COMPARISON OF LINEAR AND THRESHOLD MODELS FOR PREDICTING DIRECT AND MATERNAL GENETIC EFFECTS ON NUMBER OF LAMBS WEANED IN WESTERN AUSTRALIAN MERINO SHEEP

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INTRODUCTION
In Australia, wool quantity and quality has traditionally contributed most of the gross returns in Merino sheep enterprises. Notwithstanding, recent high prices for sheep meat are likely to increase the interest in, and importance of the reproductive rate of Merino sheep. Reproductive performance is recorded in discrete categories but analysed as a continuous trait. In theory, methods for analysing continuous data are not suitable for categorical traits (Thompson, 1979). Non-linear models such as the threshold model (TM) (Gianola and Foulley, 1983; Harville and Mee, 1984; Gilmour et al., 1985) have been proposed for estimating breeding values for categorical traits.

Advantages of threshold over linear models have been shown with simulated data (Meijering and Gianola, 1985; Hoeschele, 1988). However, variable results have been found with field data. Researchers have found either advantages of threshold over linear models (Ramirez-Valverde et al., 2001; Verona et al., 1999b), similar performance of threshold and linear models (Weller et al., 1988; Matos et al., 1997) or advantages of linear over threshold models (Hagger and Hofer, 1989).

Our objective was to compare the accuracy of a threshold animal model (TAM) to a linear animal model (LAM) for direct and maternal genetic evaluations of number of lambs weaned in Merino sheep.

MATERIAL AND METHODS
Data. The data were from a resource flock held at Katanning in Western Australia (Cloete et al., 2001). The number of lambs weaned (NLW) was recorded in two categories (1 and 2) and a total of 9850 observations were available. Most of the records fell into category 1 (78.7%) and the average number of weaned lambs was 1.2. Full pedigree records were available for all animals as well as information on year of birth (1982-1993), sex (male or female) and age of dam (2 to 4+ years).

Models of analysis. Analyses were performed using an animal model with a maternal effect, i.e. the NLW was considered as a trait of the ewe. All models included year of birth and sex effects as fixed factors and age of dam as a covariate.

Linear animal model. Number of lambs weaned was modeled as a continuous trait represented by the equation:

\[ y = X\beta + Z_1u_d + Z_2u_m + e \]
where $\beta$ is a vector associated with fixed effects; $u_d$ and $u_m$ are vectors containing direct additive and maternal effects, respectively; $e$ is a vector of residuals; and $X, Z_1,$ and $Z_2$ are incidence matrices corresponding to $\beta$, $u_d$, and $u_m$, respectively.

**Threshold animal model.** The assumed model for the underlying distribution of the number of lambs weaned ($L_{NLW}$) was the same as the linear animal model:

$$L_{NLW} = X\beta + Z_1 u_d + Z_2 u_m + e$$

but the response of number of lambs weaned was modeled with the following distribution:

$$f(y | L) = \prod_{i=1}^{2} f(y_i | L_i) = \prod_{i=1}^{2} I(L_i < t_i)I(y_i = 1)$$

where $t_i$ is the threshold that defines the two categories of response and $I$ is an indicator function that takes the value of 1 if the conditions specified are true, otherwise the value is 0.

Variance-covariance components used in the linear model were estimated by restricted maximum likelihood method (REML) (Meyer, 1997). The co-variance components used in the threshold animal model were estimated by a quasi-REML method as implemented in the CBLUP90REML program (Mizstal, 1999). The iterations were stopped when the convergence criteria was $10^{-9}$. The programs BLUP90 and BLUPthr were used to obtain solutions for linear and threshold models, respectively (Mizstal, 1999).

