

**Original article**

## Genetic parameter estimation and model selection for hot carcass weight in matebele goat

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Genetic parameter estimation for simple carcass traits has been confined to the improved goat breeds worldwide unlike in the unimproved breeds in developing countries where goats are numerous. Variance components for additive direct, additive maternal, permanent environmental maternal effects, the covariance between additive direct and maternal effects were estimated by restricted maximum likelihood, fitting five animal models from 2341 (1359 males; 982 females) hot carcass weight pedigree records collected over a period of 13 years (1984- 1997) of indigenous Matebele goat of Zimbabwe. All investigated models included a random direct genetic effect, but different combinations of random maternal genetic and permanent environmental maternal effects as well as direct-maternal genetic covariance. The analytical models included fixed effects of sex, age at slaughter and year of slaughter. The direct heritability ( $h^2_a$ ) ranged from 0.14 to 0.26 when the maternal genetic effects were included in the model, whereas  $h^2_a$  estimate was 0.26 when maternal effects were excluded. The maternal heritability ( $h^2_m$ ) was 0.00 when only maternal genetic effects were included in the model and were 0.05 and 0.10 when the permanent environmental effect of the dam was added. The permanent environmental effect of the dam was negligible. A positive covariances between direct and maternal genetic effects ( $\sigma^2_{am}$ ) was observed when maternal genetic effects and permanent environmental maternal effects were accounted for in the model. A simple animal model with direct additive genetic effects as the only random effects other than the residuals was the best model for

genetic evaluation of hot carcass weight in indigenous Matebele goat.

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## 1. Introduction

Most goats are raised in communal areas by smallholder farmers for subsistence and trading in informal markets in Zimbabwe (Agrisystems, 2000). Finishing goats in feedlot on high concentrate diets is not a wide spread practice as goats are generally used more efficiently when utilizing browse or forage (Wildeus et al 2007) a similar trend has been observed in Zimbabwe by Van Rooyen and Homman (2008) for small scale goat production. Africa's goat population increased by 75% between 1980 and 2005 and constitutes 30% of the world population (Simela and Merkel, 2008). In the country, goat population is 4.4 million and rising (CSO, 2000) of which 90% of the national flock is owned by smallholder farmers (Homann et al 2007). Globally, the number of goats has also increased even in countries with high and medium income (Mourad et al., 2001). Little has been done to improve goat productivity and management practices that might result in better quality and quantity meat production (Kebede et al 2008).

Estimates of genetic parameters for hot carcass weight using different animal models in the tropics for indigenous goats are scarce in literature. Models with maternal effects and corresponding genetic parameters have always been considered problematic (Meyer, 1997) due to the confounding contributions of direct and maternal effects. The animal models commonly used to estimate maternal effects include maternal genetic and permanent environmental effects (Willham, 1963). Genetic models, including maternal effects and the covariance of direct and maternal genetic effects, fit data better than the simple additive model (Meyer, 1992). The aim of this study was to investigate the importance of direct and maternal effects on hot carcass weight of the indigenous Matebele goat, using different animal models

## 2. Materials and methods

### 2.1. Location

Matopos Research Station (20° 23' S, 31° 30' E) situated 30 km South West of Bulawayo in Zimbabwe on an altitude of 800m above sea level which experiences low erratic rainfall of less than 450mm per annum (Homann et al., 2007). High summer temperatures, maximum and minimum mean temperatures of hottest months are 31.6 °C and 21.4 °C, respectively with a possibility of severe droughts (Hagreveas et al., 2004). The most common type of vegetation is sweet veld with comparatively high nutritional value of browse and annual grass species (Ward et al., 1968). Detailed description of the climate and vegetation type were given by Day et al (2003) and Gambiza and Nyama (2000), respectively.

### 2.2. Flock management

The does plus their progeny were grazed on an extensively managed dry land veld during the day from 0800 hours to 1500 hours and were penned at night. The major grass species in these pastures are *Hyparrhenia* spp., *Andropogon* spp., *Pennisetum purpur* and *Brachiaria mutica*. Depending on the availability of food and the severity of dry season, varying quantities of energy (maize stover) and protein (cotton seed cake) supplements were given when does grazed on standing hay or cut and stacked hay. The does were fed 0.3 kg and kids 0.2 kg of cottonseed cake meal each per day from the end of May each year until the onset of the rainy season. The nutrient composition of cotton seed cake was 930g/kg dry matter, 730g/kg total digestible nutrient, 390-450g/kg protein, 300-360g/kg digestible protein and metabolizable Energy value 10.9 megajoules/kg. Water was constantly available. Mineral licks were often *ad libitum* in the dry season. Prophylaxis deworming and de-ticking in a plunge dip were regularly carried out using organophosphates. All animals were vaccinated against Pulpy Kidney and Rift Valley Fever. Does were assigned into mating flocks each year but mating of close relatives was avoided. Does of all age categories were represented in each single buck-mating group. The breeding season was between May and June. Single sire flocks comprised of one buck to 30 does. Females were introduced to the breeding flock for mating when they attained one and half years of age and bucks were not used for service until they were over one

