ABSTRACT

Heritability estimates for growth traits were obtained in two Government owned Simmentaler stud herds in Namibia. Sires used in these herds were purchased on the basis of performance records. A derivative-free animal model REML programme was used with animals being the only random effect in the model. Estimates of heritability between the two herds were fairly consistent, but tend to be higher than mean estimates derived from literature. Estimates for birth, 100-day, 205-day and yearling masses varied from 0.40 (yearling mass in the Neudamm herd) to 0.72 (birth mass in the Uitkomst herd). No genetic trends were evident. However, a positive environmental trend (b = 0.495 ± 0.0690) was found in the Neudamm herd for birth mass. Within-herd sire selection is recommended as future breeding policy.

INTRODUCTION

The Simmentaler cattle breed was first imported to Namibia at the beginning of the last century. Although it was initially imported for dairy production purposes, it eventually became an important beef-producing breed. For many years it was considered to be the most important beef cattle breed in Namibia (Warning, 1971).

During 1952 the then Administration for South West Africa also bought Simmentaler cattle to supply milk to the Agricultural College at Neudamm. Some of these cattle were transferred to the Uitkomst Research Station during the early sixties. However, since the introduction of the National Beef Cattle Performance and Progeny Testing Scheme, when the breed was already recognized as primarily being a beef breed, the primary objective of the Government keeping these two stud herds was “to supply the commercial farming community with outstanding performance-tested genetic material” (Warning, 1971). Such an objective implicitly assumes that genetic progress would be made in these herds, otherwise there was no sense in keeping them. The purpose of the study, therefore, was to estimate heritabilities in performance recorded traits and to evaluate genetic progress in the two Government herds after 15 years of selection by means of mixed model methodology (Henderson, 1984).
Differences in performance, therefore, would be related to either a genetic difference or environmental differences mainly due to rainfall and grazing.

Observations

Records for birth, 100-day, 205-day and yearling masses as well as the respective growth rates between these masses were obtained. All mass records were adjusted to an age-constant basis. Body mass at 100-days was only recorded since 1974.

Statistical analysis

Estimates of variance components were obtained by Restricted Maximum Likelihood (REML) using the derivative-free algorithm of Graser et al. (1987) and fitted on an animal model (Meyer, 1989). The univariate model in matrix notation from Meyer's DFREML package used to analyse the data, was:

\[ y = X_1 b_1 + X_2 b_2 + Z u + e \]

where

- \( y \) = a vector of observations,
- \( b_1 \) = vectors of unknown fixed effects for year of birth, month of birth (October, November and December), age of dam (4 levels) and sex of calf,
- \( X_1 \) = known incidence matrices relating the records to the fixed effects \((b_1)(X_1-\bar{X}_1)\),
- \( u \) = vector of unknown random effects fitted which represent breeding values of the animals,
- \( Z \) = known incidence matrix relating the records to the unknown random effects \((u)\), and
- \( e \) = a vector of random residual errors.

It was assumed that the fixed effects were uncorrelated.

Since the two herds were relatively unrelated (only 3 sires were used in both herds in the early stage of the experiment), resulting in a lack of the necessary connectedness, “herds” were not included in the model.

Starting values for heritabilities of all traits were set at 0.35. The convergence was considered as being reached when the variance of the simplex function (Nelder and Mead, 1965) was less than \(0.1 \times 10^{-6}\).

Solutions for the fixed year effects of body mass traits (generalized least squares) are presented as environmental trends. Solutions for the other fixed effects (month of birth, age of dam and sex of calf) were reported by Nauhaus (1992) and follow the well-established pattern numerously presented in the literature.

Variance component estimates, obtained from this REML programme, were subsequently used to obtain genetic trends by fitting the following linear mixed model:

\[ y = X_1 b_1 + X_2 b_2 + Z u + e \]

where

- \( y, u, Z \) and \( e \) are as previously defined,
- \( b_1 \) = a vector of unknown fixed effects other than birth years and fitted as combined effects, i.e. age of dam, month of birth and sex of calf,
- \( b_2 \) = a vector of unknown birth year effects, and
- \( X_1 \) and \( X_2 \) = incidence matrices of fixed effects.

It is assumed that both \( E(u) \) and \( E(e) = 0 \) and that \( u \) and \( e \) are uncorrelated.

Furthermore that:

\[
\begin{bmatrix}
U \\
e
\end{bmatrix}
= \begin{bmatrix}
A/a & 0 \\
0 & I
\end{bmatrix} \sigma^2_e
\]

where

- \( a = \) the ratio between the error variance and additive genetic variance which is deducted from \(1-h^2\),
- \( A = \) the numerator relationship matrix, and
- \( I = \) an identity matrix.

Solutions to the mixed model equations were obtained by using the PEST computer package of Groeneveld and Kovac (1980) and Groeneveld et al. (1990). The solutions were considered to be converged when a criterion of 0.001 was reached.

Predicted breeding values (PBV) were averaged within year of birth and these averaged values, regressed on year of birth, represent the genetic trend for each trait.

