

Research Article

Genetic and Phenotypic Correlation Estimation for Growth Traits of Holstein Friesian X Boran Crossbred Dairy Cattle in the Central Highland of Ethiopia

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Abstract

Genetic factors are unique to each population and might vary over time as a result of selection and management strategies. As a result, this study sought to explore the genetic and phenotypic relationships of growth traits in Holstein Friesian (HF) x Boran (Bo) crossbred dairy cattle raised at the Holetta Agricultural Research Center (HARC) dairy farm. The performance data of 14,062 crossbred calves gathered over 22 years (1997-2018) were evaluated. The significance of fixed factors, such as year of birth, season of birth, calf sex, and genotype, was assessed using the General Linear Model (GLM) approach in SAS software (9.0). The Average Information Restricted Maximum Likelihood (AI-REML) technique was used with WOMBAT software to assess genetic and phenotypic relationships for growth traits while fitting an animal model. The most significant direct genetic correlation was identified between yearling weight and post-weaning average daily gain, with a value of 0.944 ± 0.02 . This was followed by a correlation of 0.84 ± 0.04 between weaning weight and six-month weight. In contrast, birth weight exhibited weaker genetic relationships with weaning weight (0.07 ± 0.11) and pre-weaning average daily gain (0.10 ± 0.12). The genetic correlations among various growth traits ranged from 0.94 ± 0.02 to 0.07 ± 0.11 , whereas the phenotypic correlations spanned from 0.93 ± 0.04 to -0.03 ± 0.04 . Early selection in calves is advantageous because the largely moderately positive genetic correlations imply little genetic antagonism and show that choosing for one trait is likely to enhance other growth traits.

Keywords

Correlation, Dairy Cattle, Genetic Parameter, Growth Trait

1. Introduction

The fundamental purpose of animal breeding is to determine genetic parameters for various livestock traits [1]. Recent advancements in statistical methodologies within animal breeding have broadened its scope, presenting novel opportunities for the livestock sector [1, 2]. In a multi-trait selec-

tion scheme, understanding both genetic and phenotypic correlations among traits is crucial for optimizing the anticipated gains and responses to selection [3-5]. The degree of relationship between two variables is indicated by correlations [5]. Furthermore, the magnitude and direction of genetic

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enhancement for traits are influenced by these correlations. To accurately predict both direct and correlated responses to selection, as well as to determine the appropriate selection methods, it is essential to comprehend the genetic composition of the traits involved [3, 5, 6].

Growth traits are critical components of any breed improvement strategy [7]. Cattle early growth performance has a significant impact on both fertility and production performance [8-10]. The influence of a cow's genetics on the pre-weaning weights of her calves arises from factors associated with her additive genotype related to growth potential, in addition to her genetic traits concerning milk production and maternal capabilities [3].

In order to create crossbreds that combine productivity and adaptability traits, the Holetta Agricultural Research Centre in Ethiopia has mainly crossed indigenous Boran cattle with Holstein-Friesian cattle since 1966 [11]. Diverse genetic groups were produced as a result of this extensive cross-breeding effort, and these could be helpful in evaluating the data and proposing future initiatives to strengthen the breeding program. Several researches on evaluating dairy herd growth performance were undertaken at HARC [12-14]. However, due to environmental impact variability, selection pressure, and the use of diverse sires to produce genetic diversity on the farm, the genetic parameters lack a biological constant magnitude. As a result, this study was initiated to figure out the genetic and phenotypic associations for growth traits in Holstein Friesian x Boran crossbred dairy cattle.

2. Materials and Methods

2.1. Description of the Study Area

The research was carried out at the Holetta Agricultural Research Center (HARC), situated 29 kilometers to the west of Addis Ababa, positioned at latitude of 9°00'N and a longitude of 38°30'E. This center is located at an elevation of 2400 meters above sea level, within a highland agro-ecological zone characterized by an average annual precipitation of 1144 mm. The region experiences an average temperature of 15 °C, with recorded minimum and maximum temperatures of 6 °C and 22 °C, respectively. Additionally, the monthly relative humidity averages around 60% [15, 16].

