GENETIC PARAMETERS OF GROWTH TRAITS IN NELLORE CATTLE REARED IN NORTH EAST OF BRAZIL

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INTRODUCTION
Brazil has one of the major cattle stocks in the world and even if the country is located in the tropical zone, one of the hottest parts of the world, it presents a great potential for livestock production. This is related on the one hand to its higher capacity of plant production both native and cropped, especially in the central and southern regions of the country, and on the other hand to the rearing of cattle breeds that can efficiently convert poor quality forages into beef. This latter option is more common to the northeaster areas. The use of a breed most suited to a particular environment it’s one of the choices to improve animal production everywhere, provided that animal selection could be done without interruption and genetic parameters have been estimated adequately.

The aim of this study was to estimate the genetic parameters for growth from weaning to 550 days of age in Nellore breed, reared in the North East of Brazil with extensive management.

MATERIAL AND METHODS

Data description. The data set included 5791 records for weaning weight (W205), 3348 records for yearling weight (W365) and 2292 records for weight at 550 days of age (W550), collected on Nellore animals born between 1974 and 2000. The records were collected in three States of the North East of Brazil (Ceará, Piauí, Rio Grande do Norte), where these animals were raised on natural pastures.

The original data set was obtained by Brazilian Zebu Breeders Association (ABCZ). All the herds were located in the semi arid region characterised by: predominance of nude soils, undulating profiles, shrubby vegetations, irregular rainfalls (around 700 mm/year) with periodical dry periods, high solar radiation (2,800 hour/year) with high temperatures.

Statistical analyses. Estimates of variance components and genetic parameters were performed with MTDFREML software developed by Boldman et al. (1995). Total heritability was estimated following Williams (1972). The analyses were conducted using a single trait animal model represented as follows:

\[ y = X\beta + Z_1 a + Z_2 m + Z_3 p + \epsilon \]

The linear model used included the fixed effect of contemporary group (herd-year-month-sex) and the random effects for direct, maternal and permanent environmental contributions to observations. In the model \( a \) represents a vector of additive genetic effects, \( m \) a vector of
maternal contributions, \( p \) a vector of permanent environmental contributions and \( e \) a vector of residual effects that were assumed to be distributed multivariate normally with null mean and covariance structure \( \sigma^2_e I \).

Contemporary groups were formed grouping animals of the same sex, herd, month and year of birth. The connectedness between herds was tested using the MILC program developed by Fries and Roso (1997), excluding from the analyses all the herds not connected.

RESULTS AND DISCUSSION

Estimates of variance components for W205, W365 and W550 are reported in Table 1 whereas heritabilities for the same traits are shown in Table 2.

Table 1. Estimates of variance components\(^\text{a}\) for weight at 205 (W205), 365 (W365) and 550 (W550) days of age from a single trait analysis

<table>
<thead>
<tr>
<th>Trait</th>
<th>( \sigma^2_A )</th>
<th>( \sigma^2_M )</th>
<th>( \sigma^2_{EP} )</th>
<th>( \sigma^2_E )</th>
<th>( \sigma^2_P )</th>
</tr>
</thead>
<tbody>
<tr>
<td>W205</td>
<td>23,0966</td>
<td>0.3159</td>
<td>92,8707</td>
<td>242,8504</td>
<td>359,1337</td>
</tr>
<tr>
<td>W365</td>
<td>160,4399</td>
<td>0.0103</td>
<td>38,8257</td>
<td>306,1839</td>
<td>505,4597</td>
</tr>
<tr>
<td>W550</td>
<td>100,8988</td>
<td>0.0212</td>
<td>0.0084</td>
<td>637,2182</td>
<td>738,1466</td>
</tr>
</tbody>
</table>

\( A \sigma^2_A = \) additive genetic variance; \( M \sigma^2_M = \) maternal genetic variance; \( EP \sigma^2_{EP} = \) permanent environmental variance; \( E \sigma^2_E = \) temporary environmental variance; \( P \sigma^2_P = \) phenotypic variance.