RESULTS AND DISCUSSION

Data description

Characteristics of the dataset are presented in Table 1.

The most noticeable feature of the data is the higher body mass at all ages in the Uitkomst herd compared to the Neudamm herd. It is not clear to what extent this difference is genetically determined. It may probably be related to more favourable conditions due to a higher rainfall and longer growth period of pastures at Uitkomst.

Preweaning growth rate was also higher in the Uitkomst herd compared to the calves in the Neudamm herd. However, the opposite applied to postweaning growth where calves in the Neudamm herd grew faster (25.6%) than those in the Uitkomst herd. The reason for this is also not obvious, but may be related to a higher nutritive value of winter grazing at Neudamm.
were 0.39 (number of estimates n = 84) and 0.36 (n = 20) for the two herds respectively. Mean estimates for birth mass, obtained respectively, which is higher than the mean value of 0.26 (n = 18). The same applied to preweaning ADG, where estimates of 0.41 and 0.40 were obtained respectively, which is higher than the mean value of the reviewed estimates (h² = 0.32; n = 12) by Meyer (1992), but lower than the values of 0.57 and 0.58 reported by Brown et al. (1990).

Heritabilities for 100-day mass (0.53 and 0.57 respectively) were also higher than those reported by Brown et al. (1972) (h² = 0.17) and Swanepoel and Heyns (1988) (h² = 0.21).

Both estimates for 205-day mass were 0.41 and fall within the ranges reviewed by Woldehawariat et al. (1977) and Meyer (1992), but were also higher than the respective mean values of these reviewed estimates. The mean values reported by these authors were 0.31 (n = 103) and 0.25 (n = 21) respectively. Values of 0.26, 0.25 and 0.27 were also reported by Bertrand et al. (1985), Sharma et al. (1985) and Swanepoel and Heyns (1988). Direct heritability estimates obtained by Meyer (1992) and which excluded maternal effects, varied from 0.07 to 0.59, with a mean value of 0.26 (n = 18). The ranges for 100-day mass (h² = 0.53 and 0.57 respectively) were also higher than those reported by De Nise and Torabi (1989) (h² = 0.21) and the reviewed mean values reported by Meyer (1992) (h² = 0.32; n = 2).

Table 2. Components of variance and heritability estimates (h²) for body mass and growth traits in the Neudamm and Uitkomst herds

<table>
<thead>
<tr>
<th>Traits</th>
<th>Neudamm</th>
<th>Uitkomst</th>
<th>h²</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>σ²_P</td>
<td>σ²_A</td>
<td>σ²_E</td>
</tr>
<tr>
<td>Birth mass</td>
<td>21.53</td>
<td>11.19</td>
<td>10.33</td>
</tr>
<tr>
<td>100 days mass</td>
<td>226.49</td>
<td>118.90</td>
<td>107.58</td>
</tr>
<tr>
<td>205 days mass</td>
<td>486.01</td>
<td>200.48</td>
<td>285.53</td>
</tr>
<tr>
<td>Yearling mass</td>
<td>522.82</td>
<td>209.31</td>
<td>313.12</td>
</tr>
<tr>
<td>Birth to 100-days ADG</td>
<td>0.179x10⁻¹</td>
<td>0.990x10⁻¹</td>
<td>0.803x10⁻¹</td>
</tr>
<tr>
<td>Birth to 205-days ADG</td>
<td>0.113x10⁻¹</td>
<td>0.468x10⁻¹</td>
<td>0.666x10⁻¹</td>
</tr>
<tr>
<td>Postweaning ADG</td>
<td>0.976x10⁻¹</td>
<td>0.452x10⁻¹</td>
<td>0.526x10⁻¹</td>
</tr>
<tr>
<td></td>
<td>σ²_P</td>
<td>σ²_A</td>
<td>σ²_E</td>
</tr>
<tr>
<td></td>
<td>32.83</td>
<td>23.62</td>
<td>9.21</td>
</tr>
<tr>
<td></td>
<td>335.49</td>
<td>192.12</td>
<td>143.37</td>
</tr>
<tr>
<td></td>
<td>657.51</td>
<td>271.22</td>
<td>386.29</td>
</tr>
<tr>
<td></td>
<td>961.84</td>
<td>504.47</td>
<td>456.37</td>
</tr>
<tr>
<td></td>
<td>0.252x10⁻¹</td>
<td>0.115x10⁻¹</td>
<td>0.137x10⁻¹</td>
</tr>
<tr>
<td></td>
<td>0.140x10⁻¹</td>
<td>0.561x10⁻¹</td>
<td>0.842x10⁻¹</td>
</tr>
<tr>
<td></td>
<td>0.165x10⁻¹</td>
<td>0.705x10⁻¹</td>
<td>0.942x10⁻¹</td>
</tr>
</tbody>
</table>

σ²_p = phenotypic variance; σ²_A = additive genetic variance; σ²_E = environmental variance
Table 3. Regression equations for genetic and environmental trends for mass traits in the Neudamm and Uitkomst herds

