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Original Article

Genetic parameter estimation of growth traits of Fogera cattle

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Abstract

Data collected from 1988 to 2011 at Metekel Ranch, Ethiopia was used to estimate genetic parameters of growth traits of Fogera cattle. The data set used for analysis consisted of 5513, 3223 and 3223 records for BWT, AWWT, and PADG, respectively. Four animal models were used fitting direct animal (Model1), direct animal and permanent environmental (Model2), direct and maternal genetic (Model3), and all the above random effects (Model4). Heritability values and additive variances for all traits were low. Estimates of direct heritability of growth performance traits from the best model were 0.03 ± 0.02, 0.06 ± 0.03 and 0.05 ± 0.03 for BWT, AWWT and PADG respectively. The phenotypic correlation between growth traits ranged from -0.10 ± 0.02 for BWT and PADG to 0.99 ± 0.01 for AWWT and PADG and genetic correlation ranged from 0.5 ± 0.27 for BWT and PADG to 0.99 ± 0.00 for AWWT and PADG. The low heritability estimates might be indication of low genetic control of the expression of a trait and this might also be an indication of presence of high environmental effects influence.

Keywords Ethiopia. Fogera breed. Metekel ranch. growth traits. genetic parameter

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Introduction

Efforts to improve genetic quality of cattle through selection require information on genetic parameters of cattle breed population. Without estimation of genetic parameters, breeding program setting which could be used as a tool for breed improvement program seems hardly possible. Genetic parameter estimates are needed for implementation of breeding programs and assessment of progress of ongoing programs (Bourdon 1999; Wasike 2006; Arendok *et al.*, 2010). The genetic parameters are helpful in determining the method of selection, to predict direct and correlated response to selection, choosing a breeding system to be adopted for future improvement as well as in the estimation of genetic gain (Javed *et al.*, 2001). Knowledge of the magnitude of the (co) variance components in tropical cattle is scanty. Therefore, the complete covariance structure needs to be estimated. Even in case of inadequate pedigree information and data, some attempt at estimating genetic (co) variance components and genetic parameters is better than no attempt (Wasike *et al.*, 2009). The Fogera breed, a Zebu x Sanga breed, are found in southwestern flanks of Lake Tana (*in-situ*) in Bahir Dar Zuria, Fogera and Libokemkem districts (Addisu and Getinet, 2008) and in Metekel ranch (*ex-situ*) in Guangua district. The breed is popular for its adaptation to seasonal flooding and the swampy conditions of the area. The Fogera breed population is exhibiting a decreasing trend. Metekel ranch had been established to conserve Fogera cattle genetic resource. With the view to evaluate performance of Fogera cattle, traits like growth and reproduction are being recorded since establishment of the ranch. Some efforts have been made to quantify the level of performance of the cattle for the above mentioned traits (Asheber 1992; Addisu and Hegde 2003; Melaku *et al.*, 2011a and 2011b). However, until now no effort is made to estimate genetic parameters for the recorded traits. Growth rate remains the primary selection criterion for both beef and dairy herds. Early growth of cattle has strong implications on both reproductive and production performances. It is with this underlying fact that this study was initiated with the objective of to estimate genetic parameters of growth traits of Fogera cattle.

Materials and methods

Description of the study Area

Metekel Cattle Breeding and Improvement Ranch is found in Guangua district of Awi zone in Amhara National Regional State, and is situated about 505 kilometer North-west from Addis Abeba. The annual mean relative humidity is 61.7% and it reaches to high from June to October (76.7-83.8%). The ranch receives an average annual rain fall of 1730.0 millimeter; average temperature ranges from 13.7 to 29.5^0, with monthly mean minimum-maximum occurring in January (9.4^0) and in April (35.0^0), respectively. The rain fall distribution is bi-modal, has three rainy seasons; long rainy season (June-October), short rainy season (March-May) and dry season (November-February) (Melaku *et al.*, 2011a, b and Addisu and Hegde 2003).

