Original Article

Estimation of (Co) Variance Components and Genetic Parameters of Growth Traits for Boran Cattle

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ABSTRACT

Availing information on genetic parameters of traits of interest for a given population is a prerequisite for effective genetic improvement programs. The objective of this research was to estimate the covariance components and genetic parameters of birth weight (BW), weaning weight (WW), and growth rate (ADG) traits of Boran cattle maintained at Did Tuyera cattle breeding ranch. The total number of animals considered in this study was 1162 (634 males and 528 females). The fixed effects included in the animal model for the analysis of growth traits were calf birth year, season of birth, and sex of calf. Pedigree was pruned using Relax 2 program. Covariance components were estimated using the Average Information-Restricted Maximum Likelihood (AI)-REML procedure as implemented in the DMUV.6
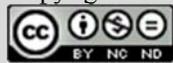
program. The data for BW (1120), WW (1144), and ADG (1144) were collected between 1999 and 2005. The estimation of the BW, WW, and ADG of Boran's calves was optimized by evaluating two models that either include or exclude the maternal genetic effects. The best model was chosen according to the log-likelihood ratio tests. The genetic parameters were estimated using bivariate models (DMU) package, fitting univariate and bivariate models with a restricted maximum likelihood algorithm. The sex of the calf significantly influenced BW and ADG ($p < 0.01$). Calf birth year and birth season significantly ($p < 0.001$) influenced BW, WW, and ADG. The direct heritability estimates for BW, WW, and ADG were 0.17, 0.38, and 0.46, respectively. A larger phenotypic correlation coefficient was found between BW and WW (0.28). The direct and maternal genetic correlations for BW, WW, and ADG were -0.47, -0.45, and -0.47, respectively. The relatively high heritability estimates observed (model 1) for WW (0.38) and ADG (0.46) indicated that reasonable genetic improvement for those traits might be possible through selection.

Keywords: Boran cattle, Correlation, Heritability, Indigenous breeds, Selection.

INTRODUCTION

Genetic improvement of animals is systematic and follows several important steps including breeding objectives, development of selection criteria, genetic evaluations, selection of animals, and lastly design of an appropriate mating system. Efforts to increase the productivity of cattle through selection require information on the genetic parameters of cattle breeds. Genetic parameter estimates are needed for the implementation of breeding programs and the assessment of the progress of ongoing programs (Arendok *et al.,* 2010; Wasike 2006). Information on the magnitude of the covariance components of growth traits in tropical cattle is scanty. The complete covariance structure needs to be estimated for growth rate remains the primary strategy for most cattle breeders around the world, thus the correct prediction of the genetic value of cattle is required for optimizing genetic gain (Archer 1998). Economically important traits in animals are affected by both genetic and environmental factors. The genetic factors are due to a random sample of genes received from the two parental gametes whereas the environmental factors include influences of climate, nutrition, health, and management (Bourdon, 1999). Genetic analysis of animal genetic resources most often aims at separating genetic and environmental effects (Falconer and Mackay, 1996).

The genetic and phenotypic parameters in quantitative genetics include heritability, genetic and phenotypic correlations, and repeatability which play a vital role in the formulation of any suitable breeding plan for a genetic improvement program (Aynalem, 2006). Ethiopian Boran cattle is one of the popular and promising indigenous cattle breeds. The breed is adaptive to and is preferable to maintain across lowland to highland ecological zones in the country. The home track for the breed is

eastern Africa, particularly in Ethiopia and Kenya. Boran, a popular cattle breed, is predominantly utilized and widely distributed across various countries of Africa (DAGRIS, 2006). The breed is well adapted to semi-arid tropical conditions, high degree of heat tolerance, diseases prevailing, ability to survive long periods of feed, and water shortage (Ojango *et al.*, 2006).

