Covariance components and genetic parameter estimation for weaning weight in local cattle breeds of Zimbabwe

Never Assan¹, ²

¹Zimbabwe Open University, Faculty of Science and Technology, Department of Agriculture Management, Bulawayo Region, Box 3550, Bulawayo, Zimbabwe
²Matopos Research Station, Bag K5137, Bulawayo, Zimbabwe
Email: neverssan@yahoo.fr

Abstract

The potential for genetic change in economically important traits in beef cattle depends to a large extent on the magnitude of the genetic variances and heritability of trait considered. Estimates of genetic parameters for weaning weight were obtained from the records of Tuli, Nguni and Afrikaner cattle collected at Matopos Research Station, Bulawayo, Zimbabwe. Genetic parameters were estimated using the Average Information Restricted Maximum Likelihood (AIREML) methodology (Gilmour, 1995) fitting additive direct genetic effects, both additive maternal and permanent environmental maternal effects and allowed for covariance between the direct and maternal effects. The analytical model included fixed effects of age of dam, sex of calf and year of birth. Direct additive genetic variance for weaning weight was higher than maternal variance in all three breeds studied. Estimates of heritability for direct genetic effects (h²A), for Tuli, Nguni and Afrikaner were 0.30, 0.25 and 0.35, respectively. Estimates of heritability for maternal genetic effects (h²A), for Tuli, Nguni and Afrikaner were 0.22, 0.17 and 0.15, respectively. The permanent maternal environmental effects were negligible in Tuli, Nguni and Afrikaner cattle for weaning weight. The genetic correlation between direct and maternal effects as a proportion of the total variance (rAM) for weaning weight were strong and negative for Tuli (-0.76) and Nguni (-0.85), while being slightly positive for Afrikaner (0.05). The heritability of direct effects were moderate in Tuli, Nguni and Afrikaner, that can favour the response to selection in breeding programs.

Keywords: Direct, Maternal, Weaning, Tuli, Nguni, Afrikaner

Introduction

Tuli, Nguni and Afrikaner are local cattle breeds in Zimbabwe that have proven remarkably suitable to survive and produce under the prevailing harsh semi arid environmental conditions. This is particularly so for tropical environments where, in the absence of resources for substantial improvement of the production environment, the most viable option is the utilization of adapted animal genetic resources (Rege, 1993). Tuli and Nguni cattle forms part of the Sanga group of cattle which includes most of the type indigenous to East, Central and Southern Africa (Faulkner and Epstein, 1957). The Afrikaner is a predominant cattle breed in southern Africa and was developed as a draft animal with little attention being given to fertility (Oliver, 1983).

Studies of various cattle breeds have shown that weaning weight is influenced not only by the genes of the individual for growth, and by the environment in which it is raised, but also by the maternal genetic composition and environment provided by the dam (Ghartouri et al., 2008). Weaning weight has been recognized as one of the most valuable trait that determine economic efficiency of beef cattle production and has been widely used as
an important selection criteria. (Wasike et al., 2006; Gunawan and Jakaria, 2011; Abera et al., 2011). Efforts to improve genetic quality of cattle through weaning weight selection require information on genetic parameters of cattle breed population so that progress of selection responses can be understood. Weaning weight has medium to high heritability this suggesting that the trait is likely to respond to selection (Buzanskas et al., 2010). The genetic parameter estimates reported for weaning weight in literature for tropical cattle are quite variable (Norris et al., 2004; Ariel-Guillen et al., 2012; Nesar et al., 2012).

Genetic parameters can differ inter- cattle breeds and from year to year. This is caused by change in management, selection program, analysis method and data structure (Koots et al., 1994; Gutierrez et al., 1997). Based on this consideration, estimation of genetic parameters of specific adapted genotypes of indigenous cattle may be recommended to provide the basis of any future objectives for sustainable use of cattle genetic resources. Very few if not, indigenous cattle breeds in Sub Saharan Africa have been introduced in modern genetic improvement programmes that aim to serve the local farming population (Bosso et al., 2009), however plans to utilize adapted genotypes, is the only way to secure a sustainable beef supply base for local population. The objective of this study was to estimate the covariance components and genetic parameters for weaning weight in local Tuli, Nguni and Afrikaner cattle of Zimbabwe.