Herd management and Breeding program

Metekel cattle Breeding and Improvement Ranch has so far been engaged in maintenance of Fogera cattle population outside their adapted environment (*ex-situ* conservation). The cattle were herded based on breed, sex and age. On the ranch, calves were weighed on the date of birth and identified within 72 hours of birth. Health management practice has prevention and control scheme. The prevention scheme focuses on vaccination against anthrax, blackleg, and pasturollosis once in every 6 to 8 months and once per year for CBPP. The control measures were taken for internal and external parasites. The breeding program has two components: selection and crossbreeding. The selection activity undertaken at Metekel ranch has never been based on quantitative traits; however, the visual appraisals made during the purchase of animals from Fogera plains might have led to a distinct cattle population. In cross breeding program; crossbred animals are produced through artificial insemination of Fogera cows with Friesian semen.

Data Source and Data management

Data collected from 1988-2011 at Metekel ranch was used for the study. Records with irregularity in pedigree information and dates were discarded. New animal identification number was generated by considering chronological order of the animals. Individuals that appear as both sire and dam and duplicate records and individuals that were parents of themselves were deleted. Parity was classified as 1, 2, 3, 4 and those parities from the fifth and above were considered as parity five because of very few observations available. Season was classified into three (dry season, short and long rainy season) based on the rain fall distribution of the area.

Traits analyzed

Data which were analyzed include birth weight (BWT), preweaning average daily gain (PADG) and adjusted weaning weight (AWWT).

$$\text{AWWT} = \frac{\text{actual weaning weight} - \text{birth weight}}{\text{No.of days from birth to weaning}} \text{ x } 240 + \text{birth weight}$$

Statistical analysis

The parameters included were heritability and correlation. They were estimated using WOMBAT (Meyer 2007). The variance components and heritability were estimated using a Uni-variate animal model using four models which fitted direct additive, dam genetic and permanent environmental effect as a random effect and the fixed effects. Correlations (genetic and phenotypic) among the different traits were estimated from bi-variate analysis by using model 1. Comparison of the different uni-variate models was made by using the log-likelihood ratio tests to determine the best model.

The model equations used were:

Model1 $y = \mathbf{X}b + \mathbf{Z_1}a + e$

Model2 $y = \mathbf{X}b + \mathbf{Z_1}a + \mathbf{Z_3}c + e$

Model3 $y = \mathbf{X}b + \mathbf{Z_1}a + \mathbf{Z_2}m + e$ (cova, m = 0)

Model4 $y = \mathbf{X}b + \mathbf{Z_1}a + \mathbf{Z_2}m + \mathbf{Z_3}c + e$ (cova, m = 0)

Where, y = the vector of records

b = vector of fixed effects

X = incidence matrix of fixed effects

a = vector of direct additive genetic effect

m = vector of maternal additive genetic effect

c = vector of permanent environmental effect

Z_1 = incidence matrix for direct additive genetic effect

Z_2 = incidence matrix for maternal additive genetic effect

Z_3 = incidence matrix for permanent environmental effect

e = vector of random errors

Table 1. Information related with pedigree, traits analyzed and sample sizes

No. of	Traits		
	BWT	AWWT	PADG
Records	5513	3223	3223
Animals	6960	4614	4691
Animals after pruning	6289	4033	3836
Animals without recording	776	810	613
Sire	73	57	61
Dam	2114	1251	1460
Dam with records and progeny	1400	661	661
Animals with unknown sires	3874	2098	2187
Animals with unknown sires with records	3098	1481	1485
Animals with both parents unknown	1097	813	925
Progeny per sire	22	19	17
Animals with paternal grand sire	635	388	323
Animals with paternal grand dam	1264	806	267
Animals with maternal grand sire	1812	961	773
Animals with maternal grand dam	2318	1118	744

Result and discussion

Effects of non genetic factor

The overall mean birth weight (BWT), adjusted weaning weight of calves (AWWT) and preweaning average daily gain (PADG) of Fogera calves is presented under Table2**.** Sex of the calves had a significant effect on BWT and AWWT but not on PADG. This sex difference in growth performance might be because of Physiological difference between male and female. Both Season and year had a significant effect on all traits considered. This might be due to the difference of rain fall and forage availability. This might be of the calves born during short rainy season gets more feed during short and the coming long rainy season and gets more weight. The dams which give birth during short rainy season get the advantage of green forage available during short and the coming long rainy season and they become in better body condition and produce more milk. Parity of birth had a significant effect on birth and adjusted weaning weight but its effect on preweaning average daily gain was not significant.

