Global Veterinaria 17 (3): 250-254, 2016
ISSN 1992-6197

DOI: 10.5829/idosi.gv.2016.17.03.10537

Estimation of Genetic Parameters for Growth Traits of Fogera and Holstein Friesian Crossbred Cattle at Metekel Ranch, Amhara Region, Ethiopia

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Abstract: The study was carried out at Metekel ranch, Amhara region, Ethiopia, with the objective of estimating genetic parameters for growth traits of Fogera and Holstein Friesian crossbreed cattle.The data used included pedigree and growth performance records of animals born from 1990 to 2012.The parameters were estimated by using Variance Component Estimation (VCE 6.0) software. Four models were used Viz. Model1: $Y= X_b+Z_1a + e$; Model2:$Y=X_b+Z_1a+Z_3c + e$; Model3: $Y=Xb+Z_1a+Z_2m+ e$; cov a,m=0 and Model4: $Y= X_b + Z_1a + Z_2m+ Z_3c + e$; cov a, m=0. Likelihood ratio was used to identify the best model; hence model 3 was the best model. Estimation of direct heritability from the best model was 0.128± 0.04 for birth weight (BWT), 0.242± 0.08 for weaning weight (WWT) and 0.158± 0.08 for pre weaning average daily gain (PADG). The phenotypic correlations between growth traits ranged from-0.021 between birth weight and pre-weaning average daily gain to 0.92 between weaning weight and pre-weaning average daily gain. Whereas, the genetic correlation between the studied traits ranged from 0.314 to 0.92 between BWT & WWT and WWT & PADG respectively. The result showed that there were low heritability estimates and it implied that selection based on phenotypic performance of animals was unlikely to bring genetic progress in the studied herd, because of the heritability of the trait. Thus, selection method, in addition to individual records, should incorporate pedigree and progeny information in the form of an index to get optimum genetic progress in the studied population.

Key words: Correlation · Crossbreed · Economic trait · Fogera X Holstein Friesian · Genetic Parameters · Growth Traits · Heritability

INTRODUCTION

The total cattle population of Ethiopia is estimated to be 53.39 million. Out of this population, about 98.95% are local breeds while the hybrids and exotic breeds account only for about 0.94% and 0.11%, respectively [1]. The dairy production in Ethiopia is based largely on indigenous breeds of cattle and breed improvement and development programs, have been directed mainly on crossbreeding activities through research stations, government stock multiplication centers and private farms [2].

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 [3]. Genetic analysis of animal genetic resources most often aims at separating genetic and environmental effects [4]. Genetic parameter estimates are needed for implementation of breeding programs and assessment of progress of ongoing programs where accuracy of their estimation is of paramount importance [5]. 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 genetic improvement program [6].

The reliability of phenotype depends upon the heritability of the trait. Heritability is critically important for selection of polygenic traits. When selection is made for trait(s), heritability decides how much genetic

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improvement is expected in the trait(s) while genetic correlation between traits selected and other correlated trait (s) decides how much response to selection can be expected for traits not selected in addition to the response for the selected traits [7]. The response to selection is the combined result of direct selection for each trait and indirect selection caused by the genetic correlation between the traits [3].

Growth trait is a function of the individual's inherent ability for growth, milk production and mothering ability of its dam [8]. Studies on estimation of genetic parameters on Ethiopian cattle are scanty which might be attributed to lack of well structured pedigree data and lack of farm record. Hence, the present study was intended to contribute its part in filling the gaps. Thus, this study was initiated with the objective Estimating genetic parameters of growth traits of Fogera and Holstein Friesian crossbred cattle population.

MATERIALS AND METHODS

Description of the Study Area: Metekel Cattle Breeding and Improvement Ranch is found in the Guangua district of Awi zone in Amhara National Regional State and is situated about 505 km North-west of Addis Ababa, 200 km from Bahir Dar town on the road to Guba. Its altitude ranges from 1500-1680 m.a.s.l. The annual mean relative humidity is 61.7% and it reaches high from June to October (76.7- 83.8%). The ranch receives an average annual rainfall of 1730.0 mm; average temperature ranges from 13.7 to 29.5^{0}C. The area has three rainy seasons; long rainy season (June-October), short rainy season (March-May) and dry season (November-February). The ranch has three types of soils viz. Red, brownish red (Latosols) and dark brown. The vegetation is mostly composed of perennial and annual grasses and a few scattered trees.