Study location
Matopos Research Station is situated in southwest Zimbabwe, an area primarily suited to semi-extensive forms of land utilization (Vincent and Thomas, 1961). The production environment is characterized by a dry tropical climate with two distinct seasons: a long dry season from October to June and a short rainy season from November to April. The climate is characterized by wide fluctuations in the quantity and distribution of rainfall within and across season. Annual biomass production is closely related to the amount of rainfall the area receives each year. Mean recorded rainfall is 609mm with a range of 257 to 1376mm. Very high summer temperatures, maximum and minimum mean temperatures of hottest months are 21.6 °C and 11.4 °C, respectively with possibility of severe droughts (Hagreveas et al., 2004). Day et al (2003) and Gambiza and Nyama (2000) give a detailed description of the climate and vegetation type, respectively.

Herd management
Animals were grazing on free range without provision of protein rich concentrate during the dry season. Routine cattle veterinary practices were followed. Cows were naturally bred and breeding season was limited to 90 d period from 1 January each year. Single sire herds comprised of one bull to 30 females were introduced to the breeding herd for mating when they had attained two years of age. Bulls were seldom used for service until they were three years old. Calves were born between late September and early January. They were numbered by means of ear tag and were weighed and recorded within 18 hours of birth. At the same time both the calf number and that of the sire were recorded thereafter all calves weighed at an average age of 210 d.

Data analysis
Fixed factors for model were determined through preliminary analyses using procedure GLM of SAS (1996) (SAS Inst. Inc., Cary, NC). The analytical model included fixed effects of age of dam, sex of calf and year of birth. Covariance components and genetic parameters were estimated using the Average Information Restricted Maximum Likelihood (AIREML) methodology (Gilmour, 1995) fitting additive direct genetic effects, both additive maternal and permanent environmental maternal effects and allowed for covariance between the direct and maternal effects. Iterations for weaning weight were stopped when the variance of twice the negative logarithm of the likelihood function (-2 log L) was less than 1* 10^-9 for single trait analyses. Initial starts used variance component estimates based on the literature, and each subsequent restart used starting values from the previous run. Convergence was declared when differences in -2 log L were small (generally less than 0.01), and ratios of variance components as a function of phenotypic variance and correlations changed by less than 0.01. The following model was used:

\[ Y = Xb + Z_d a + Z_m m + Z_c c + e \]
\[ \text{Cov}(a, m) = \sigma^2_{am} \]
where: \( y \) is the vector of observations while \( b, a, m, c \) and \( e \) are the vectors of fixed effects, direct additive genetic effects (animal), maternal genetic effects, permanent environmental effects of dam and the residual, respectively. \( X, Z_a, Z_m, Z_c \) are incidence matrices of fixed effects, direct additive genetic effects, maternal genetic effects and permanent environmental effects of the dam. \( A \) is the numerator additive genetic relationship matrix between animals, \( I \) the identity matrix

\[
V(a) = A \sigma^2_a, \quad V(m) = A \sigma^2_m, \quad V(c) = \sigma^2_c I, \quad V(e) = \sigma^2_e I \text{ and } \text{Cov}(a, m) = A \sigma_{am},
\]

where \( \sigma_{am} \) is the covariance between direct and maternal genetic effects, \( \sigma^2_a \), the direct additive genetic variance, \( \sigma^2_m \), the maternal additive genetic variance, \( \sigma^2_c \), the variance of the permanent environmental effect of the dam, and \( \sigma^2_e \), the variance of the residuals.

**Results and Discussion**

The number of records analyzed for weaning weight of Tuli, Nguni and Afrikaner cattle, as well as the average and coefficient of variation are summarized in Table 1. Coefficient of variations for weaning weight of Tuli, Nguni and Afrikaner cattle were low ranging between 13.30 to 19.20 % and is consistent with values for cattle weaning weight in other studies (Ndofor-Foleng et al., 2012; Rios-Utrera et al., 2011).

<table>
<thead>
<tr>
<th>Item</th>
<th>Tuli</th>
<th>Nguni</th>
<th>Afrikaner</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Animals</td>
<td>4090</td>
<td>5091</td>
<td>4387</td>
</tr>
<tr>
<td>Number of Sires</td>
<td>134</td>
<td>117</td>
<td>214</td>
</tr>
<tr>
<td>Number of Dams</td>
<td>1432</td>
<td>1274</td>
<td>1578</td>
</tr>
<tr>
<td>Mean (kg)</td>
<td>176.45</td>
<td>177.18</td>
<td>103.12</td>
</tr>
<tr>
<td>Standard Deviation (kg)</td>
<td>28.61</td>
<td>28.01</td>
<td>33.90</td>
</tr>
<tr>
<td>Coefficient of Variation (%)</td>
<td>15.22</td>
<td>13.30</td>
<td>19.20</td>
</tr>
<tr>
<td>R- Square</td>
<td>28</td>
<td>50</td>
<td>39</td>
</tr>
</tbody>
</table>