A nucleus breeding program have been established for Boran cattle at Dida Tuyera ranch in Borena of Ethiopia to improve the genetic potential of the breed for milk and meat produciton. In this regard, understanding the magnitude the heritability and correlation of the traits of interest are critically important to undertake a meaningful breeding program. However, estimate of genetic parameters on Ethiopian Boran cattle under its natural environment (rangeland condition) is lacking, which is decisive for the ongoing genetic improvement program in Borena. It is with this underlying fact that this study was initiated with the objective of estimating genetic parameters of birth weight, weaning weight and average daily gain of Boran cattle.

MATERIALS AND METHODS

Description of study site

The study was carried out in Borana zone, Yabello district in Oromia region, at Dida Tuyera Boran cattle improvement ranch. The ranch is situated about 550 km South of Addis Ababa and 20 km North of Yabello town, Ethiopia. It is part of the Borana plateau which covers 95,000 km², or 8.5% of the total area of Ethiopia and 14.6% of the lowland areas (Coppock, 1994). The Dida Tuyera ranch was established in 1987 and become functional in 1990. Dida Tuyera ranch is the only currently available ranch involved in the improvement of Ethiopian Boran cattle. The ranch produces pure Ethiopian Boran bulls and distributes for the local pastoralists to improve the genetic makeup of Ethiopian Boran cattle genetic resource. Besides, it supplies replacement heifers to Abernossa ranch for crossbreeding program and as demonstration center for improved husbandry practices and modern ranching system. Annual mean daily temperature varies from 19 to 24ºC. The average annual rainfall was 600 mm. The rainfall distribution is bimodal, but erratic and unreliable. About 59% of annual precipitation occurs from March to May and 27% from September to November (Coppock, 1994).

Data collection and preparation

The data were obtained from Dida Tuyera Boran cattle improvement ranch, which covers from 1999 to 2005. Data were collected from individual cow cards and case book of the ranch and were filtered. The data were cross-checked for consistency and informativeness. The growth traits analyzed included birth weight (BW), weaning weight (WW), and average daily gain (ADG). The evaluation included the records of 1,162 Boran cattle (634 male and 528 female) for growth traits. The pedigree file was

constructed containing all animals with all known relationships using RelaX2 (Strandén and Vuori, 2006). Pedigree information traits were also included for heritability and correlations calculation. After pruning the pedigree data contains a total of 1487 animals, 48 sires and 623 dams.

Statistical analysis

The general linear model (GLM) procedures of the Statistical Analysis System (SAS) computer package, version 9.1.3 was used to test the significance of fixed effects using the following model for the response variables of BW, WW and ADG. The fixed effects included in these models were season of calving, year of calving/birth and sex of the calf.

$Y_{ijkn} = \mu + Y_i + Z_j + S_k + e_{ijkn}$

where,

Y_{ijkn} = individual animal record for the trait;

μ = overall mean;

Y_i = fixed effects of ith birth year of calf; (i= 1999, 2000, 2001, 2002,2003,2004, 2005);

Z_j = effect of the jth season (j= Wet, Dry);

S_k = effect of kth sex (k= Male, Female);

e_{ijkn} = residual effects.

Estimation of variance and (co)variance components were made using the multivariate mixed model program package DMUV.6 (Madsen and Jensen, 2013) using average information restricted maximum likelihood algorithm (Gilmour *et al.,* 1995). The presence of any significant differences was checked by using Tukey Kramer multiple comparison tests. Fixed effects that were significant (p<0.05) were fitted into the model to estimate the genetic parameters. Two models were used for the estimation of variance components. Using two different models which fitted direct additive and dam's additive genetic as a random effect and the fixed effects. The significance of components was determined using a likelihood ratio test (P = 0.05) comparing models with and without the component.

Genetic parameters, heritability and genetic correlation were post processed from variance co-variance output using R Studio program (R Studio, 2016).

Model 1 is used for univariate analysis for all traits

Model 1: $Y = Xb + Z_1a + e$

Model 2 is used for bivariate analysis for all traits

Model 2: $y = Xb + Z_1a + Z_2m + e$, with Cov (a, m) =0

Where, Y = vector of observation; b = vector of fixed effects; a= a random vector for the animal own additive genetic effects; m= a random vector of maternal additive genetic effects; x=incidence matrix for fixed effects; z= incidence matrix for random effects; and e = vector of random residual effects

RESULTS

Effects of non- genetic factors on growth traits

The least squares means and standard errors for BW, WW and ADG are presented in Table 1. The overall mean birth weight, weaning weight, and Average daily gain of Boran cattle obtaind in this study was 20.5,118.81 and 0.44 respectively.