**Comparison of models.** A cross-validation method was used to assess the predictive ability of the models (Stone, 1974; Shao, 1993). The procedure used in this study was similar to that described by Ramirez-Valverde et al. (2001). The data set was duplicated and one-half of the NLW records were discarded in the first subset. The remaining NLW records were discarded in the other subset. Solutions for each model were obtained from both subsets and the correlation between predicted breeding values from the two subsets was calculated. A higher correlation estimate between subsets implied a higher stability of the model for predicting breeding values in deleted records. The reported correlations were the average of 20 replicates.

**RESULTS AND DISCUSSION**

The estimates of variance-covariance components with linear and threshold models for NLW are shown in Table 1. As expected larger estimates of heritabilities were obtained when the threshold model was employed. Similar results were reported for dystocia in cattle (Verona et al., 1999a) and for litter size in sheep (Matos et al., 1997). In these studies a substantial increase in heritability estimates was observed, whilst in our study there was only a slight increase. The estimate of the direct heritability was virtually the same as the estimates recently reported by Brown et al. (2001).
Table 1. Estimates of variance-covariance components and heritabilities with linear and threshold models

<table>
<thead>
<tr>
<th>Component</th>
<th>Linear</th>
<th>Threshold</th>
</tr>
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<tbody>
<tr>
<td>$\sigma_d^2$</td>
<td>0.0141</td>
<td>0.120</td>
</tr>
<tr>
<td>$\sigma_m^2$</td>
<td>0.0200</td>
<td>0.190</td>
</tr>
<tr>
<td>$\sigma_{dm}$</td>
<td>0.0130</td>
<td>0.118</td>
</tr>
<tr>
<td>$\sigma_e^2$</td>
<td>0.1245</td>
<td>1.0</td>
</tr>
<tr>
<td>$h_d^2$</td>
<td>0.08</td>
<td>0.12</td>
</tr>
<tr>
<td>$h_m^2$</td>
<td>0.12</td>
<td>0.16</td>
</tr>
</tbody>
</table>

The estimates of heritabilities from LAM were converted to the underlying scale by the method of Dempster and Lerner (1950). The values for converted $h_d^2$ and $h_m^2$ were 0.119 and 0.179, respectively. However, several studies (Hoeschele et al., 1987; Olausson and Ronningen, 1975; Van Vleck, 1972) have shown that the correction factor seems to overcorrect $h^2$. The averages of the correlations among breeding values for NLW from the linear and threshold models used in analysing split data sets are presented in Table 2.

Table 2. Average, minimum and maximum correlation estimates between split data sets for number of lambs weaned breeding value solutions from linear and threshold models

<table>
<thead>
<tr>
<th>Model</th>
<th>Direct genetic effect</th>
<th>Maternal genetic effect</th>
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<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>SD</td>
</tr>
<tr>
<td>LAM</td>
<td>0.52</td>
<td>0.01</td>
</tr>
<tr>
<td>TAM</td>
<td>0.57</td>
<td>0.01</td>
</tr>
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</table>

For the direct additive genetic effect the correlation from the threshold model was 10% higher than from the linear model (0.57 vs 0.52). These results were consistent for all 20 replicates and are similar to the results obtained by Verona et al. (1999b). For maternal effects the ranking of the models followed the same pattern, but the correlation estimate rose less (7%) from use of the threshold model. Our findings for both direct and maternal genetic evaluations are very close to those reported by Ramirez-Valverde et al. (2001).

Our results confirm the better performance of a threshold animal model compared to a linear animal model. The difference between the two models is small. In contrast Ramirez-Valverde et al. (2001) found that a bivariate threshold-linear model had a 30% higher correlation estimate among breeding values for dystocia in cattle than a univariate threshold model. This information suggests that bivariate models could be a good alternative to univariate models, especially for low accuracy animals.
CONCLUSION
A univariate threshold animal model performed better than a univariate linear animal model for genetic evaluation of number of lambs weaned. For practical purposes, however, the advantage of using a univariate threshold model instead of a linear model is small. Further investigation involving continuous traits such as fleece weights and/or fibre diameter is needed in order to fully assess the predictive ability of the two models.

REFERENCES