Variance component and heritability

Additive genetic effects accounted for a very small proportion of total variation for those traits. Estimates of the residual error variance, the component of phenotypic variation due to all other factors that cannot be accounted for in the analysis, were high. This high residual variation is due to both high unknown environmental effects that environmental stress highly affects the magnitude of additive genetic variance for different traits (Sendros *et al.*, 2003). It created stress and affects high producing animals and reduced the additive genetic variance of the herd on the study area. The recorded high error variance may also be associated with the data set used which recorded for long years.

The result of heritability estimates were at the lower end of the range in comparison with most other studies on tropical breeds. The low values of heritability obtained could be due to deterioration in management resulting to poor nutritional status of the animals (Mohamed 2004; Shehu *et al.*, 2008); presence of high environmental variation or high environmental stress (Bosso *et al.*, 2009 and Wasike 2006); or due to management variation through time, data record quality (Meyer 2005). Environmental influences limit the expression of genetic potential of superior animals, hence restricting difference in growth due to genetic values among animals (Mohamed 2004).

Direct heritability (h^2a) decreased when maternal genetic and permanent environmental effect was fitted (Table 3). Birth weight of an animal and its early growth rate, in particular till weaning, are determined not only by its own genetic potential but also by the maternal environment.

Table 2: Least squares means and standard error (LSM ± SE) of BWT, AWWT

Factors	BWT	AWWT	PADG
Overall	21.01 ± 0.03	88.64 ± 0.33	0.28 ± 0.001
CV (%)	10.43	17.26	18.7
SEX	***	**	NS
Female	21.37 ± 0.07a	89.76 ± 0.55b	0.28 ± 0.002
Male	22.08 ± 0.07b	91.24 ± 0.56a	0.29 ± 0.002
Season	**	***	***
Long rainy	21.77 ± 0.07a	89.03 ± 0.56b	0.28 ± 0.002b
Short rainy	21.58 ± 0.07b	92.47 ± 0.62a	0.29 ± 0.002a
Dry	21.82 ± 0.08a	89.10 ± 0.71c	0.28 ± 0.003bc
Parity	***	*	NS
1	21.05 ± 0.06a	89.66 ± 0.51ac	0.28 ± 0.002
2	21.88 ± 0.08b	90.12 ± 0.63ab	0.28 ± 0.002
3	21.88 ± 0.09b	92.28 ± 0.79a	0.29 ± 0.003
4	21.86 ± 0.11b	91.21 ± 1.02b	0.29 ± 0.004
5	21.96 ± 0.11b	89.22 ± 1.11c	0.28 ± 0.004
Year	***	***	***
1989	23.11 ± 0.77cde		
1990	25.29 ± 0.38a		
1991	23.16 ± 0.51bd		
1992	24.11 ± 0.44b		
1993	23.19 ± 0.45cb	113.74 ± 4.86a	0.38 ± 0.02a
1994	20.19 ± 0.22hij	106.12 ± 1.67b	0.35 ± 0.007b
1995	21.31 ± 0.20ghi	104.96 ± 1.54b	0.34 ± 0.006b
1996	22.26 ± 0.13def	102.40 ± 1.04b	0.33 ± 0.004b
1997	22.08 ± 0.17 def	104.49 ± 1.26b	0.34 ± 0.005b
1998	23.43 ± 0.12b	89.36 ± 0.93d	0.27 ± 0.004ef
1999	21.73 ± 0.11egf	95.70 ± 1.23c	0.31 ± 0.005cd
2000	22.29 ± 0.12cde	101.84 ± 0.91b	0.33 ± 0.003bc
2001	21.89 ± 0.11defg	92.93 ± 0.90cd	0.29 ± 0.003de
2002	20.18 ± 0.11j	83.19 ± 1.15ef	0.26 ± 0.004fgh
2003	20.05 ± 0.13j	83.41 ± 1.02e	0.26 ± 0.004fg
2004	20.72 ± 0.14hij	84.45 ± 1.14e	0.26 ± 0.004fg
2005	20.27 ± 0.12j	77.57 ± 1.06f	0.23 ± 0.004h
2006	21.16 ± 0.10fgh	69.94 ± 1.04g	0.20 ± 0.004i
2007	20.51 ± 0.10hij	78.79 ± 3.37ef	0.24 ± 0.01gh
2008	19.87 ± 0.10j	78.70 ± 1.31f	0.24 ± 0.005h
2009	21.85 ± 0.10defg	69.53 ± 0.99g	0.19 ± 0.004i
2010	20.39 ± 0.18j	90.79 ± 1.35cd	0.30 ± 0.005d
2011	19.91 ± 0.15j		