The estimated overall mean 20.5 for BWT was comparable with Fogera cattle (21) but the estimated over all mean for WW and ADG 118.81 and 0.44 respectively for Boran breed from all models was higher than with that of 88.64 and 0.28 (Zewge, A. *et al.,* (2018) for Fogera Breed. The result suggests that the trait is more heritable. Birth weight was significantly affected by the fixed effects of sex of calf (p<0.01), season of birth (p<0.001) and year of birth (p<0.001) (Table 2).

Table 1: Descriptive statistics of the data set used for the analysis

Traits	N	Mean	SD	CV (%)	Range	
					Min (kg)	Max (kg)
BW(kg)	1120	20.5	3.71	10.6	15	30
WW(kg)	1144	118.81	27	15.1	75	143
ADG(g)	1144	0.44	0.13	18.5	0.34	0.8

N, number of observations; BW, birth weight; WW, weaning weight; ADG, average daily gain

Table 2: Least squares means and standard errors (LSM ± SE) of growth traits of Boran cattle at Dida Tuyura Ranch

Factors	N	Birth weight	Weaning weight	Average daily gain
		LSM ± SE	LSM ± SE	LSM ± SE
Sex		**	NS	**
Female	528	18.48±22.38	117.62±26.12	0.45±0.15
Male	634	22.19±12.42	119.52±27.68	0.43±0.11
Season		***	***	***
Main rainy	890	20.84±17.13	117.07±28.02	0.43±0.13
Long dry	270	19.91±18.9	124.48±23.48	0.47±0.12
Year		***	***	***
1999	126	19.32±3.41	85.49±10.49	0.34±0.006
2000	128	22.62±3.92	125.41±17.44	0.52±0.09
2001	182	23.88±3.45	132.64±22.79	0.53±0.16
2002	217	24.81±2.52	135.67±14.94	0.49±0.09
2003	135	24.48±3.21	137.75±19.35	0.48±0.08
2004	194	24.26±39.24	109.25±19.82	0.38±0.10
2005	180	21.74±8.37	114.2±17.8	0.44±0.08

***p<0.001, **p< 0.01, NS: Non- Significant

Covariance components and genetic parameters from univariate analysis

The genetic correlation between direct and maternal genetic effects (r_{am}) for ADG was -0.46. The estimate was slightly lower than the estimate of -0.49 reported by Dadi *et al.,* (2004) for beef cattle. The largest negative r_{am} suggests that selection for genetically superior animals for ADG resulted in those genetically inferior for the maternal genetic components of ADG. According to Meyer (2002), there might be a number of reasons for such genetic relationship, for instance, environmental factors related to management systems and husbandry practices (Table 3 & 4).

Table 3: Estimates of covariance components (kg) and log-likelihood from univariate analysis of birth weight, weaning weight and average daily gain

Models	$\sigma^2 a$	$\sigma^2 m$	Σam	$\sigma^2 e$	$\sigma^2 p$	Log-likelihood Values (-2Log L)
Birth weight						
Model 1	1.67	-	-	8.00	9.67	3714.60
Model 2	**1.40**	0.98	-0.17	8.10	10.48	3651.20
Weaning weight						
Model 1	129.40	-	-	206.50	336	7808
Model 2	**53.10**	45.80	201	225	324	7637.10
Average daily gain						
Model 1	0.004	-	-	0.005	0.009	4249.66
Model 2	**0.002**	0.001	-0.0002	0.005	0.009	4176.94

σ^2_d: direct additive genetic variance, σ^2_m: maternal additive genetic variance, σ_{am}: covariance between direct additive and maternal additive genetic effects, $\sigma^2 e$: error variance, -2log L: log-likelihood, σ^2_p: phenotypic variance

