GENETIC PARAMETERS FOR GROWTH TRAITS IN A PURE N’DAMA BREED IN THE GAMBIA

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INTRODUCTION
The International Trypanotolerance Centre (ITC) in the Gambia has implemented a livestock improvement programme, in low input systems, in 1994. The programme aims at a better utilization of local trypanotolerant breeds in West African countries, especially in the Gambia. In the breeding programme, the performance of animals is monitored since 1995. In 1998 selection of animals based on estimated breeding values for growth rate was introduced. Estimates of genetic and phenotypic parameters in pure breed indigenous N’Dama cattle populations are scarce. A few heritability estimates are available from experiments related to trypanotolerance (e.g. Trail et al., 1991). The aim of this study was to utilise the information available from the ITC improvement programme to estimate genetic parameters for growth traits in N’Dama cattle under tsetse challenge.

MATERIAL AND METHODS
Breeding environment and animal type. The production environment at two of ITC’s research stations (Keneba and Bansang) is characterised by a subtropical climate with distinct rainy and dry seasons. ITC has monitored village cattle in several localities during a long period. Results of the monitoring study showed a mean tsetse prevalence ranging from 0.4 % to 8.4 % in low and very severe challenge areas respectively. Agyemang et al. (1997) found considerable seasonal variations in the tsetse prevalence. Annual rainfall in most parts of the country does not exceed 1,016 mm. The birth weight of the Gambian N’Dama is on average 18 kg for males and 17 kg for females. Average mature live weight is 295 kg for males and 227 kg for females. The animals in the ITC programme are maintained under a low input management system and are all year grazing on natural pasture during the day. From November to June (dry season) animals loose weight, as the quantity and quality of feed is low. Details of herds management have been described by Agyemang et al. (1988a and 1988b) and Jeannin et al. (1988).

Population structure. The ongoing breeding programme annually utilises 6 breeding bulls and 400 adult breeding females. The pedigrees file included 1300 animals born from 1987 to 1996. The breeding bulls and the breeding females with their suckling calves (around 200) are kept in one main herd in Keneba under low to medium tsetse challenge (Watcher et al., 1993). After weaning at an age of 12 months, animals (around 450) are moved to Bansang (high tsetse challenge (Watcher et al., 1993)) were they are kept in four herds. Records on weight are taken on a monthly basis for each individual animal until they are three years old, after which
selection takes place. In the genetic analysis, only animals born after 01.01.1992 are considered. Sires of individuals, for the initial generation, are often unknown, however the dam is known for all animals. Ancestors with at least two offspring are included in the relationship matrix.

**Growth traits.** The body weight records used to derive the following traits (in kg) were weight at birth (BW), weight at 12 months (W12), weight at 15 months (W15), weight at 24 months (W24), and weight at 36 months (W36).

**Statistical analysis.** Variance components and genetic parameters were estimated using ASREML (Gilmour et al., 2000) using the following model:

\[
Y_{ijklm} = \mu + a_i + b_j + c_k + d_l + e_{ijklm}
\]

where \(a\) is the animal effect (\(i = 1,450\)), \(b\) is the fixed effect of year*season (\(j=1,6\)), \(c\) is the fixed effect of sex (\(k=1,2\)), \(d\) is the fixed effect of station and herd at which animal \(i\) is produced (\(l =1,5\)), \(e\) is the random error term. Heritabilities were estimated using a univariate model, whereas bivariate models were applied to estimate genetic and phenotypic correlations.

**RESULTS AND DISCUSSION**

**Summary Statistics.** Summary statistics are presented in table 1. The number of records decreased with age. This is partly caused by censoring, i.e. the animals born in most recent years have not reached the age of 36 months yet. From 24 to 36 months of age, around 222 (out of 795) animals have died. In many cases, trypanosomiasis was not the only cause of death. There is a large variation in weight at the different ages.

