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# Genetic parameter estimates of pre-weaning weight of Horro (Zebu) and their crosses with Holstein Friesian and Jersey cattle breeds in Ethiopia

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Abstract

The present study was carried out to estimate genetic parameters of pre-weaning weight (birth, weaning and pre-weaning weight gains) of Horro cattle and their crosses (Horro-Friesian (HF) and Horro -Jersey (HJ)) at Bako Agricultural Research Center. The data used in the study included pedigree and weight records of animals born between 1980 and 2008. Genetic parameters were estimated by ASREML. Direct heritability estimates from univariate analyses of the best model for each trait were:  $0.68 \pm 0.09$  for BW,  $0.53 \pm 0.097$  for WW and  $0.29 \pm 0.08$  for DG, respectively. Direct maternal heritability estimates were BW ( $0.12 \pm 0.10$ ), WW ( $0.21 \pm 0.08$ ) and DG ( $0.21 \pm 0.07$ ), respectively. The ratio of permanent maternal environment was 0.17 to 0.18 for BW, 0.018 to 0.03 for WW, 0.016 to 0.023 for DG, respectively. Direct-maternal genetic correlations were: -0.76, -0.71 and -0.89, for BW, WW and DG, respectively. High direct heritability estimates observed for birth weight indicated that in Horro and their crosses faster genetic improvement through selection is possible for this trait. However, the results suggested that both the direct and maternal effect should be taken into account simultaneously during selection because of the high negative direct and maternal genetic correlation. From this study, it was suggested that estimation of genetic parameters for pre-weaning growth traits should be carried out separately for Horro and their crosses.

**Key words:** Genetic parameters, pre-weaning weight, Horro, Holstein Friesian, Jersey crosses.

## INTRODUCTION

Genetic parameter estimates are needed for implementation of breeding programs and assessment of progress of ongoing programs where accuracy in their estimation is of paramount importance (Wasike et al., 2006). Estimation of genetic parameters for growth traits is always considered problematic mainly due to confounding of direct and maternal effects (Baker, 1980). The genetic and phenotypic parameters in the field of quantitative genetics include heritability, genetic and phenotypic correlation and repeatability, which play vital role in formation of any suitable breeding plan for genetic

improvement program (Aynalem, 2006). Additionally, crossbreeding parameters, which arise from non-additive genetic components, are useful in this regard. The genetic parameters could vary for different models of analysis, numbers of relationships accounted for, size of the data set and the nature of cleaning of the data (Mohamed, 2004). In estimating genetic parameters appropriate identification of sources of variation and their magnitude is required. Separately from the direct genetic effect of an animal the confounding of the maternal effect of the dam and her genetic contribution to the phenotypic value of her offspring and the possibility of a negative genetic correlation between the direct and maternal effect are the two most important aspects in estimation of genetic parameters. Therefore, in order to decide upon a

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feasible selection strategy, estimation of the genetic parameters and the correlations between direct and maternal additive genetic effects are necessary (Gemedu et al., 2003). Pandya et al. (1985) reported that the estimated heritability of birth weight for Jersey calf in India was  $0.36 \pm 0.02$ . The usually accepted range of heritability for birth weight in cattle is 0.4 to 0.45 (Woldehawariate et al., 1977). Heritability estimates for birth weight of Holstein Friesian calves in Ethiopia using animal model and sire model were  $0.22 \pm 0.064$  and  $0.27 \pm 0.111$ , respectively (Mohamed, 2004). The lower estimate of heritability was evident that selection for birth weight could not improve body size of the calves significantly; rather improvement in feeding and management can play a major role (Demeke et al., 2003a). Demeke et al. (2003a) found lower estimates of direct heritability for weaning weight (7 to 11%), pre-weaning average daily gain (6 to 9%) for a mixed population of purebred (*Bos indicus*) and crossbred cattle in Ethiopia. Direct heritabilities of weaning weight fitting univariate models were 0.54 for Hereford breed in a multibreed composite beef cattle population (Skrypzeck et al., 2000) and 0.61 to 0.64 in Kenyan Boran cattle (Wasike et al., 2006). The high estimates are attributable to the high variances, which imply a high genetic variability in the population considered thus presenting a wide scope of genetic selection for improvement.