2.2. Herd Management

Cattle are managed in the center according to their

physiological status such as pregnancy stage and lactation stage, as well as breed, sex, and age. The main feed sources are natural grass, hay, and concentrate supplements. In the center, newborns are permitted to suckle their mother for four days after birth to collect colostrum. Weighting and ear tagging were also done during the first 24 hours after birth. After four days, the calves were moved to a calf raising housing and fed a fixed amount of milk (260 L of whole milk) for around three months using bucket feeding. Once weaned, the calves are moved to a separate indoor pen until they reach six months of age, during which they receive a diet of concentrate and roughage based on their weight and age. Upon reaching six months, they transition to the heifer management room, where comprehensive care protocols are implemented. Routine health management practices are in place to address any disease outbreaks, and seasonal patterns of prevalent illnesses are monitored, with control measures enacted in line with the guidelines established by the animal health research division.

2.3. Breeding Program

Pure Holstein Friesian semen is used as a sire for Pure Boran dams, producing 50% F1 and 50% F1 HF x Boran crosses. Backcrossing the 50% F1 HF x Ethiopian Boran crossbred dam with pure Holstein Friesian semen generates the 75% F1 HF x Ethiopian Boran first generation crossings. Inter-mating with 50% male and 50% female and 75% male and 75% female resulted in 50% and 75% F2 and F3 offspring, respectively. Throughout the year, artificial insemination served as the farm's major breeding strategy. In addition to herders, a teaser bull was reared among the cows every day to detect heat. A professional inseminator used artificial insemination on the cows when they were in heat.

2.4. Data Source and Management

The data utilized in this research was sourced from the dairy cattle herd maintained at the Holetta Agricultural Research Center (HARC), specifically focusing on Holstein Friesian x Ethiopian Boran crossbred cattle with varying levels of Holstein Friesian gene/blood level. Adjustments were made to the data in order to maintain the uniformity of pedigree information. Regular checks were conducted to verify the identification of animals and their respective pedigrees. The comprehensive data set included 14,062 entries for the analysis of growth traits (Table 1).

Table 1. Description of data structure for growth traits of HF x Boran crossbred calves.

Items	Traits					
	BW	WW	SMW	YW	PrWADG	PoWADG
No. records	3144	2763	2315	1542	2757	1541
No. sires	101	100	100	98	100	98
No. dam	965	923	852	720	922	720
No. of progeny/sire	31	27	23	15	27	15
No. of progeny/dam	3	3	3	2	3	2
Lsmean	28.5	60.56	84.49	138.44	359.61	279.94
SE	0.11	0.27	0.50	1.17	2.72	3.60
Mean	27.61	62.31	89.57	145.28	384.99	297.86
SD	5.12	11.96	21.70	39.03	127.86	121.33
Minimum	15	25	41	60	0.008	54.55
Maximum	45	102	167	256	0.798	672.73
CV (%)	18.53	19.2	24.23	26.87	33.21	27.98

BW, birth weight; WW, weaning weight; SMW, six months weight; YW, yearling weight, PrWADG, birth to weaning date weight gain; PoWADG, three months to yearling age weight gain; HF, Holstein Friesian; BO, Boran Lsmean, least squares mean; SD, standard deviation; SE, standard error; CV, coefficient of variation

2.5. Traits Studied

The analysis focused on several growth-related traits, including birth weight, weaning weight, weight at six months, yearling weight, and daily body weight gains calculated between birth and weaning, as well as between weaning and yearling.