and half years. Initial buck selection was based on birth weights with male singles of over 3 kg and twins over 2.5 kg weights being retained entire, while the rest of the males were castrated using rubber ring. Most kids were born between late October and early November, which is the start of the rainy season. Kids were weighed using an electronic scale and ear tagged soon after birth and left to suckle their dams during grazing until weaning at approximately 3 months of age. Kids were separated by sex at weaning into different weaner flocks.

### 2.3. Slaughter Method

Goats of an average age of 21 months raised on range were slaughtered without being fattened. The animals were humanely slaughtered at a commercial slaughtering facility. The weight of the head, feet and skins were recorded separately. The entire gastro-intestinal tract was removed from each slaughtered goat and weighed with and without contents. A hot carcass weight of each animal was prepared by removing head, feet, skin, thoracic cavity contents, abdominal cavity contents, pleural cavity contents and cannons. This was weighed within one hour of slaughter. Liver, lungs, heart, kidneys, kidney fat were removed from the body cavity and weighed separately. The dressed carcasses were chilled at  $-20^{\circ}\text{C}$  for 24 hours which led to shrinkage in carcass. Cold carcass was obtained before cutting the carcass into different prime cuts. The weight of prime cuts (front barrel and hind barrel) was also recorded. The last rib was left attached to the hind barrel. The chilled carcass was split between the 6<sup>th</sup> and 7<sup>th</sup> ribs to obtain the rib barrel. Fat score on back fat was done by visual assessment using a scale of 1 to 3.5 designed by International Livestock Centre for Africa.

### 2.4. Statistical methods

Data on hot carcass weight were obtained from Matopos Research Station, Bulawayo, Zimbabwe on indigenous Matebele goat. The data included a total of 2341(1359 males and 982 females) pedigree hot carcass weight records from 37 sires and 218 dams of the indigenous Matebele goat. Genetic parameters were estimated using the Average Information Restricted Maximum Likelihood (AIREML) methodology (Gilmour, 1995) using an Animal Model. The analytical models included fixed effects of sex, age at slaughter and year of slaughter. Fixed factors for models for all traits were determined through preliminary analyses using procedure GLM of SAS (1996) (SAS Inst. Inc., Cary, NC). Fixed factors (main effects and interactions) and covariates were tested and removed from the model if found non-significant ( $P > 0.01$ ), with non-significant effects rejected sequentially. A simplex algorithm is used to search for variance components to minimize the function,  $-2\log$  likelihood (L). Convergence was assumed when the variance of the function values ( $-2\log L$ ) of the simplex was  $< 10^{-8}$ . A log likelihood ratio test was used to choose the most suitable random effects model for post weaning growth. The reduction in  $-2 \log L$  when a random effect was added to the model was calculated. If this reduction was greater than the value of the Chi-square distribution with one degree of freedom ( $p < 0.05$ ) the additional random effect fitted was considered significant. When log likelihood did not differ significantly ( $p > 0.05$ ), the model that had the fewer number of parameters was selected as the most appropriate. Five different single trait animal models were fitted for mature weight by ignoring or including maternal genetic effect, covariance between direct-maternal effects, maternal environmental effect that the five different models were:

Model 1 was a model with animal additive genetic effects as the only random effect other than the residuals:

$$y = Xb + Z_a a + e \quad (1)$$

Model 2 allowed for genetic maternal effect to those of model 1

$$y = Xb + Z_a a + Z_m m + e \quad (2)$$

Model 3 included random effect of permanent maternal environment

$$y = Xb + Z_a a + Z_c c + e \quad (3)$$

Model 4 was the same as model 2 but assumed correlation between direct and maternal genetic random effects.

$$y = Xb + Z_a a + Z_m m + e \quad \text{Cov}(a,m) = A\sigma_a m \quad (4)$$

Model 5 included both permanent environmental and genetic maternal effects but allowed correlation between direct and maternal genetic random effects.

