GENETIC PARAMETERS FOR GROWTH TRAITS OF ZEBU CATTLE IN THE SEMI-ARID REGION OF BRAZIL

(Parâmetros genéticos para características de crescimento de bovinos zebus na região semi-árida do Brasil)

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ABSTRACT

Estimates of covariance components of weaning (WW), yearling (YW) and post yearling weight (PW) of Guzera cattle were obtained from a series of bivariate Restricted Maximum Likelihood analysis (REML), fitting an animal model incorporating direct and maternal genetic effects and permanent environmental effects. The model included fixed effects of contemporary group (herd-year-season), calf sex and age at calving of cow class. Two groups of analysis were conducted considering or not the covariance between direct and maternal effects. The results indicate caution when studying maternal effects, with regard to the covariance between maternal and direct genetic effects. Possibly the best route should be to impose a zero value for this covariance.

KEY WORDS: cattle, zebu, animal model, genetic parameter, growth, maternal effect, semi-arid region

RESUMO

Estimativas de componentes de covariância dos pesos corporais a desmama (PD), a um ano de idade (PA) e ao sobreano (PS) de bovinos da raça Guzerá foram obtidas de uma série de análises bivariadas, através do método de Máxima Verossimilhança Restrita (REML), usando um modelo animal incorporando efeitos genéticos diretos e maternos e efeitos de ambiente permanente. O modelo incluiu efeitos fixos de grupo contemporâneo (propriedade-ano-estação), sexo da cria e classe da idade da vaca. Dois grupos de análises foram conduzidas considerando ou não a covariância entre o efeito genético direto e materno. Os resultados indicam cautela quanto ao estudo dos efeitos maternos, no que se refere ao valor da covariância entre os efeitos direto e materno, sendo melhor em muitos casos a imposição de um valor zero para a referida covariância.

PALAVRAS-CHAVE: bovinos, zebu, modelo animal, parâmetros genéticos, crescimento, efeito materno, região semi-árida

INTRODUCTION

Herds in the northwest semi-arid regions present particularity and differ from others located in the most of regions of Brazil. The critical capacity of production and the small survival in dry periods are important parameters. The Guzera is one of the principal zebu breeds in this region, due to its heat resistance and tolerance and ability to survive under limited food resources in the dry periods of year. Literature concerning genetic parameters in these harsh conditions found in the semi-arid region of the Northeast Brazil is scarce.

According to BOLDMAN & VAN VLECK (1991), Restricted Maximum Likelihood (REML) estimation of (co) variance components and breeding value prediction with BLUP

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properties, were the best methods for unbalanced animal breeding data. In this way, the estimates of covariance and the genetic parameters, essential to animal breeding research, were necessary as assistance tools for selection of these populations as yet unstudied by this modern method.

The objectives of this study were to obtain estimates of (co)variance, heritabilities and correlations for weights of Guzera cattle from weaning to 550 days of age, raised on the pastures of the semi-arid region of Ceará State, Brazil, and to verify the result when considering null the covariance between direct-maternal covariance.

**MATERIALS AND METHODS**

*Data*

Records for weaning weight (WW), yearling weight (YW) and post yearling weight (PW) were obtained from 1975 to 1995 from Brazilian Zebu Breeders Association (ABCZ) collected from five herds located in the semi-arid region of Ceará State. Animals were grazed on native pasture and were the progeny of 102 sires.

Data used in this study consist of about four generations, with a minimum of five animals per sire, three sires per year and four animals per contemporary group.

Further details on the herds, environmental conditions and breeding system can be found in LÔBO (1998).

*Statistical analysis*

Estimates of covariance components were obtained by Derivative Free Restricted Maximum Likelihood (DFREML) using Multiple Trait Derivative Free Restricted Maximum Likelihood (MTDFREML) software developed by BOLDMAN et al. (1993). One, Two and Three-trait analyses were run. Fixed effects of contemporary group (herd-year-season), calf sex and age at calving of cow class (22-36 months, 37-60 months, 61-84 months, 85-108 months, 109-132 months and above 132 months) were fitted on model, beyond direct and maternal genetic effects, environmental permanent effects and residual error.

Initially, a small *a priori* value (0.001) was considered for the covariance between direct and maternal genetic effects. Later, single trait analyses were carried out by considering this covariance as null.

**RESULTS AND DISCUSSION**

The number of records, mean weights and standard deviations for studied traits are presented in Tab. 1. Mean weights were lower than zebu weights raised in the other regions of Brazil, maybe due to food restriction mainly in the dry periods of year (July to December).

Tab. 2 presents estimates of (co)variance and genetic parameters, results of analyses considering the covariance between genetic and maternal effects.