Herd Management: The Ranch has been engaged in maintenance of Fogera cattle population outside their adapted environment (*Ex-situ conservation*). The cattle herded based on breed and age. During the day time animals graze on natural pasture and were provided with hay in addition to grazing during dry season. Crossbred female calves above three months of age and sick animals were supplemented with Desmodium (*Desmodium triflorum*), Rohodus (*Chloris gayana*) and Elephant grass (*Pennisetum purpureum*) both in wet and dry seasons through cut and carry system. The main source of water was a year-round river. Tap-water has been provided to lactating Fogera cows, crossbred stock and sick animals. Health management practice includes the prevention and control scheme. The prevention scheme focused on vaccination against anthrax, blackleg and pasturollosis once in every 6 to 8 months and once per year for CBPP. Whereas, control measures focused on internal and external parasites. De-worming was conducted twice a year, at the start and end of the rainy seasons.

Study Design, Source and Nature of the Data: A retrospective type of study was carried out to evaluate the growth performances of Fogera X Holstein Friesian crossbred cattle in the ranch. At the ranch, records of individual animals were kept on individual animal cards. Therefore, a 23 year old farm records (i.e. All records of animals born and cows that calved between 1990 and 2012 were included). The main problem encountered was the challenge of the pedigree record screening procedure. Therefore, consistency checks were performed on identification of animals and their pedigrees.

Data Analyzed: After clearing the data for consistency of pedigree information a final data set comprising of 3404, 1806 and 1747 records of BWT, WWT and PADG respectively were used for analysis.

Statistical Analysis: The statistical analysis had two parts. In the preliminary analysis General Linear Model (GLM) procedures of the Statistical Analysis System [9] were employed to determine the fixed effects. The presence of any significant differences was checked by using TUKEY Kramer multiple comparison tests. Fixed effects which were significant ($p<0.05$) were fitted into the model to estimate the genetic parameters.

Model Used in the Preliminary Analysis:

$$Y_{ijkmn} = \mu + Y_{i} + S_{j} + Se_{k} + G_{m} + e_{ijkmn}$$

where, Y_{ijklmn} = n^{th} record of k^{th} sex in the i^{th} year, j^{th} season and m^{th} genetic group
μ = overall mean
Y_{i} = effect of i^{th} year of birth (i= 1990-2012)
S_{j} = effect of j^{th} season of birth (j= 1, 2, 3)
Se_{k} = effect of k^{th} sex (l= 1, 2)
G_{m} = effect of m^{th} genetic group (m= 1, 2, 3)
e_{ijkmn} = random error associated with each observation

The genetic parameters estimated were heritability and correlation. They were estimated using variance component estimation (VCE) procedure which is a software program package to estimate dispersion parameters under a general linear model for quantitative genetic analysis of continuous traits, fitting a linear mixed model for estimation of covariance components [10]. The resulting genetic parameters were obtained by restricted maximum likelihood. It was assumed that traits analyzed were continuous and had a multivariate normal distribution.

The genetic parameters i.e. Heritability and correlations (genetic and phenotypic) were estimated using a Uni-variate, bi-variate and multivariate animal model using four different models which fitted direct additive, dam's additive genetic and permanent environmental effect as a random effect and the fixed effects. The Likelihood ratio tests were conducted to determine the most suitable model.

The model equations used for the analysis were:

Model$_1$ $Y= Xb + Z_1a + e$; Model$_2$ $Y= Xb + Z_1a + Z_3c + e$; Model$_3$ $Y= Xb + Z_1a + Z_2m + e$ ($cov_{a,m} = 0$); Model$_4$ $Y= Xb + Z_1a + Z_2m + Z_3c + e$ ($cov_{a,m} = 0$)

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 and Z_1, Z_2 and Z_3= incidence matrix for direct additive genetic effect, maternal additive genetic effect and permanent environmental effects respectively; e = vector of random errors.