$$y = Xb + Z_a a + Z_m m + Z_c c + e \quad \text{Cov}(a,m) = A\sigma_a m \quad (5)$$

where Y is the vector of observations b, a, m, c and e are the vectors of fixed effects, direct additive genetic effects (animal), maternal genetic effects, permanent environmental effect of dam and the residual, respectively. X, Z<sub>a</sub>, Z<sub>m</sub>, and Z<sub>c</sub>, are the incidence matrices of fixed effects, direct additive genetic effects, maternal genetic effects and permanent environmental effect of dam. (Co) variances were described as:  $V(a) = \sigma_a^2 A$ ,  $V(m) = \sigma_m^2 A$ ,

$V(c) = \sigma_c^2 I$ ,  $V(e) = \sigma_e^2 I$  and  $\text{Cov}(a,m) = \sigma_{am} A$ , where  $\sigma_{am}$  is the covariance between direct and maternal genetic effects,  $\sigma_a^2$  the direct additive genetic variance,  $\sigma_m^2$  the maternal genetic variance,  $\sigma_c^2$  the variance of the permanent environmental effect of the dam and  $\sigma_e^2$  the variance of the residuals.  $A$  is the numerator relationship matrix between animals,  $I$  the identity matrix. In the present study the fixed part of the model included age at slaughter, sex and year of slaughter of progeny. Heritability of total additive genetic contribution to a maternally influenced trait was calculated according to the following equation (Willham, 1972).

$$h_T^2 = \frac{\sigma_a^2 + 0.5\sigma_m^2 + 1.5\sigma_{am}^2}{\sigma_p^2}$$

### 3. Results and discussion

The descriptive statistics of the data set, covariance components and log likelihood values under five different single trait models regarding hot carcass weight are shown Table 1 and 2, respectively. It is evident that the model used in the analysis influenced the relative values of direct heritability and maternal heritability. Estimates of the direct heritability had a range of 0.15 to 0.64 and estimates of the maternal heritability ranged from 0.02 to 0.07. Maternal heritability was lower than direct heritability in all models which was an indication that hot carcass weight was largely influenced by the individual genetic potential than the maternal genetic potential. In current study on hot carcass weight of Matebele goat the inclusion of both maternal genetic and permanent environmental maternal effects, with a covariance between direct and maternal effects reduced the log likelihood values. In Model 3 the permanent environmental maternal effects ( $\sigma_{pe}^2$ ) was non significant and therefore this model was could not be considered appropriate for hot carcass weight. Including maternal genetic effects in Model 2 resulted in a decrease in direct heritability by 50% compared to Model 1 with direct genetic effects alone. In fact in Model 4 in which both direct and maternal genetic effects were taken into account, 18% and 2% of the total phenotypic variance was attributable to direct and maternal effects, respectively. When one of the maternal effects was ignored the total variance was more attributed to the direct genetic variance resulting in overestimating of direct heritability. Inclusion of a covariance between direct and maternal effects in Model 4 and 5 resulted in low and high total genetic effects, respectively. The high total genetic effects in Model 5 could have been caused by the low positive correlation ( $r_{AM}$ ) of direct and maternal genetic effects. The nature of the correlations which may be positive or negative can sometimes be attributed to structure of the data (Lee and Pollack, 1997; Robinson, 1996). In the present study Model 1 with only direct additive genetic effects as the only random effect was found to be appropriate for genetic evaluation of hot carcass weight in this population as indicated by the highest log likelihood value (Table 2)

**Table 1**

Structure and descriptive statistics of the data set of hot carcass weight of Matebele goats of Zimbabwe.

| Item                             |       |
|----------------------------------|-------|
| Pedigree records                 | 2341  |
| No base parents                  | 255   |
| No animals                       | 2596  |
| No sires                         | 37    |
| No dams                          | 218   |
| Mean (kg)                        | 12.81 |
| Coefficient of Determination (%) | 57    |
| Coefficient of Variation (%)     | 20.97 |
| Standard Deviation (kg)          | 2.93  |

