.* (2018) in Brazil.

The year of birth was a significant source of variation ($P < 0.0001$) for growth traits. However, the variation was inconsistent, with no clear trend detected. This might be mainly related to differences in management

(feeding, health management, and other husbandry practices) across years. It could also be partly associated with a change in breeding program at HARC, as some genotypes were not uniformly available throughout the study period. The use of J sires was interrupted in the last 15 years, and upgrading to $\frac{3}{4}$ F and $\frac{1}{4}$ B was

restarted after 10 years in between. The effect of birth year on growth traits observed in this study is supported by literature from tropical countries (Mulindwa *et al.*, 2012; Fialho *et al.*, 2015; Rahman *et al.*, 2015; Babigumira *et al.*, 2018; Tazeb *et al.*, 2022).

Table 4. Estimates and standard error of growth performance.

Factors	N	BW	WW	SMW	YW	PRWWG	PTWWG
Overall	4035	27.09±0.1	64.42±0.2	88.87±0.4	142.10±0.8	385.35±2	284.75±2
Genotype		***	***	***	***	***	***
Boran (B)	69	23.78±0.7 ^d	61.37±2 ^{cd}	91.34±3 ^b	135.83±6 ^b	388.21±18 ^{bc}	262.13±20 ^{bc}
1/2F:1/2B (F1)	1267	24.89±0.3 ^d	72.35±1 ^a	107.01±2 ^a	170.38±3 ^a	490.24±9 ^a	353.30±10 ^a
1/2F:1/2B (F2)	712	27.75±0.4 ^b	60.04±1 ^d	77.47±2 ^{def}	120.08±3 ^c	336.33±9 ^d	215.91±11 ^d
1/2F:1/2B (F3)	303	26.36±0.4 ^c	60.31±1 ^d	80.96±2 ^{cde}	123.39±4 ^c	353.00±10 ^d	227.78±12 ^{cd}
3/4F:1/4B (F1)	935	30.42±0.4 ^a	68.30±1 ^b	88.58±2 ^b	140.73±3 ^b	391.99±10 ^b	270.67±11 ^b
3/4F:1/4B (F2)	369	30.39±0.4 ^a	64.79±1 ^c	82.34±2 ^{cde}	122.95±4 ^c	355.45±12 ^{cd}	221.10±14 ^{cd}
5/8F:3/8B	37	29.30±0.8 ^{ab}	63.13±2 ^{cd}	87.74±4 ^{bc}	123.24±7 ^c	345.73±22 ^d	235.05±25 ^{bcd}
1/2J:1/2B (F1)	57	21.57±0.7 ^e	57.41±2 ^{de}	85.07±3 ^{bcd}	122.30±7 ^c	358.53±20 ^{bcd}	234.29±22 ^{bcd}
1/2J:1/2B (F2)	78	22.62±0.6 ^e	55.11±2 ^{cd}	77.48±3 ^{def}	114.35±5 ^c	337.68±16 ^d	214.49±18 ^d
1/2J:1/2B (F3)	163	21.45±0.5 ^e	51.48±1 ^d	72.09±2 ^f	113.88±5 ^c	313.63±13 ^d	215.21±16 ^d
3/4J:1/4B (F1)	25	21.33±1 ^e	54.24±3 ^{ed}	67.75±5 ^f	107.25±10 ^c	330.20±31 ^d	194.62±32 ^d
5/8J:3/8B	20	20.50±1 ^e	53.53±3 ^{ed}	72.27±5 ^{ef}	108.82±9 ^c	342.60±28 ^d	200.49±29 ^d
Birth years		***	***	***	***	***	***
1978-1982	41	25.13±1 ^b	70.10±3 ^a	101.34±5 ^a	143.60±9 ^a	472.63±28 ^a	279.53±29 ^{ab}
1983-1987	12	22.53±2 ^b	59.17±4 ^{bc}	80.89±7 ^{bc}	112.84±13 ^{bcd}	385.89±40 ^b	191.54±43 ^{cd}
1988-1992	68	25.20±0.6 ^b	60.75±2 ^b	85.60±3 ^b	118.26±5 ^{bc}	360.62±16 ^b	212.61±16 ^{cd}
1993-1997	203	25.46±0.4 ^{ab}	58.10±1 ^{bcd}	80.27±7 ^{bc}	125.53±3 ^b	333.16±10 ^c	256.39±11 ^b
1998-2002	767	26.06±0.3 ^a	59.30±0.9 ^{bc}	79.46±1 ^c	123.76±3 ^b	339.89±8 ^c	243.55±9 ^{bc}
2003-2007	754	24.93±0.3 ^b	56.48±0.9 ^d	73.84±1 ^d	106.67±3 ^d	324.32±8 ^c	183.92±10 ^d
2008-2012	936	25.36±0.3 ^b	60.67±0.9 ^b	83.41±1 ^b	141.84±3 ^a	355.87±8 ^b	291.36±10 ^a
2013-2017	866	24.24±0.3 ^b	59.38±1 ^b	83.37±2 ^b	142.65±3 ^a	360.63±9 ^b	299.02±10 ^a
2018-2020	388	26.36±0.4 ^a	57.61±1 ^{cd}	74.40±2 ^d	112.25±5 ^{cd}	324.70±11 ^c	175.85±15 ^d
Birth season		***	***	*	***	***	***
Dry	1921	24.37±0.2 ^c	59.13±0.7 ^b	83.17±1 ^a	129.99±2 ^a	348.96±7 ^b	258.32±7 ^a
Short rain	1146	24.76±0.3 ^b	61.73±0.8 ^a	83.55±1 ^a	124.38±2 ^b	381.14±7 ^a	229.32±8 ^b
Main Rain	968	25.95±0.3 ^a	59.66±0.8 ^b	80.81±1 ^b	121.43±3 ^b	355.81±6 ^b	223.62±8 ^b
Calves sex		***	NS	***	***	***	***
Male	1984	25.75±0.2 ^a	59.83±0.7	79.63±1 ^b	130.64±3 ^a	351.40±6 ^b	253.96±9 ^a
Female	2051	24.31±0.2 ^b	60.51±0.7	85.39±1 ^a	119.89±3 ^b	372.53±6 ^a	220.22±7 ^b