Variance --covariance components and genetic parameter estimates for weaning weight in Tuli, Nguni and Afrikaner cattle are shown in Table 2. Additive direct variance were consistently higher than additive maternal variance in Tuli, Nguni and Afrikaner cattle. Similar results have been reported in the study of Australian beef cattle by Duangjinda et al., (2001) and Azizi et al., (2005) in Japanese Black cattle. In contrast, Rios-Utrera et al., (2011) in a study of Mexican Limousine cattle and Elzo et al., (1988) in a study of Romosinuno-Zebu cattle, observed that the additive genetic variance were lower than maternal genetic variance for weaning weight of (133.60 and 199.80 kg² ) and (100.46 and 166.52 kg²), respectively. The error variance as a proportion of total phenotypic variance was highest in Nguni cattle. Lee et al., (1997) reported that error variance for estimated genetic values increases as the differences between true and estimated variance components decreases.

Direct heritability for weaning weight in the present study were 0.30, 0.25 and 0.35 for Tuli, Nguni and Afrikaner cattle, respectively. Estimates of heritability for weaning weight in Tuli, Nguni and Afrikaner in the present study were within the expected range in beef cattle, although weaning weight heritabilities reported in literature are very diverse. In a comprehensive review for similar analysis with an animal model Mohuiddin (1993) reported weaning weight heritabilities ranging from 0.14 to 0.58, and Praharani (2009) reported heritability of weaning weight using a single trait or multiple trait analysis with range of 0.30 to 0.39.

Maternal heritability for weaning weight in the present study were 0.22, 0.17 and 0.15 for Tuli, Nguni and Afrikaner cattle, respectively. These estimates were slightly lower than those reported by Wasike et al., (2006) and For Zebu breeds in the tropics, Mercadante et al., (1995), found weighted means of maternal heritability estimates for weaning weight of 0.18, which is within the range found in the present study. However, current estimates for maternal heritability were lower than Mohuiddin (1993) reported that maternal heritabilities for weaning weight tended to be lower than direct heritabilities, indicating a greater genetic influence of the calf than its dam for weaning weight. Maternal effects are significant sources of variation for weaning weight and ignoring maternal effects in the model would cause inaccurate genetic evaluation of calves. The importance of maternal
effects in beef cattle has been widely reported (Koch, 1972; Baker, 1980; Robison, 1981; Meyer, 1992). Studies on African cattle populations have reported a strong maternal influence on growth traits (Tawah et al., 1993; Khombe et al., 1995; Diop and Van Vleck, 1998). Animal models used to estimate maternal effects typically include direct and maternal genetic effects and maternal permanent environmental effects and consider the covariance between genetic effects. Meyer (1992) pointed out that such models may be suboptimal and need to be improved. The fitting of models that account for maternal additive genetic effects for traits up to weaning is important (Vaez et al., 1996).

The estimate of the ratio of maternal permanent environmental variance to the phenotypic variance were negligible for weaning weight in all breeds studied, as also reported by Aynalem (2006) and Migose et al (2007). Permanent environmental effects result from incidents that affect all progeny of the same cow. The effects before weaning may be caused by sequels of diseases or accidents to the udder, which will affect the milk production of the dam, whereas the estimate of permanent environmental maternal effects at later ages may reflect a carry-over effect on weaning weight. Meyer (2001) reported that breeds differences in the importance of maternal environmental effects are important and in some breeds permanent environmental effects is due to earlier decline of lactation curve than in other breeds.

Total heritability estimates are useful in estimating response to selection based on phenotypic value and the estimates can be affected by data size, model used and breeds (Solomon, 2002). Total heritability estimates for weaning weight lie within the range of literature estimates of Mohiuddin (1993), which vary from 0.02 to 0.82.