Table 1. Number of animals, mean, standard deviation minimum and maximum for the data used for the estimation of genetic parameters

<table>
<thead>
<tr>
<th>Traits</th>
<th>Animals</th>
<th>Mean</th>
<th>Std. dev.</th>
<th>Min.</th>
<th>Max.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth weight (kg)</td>
<td>1099</td>
<td>16.28</td>
<td>2.68</td>
<td>5</td>
<td>30</td>
</tr>
<tr>
<td>Weaning weight (kg)</td>
<td>752</td>
<td>79.78</td>
<td>13.46</td>
<td>33</td>
<td>131</td>
</tr>
<tr>
<td>Weight 15 months (kg)</td>
<td>795</td>
<td>87.96</td>
<td>15.17</td>
<td>49</td>
<td>150</td>
</tr>
<tr>
<td>Weight 24 months (kg)</td>
<td>707</td>
<td>123.91</td>
<td>20.63</td>
<td>70</td>
<td>193</td>
</tr>
<tr>
<td>Weight 36 months (kg)</td>
<td>532</td>
<td>165.29</td>
<td>23.6</td>
<td>83</td>
<td>258</td>
</tr>
</tbody>
</table>

**Genetic parameters of growth traits.** Estimates of heritabilities and genetic and phenotypic correlations for the traits BW, W12, W15, W24 and W36 are given in table 2. Heritabilities ranged from 0.11 for W24 to 0.40 for W36. The estimates for BW are in the range of estimates found in previous studies (Koots et al., 1994; Maiwashe et al., 2001) for different breeds. The heritability estimate for W12 is higher compared with those found in other similar studies (Mackinnon et al., 1991; Eler et al., 1995; Diop et al., 1998). Maternal genetic effects were ignored in our calculations. Accounting for maternal genetic effects is expected to lead to a lower estimate of the heritability for body weight measured early in the life of the animals (Meyer, 1992). After weaning the animals were moved to the high challenge area. Heritabilities for weight at 24 and 36 months were lower than for earlier weights. It is important to realize...
that the weight of an animal under high tsetse challenge is determined by its genetic potential for growth, but also by its level of trypanotolerance (e.g. Trail et al., 1992), and, therefore, may have a different genetic background compared to weights under low tsetse challenge. In addition, the variation in tsetse prevalence will contribute to a higher environmental variance.

Genetic correlations between birth weight and weights at later ages were moderate to high. This indicates that animals with higher birth weight usually also have a faster postnatal growth. Olutogun (1976) reported phenotypic correlations between birth weight and weaning weight of 0.19, which is slightly lower than the 0.26 that was estimated in this study. The genetic correlation between weaning weight and W36 was moderate (0.45). This correlation demonstrates that these two weights should be treated as separate traits. This was to be expected given the difference in environment (i.e. suckling under low challenge vs. weight under high challenge).

Table 2. Estimates of genetic parameters (s.e.) for growth traits with heritabilities on the diagonal, genetic correlations below and phenotypic correlations above the diagonal

<table>
<thead>
<tr>
<th></th>
<th>BW</th>
<th>W12</th>
<th>W15</th>
<th>W24</th>
<th>W36</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW</td>
<td>0.32 (0.09)</td>
<td>0.26 (0.04)</td>
<td>0.23 (0.03)</td>
<td>0.17 (0.04)</td>
<td>0.11 (0.05)</td>
</tr>
<tr>
<td>W12</td>
<td>0.51 (0.26)</td>
<td>0.37 (0.14)</td>
<td>0.8 (0.01)</td>
<td>0.62 (0.03)</td>
<td>0.40 (0.04)</td>
</tr>
<tr>
<td>W15</td>
<td>0.60 (0.28)</td>
<td>0.86 (0.07)</td>
<td>0.31 (0.13)</td>
<td>0.64 (0.02)</td>
<td>0.43 (0.03)</td>
</tr>
<tr>
<td>W24</td>
<td>n.e</td>
<td>0.58 (0.18)</td>
<td>n.e</td>
<td>0.11 (0.13)</td>
<td>0.57 (0.03)</td>
</tr>
<tr>
<td>W36</td>
<td>0.21 (0.29)</td>
<td>0.45 (0.26)</td>
<td>0.56 (0.31)</td>
<td>n.e</td>
<td>0.40 (0.22)</td>
</tr>
</tbody>
</table>

n.e = non estimable

CONCLUSION
Estimates of heritabilities indicate that additive genetic variance exists for these traits. Selection for these traits, therefore, is likely to result in genetic gain for growth in N’Dama cattle under tsetse infection pressure in the Gambia and in the humid zone of Africa in general. The high genetic correlations between traits indicate that not all traits need to be included in a selection scheme.

REFERENCES

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