2.6. Statistical Analysis

The estimation of genetic and phenotypic correlations was conducted utilizing WOMBAT software [17], which implemented an animal model through bivariate analysis. Fixed effects, including year of birth, season of birth, calf sex, and calf genotype, were incorporated into the model following their significance testing ($p < 0.05$) via Tukey-Kramer tests implemented through the GLM procedure in SAS [18]. The notation for the model employed in the bivariate analysis of growth traits is as follows:

$$\text{Model 1: } Y = Xb + Z_1a + e \quad (1)$$

Where

Y is a vector of observations on the specific trait of the animal;

b is the vector of fixed effect

a is the vector of direct additive genetic effects

Z₁ is the incidence matrix of direct additive genetic effects,

X is the incidence matrix of fixed effects,
e is the vector of residual error.

3. Results

Genetic and Phenotypic correlations

The estimation of genetic and phenotypic correlations among growth traits include birth weight (BW), weaning weight (WW), six-months weight (SMW), yearling weight (YW), pre-weaning average daily weight gain (PrWADG), and post-weaning average daily weight gain (PoWADG) from bivariate animal model analysis are summarized and presented in Table 2. Most genetic correlations between traits of growth were positive and greater than corresponding phenotypic correlations. The lesser phenotypic correlation might be explained by the fact that the genetic correlation only examines shared genetic contributions, but the phenotypic correlation considers both genetic and environmental factors [4].

A genetic association measures the significance of pleiotropic impacts on two characteristics. The strongest direct additive association was observed among yearling weight and post-weaning average daily weight gain (0.944 ± 0.02), followed by weaning weight and six months weight (0.84 ± 0.04), but the weakest genetic correlation value was observed between birth weight and post-weaning average daily weight gain (0.07 ± 0.11) and birth weight and pre-weaning average daily weight gain (0.10 ± 0.12) (Table 2).

The genetic correlation between pre-weaning and post-weaning average daily weight gain was found to be small in the current study.

Phenotypic relationships were evaluated from a bivariate animal model for growth traits taking two traits at a time (Table 2). The phenotypic correlation among birth weight and pre-weaning average daily weight gain (PrWADWG) (-

0.03±0.02) and post-weaning average daily weight gain (PoWADWG) (-0.02±0.03) was negative and a minimum, whereas the correlation between weaning weight (WW) and six-months weight (SMW) (0.82±0.07) and pre-weaning average daily weight gain (PrWADWG) and yearling with post-weaning average daily weight gain (PoWADWG) (0.93±0.04) was positive and the maximum.

Table 2. Estimates of genetic correlations (below diagonal) and phenotypic correlations (above diagonal) among growth traits of HF x Boran cross calf.

Traits	BW	WW	SMW	YW	PrWADG	POWADG
BW		0.41±0.02	0.27±0.02	0.15±0.03	-0.03±0.02	-0.02±0.03
WW	0.66±0.07		0.82±0.07	0.59±0.02	0.90±0.004	0.24±0.03
SMW	0.55±0.10	0.84±0.04		0.74±0.01	0.77±0.01	0.52±0.02
YW	0.31±0.11	0.52±0.10	0.76±0.01		0.58±0.02	0.93±0.04
PrWADG	0.10±0.12	0.46±0.12	0.70±0.08	0.46±0.12		0.28±0.03
POWADG	0.07±0.11	0.16±0.14	0.52±0.012	0.94±0.02	0.18±0.15	

BW, birth weight; WW, weaning weight; SMW, six months weight; YW, yearling weight, PrWADG, birth to three month weight gain; PoWADG, weaning to yearling age weight gain

4. Discussion

4.1. Genetic Correlations

The direct genetic correlation among birth weight and weaning weight was 0.66±0.07, which was similar to the reported values for multi breeds, which including both local and crossbred dairy cattle (0.66±0.08) [12] and for Fogera breed (0.6±0.23) [19]. However, it was greater than the results (0.03±0.12) for HF x Boran and Boran [13] and for HF x Fogera (0.314) [5]. The genetic association among birth weight and six months weight (0.55±0.010) was greater than the 0.21±0.03 for HF x Boran crossbred calves [13]. This difference could be attributed to the number of observations and the data structure utilized.