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

These represent mainly the dam's milk production and mothering ability, though effects of the uterine environment and extra-chromosomal inheritance may contribute. The genotype of the dam therefore affects the phenotype of the young through a sample of half her direct additive genes for growth as well as through her genotype for maternal effects on growth (Meyer 1992; Habtamu *et al.*, 2011). Estimates of direct heritability were comparatively higher when maternal effects were ignored. Omitting maternal effects result in an upward bias of direct heritability estimates (Meyer 1992).

The proportion of phenotypic variance due to maternal permanent environmental effect of the dam was slightly higher at birth and decreased thereafter, the maternal effect at birth is due to the prenatal maternal environment and cytoplasmic effect of dam on pre natal growth of fetus (Wasike 2006). Permanent environmental effect is due to uterine environment and the maternal behavior of the dam (Habtamu *et al.*, 2011). Maternal effects were found less important for the adjusted weaning and pre weaning average daily gain. It might be due to Fogera cattle at Metekel ranch have less variability in milk production performance to cause less maternal effects at weaning weight and on daily gain of the calves. Maternal and permanent environmental heritability decreases for AWWT and PADG. The maternal heritability was estimated zero for AWWT and PADG. It is consistent with the result of Aynalem *et al.*, (2010) who found values of 0.001 ± 0.04 permanent environmental heritability for WWT and 0.00 ± 0.03 for maternal genetic effect and 0.0001 ± 0.03 for permanent environmental heritability for PADG for Boran crosses and Habtamu *et al.*, (2011) estimated zero maternal genetic effect on weaning weight and pre weaning average daily gain of Horro cattle and their crosses. It could arouse from high environmental effect which reduce the mothering performance of high producing dams and results similarity among dams.

The estimated direct heritability 0.06 ± 0.02 for BWT was comparable with the result obtained by Diop and Van Vleck (1998) for Gobra cattle (0.07 ± 0.03), Sendros *et al.*, (2003) for a mixed population (0.14) and Gunawan and Jakaria (2011) for Bali cattle (0.09 ± 0.07) and it is slightly less than 0.10 ± 0.05 reported by Abdullah and Olutogun (2006) for N'Dama cattle and 0.10 ± 0.002 by Shehu *et al.*, (2008) in Nigerian cattle. Estimated direct heritability for BWT from all models was less than 0.28 for South African Brahman cattle (Pico, 2004), 0.34 for Kenyan Boran cattle (Wasike 2006), 0.25 ± 0.05 (Aynalem *et al.*, 2010) reported for Ethiopian Boran 0.68 ± 0.09 (Habtamu *et al.*, 2011) for Horro and their crosses and 0.25 ± 0.003 (Assan 2012) for Tuli breed. The result suggests that the trait is less heritable.

Table 3 Estimates of variance components and heritability measurements with their standard errors (SE) for growth traits