Estimates of (co)variance components and genetics parameters among different analyses (one, two- and three-trait analyses) for weaning weight (WW) on the whole were very similar. Variation among analyses for yearling weight (YW) and post yearling weight (PW) occurred mainly in genetic and total variance. There was an increase for these components in the two- and three-trait analyses. This reflects the elimination in multiple trait analyses of part of the selection effects based on age-related culling of animals with low growth tax. MEYER (1994) observed a similar result in beef cattle in Australia. It is important to emphasise the natural selection affecting these populations, where the effect of adverse conditions on animals with reduced growth is superior.

Phenotypic variance components were similar among one- and multiple trait analyses, reflecting a standard behaviour for results according to the analyses carried out.

There is a similarity between the heritability estimates in this study and those estimated for the same populations by MARTINS FILHO et al. (1997) by intra class correlation method. Higher estimates were obtained to Nellore breed by CUNHA et al. (1996), in Ceará State, and by MARTINS et al. (1996), in Maranhão State, both
by intra class correlation method. Similar results were also obtained by MAGNABOSCO et al. (1996), using an animal model in the study of body weight of Nellore breed.

The direct heritability estimates observed are within the range of 0.05 to 0.58 (WW), -0.06 to 1.21 (YW) and 0.09 to 0.79 (PW) observed by MERCADANTE et al. (1995) from a review of several papers in the literature. Weighted means for heritability of WW (0.24) and YW (0.33) from a review reported by KOOTS et al. (1994) were higher than estimates in this study for the same traits.

Maternal heritability estimates were lower than weighted means from studies of literature reported by MERCADANTE et al. (1995). However, the values estimated in the different analyses for WW were similar to mean value reported by KOOTS et al. (1994). In analysis of YW with WW a maternal heritability for YW (0.11) equal to mean observed by KOOTS et al. (1994) was observed.

WILLHAM (1972) defined total heritability as the determinant of the selection result for traits subject to maternal effect. Estimates of this parameter in this paper were low, reflecting a limited potential of genetic variability to be explored through the selection in the studied populations.

Different estimates of heritability can be observed for the same trait according to estimate method. SCHAEFFER (1993) reported that its use in the genetic evaluation of animals should be a last resort, because of the many assumptions that are implied by the sire model when compared to an animal model. Thus, the requirement of the sire model to attend to more assumptions can produce errors in genetic variance estimates, and these errors will be enlarged when multiplied by four. KOOTS et al. (1994) studied the method effect in the heritability estimate for the same trait and observed higher values of estimates realised by intra class correlation method when compared to estimates realised by progeny-parent regression method. The authors were intrigued because there is a tendency of the regression method to produce higher estimates than intra class correlation method in selected populations. They hoped too that estimates realised by animal model were highest, because this method estimates the variances before the selection, due to use of relationship matrix. However, there was no tendency of highest estimates, leading to an absence of reduction in genetic variance, as supposed by the authors because of insufficient data on pedigree or absence of effective selection in herds.

High and positive genetic correlation between studied weights indicate the possibility of early selection for studied populations, despite the influence of the maternal effect. ELER et al. (1996), using a similar method, observed a genetic correlation of 0.77 between weaning weight and post yearling weight. This value is similar to 0.70 reported in our present study.

MERCADANTE et al. (1995) examining several papers in literature observed weighted means of 0.68 and 0.78 for genetic and phenotypic correlations, respectively, between WW and YW. Between WW and PW these means for genetic and phenotypic correlations were equal to 0.64 and 0.71, respectively, and 0.77 and 0.85, respectively, between YW and PW. These values of genetic correlation were similar to arithmetic means for genetic

Table 1. Number of observations (N), means and standard deviations for growth traits in Guzera cattle in the Northeast of Brazil.

<table>
<thead>
<tr>
<th>Traits</th>
<th>N</th>
<th>Mean</th>
<th>Standard deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Weaning weight (WW)</td>
<td>4.10</td>
<td>32.87</td>
<td>33.92</td>
</tr>
<tr>
<td>Yearling weight (YW)</td>
<td>3.12</td>
<td>78.76</td>
<td>52.74</td>
</tr>
<tr>
<td>Post Yearling weight (PW)</td>
<td>1.95</td>
<td>222.93</td>
<td>69.32</td>
</tr>
</tbody>
</table>


Table 2. (Co) variances and genetics parameters according to single, two and three-trait analysis for liveweight traits in Guzera cattle in the Northeast of Brazil.