Global, there is a paucity of reported genetic parameter estimates for purebred indigenous tropical cattle and their crosses (Lobo et al., 2000). Genetic parameters are unique to the population in which they were estimated and they may change over time due to selection and management decisions (Koots et al., 1994a; Lobo et al., 2000). However, in practical breeding programs, estimates are used to improve not only purebreds but also animals of diverse genetic composition (Demeke et al., 2003a). According to Jiregna (2007) estimation of genetic parameters for Horro cattle breed in Western Oromia was recommended and they provide the basis of future objectives for sustainable use of cattle genetic resources. In general, information on the genetic parameters of growth traits of Horro and crossbred are scanty in Ethiopia. Knowing of this fact this study was initiated on Horro cattle and its crosses (Horro-Friesian and Horro- Jersey cattle) with the objectives to estimate genetic parameters for pre-weaning weight of Horro, Horro-Friesian and Horro- Jersey cattle

## MATERIALS AND METHODS

### Description of the study area

#### Location

The data used in this study was generated from Horro cattle and

their crosses kept at Bako Agricultural Research Centre. The center is located at about 250 km West of Addis Ababa at an altitude of 1650 m above sea level. The center is at 37°09'E. The area has a hot and semi-arid climate with a mean annual rainfall of about 1220 mm, of which more than 80%

falls in the months of May to September. Mean monthly minimum and maximum temperatures are about 14°C and 28°C, respectively, with an average monthly temperature of 21°C. The daily mean minimum and maximum temperatures are 9.4 and 31.3°C respectively.

### Breeding system

At Bako Agricultural Research Center, heifers bred at least two years of age when they attained a body weight of 200 kg. Heat detection was done visually every day from 06:00 to 08:00 h in the morning and from 17:00 to 18:00 h in the afternoon by trained inseminator, teaser bulls and the herdsmen. Cows and heifers observed in heat were bred either naturally (local or crossbred bull) or inseminated with frozen semen (Holstein Friesian and Jersey) purchased from Kality National Artificial Insemination center within 24 h after heat.

### Management of calves at Bako agricultural research center

Calves were separated from their dams at birth, weighed and fed colostrums from a bucket for the first five days of life. A total of 227 liter of milk was fed to each calf and a concentrate mix (49.5% ground maize, 49.5% Noug seed cake and 1% Salt) were offered until weaning (three months), then after both calves (male and female) were kept indoors (day and night) until six months of age in individual pens except for about two hours of exercise in a nearby paddock every day. After six months of age, weaned calves were maintained on natural pastures for approximately eight hours a day and supplemented with silage or hay *ad libitum* during the night and were kept as a group (male and female separately), where concentrate were supplemented to heifer calves only on availability. Vegetation cover of the area is woodland and open wood grassland types. The dominant grass species include hyperheniya (*Hyperhenia anamesa*) and sporobolus (*Sporobolus praminidals*) grass and the legumes include Neonotonia (*Neonotonia wights*).

### Data collection and preparation

The data used for this study include pedigree and weight records of animals born between 1980 and 2008. Data were extracted from various growth records (birth and weaning) of Horro and its crossbred animals at Bako Agricultural Research center. A total of 2359 calves' records were used sires in were used during the whole experimental year along with 710 dams' age of the calves at weights.