Correlation between direct and maternal genetic effects ($r_{AM}$) in Tuli (-0.76), Nguni (-0.85) and Afrikaner (0.05) ranged from relatively large negative value to small positive for weaning weight, indicating important tradeoffs between direct and maternal effects in Tuli and Nguni cattle. Numerous studies have found a negative correlation between direct and maternal effects for weaning weight of various beef cattle. However, positive relationships have also been reported for weaning weight concluding that selection for increased weights will also improve the maternal ability in the case of positive correlation between direct and maternal effects (Dodenhoff et al., 1999). Sign and magnitude of correlation between direct and maternal genetic effects seemed to differ among pure breeds and were reflected in composites from the parent breeds (Van Vleck et al., 1996). The strong and negative correlation between direct and maternal genetic effects for weaning weight in Tuli and Nguni were higher than those reported by Koots et al., 1994b, who reported unweighted and weighted correlation between direct and maternal genetic effects of -0.30 and -0.16, respectively. Weaker correlation between direct and maternal genetic effects than in the present study of -0.23 and -0.34 were reported for weaning weight by Rios-Utrera (2008) in Mexican Limousine cattle and Garcia (2007) in Colombian Romosinuano cattle, respectively. However, the correlation of direct and maternal genetic effects reported in the present study where within the range reported by Cheverud (2003) and Campelo et al., (2004) of -0.90 to -0.31 for weaning weight, while being comparable with values of -0.64 and -0.78 reported by Segura-Correa et al., (2012) in Brown Swiss cattle in Mexico and Meyer (1992) for Zebu crosses, respectively. It seems most of the estimates of correlation between direct and maternal genetic effects reported by Mohiuddin (1993) were negative, although they ranged from -0.78 to 0.25. Matos et al., (2000) and Iwaisaki et al., (2005) postulated that high negative correlation between direct and maternal genetic effects was caused by negative environment correlation between dam and calf, where heifer and superior dams did not give conducive environment (good care) for their calves. Meyer (1993) and Swalve (1993) compared results from different studies of correlation of direct and maternal genetic effects for weaning weight in beef cattle and argued that less than sufficient environment may impose a negative correlation. Robinson (1996) explained that negative correlation estimates of beef cattle might be caused by other non-genetic factors such as interaction between sire and cattle herd. However, an investigation conducted by Dodenhoff et al., (1999) on several breeds of beef cattle indicates the dependences between direct and maternal genetic effects are determined by breed. Moreover, Pribyl et al., (2008) showed that editing the database plays a role in estimating genetic parameters and includes a more complex pedigree as well as produces different results. Due to antagonism of direct and maternal genetic effects in evaluation of weaning weight in Tuli and Nguni, maternal effects should be included in genetic analysis model. Meyer (1997) suggested maternal effect was included in analysis model to reduce bias of genetic variance estimation. While Lee et al., (2000) recommended to consider the correlation between direct and maternal genetic effects in selection program.
because selection on growth trait would contradictory with its maternal. Apart from discrepancies caused by different models applied and real differences between population analyzed, differences in data structure and size could play an important role. According to Maniatis and Pollot (2003) the estimation of the correlation between direct and maternal genetic effects is dependent on key pedigree relationships where a high proportion of both dams and maternal grand dam with their own records are essential. Gutierrez et al., (1997) reported antagonism between direct and maternal genetic effects for weaning weight for Zebu cattle and suggested that this antagonistic relationship should be compensated by improving managerial practices and using supplementary feeding when necessary.

Table 2. (Co) variance components and genetic parameters for weaning weight in Tuli, Nguni and Afrikaner cattle of Zimbabwe

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Tuli</th>
<th>Nguni</th>
<th>Afrikaner</th>
</tr>
</thead>
<tbody>
<tr>
<td>σ²a</td>
<td>283.40</td>
<td>219.00</td>
<td>443.20</td>
</tr>
<tr>
<td>σ²m</td>
<td>209.60</td>
<td>149.20</td>
<td>189.20</td>
</tr>
<tr>
<td>σ²am</td>
<td>186.60</td>
<td>-0.15</td>
<td>62.56</td>
</tr>
<tr>
<td>σ²pe</td>
<td>0.02</td>
<td>0.03</td>
<td>0.01</td>
</tr>
<tr>
<td>σ²e</td>
<td>306.96</td>
<td>627.30</td>
<td>560.80</td>
</tr>
<tr>
<td>σ²p</td>
<td>613.20</td>
<td>869.44</td>
<td>1263.86</td>
</tr>
<tr>
<td>h²a</td>
<td>0.30</td>
<td>0.25</td>
<td>0.35</td>
</tr>
<tr>
<td>h²m</td>
<td>0.22</td>
<td>0.17</td>
<td>0.15</td>
</tr>
<tr>
<td>h²T</td>
<td>0.18</td>
<td>0.34</td>
<td>0.50</td>
</tr>
<tr>
<td>r²am</td>
<td>-0.76</td>
<td>-0.85</td>
<td>0.05</td>
</tr>
</tbody>
</table>

Conclusion

It is concluded that the direct heritability of weaning weight in Tuli, Nguni and Afrikaner were moderate, which favor the response to selection in breeding programs. Due to negative genetic correlation between direct and maternal effects for weaning weight in Tuli and Nguni, selection for both the direct and maternal components of weaning weight is advisable. Magnitude of correlation between direct and maternal genetic effects seemed to differ among pure breeds, despite being kept in the same environment and under the same management.

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References