RESULTS AND DISCUSSIONS

Heritability of Growth Traits: Birth weight (BWT): Heritability is critically important for selection of polygenic traits. Growth trait is a function of the individual's inherent ability for growth, milk production and mothering ability of its dam [8]. The result of heritability estimation for growth traits is summarized in Table 1. Heritability of birth weight in this study (0.128) was less than the so called accepted range estimate for birth weight of 0.4 - 0.45 by Woldehawariate *et al.* [11]. Although the estimate was very low, it still showed the existence of variability. The Estimated direct heritability was less than the report of Deb [12] for Local, Friesian x Local and Jersey x Local: 0.37, 0.50 and 0.49, respectively. Heritability of birth weight trait of different breeds has been estimated by Aynalem *et al.* [13], Habtamu et *al.* [14] and Assan [15].

Table 1: Estimated heritability values with their standard errors (SE) for growth traits

	Traits		
Parameters	BWT	WWT	PADG
h^2_a	0.128±0.04	0.242 ± 0.07	0.158± 0.07
h^2_m	0.166±0.02	0.015± 0.02	0.0103± 0.03
e^2	0.715±0.03	0.743± 0.07	0.832± 0.07

BWT = birth weight, WWT= weaning weight, PADG = pre-weaning average daily gain

The 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. 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 [14, 16]. Unlike the direct heritability, the estimated maternal heritability 0.166 for BWT was higher than the result 0.04 ± 0.02 obtained by Diop and Van Vleck [17], 0.08 and 0.07 Plasse *et al* [18, 19] respectively and 0.07 Sendros *et al* [20].

Weaning Weight (WWT): The result of direct heritability (**0.242)** for WWT was higher than 0.19±0.05 [21] and 0.12 [5]. However, it was less than report of Aynalem *et al.* [13] 0.43 ± 0.04 and 0.34±0.05 for boran and their crosses and 0.53 ± 0.097 for Horro cattle and their crosses [14]. In addition, the result was lower than the expected range for growth traits. The low direct heritability for weaning weight could be due to the stressful environment after birth. It indicates the trait had low response to selection and improvement of weaning weight could be effective through improvement of production environments and by repeated cross breeding.

Pre Weaning Average Daily Gain (PADG): The current finding for direct heritability of PADG (0.158) was less than 0.29± 0.04 [6] for Boran crosses and greater than 0.07±0.04 for pure Boran breeds [6] 0.062±0.03 [22] for Fogera breed [23]. Also found lower estimates of direct heritabilities for pre-weaning average daily gain (6-9%).

The low values of heritability obtained could be due to deterioration in management resulting to poor nutritional status of the animals [24, 25] presence of high environmental variation or high environmental stress [5, 26] or due to management variation through time and data record quality.

Table 2: Phenotypic (Above diagonal) and genetic correlation (Below diagonal) for growth traits

Parameters	BWT	WWT	PADG
BWT	*	0.0972	-0.021
WWT	0.314	*	0.917
ADG	0.732	0.918	*

Correlations Between Growth Traits: Since livestock are usually bred for multiple rather than single traits to bring about production efficiency in their lifetime, there is always bound to be a relationship between traits. This relationship can be shown through the correlation of trait values positively or negatively on the individual of a population [27].

The phenotypic correlation between two characters can be influenced by inheritance, environmental or both [7]. As indicated in Table 2, the phenotypic correlation between the birth weight (BWT) with weaning weight (WWT) and pre weaning average daily gain (PADG) were low. The reason could be the BWT of calf depend on the intra uterine environment of the dam, health status of the dam and nutrition of the dam before birth. However, PADG and WWT were having high phenotypic correlation. Similarly, high phenotypic correlations were reported by Lobo *et al.* [28] 0.96, Cucco *et al.* [29] 0.91 ± 0.027, Habtamu [21] 0.91±0.04 and Almaz [22] 0.99 ± 0.01. But it was opposite to the reports of Wasike [5] and Aynalem [6] who found a low phenotypic correlation for growth traits. On the other hand, strong and moderately high genetic correlation was observed between WWT and ADG and between BWT and PADG respectively. Similarly [18, 30] reported high genetic correlation between growth traits.

CONCLUSIONS

The low direct heritability estimate for the growth traits indicated that there was low additive genetic variance in the study population. In other words the estimates showed low genetic control of the expression of the traits. So the variation in these traits was greatly influenced by environmental effects. This was indicative of the fact that selections based on phenotypic performance of animals were not effective in the studied herd or the population had low response to selection. Therefore, one may decide on for a long-term strategy of achieving change in these traits firstly through improvement of the production environment and then by gene transfer through crossbreeding.

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