### Estimation of genetic parameters

Co-variance components were estimated using different models which, differed in their inclusion or exclusion of maternal genetic effects, permanent maternal effects and the correlation between direct and maternal genetic effects as adopted by Meyer (1989; 1992). Three variables were analyzed for genetic parameters using a univariate REML procedure: birth weight (BW), weaning weight (WW) and pre-weaning average daily gain (DG). Comparison of the

**Table 1.** (Co) variance components and genetic parameters for birth weight of Horro and their crosses.

Items	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
$\sigma_a^2$	8.8±11.2	7.42±8	7.0±7.8	10.45±6.9	7.4±8	9.98±6.9
$\sigma_m^2$			2.54±5.6	5.7±5.5	0.00	2.71±2.7
$\sigma_c^2$		2.49±6			2.49±6	1.74±6.9
$\sigma_e^2$	5.4±10.3	4.74±8.4	5.14±9.3	3.2±3.9	4.74±8.4	3.37±4.2
$\sigma_p^2$	14.26±0.48	14.7±0.52	14.74±0.53	14.79±0.92	14.66±0.52	14.65±0.7
$\sigma_{am}$				-4.6±3.9		-3.14±-2.7
$r_{am}$				-0.59±0.11		-0.76±0.2
$h_a^2$	0.62±0.042	0.51±0.54	0.48±0.054	0.71±0.09	0.51±0.054	0.68±0.09
$h_m^2$			0.17±0.029	0.39±0.08	0.00±0.00	0.12±0.1
$h_c^2$		0.17±0.027			0.17±0.03	0.18±0.07
$h_t^2$	0.62±0.042	0.51±0.54	0.56±0.054	0.84±0.09	0.51±0.054	0.75±0.09
-2 Log L	-4163.19	-4130.59	-4139.49	-4128.91	-4130.6	-4124.93

$\sigma_a^2$ =direct additive genetic variance;  $\sigma_p^2$ =Phenotypic variance;  $\sigma_{am}$ =Covariance between direct additive and maternal genetic effect;  $r_{am}$ =genetic correlation between direct additive and maternal additive effects;  $h_a^2$ =direct additive heritability;  $h_m^2$ =maternal additive heritability;  $h_c^2$ =heritability of permanent environment;  $h_t^2$ =total heritability; -2LogL =-log likelihood and  $\sigma_e^2$  = error variance.

different univariate models was made using the log-likelihood ratio tests to determine the best model to fit the growth data. The difference in log likelihood ratio between pairs of model were doubled and tested against chi-square value with degree of freedom being the difference in number of variance or (co)variance component in the model. This was based on what Swalve (1993) suggested, where a likelihood ratio test can be applied by multiplying the difference by -2 and then compare it to a chi-square test statistics with the number of parameters taken as the degrees

of freedom. Direct ( $h_a^2$ ) and maternal ( $h_m^2$ ) heritability, ratio of permanent environmental variance, and the direct and maternal additive covariance were calculated as (where  $\sigma_p^2$  is total phenotypic variance)  $\sigma_a^2 / \sigma_p^2$ ,  $\sigma_m^2 / \sigma_p^2$ ,  $\sigma_c^2 / \sigma_p^2$ , and  $\sigma_{am} / \sigma_p^2$ , respectively. Total heritability were calculated as  $(\sigma_a^2 + 0.5 \sigma_m^2 + \sigma_{am} / \sigma_p^2)$ , while direct and maternal additive correlation was expressed as a ratio of the covariance to the square root of the product of direct and maternal variance ( $r_{am} = \sigma_{am} / (\sigma_a \sigma_m)^{1/2}$ ). The models are numbered, according to Meyer (1994a) as follows:

- Model 1:  $Y = X\beta + Z_1a + e$
- 2:  $Y = X\beta + Z_1a + Z_3c + e$ ,  $Cov(a, m) = 0$
- 3:  $Y = X\beta + Z_1a + Z_2m + e$ ,  $Cov(a, m) = 0$
- 4:  $Y = X\beta + Z_1a + Z_2m + e$ ,  $Cov(a, m) \neq 0$
- 5:  $Y = X\beta + Z_1a + Z_2m + Z_3c + e$ ,  $Cov(a, m) = 0$ .
- 6:  $Y = X\beta + Z_1a + Z_2m + Z_3c + e$ ,  $Cov(a, m) \neq 0$

Where: Y is the vector of observations;  
 $\beta$  is the vector of fixed effects;  
 X is the incidence matrix that associates  $\beta$  with Y;  
 a is the vector of breeding values for direct genetic effects;  
 m is the vector of breeding values for maternal genetic effects; c  
 is the vector of permanent environmental effects due to dam;  
 $Z_1$ ,  $Z_2$  and  $Z_3$  are the incidence matrices that associate a, m and c  
 with Y; and e is the vector of residual effects.