Traits	Models			
	1	2	3	4
B BWT				
V_a	0.3	0.16	0.13	0.13
V_m			0.32	0.3
V_c		0.31		0.03
V_e	4.53	4.34	4.37	4.4
V_p	4.82	4.81	4.82	4.8
h^2a	0.06 ± 0.02	0.03 ± 0.02	0.03 ± 0.017	0.03 ± 0.02
h^2m			0.07 ± 0.016	0.06 ± 0.02
C^2		0.065 ± 0.02		0.01 ± 0.03
e^2	0.94 ± 0.02	0.90 ± 0.02	0.90 ± 0.02	0.90 ± 0.02
Max. log L	-7116.653	-7109.407	-7103.925	-7103.891
AWWT				
V_a	17.8	14.2	16.04	14.20
V_m			2.602	0.003
V_c		8.06		
V_e	213.5	208.9	212.57	208.9
V_p	231.3	231.2	231.2	231.2
h^2a	0.08 ± 0.03	0.06 ± 0.03	0.07± 0.034	0.06 ± 0.03
h^2m			0.01± 0.020	0.00 ± 0.02
C^2		0.04 ± 0.03		0.04 ± 0.03
e^2	0.92 ± 0.03	0.90 ± 0.03	0.92± 0.32	0.90 ± 0.03
Max. log L	-10358.787	-10352.723	-10358.629	-10352.723
PADG				
V_a	0.003	0.002	0.002	0.002
V_m			0.00063	0.00001
V_c		0.002		0.001
V_e	0.04	0.04	0.04	0.04
V_p	0.04	0.04	0.041	0.04
h^2a	0.06 ± 0.03	0.05 ± 0.03	0.06 ± 0.030	0.05 ± 0.03
h^2m			0.02 ± 0.02	0.00 ± 0.02
C^2		0.04 ± 0.03		0.04 ± 0.03
e^2	0.94 ± 0.03	0.91 ± 0.03		0.91 ± 0.03
Max. log L	7176.265	7177.835	7177.040	7177.830

V_a = direct genetic variance; V_m = maternal genetic variance; V_c = maternal permanent environmental variance; V_e = the residual variance; V_p = phenotypic variance; h^2a = direct heritability; h^2m = maternal heritability; C^2 = the fraction of total variance that corresponds to maternal permanent environmental effect; e2 = the fraction of total variance that corresponds to environmental variance; Max. log L log likelihood value.

The present result of direct heritability 0.08 ± 0.03 for AWWT was comparable with 0.06 for Boran cattle (Ronningen *et al.*, 1972), 0.07 and 0.08 for Brahman cattle (Plasse *et al.*, 2002a; 2002b), 0.07 for a mixed population (Sendros *et al.*, 2003), and 0.06 ± 0.01 for Cuban zebu cattle (Trujillo *et al.*, 2011). It is slightly less than 0.12 for Kenyan Boran cattle (Wasike 2006) and 0.12 ± 0.04 for Kenyan Boran (Wasike *et al.*, 2009). Low estimates indicated that the variation due to additive gene action was probably small and that the variation due to environmental factors was more important. It suggested that selection on the basis of individual performance will not be effective in achieving increased gain in growth weights (Goyache and Guiterez 2001; Javed *et al.*, 2001; Gunawan and Jakaria 2011 and Rabaya *et al.*, 2009).

Correlations

The phenotypic correlation between growth traits is summarized in Table 4. The phenotypic correlation between BWT with AWWT and PADG were low and it might because of BWT of calf depends on the intra uterine environment of the dam, health status of dam and nutrition of dam before birth but PADG and AWWT were having high phenotypic correlation. Similarly low phenotypic correlation were reported in the review by Lôbo *et al.*, (2000) (0.96) and Cucco *et al.*, (2009) (0.91 ± 0.027). But it is opposite to the reports of Wasike (2006), Aynalem *et al.*, (2010) who found low phenotypic correlation for those traits. Genetic correlations between the traits studied were favorable, indicating that selection for one trait will improve others in a desired direction, helping the breeding process as a whole. The highest genetic correlations were observed between the AWWT and PADG (0.99 ± 0.00) and the genetic correlation between BWT and AWWT and PADG were moderately high 0.6 ± 0.23 and 0.5± 0.27, respectively (Table 3). Similarly Plasse *et al.*, (2002a) and Pico (2004) reported a high genetic correlation of 0.64 and 0.62 between BWT and WWT, respectively. It is quite similar to the present result. The result found by Cucco *et al.*, (2009) also confirms the present result.

Table 4 Phenotypic (above diagonal) and genetic correlation (below diagonal) for growth traits

Parameter	BWT	AWWT	PADG
BWT		0.05 ± 0.02	-0.10 ± 0.02
AWWT	0.6 ± 0.23		0.99 ± 0.01
PADG	0.5 ± 0.27	0.99 ± 0.00	

Conclusion

Poor control of the production environment can increase environmental variation and mask genetic differences among animals. The low heritability estimates indicate that selection based on early stages phenotypic performance of animals could not be effective in the population studied or the population has low response to selection. Therefore, producers, in the study area alongside with improvement of the data management, should improve these traits firstly through improvement of the production environment and then by crossbreeding.

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