Table 4: Estimates of direct and maternal heritability and genetic correlation for Boran cattle breed under a univariate animal model

Models	Parameters					
	$h^2 a$	SE	$h^2 m$	SE	Ram	$h^2 T$
Birth weight						
Model 1	0.17	0.51	-		-	
Model 2	0.15	0.43	0.10	0.20	0.47	0.15
Weaning weight						
Model 1	0.38	0.52	-		-	
Model 2	0.19	0.43	0.17	0.22	-0.45	0.69
Average daily gain						
Model 1	0.46	0.56	-		-	
Model 2	0.30	0.46	0.15	0.20	-0.47	0.0028

h^2_T: total heritability ($h^2_T = (\sigma^2_d + 0.5\sigma^2_m + 1.5\sigma_{dm})/\sigma^2 p$ estimated according to Willham (1972) S.E.: Standard error, h^2_d: direct heritability, h^2_m: maternal heritability

Bivariate analysis

Estimates of covariance components, direct, maternal and total heritability from bivariate analyses were presented in Table 5. Bivariate analyses were completed for all combinations of the trait.

Table 5: Estimates of covariance components, direct and maternal heritability and total heritability from bivariate analyses of BW, WW and ADG fitting two animal models

Models	Variance components				Genetic parameter			
	σ^2a	σ^2m	σ^2e	σ^2p	h^2d	h^2m	r_{am}	h^2_T
Birth weight								
Model 1	1.65	-	8.00	9.650	0.17		-	0.17
Model 2	1.93	0.046	7.71	9.670	0.20	0.005	-0.45	0.17
Weaning weight								
Model 1	127.17	-	208.73	336.00	0.41		-	0.37
Model 2	82.33	38.000	213.25	333.60	0.32	0.150	-0.46	0.64
Average daily gain								
Model 1	0.004	-	0.005	0.009	0.43		-0.48	0.43
Model 2	0.002	0.001	0.0057	0.0087	0.35	0.140		0.28

h^2T: total heritability, h^2a: direct heritability, h^2m: maternal heritability, σ^2a: direct additive genetic variance, σ^2m: maternal additive genetic variance, σ^2e: error variance, σ^2p: phenotypic variance

Phenotypic and genetsic correlations of growth traits

Phenotypic and genetic correlations for growth traits are shown in (Table 6). The phenotypic correlation between two traits can be influenced by inheritance, environmental or both.

Table 6: Phenotypic (above diagonal) and genetic (below diagonal) correlations for growth traits for Boran cattle from the bivariate analyses

Parameters	BW	WW	ADG
BW	*	0.28	0.21
WW	0.96	*	0.65
ADG	-	1.00	*

DISCUSSION

The sex of the calves had a significant effect (p<0.01) on BW and ADG but not on WW. The sex difference in growth performance might be because of physiological differences between males and females. Year and season had a highly significant effect (p<0.001) on all traits considered in this study. The significant effect of the year on growth traits might be due to the difference in amount of rainfall, forage availability and management differences. Birth year and sex had reported significant effects on birth weight, weaning weight and average daily gain in Boran cattle (Banjaw and Haile-Mariam 1994; Demeke *et al.,* 2003).

The number of observations by sex and season are not equal because it is natural breeding system that we used in this experiment, there is no human interference and the experiment was conducted under rangeland conditions using bulls, so the difference that we observed is absolutely a matter of chance for X and Y chromosomes.

Covariance components and genetic parameters from univariate analysis
Birth weight
Estimates of direct and maternal heritability and genetic correlation for Boran cattle breed using univariate animal model is indicated in Table 3. The estimated direct heritability (h^2_d)) for BW ranged from 0.15 to 0.17, which was lower than the heritability estimates of 0.22 reported for Nellore cattle in Brazil (Eler *et al.,* 1995), 0.41 in Australian breed (Meyer 1992), 0.33, (Plasse *et al.,* 2002) in Brahman breed in Venezuela, and 0.34 reported in Kenyan Boran cattle (Wasike 2006). Haile-Mariam and Kassa (1995), Haile *et al.,* (2011) and Banjaw and Haile-Mariam (1994) reported direct heritability estimates of 0.24, 0.25 and 0.32, respectively for the same breed in Ethiopia. The corresponding maternal heritability (h^2_m) for BW was ranged from 0.10 to 0.17 (Table 3). The present estimates are higher than h^2_m of 0.09 obtained by Haile-Mariam and Kassa (1995) for Boran breed in Ethiopia.