Furthermore, with A, the numerator relationship matrix between animals, I<sub>n</sub>, an identity matrix with order n, the number of dams, and I, an identity matrix with order of the number of records the (co)variance structure of random effects can be described as:  $V(a) = \sigma_a^2 A$ ,  $V(m) = \sigma_m^2 A$ ,  $V(c) = \sigma_c^2 I_n$ ,  $V(e) = \sigma_e^2 I$ , where  $\sigma_a^2$  is the direct

genetic variance;  $\sigma_m^2$  is the maternal genetic variance;  $\sigma_c^2$  is the maternal permanent environment variance;  $\sigma_e^2$  is the residual variance and  $\sigma_{am}$  is the genetic covariance between direct and maternal effects. All calculations were done using the options available in ASREML (Gilmour et al., 1999) for parameter and sampling error estimation.

## RESULTS AND DISCUSSION

The estimated (co)variance components and genetic parameters using univariate analysis for birth, weaning and pre-weaning average daily gains are presented in Table 1 to 3. The direct additive variances were larger than maternal genetic variance for all traits. Larger values of direct variances were found for pre-weaning average daily gains. Generally, the maternal genetic variance is smaller than the direct genetic variance resulting in higher estimates of direct heritability than maternal heritability. Direct heritability did decrease when maternal effects or permanent maternal effects were fitted but including direct-maternal covariance in the model substantially increase the direct heritability estimates but did not improve the log likelihood in the model. The bold column in Tables 1 to 3 indicate the best model.

### Birth weight

Table 1 presents estimates of (co)variance components and genetic parameters for birth weight. Estimates of additive genetic variance were highest in model 4 and lowest in model 3. Model 4 had the lowest estimates of residual error variance. Estimates of maternal genetic

**Table 2.** (Co) variance components and genetic parameters for weaning weight of Horro cattle and their crosses.

Items	Model 1	Model 2	Model 3	Model 4	Model 5	Model6
$\sigma_a^2$	31.6±6.79	29.2±5.7	29.4±5.4	42.2±4.1	29.2±5.7	42.1±4.9
$\sigma_m^2$	-		1.81±0.08	17.1±2.8	0.00002±12.8	15.4±1.8
$\sigma_c^2$	-	2.39±1.14			2.4±1.1	1.4±0.3
$\sigma_e^2$	47.9±12.7	47.88±12.8	48.28±12.8	40.2±7.7	47.8±12.8	40.2±7.7
$\sigma_p^2$	79.6±2.9	79.5±2.9	79.5±2.9	80.4±3.3	79.41±2.85	80.38±3.3
$\sigma_{am}^2$				-19.2±-2.7		-18.7±-2.6
$\sigma_{fam}^2$				-0.71±0.011		-0.73±0.14
$h_a^2$	0.40±0.052	0.37±0.058	0.37±0.063	0.53±0.097	0.37±0.059	0.52±0.1
$h_m^2$			0.023±0.028	0.213±0.075	0.00±0.00	0.19±0.01
$h_c^2$		0.0301±0.027			0.0301±0.027	0.018±0.06
$h_t^2$	0.397±0.052	0.37±0.058	0.38±0.063	0.62±0.097	0.37±0.059	0.53±0.1
-2Log L	-4962.77	-4962.08	-4962.43	-4958.16	-4962.08	-4958.11

variance were highest in model 4 and lowest in model 5 and almost equal for model 3 and 6 because of partitioning of maternal effects into genetic and permanent environmental effects. Phenotypic variance was comparable for each of the model. Direct heritability of birth weight was  $0.62 \pm 0.042$ ,  $0.51 \pm 0.54$ ,  $0.48 \pm 0.054$ ,  $0.71 \pm 0.09$ ,  $0.51 \pm 0.054$  and  $0.68 \pm 0.09$ , for models 1, 2, 3, 4, 5 and 6, respectively. Model 6 (complete model), which included covariance between direct and maternal effects is significantly the best model in comparison to the rest of the models when judged by the -2 log likelihood (-2Log L).