N= Number of records; B= Boran breed; F= Friesian breed; J= Jersey breed. Fraction values are the proportion of respective breeds to the genotypes. BW, WW, SMW, and YW denote birth weight, weaning weight, six-month weight, and yearling weight, respectively. Least squares mean values across the column with the same superscript indicate non-significant association ($p > 0.05$); NS= Non-significant; * = $p < 0.05$; ***= $p < 0.0001$.

Season of birth had a substantial effect ($P < 0.05$) on all growth traits, with major differences detected for YW and PTWWG. Calves born during the dry season gained 5.6 kg and 8.5 kg more YW, resulting in 29 g and 34 g higher PTWWG than calves born during the short rain and main rainy season, respectively. Although calves born during the main rainy season were heavier in BW than the others, they could not sustain this superiority in subsequent growth stages. This is probably attributed to feed availability and weather conditions. Better feed resources were available during dry and short rainy seasons as animals grazed in the farm pastureland. All animals were restricted from grazing during the main rainy season to protect pasturelands for hay production. In addition, supplemental feed was more available

during the dry and short rainy seasons. The better BW for calves born during the main rainy season might be due to greater feed availability for dams during the preceding dry and short rainy seasons, leading to better fetal growth. The lower growth rate of calves born during the main rainy season might be associated with cold weather that forced the calves to use high nutrients to keep their body warmth rather than for weight gain. Consistent with the present study, several previous studies have noted similar effects of season on growth traits (Tesfa and Garikipati, 2014; Ali *et al.*, 2015; Fialho *et al.*, 2015; Mostari *et al.*, 2017; Tazeb *et al.*, 2022).

A Significant weight difference ($P < 0.001$) was obtained between male and female calves for all traits except WW. Male calves were significantly heavier in BW and YW,

and superior in PTWWG. Conversely, female calves were better for SMW and PRWWG. Better feeding and husbandry practices were provided for female calves during the pre-weaning period, as they are essential for cow replacement and on-farm demonstration activities. There was high selection pressure on weaned male calves, and most were culled shortly after weaning. The farm kept some male calves after weaning for use as bull calves or for feeding experiments. Thus, the better YW and PTWWG of male calves resulted from intensive selection and the provision of better feed during the experiments, allowing them to express their genetic potential (Manzi *et al.*, 2012; Tesfa and Garikipati, 2014; Fialho *et al.*, 2015; Tazeb *et al.*, 2022).