In this research, the genetic correlation estimated value of birth weight and yearling weight (0.31±0.11) for HF x Boran crossbred cattle was greater than the published value for HF x Boran (-0.15±0.20) but lower than the value for Jersey x Boran crossbred (0.56±0.37) [20]. It was also greater than the reported value of 0.01±0.13 for HF x Boran [13] and lower than the reported value of 0.05±0.13 [12]. The genetic association among birth weight (BW) and pre-weaning average daily weight gain (PrWADG) (0.10±0.12) was lower than the results of other studies (0.55±0.19) [12], (0.73) [5], and (0.5±0.27) [19].

Haile *et al.* [13] found a weaker genetic correlation be-

tween weaning weight (WW) and six-month weight on HF Boran (0.75±0.06) than the present research finding (0.84±0.04). However, the correlation between weaning weight (WW) and yearling weight (YW) (0.52±0.10) was greater than the genetic relationship of HF x Boran (0.459±0.10) [13]. However, it is lower than the 0.89±0.09 [12]. The correlation between weaning weight and pre-weaning average daily weight gain (0.46±0.12) in the result of this present was lower than other researchers' results (0.99±0.01 for Fogera [19], 0.92 for HF x Boran [4], and 0.97±0.01 for multi-breed) [12]. A lower direct genetic correlation between six-month weight and yearling weight were found 0.43±0.01 [4] than (0.74±0.01) (Table 2).

Post-weaning average daily weight gain (PoWADG) had a poor genetic relationship with birth weight (BW) (0.07±0.11), weaning weight (0.16±0.14), and pre-weaning average daily weight gain (0.18±0.15). The post-weaning average daily weight gain (PoWADG), on the other hand, had a moderate and high genetic association with six months weight (0.52±0.012) and yearling weight (0.94±0.02), respectively. The genetic foundation for these strongest evaluations of direct genetic association is the huge number of comparable loci affecting the expression of these traits [21]. The genetic correlation among most of the growth traits studied in this research was found to be moderate to highly strongest. Thus, selecting for any of these traits would enhance the other traits and could be profitable for cattle selection at an early age. This would aid in the early killing of animals, lowering the related costs.

4.2. Phenotypic Correlations

The phenotypic correlation between birth weight and weaning weight were found the value of 0.26 ± 0.02 [12], 0.29 ± 0.02 [13], and 0.097 [5], which were not comparable with this study (0.41 ± 0.02). The phenotypic correlation among birth weight and six months weight (0.003 ± 0.13) was smaller to the stated value of 0.27 ± 0.02 [4]. The phenotypic association of birth weight and yearling weight (0.15 ± 0.03) was lower than the value of 0.22 ± 0.43 for HF x Boran cross-bred cattle [20] and for multi-bred cattle (pooled) [12]. The present result was higher than the stated value (0.13 ± 0.03) for HF x Boran [4]. This difference could be attributed to the number of observations and the data structure used. The phenotypic relationship of birth weight with pre-weaning average daily weight growth and post-weaning average daily weight gain was -0.03 ± 0.02 and $-0.020.03$, respectively. This matches the previously reported value of Belay [5] and Almaz *et al.* [19]. This could be because calves' birth weight is affected by the dam's intrauterine environment, health status, and nutrition before delivery.

The phenotypic correlation between weaning weight and six-month weight (0.82 ± 0.07) was similar to Molla *et al.* [22] reports (0.82) and greater than Aynalem [5] reports (0.67 ± 0.01). The lower phenotypic correlations between weaning weight and yearling weight was reported for Boran (0.27 ± 0.02) [4] and HF x Bo (0.45 ± 0.02) [4] than the present research finding (0.59 ± 0.02). However, it was highly similar to the finding of Demeke *et al.* [12] with the reported value of 0.57 ± 0.01 for multi-breed (pooled).