Inclusion of the covariance between direct and maternal effects, increased the estimate of direct heritability for birth weight from 0.48 (model 3) to 0.71 (model 4) and 0.68 (model 6). This is in agreement with the findings of Schoeman and Jordaan (1999) who reported that including covariance between direct and maternal effects increase direct heritability of birth weight due to small number of observation. Direct heritability estimates in all models were higher than the usually accepted range of heritability of 0.4 to 0.45 for birth weight in cattle (Woldehawariate et al., 1977). Using animal model and sire model, Mohamed (2004) reported heritability estimates for birth weight for Holstein Friesian calf in Ethiopia at  $0.22 \pm 0.064$  and  $0.27 \pm 0.11$ , while Demeke et al. (2003a) reported direct heritability estimates of  $0.14 \pm 0.03$  for birth weight of purebred and crossbred cattle in Ethiopia. Values lower than those found in the current study were reported for *Bos taurus* and *Bos taurus* × *Bos indicus* crosses by Meyer (1992). The higher heritability obtained in this study is in agreement with the findings of Schoeman and Jordaan (1999) and Skrypzeck et al. (2000) who found a higher direct heritability estimates of 0.62 and 0.72 for birth weight, respectively. Both authors mentioned that fairly high heritability, arising from large genetic variances due

to the multibreed composition of the herd could have been expected, since the population consists of 15 breeds and this effect was not accounted for by the model. Similarly, in the current study large numbers of genetic groups were categorized into only three groups to have reasonable number of observations in each category. This would create a high level of genetic variability within a group and inflating the estimate of heritability. Rodriguez-Almeida et al. (1995) reported quite variable estimates in different herd-line combinations and suggested that the variable estimates might be due to the inclusion of non-additive genetic variances. That is not due to fitting dominance and epistatic effects in the model. Being a crossbred population, dominance and epistatic effect could be a possible contributor to the higher and possibly biased estimates. Bennett and Gregory (1996) and Tosh et al. (1999) also reported heritability estimates for early growth traits in composite populations, which were larger than literature means. In model one, where maternal effect is ignored higher and most likely inflated, heritability estimate was obtained. Similarly higher heritability estimates for birth weight from model one have been reported for Austrian beef cattle (Gutierrez et al., 1997), for Merino sheep (Gemedda, 2001), for Horro sheep (Solomon, 2002), for tropical cattle (Mackinnon et al., 1991) and for multi breed beef cattle (Hailu et al., 2003). The total heritability in the current study ranges between 0.62 to 0.84 for birth weight. Hailu et al. (2003) reported lower total heritability estimates which varied from 0.15 to 0.59 for beef cattle. Similarly, Mokennen (1994) and Demeke et al. (2003a) reported lower total heritability for Boran and mixed purebred cattle and crosses, respectively, while Mohiuddin (1993) reported total heritability estimates of -0.02 to 0.68 which partially agree with estimates in this study. Total heritability estimates are useful in estimating response to selection based on

**Table 3.** (Co) variance components and genetic parameters for pre-weaning average daily gain of Horro cattle and their crosses.

Items	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
$\sigma_a^2$	2131.0±4.1	1896.5±3.4	1891.3±3.3	2924±3.5	1899.7±3.4	2929.3±3.5
$\sigma_m^2$			219.4±0.81	218.9±2.9	0.0000001±16	2002.4±1.9
$\sigma_c^2$		246.28±0.93			246.3±0.93	168.4±0.3
$\sigma_e^2$	8427.4±16.6	8403.2±16.97	8438.0±17	7750.4±13	8406.3±0.93	7730.6±12.9
$\sigma_p^2$	10558±360	10546 ±359.7	10549±359	10590±374	10550±358.7	10589±373
$\sigma_{am}$				-2267±-2.8		-2241±-2.7
$r_{am}$				-0.89±0.12		-0.93±0.16
$h_a^2$	0.202±0.05	0.18±0.05	0.18±0.053	0.28±0.08	0.18±0.08	0.29±0.8
$h_m^2$			0.0208±0.026	0.206±0.07	0.00±0.00	0.19±0.09
$h_c^2$		0.0234±0.03			0.023±0.025	0.016±0.6
$h_t^2$	0.202±0.05	0.18±0.05	0.19±0.053	0.29±0.08	0.28±0.08	0.37±0.8
-2Log	-9493.19	-9492.73	-9492.85	-9488.27	-9492.73	-9488.24