Crossbreeding Parameters

Table 5 displays the estimates of additive, heterosis, and recombination loss effects for growth traits. The contribution of the additive effect of the F breed was positive and significant ($P < 0.001$) for BW and WW. Likewise, heterosis from F and B resulted in substantial improvement for all traits ($P < 0.01$). The additive effect of F (deviation from B) on BW (11.99 ± 0.7 kg) and WW (12.64 ± 2 kg) was more important than the heterosis effect for these traits (-4.76 ± 0.5 kg and 4.68 ± 1.53 kg). However, for SMW, YW, and weight gain traits, heterosis was more important than the additive effect. This indicates that calves were exposed to environmental stress after weaning, which favored the expression of heterosis over additive effects. The weight gain obtained through heterosis could not be sustained in the next generations of F x B crossed due to recombination loss for all traits except BW. Estimates of recombination loss varied from -19.92 ± 2 kg for WW to -68.49 ± 7 kg for YW. Additionally, a loss of

approximately 180- 200 g per day was recorded due to recombination in F x B crosses. Hence, crossing these two breeds was found to be beneficial mainly for the growth performance of the first generation, implying the need for interventions such as enhanced management and appropriate breeding programs to reduce the effect of recombination loss.

On the other hand, the additive effect of J breed was negligible ($p > 0.05$) in most traits and undesirably negative for SMW ($P < 0.01$). Heterosis from the J x B cross did not have a significant effect on all traits ($P > 0.05$). This could be attributed to the naturally smaller physical characteristics of the J breed. The lower estimates of additive and heterosis effects for J crosses do not mean this genotype is inferior for dairy growth performance, as they reach puberty at lighter weights than F crosses. The study by Direba *et al.* (2022) showed that J crosses attain AFC approximately 4 to 5 months earlier than F crosses and the B breed.

The additive and heterosis effects for F x B breeds are consistent with those reported in other studies (Schiermiester *et al.*, 2015; Babigumira *et al.*, 2018; Bunning *et al.*, 2019). Aynalem *et al.* (2011) reported additive and heterosis effects of 4.8 kg and 1.4 for WW, 12.3 and 7.4 kg for SMW, and 35.6 kg and 17.9 kg for YW in Ethiopia, respectively. Figures of 0.71, 2.06, and 0.03 for additive and 0.81, 4.31, and 0.02 for heterosis of BW, WW, and PRWWG in Brazil, respectively (Leal *et al.*, 2018), are comparable with the values from the present study. Similarly, Schiermiester *et al.* (2015) calculated heterosis effects of approximately 0.47-0.75 kg for BW, 5.86-8.65 kg for WW, and 9.12-13.88 kg for YW in crossbred cattle in America. Differences in estimates may be due to the breed differences, data size, and farm breeding programs.

Table 5. Estimates of additive, heterosis and recombination loss for growth traits.

Breed group	BW (kg)	WW (kg)	SMW (kg)	YW (kg)	PRWWG (g)	PTWWG (g)
B	23.78 ± 0.7	61.37 ± 2	91.34 ± 3	135.83 ± 6	388.21 ± 18	262.13 ± 20
gF	$11.99 \pm 0.7^{***}$	$12.64 \pm 2^{***}$	0.23 ± 4	7.24 ± 7	4.24 ± 21	12.26 ± 25
gJ	-3.56 ± 3	-4.54 ± 8.8	$-37.55 \pm 14^{**}$	-38.41 ± 26	-25.88 ± 80.27	-103.74 ± 84
hFB	$-4.76 \pm 0.5^{***}$	$4.68 \pm 1.53^{**}$	$15.38 \pm 3^{***}$	$30.99 \pm 5^{***}$	$98.95 \pm 14^{***}$	$85.14 \pm 17^{***}$
hJB	-0.43 ± 0.5	-1.92 ± 4	10.55 ± 7	5.64 ± 13	-17.95 ± 41	21.55 ± 43
RFB	-0.03 ± 0.7	$-19.92 \pm 2^{***}$	$-41.34 \pm 3^{***}$	$-68.49 \pm 7^{***}$	$-199.34 \pm 18^{***}$	$-184.64 \pm 22^{***}$
RJB	0.32 ± 2	-10.98 ± 6	-9.34 ± 10	-11.44 ± 19	-91.75 ± 58	$-16.22 \pm 64^{***}$

B= Boran breed; F= Friesian breed; J = Jersey breed; gF and gJ are F and J breed additive contributions relative to B; hFB and hJB are heterosis effects for crossing F and J with B, respectively. RFB and RJB are recombination losses when crossing F and J with B breeds, respectively. The BW, WW, SMW, YW, PRWWG, and PTWWG denote birth weight, weaning weight, six-month weight, yearling weight, pre-weaning weight gain, and post-weaning weight gain, respectively. ** and *** represent $p < 0.01$ and $p < 0.0001$, respectively. Values with no asterisk superscript denote $p > 0.05$.