The genetic correlation (r_{am}) between direct and maternal genetic effects for BW was negative -0.47. The current estimate was lower than the estimate of -0.35 reported by Banjaw and Haile/Mariam (1994) and slightly higher than the estimates of -0.55 obtained by Haile-Mariam & Kassa (1995) for the same breed. In other studies, genetic correlations between direct and maternal genetic effects for BW were -0.42 and -0.17 for Fogera Assemu *et al.,* (2015) and Gobra cattle Diop & Van Vleck (1998) respectively. In contrast the above studies, positive correlations for direct and maternal genetic effects for BW were reported in Nellore cattle Eler *et al.,* (1995) r_{am} = 0.72; Plasse *et al.,* (2002) r_{am} = 0.22. The total heritability for BW was 0.17 which is similar to the estimates of 0.17 Haile -Mariam & Kassa (1995) for Boran breed and less than the estimates of a 0.28 and 0.30 obtained by Plasse *et al.,* (2002) in Brahman cattle. But, higher than the estimates of a 0.10 for Nellore Eler *et al.,* (1995) and 0.08 value obtained for Gobra Diop & Van Vleck (1998).

Weaning weight
The direct heritability for WW was 0.38 higher than the direct heritability estimates Arnason and Kassa (1987); Banjaw and Haile-Mariam (1994); Kassa Mersha and Haile-Mariam (1995) for Boran breed, but lower than the estimate reported by Haile *et al.,* (2011) for the same breed. For Ethiopian Fogera cattle breed, direct heritability of 0.24 was reported Zeleke *et al.,* (2016). The relatively high direct heritability estimate for WW in this study denotes the fact that direct genetic effects constitute a significant

portion of the phenotypic variance for WW of Boran breed; suggesting that better genetic progress would be expected through direct genetic selection. The maternal heritability of WW was 0.19. The estimate of maternal heritability we found in this study was higher than maternal heritability of 0.06 estimated in Boran cattle Haile-mariam & Kassa (1995) and 0.016 in Fogera cattle Assemu *et al.,* (2016) but lower than the maternal heritability estimates of 0.25 in Brahman cattle Mostert *et al.,* (1998). Maternal genetic effect had a medium contribution in expression of WW trait in Boran cattle at Dida Tiyura Ranch. Genetic correlation (r_{am}), the genetic correlation between direct and maternal genetic effects (r_{am}) for WW was -0.45. The estimate was higher than with a negative value of -0.57 reported by Haile-Mariam and Mersha (1995) for the same cattle. In contrast, the genetic correlation between direct and maternal genetic effects was positive for WW ($r_{am} = 0.11$) in Brahman breed (Plasse *et al.,* (2002).

The total heritability estimate was 0.38 for WW in Boran cattle in this study. This value for WW was higher than the estimates of 0.21 in the same breed Haile-mariam and Mersha, 1995). In other studies, such as Plasse *et al.,* (2002), Eler *et al.,* (1995), and Diop &Van Vleck (1998), reported total heritability of 0.12, 0.14 and 0.12, respectively. The difference in heritability estimates might be associated with the data size Yosef (2006).