phenotypic value and the estimates can be affected by data size, model used and breeds (Solomon, 2002).

Maternal heritability estimates of birth weight were  $0.17 \pm 0.02$ ,  $0.39 \pm 0.08$ ,  $0.00 \pm 0.00$  and  $0.12 \pm 0.1$  for model 3, 4, 5 and 6, respectively. The maternal heritability estimates for birth weight from the best model (model 6) were  $0.12 \pm 0.1$ . Similarly, Demeke *et al.* (2003a) reported very small, though significantly different from zero direct maternal heritability estimates for birth weight. Pico (2004) and Plasse *et al.* (2002a; 2002b) reported that maternal heritability for birth weight of Brahman cattle were 0.11, 0.08 and 0.07, values which are lower than the current findings. Similar figures were also obtained by Eler *et al.* (1995) and Diop and Van Vleck (1998) who reported very low estimates (0.04) for maternal heritability, which is by far lower than the current estimates. Aynalem (2006) reported maternal heritability estimates of  $0.25 \pm 0.05$  and  $0.18 \pm 0.05$  for Boran and their crosses, which are comparable to the current estimates. The low or absence of maternal effects on growth traits shows that improvement in these traits would be more efficiently achieved if selection is based on the animal's direct genetic than a true potential negative genetic relationship. Maternal contradictions effect at birth are generally as a result of the prenatal maternal environment and cytoplasmic effect (Wasike, 2006). However, lack of maternal influence on birth weight of Boran breed was reported by Wasike *et al.* (2006).

Permanent maternal environmental effects ranged from 0.17 to 0.18 for birth weight. Permanent maternal environmental effects of birth weight from the best model were higher than direct maternal heritability effects. Gameda *et al.* (2003) reported that a permanent environmental effect of the dam in birth weight was attributed to uterine environment provided by the dam. The same authors also indicated that permanent environmental effect is due to uterine capacity, feeding level during late gestation and the maternal behavior of

the dam. Maternal behavior is likely to be associated with the rearing ability of a dam.

The correlation between direct and maternal genetic effects for birth weight was high and negative ( $-0.59 \pm 0.11$  for model 4 and  $-0.76 \pm 0.23$  for model six). However, lower (in absolute value) direct-maternal correlation estimates ( $-0.35$  to  $-0.37$ ) than obtained in the current study were reported for Brahman cattle (Plasse *et al.*, 2002a; Pico, 2004), while comparable estimates were reported for Boran cattle ( $-0.55$ , Haile-Mariam and Kassa-Mersha, 1995) and Nellore cattle ( $-0.72$ , Eler *et al.*, 1995). The negative correlation between direct and maternal genetic effects could be an indication of genetic antagonism between genes and it may, therefore, be important to consider the genetic correlation in selection programs. Both Meyer (1992) and Swalve (1993) suggested that environmental covariances between dam and offspring that is not accounted for may bias the direct and maternal genetic correlation downwards. In beef cattle, Robinson (1996b) indicated that the negative correlation between direct and maternal genetic variances could result from other effects in the data rather than the present result. Demeke *et al.* (2003a) reported that large positive (0.48) correlation between direct and maternal genetic effects this might be biased due to breed additive and no additive effects in the dam not account for.