Genetic Parameters

A summary of the additive genetic variance, phenotypic variance, residual variance, and associated standard errors for the studied traits is shown in Table 6. The highest heritability (h^2) was obtained for BW (0.46 ± 0.04) and PTWWG (0.34 ± 0.04) followed by YW (0.30 ± 0.04). These h^2 results imply that these traits can be improved through selection. The observed variance figures also

showed sufficient genetic variation within the population for selection. However, the h^2 value was reduced by approximately 26% to 56% for all traits expressed after BW. This might indicate that growth traits are highly influenced by environmental factors such as feed, animal health management and other husbandry practices, highlighting the need for management interventions.

The h^2 estimates for growth traits in this study are within the range reported in other tropical studies. For instance, h^2 of 0.41 for BW and 0.36 for PRWWG of crossbred cattle in Uganda (Mulindwa *et al.*, 2012), 0.28 for YW in Sahiwal cattle in Kenya (Ilatsia *et al.*, 2011), and 0.23 and 0.22 for WW and YW in Brangus cattle in South Africa (Neser *et al.*, 2012) concur with this study. In contrast, the values of this study differ from some other reports. Aynalem *et al.* (2011) and Almaz *et al.* (2016) estimated h^2 values of 0.25 and 0.03 for BW in crossbred and

Fogera cattle in Ethiopia, respectively. Similarly, Ilatsia *et al.* (2011) reported h^2 values of 0.23 for BW and 0.39 for WW in Sahiwal cattle in Kenya, and Bignardi *et al.* (2014) reported 0.26 for BW in Bonsmara cattle in Brazil. Brito *et al.* (2020) found higher h^2 for WW (0.42) and YW (0.49) in Brazilian Guzera cattle than the present figures. Variation in estimates is likely due to the difference in genotype, data size, model fitted, and environment in which the animals were managed.

Table 6. Estimate of variance components and heritabilities for growth traits.

Estimate	BW	WW	SMW	YW	PRWWG	PTWWG
V _a	10.64±1	40.09±6	107.99±16	346.35±51	2747.92±475	3863.54±551
V _e	12.55±0.69	132.44±5	313.32±13	792.54±43	11331.10±437	7470.86±445
V _p	23.19±0.65	172.53±4	421.30±11	1138.89±38	14079.00±366	11334.40±397
h^2	0.46±0.04	0.23±0.03	0.26±0.04	0.30±0.04	0.20±0.03	0.34±0.04

V_a = Additive genetic variance; V_e = Residual variance; V_p = Phenotypic variance; h^2 = Heritability. The BW, WW, SMW, YW, PRWWG, and PTWWG indicate birth weight, weaning weight, six-month weight, yearling weight, pre-weaning weight gain, and post-weaning weight gain, respectively.

Table 7 contains phenotypic and genetic correlations between growth traits and their correlations with AFC. The phenotypic correlations varied from 0.02 (between BW and weight gain traits) to 0.93 (between YW and PTWWG). Low phenotypic correlations were observed between BW and all other growth traits (0.02 to 0.39), implying that the phenotypic value of BW is less

indicative of later growth. However, genetic correlations of BW with WW (0.57±0.07), SMW (0.36±0.08), and YW (0.22±0.08) traits were stronger than phenotypic correlations. Thus, selection based on breeding value rather than phenotypic BW could lead to better WW and YW.

Table 7. Genetic and phenotypic correlation of production, reproduction, and herd life traits.

Traits	Traits						
	BW	WW	SMW	YW	PRWWG	PTWWG	AFC
BW		0.57±0.07	0.36±0.08	0.22±0.08	0.03±0.09	0.04±0.08	0.26±0.10
WW	0.39±0.02		0.86±0.03	0.47±0.08	0.84±0.03	0.15±0.10	0.13±0.14
SMW	0.27±0.02	0.78±0.01		0.67±0.06	0.80±0.04	0.43±0.09	-0.14±0.15
YW	0.18±0.02	0.53±0.02	0.70±0.01		0.39±0.09	0.94±0.10	-0.77±0.09
PRWWG	0.02±0.02	0.89±0.00	0.77±0.01	0.53±0.02		0.13±0.11	-0.04±0.15
PTWWG	0.03±0.03	0.19±0.02	0.46±0.02	0.93±0.00	0.22±0.02		-0.80±0.09
AFC	0.10±0.04	-0.11±0.04	-0.18±0.04	-0.49±0.03	-0.17±0.03	-0.50±0.03	

BW, WW, SMW, YW, PRWWG, PTWWG, and AFC indicate birth weight, weaning weight, six-month weight, yearling weight, pre-weaning weight gain, post-weaning weight gain, and age at first calving, respectively. Above diagonal indicates genetic correlation, while below diagonal indicates phenotypic correlation.