Table 2. Estimates of genetic parameters\(^\text{a}\) (±s.e.) for weight at 205 (W205), 365 (W365) and 550 (W550) days of age from a single trait analysis

<table>
<thead>
<tr>
<th>Trait</th>
<th>( h^2_A )</th>
<th>( h^2_M )</th>
<th>( h^2_T )</th>
</tr>
</thead>
<tbody>
<tr>
<td>W205</td>
<td>0.06 ± 0.03</td>
<td>0.00 ± 0.05</td>
<td>0.06</td>
</tr>
<tr>
<td>W365</td>
<td>0.32 ± 0.09</td>
<td>0.00 ± 0.10</td>
<td>0.32</td>
</tr>
<tr>
<td>W550</td>
<td>0.14 ± 0.07</td>
<td>0.00 ± 0.11</td>
<td>0.14</td>
</tr>
</tbody>
</table>

\( A h^2_A = \) estimate of direct heritability; \( M h^2_M = \) estimate of maternal heritability; \( T h^2_T = \) total heritability.

Direct genetic variance for W205 was low and thus its contribution to the phenotypic variance was reduced. This value is lower than that reported by Sarmento et al. (2000) and Biffani (1997). The results regarding W365 and W550 were similar to the ones related by Garnero et al. (1998) and Lôbo et al. (2000a) all of them on zebu breeds. Estimate of maternal genetic variance was negligible and, as expected, it decreased as age increased, attaining values close to zero at W365 and W550. These results were lower than those reported by Garnero et al. (1998), Lôbo et al. (2000b) and Sarmento et al. (2000). In terms of heritability, the maternal effect was close to zero but with a high standard error. Temporary environmental variance accounted for 60 to 87 % of the total variation showing the strong influence of the environment, in terms of nutritional and climatic conditions, in the studied area. Estimate of direct heritability increased considerably from W205 to W365 and decreased smoothly from W365 to W550. Similar results in Nellore cattle were related by Albuquerque and Meyer (2001), who using a RRM, found a non-linear trend for direct heritability from birth to 600 d of age. These findings suggest that direct selection for growth is more efficient at older ages. Estimated values for total heritability, excepting for W205, are

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included in the range reported for Mohiuddin (1993), Koots et al. (1994) and Mercadante et al. (1995). However, all the estimates were lower than those found by Lôbo et al. (2000a) working in a tropical zone and even lower than the values reported by Biffani (1997) and Martins Filho et al. (1998), both working on the same region and breed. These results could be the consequence of the more rigorous criteria used in the data edits. Herds not connected through dams or sires were eliminated. Considering that in Brazil only 4% of total insemination is by means of A.I. (Heimerink, 2000), the herds analysed in the present study were connected through a small number of high selected bulls. This situation might have decreased genetic variability. Another factor which could have affect genetic and environmental estimates was the size of each contemporary group. Animals were grouped by month of birth, reducing the number of records per group. In previous studies developed on the same region and breed (Biffani, 1997; Martins Filho et al., 1998) the contemporary groups included all the animals born during the same season, dry or humid. In this case the authors found a higher direct genetic variance and a higher direct heritability.

CONCLUSION

The estimates of heritability found in the present study were of low to intermediate magnitude, even if below the values found in previous studies based on Nellore cattle and more similar to estimates from North European cattle. These results seem to confirm that phenotypic selection for these traits can still be used but in order to obtain greater selection responses it needs a larger diffusion of A.I., a wider pool of selected bulls and their intense use across the herds. Nevertheless, the great contribution of temporary environmental variance to the total variance leads to put special attention on the environment and on the management system when the animals are reared on natural pastures. At the same time a critical point is the definition of the contemporary group as its structure and size seems to affect the analyses and could lead to under or overestimation of genetic and environmental estimates.

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REFERENCES