### Weaning weight

The direct additive genetic variance estimates were found to be larger than estimates for maternal additive variance, which was also observed by Lee *et al.* (2000) in Native Korean cattle and Meyer *et al.* (1993) in Australian multibreed beef cattle. Environmental stress highly affects

the magnitude of additive genetic variance for different traits (Demeke et al., 2003a). Direct heritability of weaning weight was lower than birth weight (Table 2). Banjaw and Haile-Mariam, (1994), Demeke et al. (2003a) and Aynalem (2006) have reported lower direct heritability estimates for weaning weight of cattle in Ethiopia. Direct heritability of weaning weight was  $0.40 \pm 0.052$ ,  $0.37 \pm 0.058$ ,  $0.37 \pm 0.063$ ,  $0.53 \pm 0.097$ ,  $0.37 \pm 0.059$  and  $0.52 \pm 0.1$ , for model 1, 2, 3, 4, 5 and 6, respectively (Table 2).

Demeke et al. (2003a) found lower estimates of direct heritability for weaning weight (7 to 11%) and pre-weaning average daily gain (6 to 9%) than the present results for a mixed population of purebred (*Bos indicus*) and crossbred cattle in Ethiopia. Hailu et al. (2003) worked with multi-breed beef cattle herd in South African and reported lower direct heritability values for weaning weight and pre-weaning average daily gain than this study. In contrast with the current findings direct heritability increased from birth to weaning for Braunvieh cattle in Brazil (Cucco et al., 2009). Heritability estimate for weaning weight computed from the best model was in agreement with a value 0.54 reported by Skrypzeck et al. (2000) for Hereford breed in a multibreed composite beef cattle population and 0.61 to 0.64 for Kenyan Boran cattle (Wasike et al., 2006). The direct heritability for weaning weight (0.52) is considerably higher than the mean estimates of 0.14 obtained by Pico (2004) for Brahman cattle breeds in South Africa, as well as those reported by Plasse et al. (2002a; 2002b) for Brahman cattle, Diop and Van Vleck (1998) for Gobra (*Bos indicus*) cattle. The high estimates are attributable to the high variability of population stated earlier. The low heritability results of model one in the present study is in disagreement with Mackinnon et al. (1991) who reported heritability estimates of 0.56 for weaning and 0.50 for pre-weaning average daily gain in tropical cattle when fitting a model accounting for direct genetic effects only. Total heritability estimates for the traits lie within the range of literature estimates of Mohiuddin (1993), which vary from 0.02 to 0.81 for weaning weight.

Maternal heritability for weaning weight in the present study was:  $0.023 \pm 0.028$ ,  $0.213 \pm 0.075$ ,  $0.00 \pm 0.00$  and  $0.19 \pm 0.01$ , for model 3, 4, 5 and 6, respectively. Maternal heritability was higher than permanent environmental effect for weaning weight. Evidence for maternal effects in cattle can be seen in crossbreeding experiments due to the differences in performance among the reciprocal crosses, however, these do not help in quantifying the relative variation due to maternal effects (Wasike, 2006). Maternal genetic effects have been demonstrated to be significant for growth up to weaning after which it declines; however the upper age limit at which this effect dies out varies among the reported results (Meyer, 1992). Therefore, fitting of

models that account for maternal additive genetic effects for traits up to weaning is important (Vaez et al., 1996). The results of this study are consistent with studies done on suckling beef cattle that reported effects of maternal influence on weaning weight (Meyer, 1992; Gutierrez et al. 1997; Ferreira et al. 1999). This could be due to the fact that the calves in the present study were artificially fed and maternal environment removed at birth and any presence of maternal effects could only be explained the carryover effects from the residual prenatal care of the dam or to the compound effects of the residual prenatal care plus additive and non-additive effects in the dam, which could not be accounted for in this analysis. These results also were confirmed by Demeke et al. (2003a).