<table>
<thead>
<tr>
<th>Traits</th>
<th>$\sigma^2_A$</th>
<th>$\sigma^2_M$</th>
<th>$\sigma_{AM}$</th>
<th>$\sigma^2_E$</th>
<th>$\sigma^2_T$</th>
<th>$h^2_A$</th>
<th>$h^2_M$</th>
<th>$\gamma_{AM}$</th>
<th>$\gamma_{A1}$</th>
<th>$\gamma_{A2}$</th>
<th>$h^2_T$</th>
</tr>
</thead>
<tbody>
<tr>
<td>WW</td>
<td>155.31</td>
<td>113.11</td>
<td>-66.86</td>
<td>111.57</td>
<td>530.12</td>
<td>827.52</td>
<td>0.19</td>
<td>0.14</td>
<td>-0.50</td>
<td>-</td>
<td>0.13</td>
</tr>
<tr>
<td>+YW</td>
<td>139.74</td>
<td>86.73</td>
<td>-58.39</td>
<td>95.52</td>
<td>511.10</td>
<td>819.72</td>
<td>0.17</td>
<td>0.11</td>
<td>-0.53</td>
<td>0.67</td>
<td>-0.12</td>
</tr>
<tr>
<td>+FW</td>
<td>174.88</td>
<td>98.45</td>
<td>-43.31</td>
<td>159.14</td>
<td>522.33</td>
<td>824.31</td>
<td>0.21</td>
<td>0.12</td>
<td>-0.33</td>
<td>0.70</td>
<td>-0.19</td>
</tr>
<tr>
<td>+YW+FW</td>
<td>200.74</td>
<td>107.49</td>
<td>-70.74</td>
<td>148.37</td>
<td>540.53</td>
<td>860.76</td>
<td>0.23</td>
<td>0.12</td>
<td>-0.48</td>
<td>0.68</td>
<td>0.74</td>
</tr>
<tr>
<td>YW</td>
<td>214.39</td>
<td>90.13</td>
<td>-38.58</td>
<td>201.58</td>
<td>1,342.63</td>
<td>2,099.22</td>
<td>0.10</td>
<td>0.04</td>
<td>-0.28</td>
<td>-</td>
<td>-0.10</td>
</tr>
<tr>
<td>+YW</td>
<td>237.59</td>
<td>216.77</td>
<td>-48.62</td>
<td>273.04</td>
<td>1,323.15</td>
<td>2,063.36</td>
<td>0.12</td>
<td>0.11</td>
<td>-0.21</td>
<td>0.83</td>
<td>-0.13</td>
</tr>
<tr>
<td>+FW</td>
<td>323.40</td>
<td>57.35</td>
<td>-24.07</td>
<td>315.97</td>
<td>1,330.96</td>
<td>2,072.94</td>
<td>0.16</td>
<td>0.03</td>
<td>-0.18</td>
<td>0.99</td>
<td>-0.15</td>
</tr>
<tr>
<td>+YW+FW</td>
<td>416.25</td>
<td>63.74</td>
<td>-33.36</td>
<td>398.08</td>
<td>1,520.46</td>
<td>2,188.45</td>
<td>0.19</td>
<td>0.03</td>
<td>-0.20</td>
<td>0.80</td>
<td>0.95</td>
</tr>
<tr>
<td>PW</td>
<td>687.76</td>
<td>969.28</td>
<td>-634.00</td>
<td>221.40</td>
<td>2,610.37</td>
<td>3,388.13</td>
<td>0.20</td>
<td>0.29</td>
<td>-0.78</td>
<td>-</td>
<td>-0.06</td>
</tr>
<tr>
<td>+YW</td>
<td>563.81</td>
<td>626.52</td>
<td>-293.29</td>
<td>437.13</td>
<td>2,797.43</td>
<td>3,630.93</td>
<td>0.16</td>
<td>0.17</td>
<td>-0.49</td>
<td>0.40</td>
<td>-0.12</td>
</tr>
<tr>
<td>+YW</td>
<td>857.26</td>
<td>702.20</td>
<td>-504.01</td>
<td>452.34</td>
<td>2,812.87</td>
<td>3,748.80</td>
<td>0.23</td>
<td>0.19</td>
<td>-0.65</td>
<td>0.24</td>
<td>-0.12</td>
</tr>
<tr>
<td>+YW+YW</td>
<td>669.87</td>
<td>55.76</td>
<td>4.33</td>
<td>704.24</td>
<td>2,791.64</td>
<td>3,676.73</td>
<td>0.18</td>
<td>0.02</td>
<td>0.02</td>
<td>0.76</td>
<td>0.96</td>
</tr>
</tbody>
</table>