The phenotypic association of weaning weight with pre-weaning average daily weight gain had a positive correlation value (0.90 ± 0.004), which was consistent with the previously reported values of 0.92 for HF x Fogera [5] and 0.99 ± 0.01 for Fogera cattle [19]. The average daily weight gain after weaning had a negative and moderate phenotypic correlation with birth weight (-0.02 ± 0.03). Post-weaning average daily weight gain, on the other hand, had a moderate phenotypic association with weaning weight (0.24 ± 0.03), six-month weight (0.52 ± 0.02), and pre-weaning average daily weight gain (0.28 ± 0.03). Average daily weight increase after weaning had a significant favorable phenotypic correlation with other growth performance characteristics.

5. Conclusions

The genetic correlations among growth traits were generally stronger than their phenotypic counterparts, indicating a substantial shared genetic basis for these traits. The strongest genetic associations were observed between yearling weight and post-weaning average daily weight gain, and between weaning weight and six-month weight, while the weakest correlations involved birth weight. Phenotypic correlations varied, with positive and strong associations for most traits but negative and minimal relationships involving birth

weight. These findings suggest that selection based on early growth traits can effectively enhance other related traits, supporting the potential for genetic improvement in cattle growth performance.

Abbreviations

BW	Birth Weight
HARC	Holetta Agricultural Research Center
PrWADG	Birth to Three Month Weight Gain
PoWADG	Weaning to Yearling Age Weight Gain
SMW	Six Months Weight
WW	Weaning Weight
YW	Yearling Weight

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Author Contributions

Fikadu Wodajo: Conceptualization, Data curation, Formal Analysis, Investigation, Methodology, Project administration, Resources, Supervision, Validation, Visualization, Writing original draft, Writing review & editing

Damitie Kebede: Data curation, Methodology, Validation, Writing review & editing

Mengistie Taye: Data curation, Methodology, Validation, Writing review & editing

Data Availability Statement

The data supporting the findings of the current study are available from the corresponding author upon request.

Conflicts of Interest

The authors declare no conflicts of interest.

References

- [1] Damitie Kebede and I Komlosi. Evaluation of genetic parameters and growth of Hungarian Simmental cattle breed. LRRD. 2015; 27(9).
- [2] Sang Hyon O H. Estimation of genetic parameters for Boar semen traits. PhD. Dissertation, North Carolina State University. Raleigh. 2003.