Average daily gain
The estimated direct heritability for ADG in the present study was 0.46. In other studies, direct heritability estimates of 0.07 was found in Boran breed Aynalem (2006). The present estimate of direct heritability of ADG was comparable with the estimate of 0.50 reported in different breeds Banjaw and H/Mariam (1994); F. Goyache *et al.,* (1997); Dadi *et al.,* (2004) but higher than the direct heritability estimate reported by Haile *et al.,* (2011) for Boran and Zeleke *et al.,* (2016) for Fogera cattle. The maternal heritability of ADG was 0.14 which was higher than the estimates of 0.05 and 0.06 reported in Gobra Diop & Van Vleck (1998) but, lower than the estimate of 0.35 Dadi *et al.,* (2004). The results showed that the inclusion of maternal effects in genetic evaluation of early growth traits in Boran cattle is of crucial importance. The exclusion of maternal effects (model 1) leads to upward biased estimates for covariance components. As a result, accurate estimation of covariance components is a prerequisite for designing Boran cattle genetic improvement program and genetic evaluation system. The total heritability was 0.46 for ADG, which was lower than the ADG (0.48) estimate reported by Dadi *et al.,* (2004). When the h^2 of a trait is high, a correlation between the phenotype and genotype of individuals, on average, should also be high, and selection on the basis of own phenotype should be effective. The heritability value for growth traits is variable depending on the breed, the production system and the method of estimation.

Bivariate analysis

The direct heritability estimates from bivariate analysis varied from 0.17 to 0.43 for BW, WW and ADG. The corresponding maternal heritability of BW, WW and ADG were 0.005, 0.15 and 0.14, respectively. Our estimates lie within the range of previous scholars' reports Haile-Mariam and Kassa-Mersha (1995) and Aynalem (2006) for Boran cattle and Zeleke *et al.,* (2016) for Fogera cattle. The genetic correlations between the direct and maternal effects (r_{am}) were large and negative for BW (-0.45). This value for BW was in contrast to the estimates from previous studies Meyer (1992). Negative (r_{am}) estimates may arise from the same genes tending to possess the different effects on direct and maternal genetic effects of BW. Estimates of r_{am} for WW and ADG were negative (Table 5). Corresponding large negative genetic correlations were reported for WW in other beef cattle studies Cantet *et al.,* (1993) and Schoeman *et al.,* (2000). The large negative estimates obtained in this study as well as those reported estimates are thus most likely not reflecting a true antagonism but are biased estimates of the true relationship between direct and maternal genetic effects. The bivariate estimates of genetic correlations between direct and maternal effects (Table 5) for BW (- 0.45), WW (-0.46) and for ADG (0.48) were comparable estimates with that of the univariate analysis.

Phenotypic and genetic correlations of growth traits

The phenotypic correlation between BW and WW were (0.28) and between BW and ADG were 0.21 in this study. Zeleke *et al.,* (2016) reported a 0.09 phenotypic correlation between BW and WW and -0.021 between BW and ADG. Bekele *et al.,* (2017) reported a negative correlations value for both of -0.04 between BW and WW and -0.04 between BW and ADG and phenotypic correlation between ADG and WW was positive and moderately high (0.65) this result was comparable with the phenotypic correlation of 0.64 Plasse *et al.,* (2002) and 0.62 Pico (2004) were reported for BW and WW in Brahman breed. Selection for increased ADG in Boran cattle would lead to an increased WW. So, there is scope for simultaneous improvement of these WW and ADG through the improvement of the production environment Bekele *et al.,* (2016). Phenotypic correlation for all traits was lower than genetic correlation, which is consistent with the majority of reported results Gizaw *et al.,* (2004). The genetic correlation estimates between BW and WW (0.62) and between ADG and WW (0.96). The current result was comparable with 0.6 reported by Almaz (2012) for Fogera cattle. Due to the strong genetic relationship between these traits, selection of one of them could have high effect on the other through correlated responses Zeleke *et al.,* (2016).

CONCLUSION

- All non-genetic factors considered in the study affected the growth performances of the breed under the ranch management system.

- Our heritability and genetic correlation estimate for BW and WW for Boran cattle breeds were comparable to other reports of the same breed.
- Results from the current study, as expected, show that both ADG and WW would respond favorably to selection.
- Particularly, the genetic improvement through selection would be more effective for ADG compared to WW because of higher heritability estimates.
- Furthermore, the information generated from this study should be supported with a large number of animals.

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CONFLICT OF INTERESTS

The authors declare that they have no competing interests.

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