a

- $\sigma^2_A$ = direct genetic variance, $\sigma^2_M$ = maternal genetic variance, $\sigma_{AM}$ = direct-maternal covariance, $\sigma^2_E$ = total genetic variance ($\sigma^2_A + 0.5 \sigma^2_M + 1.5 \sigma_{AM}$), $\sigma^2_E$ = environmental permanent variance, $\sigma^2_T$ = phenotypic variance, $h^2_A$ = direct heritability, $h^2_M$ = maternal heritability, $\gamma_{AM}$ = direct-maternal genetic correlation, $\gamma_{A1}$ = direct genetic correlation with the 1st. trait, $\gamma_{A2}$ = direct genetic correlation with the 2nd. trait, $h^2_T$ = total heritability

b

For abbreviations, see text. First row = single-trait analysis, following row, multiple-traits analysis
correlations of all analyses in the present study: 0.74 between WW and YW, 0.65 between WW and PW and 0.78 between YW and PW.

Tab. 3 presents analyses considering the covariance between direct and maternal genetic effects as null. There was a reduced maternal effect on WW, that was not observed at other weights. In Tab. 2, however, the maternal effect on studied animals was considerable and extended in the post weaning period, except in analyses for PW with other weights. There was an antagonism between direct and maternal genetic effects, which is in accordance with results in the literature. (MEYER, 1994; REYES et al., 1994).

Considering null the covariance between direct and maternal effects in this data, the estimates of direct genetic, environmental and phenotypic variances, beyond direct heritability showed no great alterations. There was only a small decrease when the results of analyses with one trait in the Tab. 2 are compared with the results in the Tab. 3, with the exception of PW. There was a considerable reduction in genetic variance and proportional increase in environmental and phenotypic variances at this weight. This probably occurred due to a decrease in the number of records for PW. However, estimates of maternal variance and heritability decreased sufficiently towards zero for all studied weights. A strong connection appears to exist between the direct-maternal genetic covariance and the maternal variance for this data, since when the covariance was considered null the maternal variance was lost without great changes in other components.

It is important to consider some aspects in studies with maternal effects: a) it is important to measure connectability amongst data; b) to value dependence of results to direct-maternal genetic covariance imposed; and, c) if there is contradiction maybe it is better to not consider direct-maternal covariance. FRIES & ALBUQUERQUE (personal communication) reported that estimates different of zero for direct-maternal covariance could be product of data structure or deficiency in this structure. The authors recommend the utilisation of zero value in some cases or to consider the effect of the cow as a whole without worrying whether it is direct or maternal.

**CONCLUSIONS**

An increase of variance components in multiple trait analyses justifies the realisation of these analyses since they remove the effects of selection for growth in precedent period.

The small value of heritability demonstrates a reduced genetic variability to be exploited in Guzera cattle raised on pasture in Ceara State.

Studies with direct-maternal covariance

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Table 3. (Co) variances and genetics parameters\(^a\) according to single-trait analysis for liveweight traits considering null covariance between direct and maternal effect in Guzera cattle in the Northeast of Brazil.

<table>
<thead>
<tr>
<th>(\tau)traits(^b)</th>
<th>(\sigma^2_A)</th>
<th>(\sigma^2_M)</th>
<th>(\sigma^2_G)</th>
<th>(\sigma^2_E)</th>
<th>(h^2_A)</th>
<th>(h^2_M)</th>
<th>(h^2_T)</th>
</tr>
</thead>
<tbody>
<tr>
<td>WW  (\sigma^2)</td>
<td>136.49  1.53</td>
<td>137.15  0.75</td>
<td>824.49  0.17</td>
<td>0.00  0.17</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>YW  (\sigma^2)</td>
<td>202.00  0.0018</td>
<td>202.00  1.575.40</td>
<td>2.097.30  0.10</td>
<td>0.00  0.10</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PW  (\sigma^2)</td>
<td>435.47  0.03</td>
<td>435.48  3.721.29</td>
<td>3.577.39  0.12</td>
<td>0.00  0.12</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

\(^a\)\(\sigma^2_A\) = direct genetic variance, \(\sigma^2_M\) = maternal genetic variance, \(\sigma^2_G\) = total genetic variance (\(\sigma^2_A + 0.5\sigma^2_M + 1.5\sigma_{AM}\)), \(\sigma^2_E\) = environmental variance, \(\sigma^2_P\) = phenotypic variance, \(h^2_A\) = direct heritability, \(h^2_M\) = maternal heritability, \(h^2_T\) = total heritability

\(^b\)For abbreviations, see text.
must be treated with caution since there is a possibility that this covariance may be the product of available data structure.

REFERENCES