<table>
<thead>
<tr>
<th>Traits</th>
<th>Neudamm</th>
<th></th>
<th></th>
<th></th>
<th>Uitkomst</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Genetic</td>
<td>R² (%)</td>
<td>Environmental</td>
<td>R² (%)</td>
<td>Genetic</td>
<td>R² (%)</td>
<td>Environmental</td>
<td>R² (%)</td>
</tr>
<tr>
<td>Birth mass</td>
<td>Y=-1.71+0.023X (± 1.56) (± 0.020)</td>
<td>7.97</td>
<td>Y=-37.80+0.495X (± 5.28) (± 0.069)</td>
<td>78.63</td>
<td>Y=-1.30-0.016X (± 1.77) (± 0.023)</td>
<td>3.35</td>
<td>Y=-8.25+0.106X (± 6.37) (± 0.083)</td>
<td>10.34</td>
</tr>
<tr>
<td>100-day mass</td>
<td>Y=-4.66+0.060X (± 4.02) (± 0.051)</td>
<td>12.22</td>
<td>Y=-69.93+0.911X (± 74.93) (± 0.953)</td>
<td>8.36</td>
<td>Y=-1.77+0.023X (± 6.09) (± 0.077)</td>
<td>0.91</td>
<td>Y=-38.54+0.500X (± 49.62) (± 0.631)</td>
<td>5.90</td>
</tr>
<tr>
<td>205-day mass</td>
<td>Y=2.40+0.034X (± 5.56) (± 0.072)</td>
<td>1.52</td>
<td>Y=-116.54+1.572X (± 69.21) (± 0.903)</td>
<td>17.80</td>
<td>Y=-4.88+0.062X (± 5.58) (± 0.073)</td>
<td>4.89</td>
<td>Y=-87.24+1.161X (± 58.74) (± 0.786)</td>
<td>14.08</td>
</tr>
<tr>
<td>Yearling mass</td>
<td>Y=-0.10+1.40x10⁻³X (± 0.23) (± 3.05x10⁻³)</td>
<td>1.47</td>
<td>Y=-53.72+0.729X (± 64.30) (± 0.839)</td>
<td>5.11</td>
<td>Y=-22.27+0.281X (± 10.63) (± 0.138)</td>
<td>22.71</td>
<td>Y=-97.65+1.311X (± 117.98) (± 1.539)</td>
<td>4.93</td>
</tr>
</tbody>
</table>

Heritabilities for all traits seem to be biased upwards. Reasons for this are not clear. Although heritabilities in good environments tend to be higher than in poor environments (Garrick and Van Vleck, 1987; De Nise et al., 1988; De Nise and Torabi, 1989), there may be other reasons as well. Since only the additive genetic component was considered in the model fitted, both maternal genetic and maternal permanent environmental effects could be confounded with the additive effect giving rise to an 'inflated' estimate (Thompson, 1976; Bertrand and Benyshek, 1987; Brown et al., 1990; Mrode and Thompson, 1990; Meyer, 1992). However, since the main objective of the study was to assess genetic response in the herds and on account of the finding by Erasmus (1988), namely that by using different heritabilities, it does not have a serious effect on the response curve, it was decided to use the obtained estimates.

Genetic and environmental trends

Regression equations expressing genetic and environmental trends for birth, 100-day, 205-day and yearling masses are presented in Table 3.

Although both genetic and environmental trends were in almost all cases characterized by positive slopes, R² values were, with the exception of the environmental trend for birth mass in the Neudamm herd, extremely low. In all cases large year-to-year fluctuations were evident. This is illustrated in Figures 1 and 2 for birth mass only. The same, however, applied to the other traits.

![Figure 1. Genetic trends for birth mass.](image1)

![Figure 2. Generalized least squares by year for birth mass.](image2)
Only a slight tendency of genetic change was found in yearling mass in the Utikomist herd, indicated by a regression coefficient of 0.281 kg/yr (R² = 0.22711). A positive environmental trend in 205-day mass, indicated by a slope of 1.572 kg/yr (R² = 0.1780%) was evident in the Uitkomst herd. All other traits exhibit, both genetically and environmentally, a highly fluctuating nature. In the case of the genetic trends it could possibly be related to variable genetic merit of sires which were purchased and used in these herds.

CONCLUSIONS

Although heritabilities differ among populations and are also affected by environmental conditions, the relatively high estimates obtained in this study may also be related to maternal genetic and environmental effects confounded into the additive component. One is further inclined to expect some genetic progress with heritabilities of this magnitude and especially where selection was based on performance recorded traits. However, in both herds no genetic change worth mentioning was evident for any trait. If sire replacements were selected from within the respective herds, more genetic progress could have been possible. No genetic change was also obtained by Van der Westhuizen (1990) in a Bonsmara herd where sire replacements were purchased. It is therefore recommended that the now combined Simmentaler herd of the Namibian Department of Agriculture should either be closed or sires with proven high breeding values be used (e.g. AI sires).

REFERENCES