Notably higher phenotypic correlations were recorded between WW and SMW (0.78±0.01), WW and PRWWG (0.89±0.00), SMW and PRWWG (0.77±0.01), and YW and PTWWG (0.93±0.00). Likewise, high genetic correlations were obtained between WW and SMW (0.86±0.03), WW and PRWWG (0.84±0.03), PRWWG and SMW (0.80±0.04), and YW and PTWWG (0.94±0.10). On the other hand, all growth traits except BW had a negative phenotypic correlation with AFC. The phenotypic correlations of YW and PTWWG with AFC were desirably high (-0.49 to -0.50) compared to other traits. Similarly, desirably high negative genetic correlations between PTWWG and AFC (0.80±0.09) and YW and AFC (0.77) were found. These results suggest that selection using the breeding value of one of these highly correlated traits can result in genetic

improvement for the other. Furthermore, growth traits expressed at later ages, particularly YW and PTWWG, were better indicators of heifers with lower AFC. Likewise, selecting heifers with lower breeding values for AFC could result in better YW and PTWWG.

Consistent with this study, Bignardi *et al.* (2014) found phenotypic and genetic correlations of 0.37 and 0.60, respectively, between BW and WW in Brazil. The obtained results are comparable to a genetic correlation of -0.62 between YW and AFC in Brazil (Brito *et al.*, 2020), genetic and phenotypic correlations of 0.48 and 0.59 between WW and YW for Sahiwal cattle in Kenya (Ilatsia *et al.*, 2011), and a phenotypic correlation of 0.53 between WW and YW in Ethiopia (Aynalem *et al.*, 2011). However, the values from the present study are higher than genetic (0.03 to 0.04) and phenotypic (0.003 to

0.01) correlations for BW with WW and YW, and genetic correlation between WW and YW (0.29) found by Aynalem *et al.* (2011) for crossbred calves in Ethiopia. Nesar *et al.* (2012) reported higher genetic correlations for BW and WW (0.78), BW and YW (0.57), and WW and YW (0.86) in Brangus cattle in South Africa.

Conclusion

The analysis revealed that first-generation F × B crossbred calves exhibited superior performance across all measured growth traits, except birth weight (BW). The additive genetic contribution from breed F was both positive and significant for BW and weaning weight (WW), indicating its potential for enhancing early growth performance. Similarly, heterosis arising from the gene combination of F and B resulted in notable improvements across traits. However, these heterotic advantages diminished in subsequent generations due to recombination loss, limiting the long-term benefit of such crosses. In contrast, the additive effect of breed J, along with the heterosis from J × B crosses, showed minimal influence on most traits. This suggests that incorporating J into crossbreeding programs with B breed may not yield substantial improvements in growth performance. Heritability estimates (h^2) were relatively high for BW, post-weaning weight gain (PTWWG), and yearling weight (YW). Nonetheless, heritability declined by approximately 26% to 56% for traits expressed after BW, highlighting potential environmental influences and genetic complexity in later growth stages. Strong genetic correlations were identified between WW and six-month weight (SMW), WW and pre-weaning weight gain (PRWWG), PRWWG and SMW, and YW and PTWWG. These relationships suggest that selection based on the breeding value of one trait could effectively lead to genetic improvements in the others. Traits expressed at later ages, particularly YW and PTWWG, were found to be more reliable indicators for selecting heifers with earlier age at first calving (AFC). Furthermore, the moderate to high estimated heritabilities and variances imply ample genetic variation within the population, underscoring the feasibility of achieving genetic progress through a structured breeding program. Nevertheless, the significant effects of calving year and season, along with reduced heritability in later-expressed traits, stress the importance of addressing environmental influences in growth traits. Appropriate management and environmental interventions should therefore complement genetic strategies to optimize performance.

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Conflict of Interests

The authors declare that they have no competing interests.

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