Permanent environmental effects for weaning weight in the current study was  $0.0301 \pm 0.027$ ,  $0.0301 \pm 0.027$  and  $0.018 \pm 0.06$  for model 2, 5 and 6, respectively. The proportion of permanent maternal environmental effect was less than the results obtained by Meyer (1992) for Hereford cattle (0.23) and Haile-Mariam and Kassa-Mersha (1995). Similarly, Pico (2004) reported a permanent maternal environmental effect of 0.07 for South African Brahman and concluded that permanent maternal environmental effects are not as important as the maternal genetic effects. This is in agreement with the results of Haile-Mariam and Kassa-Mersha (1995) in Boran cattle, Robinson (1996a) for Angus in Australia and Plasse et al. (2002a and b) for Brahman cattle who found that the contribution of permanent maternal environmental effects and maternal genetic effects are equally important. But in contrast to the present study, Hailu et al. (2003) suggested that only permanent environmental effect plays an important role in the pre-weaning growth traits of beef cattle population.

The genetic correlations between direct and maternal genetic effects of weaning weight were negative and high in the present study ( $-0.71 \pm 0.11$  and  $-0.73 \pm 0.14$  under model 4 and 6 respectively). Higher weaning weight values of  $-0.34 \pm 0.133$  has been reported for Romosinuano cattle in the Colombian humid tropics (Sarmiento and Garcia, 2007), while it is comparable with a value of -0.78 reported by Meyer (1992) for Zebu crosses. Antagonism between direct and maternal effects has been reported for weaning for zebu beef cattle (Gutierrez et al., 1997). This antagonistic relationship should be compensated by improving managerial practices and using supplemental feeding when necessary.

Direct heritability of pre-weaning average daily gain was  $0.202 \pm 0.05$ ,  $0.18 \pm 0.05$ ,  $0.18 \pm 0.053$ ,  $0.28 \pm 0.08$ ,  $0.18 \pm 0.08$  and  $0.29 \pm 0.8$  for model 1, 2, 3, 4, 5 and 6, respectively. Direct heritability estimate from the best model (model 4) was 0.28 and which higher than the result reported by Migose et al. (2007). Direct additive heritability of pre-weaning average daily gain was lower

than direct additive heritability of birth and weaning weight. Similar results to the present study were reported by (Aynalem, 2006) for pre-weaning average daily gains of Boran cattle (0.29) and the crosses (0.28) in Ethiopia. The results were also in agreement with the reports of Demeke et al. (2003a) who reported that the presence of maternal effects on pre-weaning gains in bucket fed mixed purebred and crossbred cattle. Permanent maternal effects in the current study were 0.016 to 0.023 and these are in agreement with the findings of Aynalem (2006) and Migose et al. (2007).

## CONCLUSION AND RECOMMENDATION

Estimates of direct and maternal heritability in this study tended to be larger under the different model used. This appears to be due categorization of large number of genetic groups into only three groups to have reasonable number of observations in each category. The result also suggests that model choice is an important aspect for obtaining reliable parameter estimates to be used in genetic improvement. It seems that ignoring maternal effects, both maternal genetic and environmental, leads to overestimations of the heritability estimates, particularly for birth weight. This study has shown that birth weight is highly heritable and under the influence of maternal effects. Relatively, low values of direct heritability for weaning weight and pre-weaning average daily gains obtained in this study means there is sizeable maternal variance both on the genetic and environmental side. It is therefore, suggested that the maternal genetic and the management aspects during the pre-weaning period needs attention. Maternal effects were important in influencing weight upto weaning age. Artificial calf rearing system was used and it is difficult to explain why the maternal effect persisted to weaning age. Carryover effect of variation in the size of the Horro dams and the uterine environment they provide along with possible cytoplasmic effect may play a role in influencing the persistence of the maternal effect. This study has also shown higher estimates genetic parameters when models accounting for direct-maternal genetic covariance were used. Selection programmes for genetic improvement of growth performance should therefore be based on genetic models where direct-maternal genetic correlation has been well taken care of, if high and sustainable genetic progress is expected. However reliable estimation of direct and maternal genetic parameters accounting for direct maternal genetic covariance requires data with a sufficient amount of reliable records and good pedigree information. This was a major limitation in this study, since Artificial Insemination was used in most of the cases and pedigree information for AI sires is not accessible.

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