- [3] Abdullah A R and O Olutogun. Estimates of genetic and phenotypic parameters for preweaning growth traits of N'Dama (*Bos taurus*) calves in the humid tropics of Nigeria. *LRRD*. 2006; 18(8).
- [4] Aynalem Haile, A. Genetic and Economic Analysis of Ethiopian Boran Cattle and Their Crosses with Holstein Friesian in Central Ethiopia. PhD. Dissertation, Deemed University, Haryana, India. 2006.
- [5] Belay Zeleke. Estimation of Genetic Parameters for Growth and reproductive Traits of Fogera and HolsteinFriesian Crossbred Cattle at Metekel Ranch, Amhara Region, Ethiopia. (MSc Thesis), Haramaya university, Ethiopia. 2014.
- [6] Mohiuddin G. Estimates of genetic and phenotypic parameters of some performance traits in beef cattle. *Animal Breeding Abstracts*. 1993; 61(8), 495-522.
- [7] Pires, B. C., Tholon, P., Buzanskas, M. E., Sbardella, A. P., Rosa, J. O., da Silva, L. O. C., de Almeida Torres, R. A., Munari, D. P., & de Alencar, M. M. Genetic analyses on body weight, reproductive, and carcass traits in composite beef cattle. *Animal Production Science*. 2016; 57(3), 415-421.
- [8] Zeleke, B., Kebede, K., & Kumar, B. Estimation of genetic parameters for reproductive traits of Fogera and Holstein Friesian crossbred cattle at Metekel Ranch, Amhara region, Ethiopia. *Online Journal of Animal and Feed Research*. 2016; 6, 90-95.
- [9] Kumar, S., Kumar, V., Gangaraju, G., Nath, S., & Thiruvankadan, A. Estimates of direct and maternal (co) variance components as well as genetic parameters of growth traits in Nellore sheep. *Tropical Animal Health and Production*. 2017; 49(7), 1431-1438.
- [10] Kassahun, D., Taye, M., Kebede, D., Tilahun, M., Tesfa, A., Bitew, A., Kebede, A., Meseret, M., Lakew, E., Bimrow, T., & Haile, A. Phenotypic and genetic parameter estimates for early growth, growth rate, and growth efficiency-related traits of Fogera cattle in Ethiopia. *Veterinary Medicine and Science*. 2022. 8, 387-397. <https://doi.org/10.1002/vms3.628>
- [11] Kefena Effa, Mengistu Alemayehu, Zewdie Wondatir, Diriba Hunde, Getnet Assefa and Getu Kita. Achievements, Status and Prospects in Dairy Research and Development. *Ethiopian journal of agricultural sciences*. EIAR 50th Year Jubilee Anniversary Special Issue: 2016; 51-65.
- [12] Demeke, S., Neser, F. W. C., & Schoeman, S. J. Early growth performance of Bos Taurus x Bos indicus cattle crosses in Ethiopia: Evaluation of different crossbreeding models. *J. Anim. Breed. Genet*. 2003; 120, 39-50.
- [13] Haile, A., Joshi, B., Ayalew, W., Tegegne, A., & Singh, A. Genetic evaluation of Ethiopian Boran cattle and their crosses with Holstein Friesian for growth performance in central Ethiopia. *Journal of Animal Breeding and Genetics*. 2011; 128(2), 133-140.
- [14] Molla Shumye. Genetic analysis of early growth curve of crossbred dairy cattle at Holetta research farm using random regression analysis. MSc Thesis, Haramaya University, Haramaya, Ethiopia. 2014.
- [15] Gojam, Y., Tadesse, M., Effa, K., & Hunde, D. Performance of Crossbred Dairy Cows Suitable for Smallholder Production Systems at Holetta Agricultural Research Centre. *Ethiop. J. Agric. Sci*. 2017; 27(1), 121-131.
- [16] Getahun, Kefale. Genetic and non-genetic parameter estimation for productive and reproductive performances of crossbred dairy cattle at Holetta research center. MSc Thesis, Haramaya University, Haramaya, Ethiopia. 2018.
- [17] Meyer K. WOMBAT, A program for mixed model analyses by restricted maximum likelihood. User notes. *Animal Genetics and Breeding Unit, University of New England Armidale, Australia*. 2012.
- [18] SAS. SAS User's Guide Version 9.0: Statistics, SAS Institute Inc, Cary, NC, USA. 2004.
- [19] Almaz, B., Wuletaw, Z., Haile, A., Gizaw, S., & Mekuriaw, G. (2016). Genetic parameter estimation of pre weaning growth trait of Fogera cattle at Metekel ranch, North West Ethiopia. *International journal of scientific research in science and technology*. 2016; 2(5), 15-21.
- [20] Berhanu Belay. Genetic Evaluation of Dairy Cattle Sires in Central Highlands of Ethiopia. PhD Dissertation, Deemed University, Haryana, India. 2008.
- [21] Wasike, C. B. Genetic evaluation of growth and reproductive performance of the Kenya Boran cattle. MSc. Thesis, Egerton University. 2006.
- [22] Molla Shumye, Kefelegn Kebede, Kefena Effa. Genetic Analysis of Early Growth of Crossbred Dairy Cattle in Central Ethiopia Using Random Regression Model. *Ethiop. J. Agric. Sci*. 2018, 28(3), 19-34.
- [23] Fikadu W. Phenotypic and genetic parameters estimation for growth traits of Holstein Friesian x Boran crossbred dairy cattle at Holletta agricultural research center, Ethiopia. MSc Thesis, Bahir Dar University, Bahir Dar, Ethiopia. 2020.