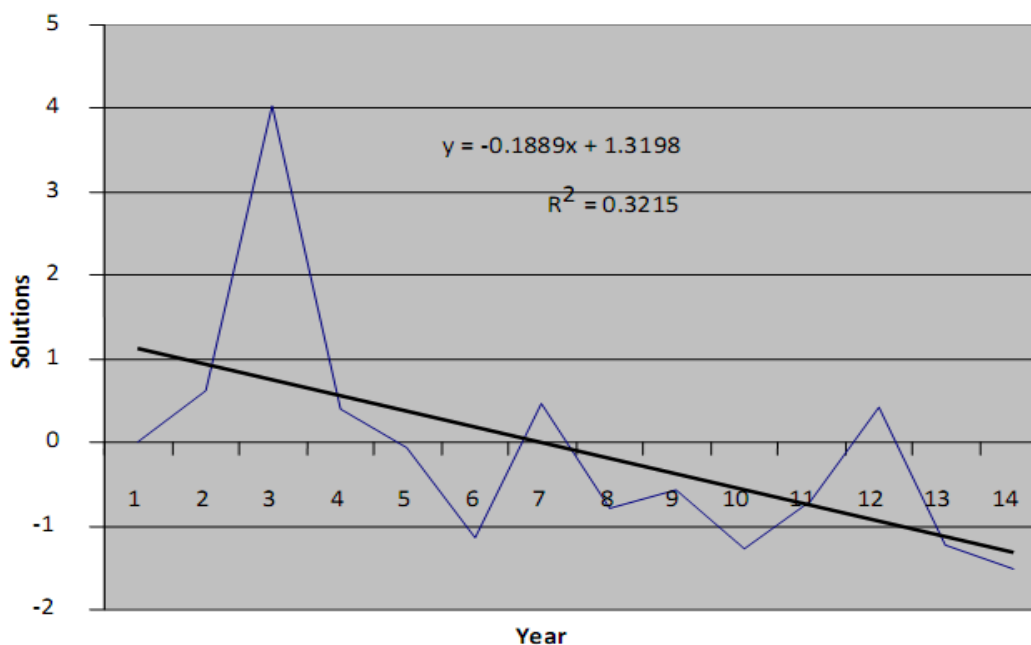
The results of the linear regression analysis of environmental values on year of slaughter for hot carcass weight are presented in figure 1, the trend was negative however non significant which can conclude that year of slaughter had no influence on hot carcass weight in indigenous Matebele goats.

**Table 2**

Estimates of covariance components and genetic parameters of hot carcass weight in Matebele goat of Zimbabwe.

| Item            | Model 1 | Model 2 | Model 3 | Model 4 | Model 5 |
|-----------------|---------|---------|---------|---------|---------|
| $\sigma_a^2$    | 6.66    | 2.73    | 1.24    | 1.51    | 1.30    |
| $\sigma_m^2$    |         | 0.20    |         | 0.19    | 0.57    |
| $\sigma_{am}^2$ |         |         |         | -0.53   | 0.05    |
| $\sigma_{pe}^2$ |         |         | 0.00    |         | 0.00    |
| $\sigma_e^2$    | 3.68    | 5.95    | 7.06    | 7.13    | 6.69    |
| $\sigma_p^2$    | 10.34   | 8.88    | 8.30    | 8.30    | 8.61    |
| $h_a^2$         | 0.64    | 0.31    | 0.15    | 0.18    | 0.15    |
| $h_m^2$         |         | 0.02    |         | 0.02    | 0.07    |
| $r_{am}$        |         |         |         | -1.00   | 0.06    |
| $h_T^2$         | 0.64    | 0.32    | 0.15    | 0.09    | 0.19    |
| -2LogL          | 1574    | 1869    | 1879    | 1868    | 1868    |

$\sigma_a^2$  = direct additive genetic  
 $\sigma_m^2$  = maternal additive genetic variance  
 $\sigma_{am}^2$  = direct and additive variance  
 $\sigma_{pe}^2$  = permanent environmental dam variance  
 $\sigma_p^2$  = phenotypic variance = sum of variance and covariance components  
 $\sigma_e^2$  = error variance  
 $h_a^2$  = direct heritability  
 $h_m^2$  = maternal heritability  
 $h_T^2$  = total heritability (total genetic effect)  
 $r_{am}$  = direct and maternal genetic correlation



**Fig. 1.** Fixed effects solutions of hot carcass weight for year of slaughter in Matebele goat.

#### 4. Conclusion

The study shows that inclusion of maternal genetic and/or permanent environmental effects in animal models for hot carcass weight of indigenous Matebele goat will influence the magnitude of direct heritability. Maternal heritability was lower than direct heritability estimates, indicating a greater genetic influence of

individual animal's genetic potential than the influence of maternal effects on this trait. In general due to the contribution of maternal effects to phenotypic variance analyzed trait, maternal genetic and maternal environmental effects should not be taken into account in genetic evaluation for hot carcass weight.

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