

DEVELOPMENT OF A GENETIC EVALUATION SYSTEM FOR STRUCTURAL SOUNDNESS TRAITS IN ANGUS CATTLE

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SUMMARY

Three options comprising a generalized threshold model and two linear animal models were explored to predict and express breeding values for structural soundness traits in Angus cattle, using front feet angle as an example trait. Front feet angle scores (scored on a 1 to 9 scale, with 5 being the most desirable score) from 2926 Angus cattle under three years of age were used. Estimated breeding values (EBVs) predicted from a generalized threshold model by grouping animals with scores 1 to 4 as category 1, representing steep foot angle (%STE), category 2 with score of 5, representing desirable score (%DESI) and category 3 with scores 6 to 9, representing shallow foot angle (%SHA). These were compared with EBVs from a conventional linear animal model with the original scores of 1 to 9 or after assigning scores according to Snell's procedure to differentiate desirable scores. EBVs obtained as %DESI was identified as an appropriate way to express EBVs in a manner that would allow breeders to identify differences in Angus cattle for expected progeny structural soundness.

INTRODUCTION

Structural soundness (SS) traits play a major role in determining the length of productive life of a breeding cow and the incidence of bull breakdown in breeding herds. Structural soundness traits in young animals are used as early predictors of longevity in dairy cattle and may also be useful in beef cattle to reduce the replacement costs in the breeding herds. Therefore, it is important to develop a genetic evaluation system to assist beef breeders in selecting replacement sires with desirable SS. In the BeefClass Structural Assessment system (Angus Australia, 2003), SS traits are scored on a 1 to 9 scale with 5 being the most desirable score. Therefore, expression of EBVs based on conventional linear animal model evaluation may not give clear direction in identifying replacement animals with desirable SS. Threshold models have been suggested by Gianola and Foulley (1983) as a more appropriate means of analyzing traits that are scored as one of several ordered categories. The advantage of using threshold models over the conventional linear animal models is mostly determined by the distribution of observations across the identified scores (Jamrozik *et al.* 1990). For SS traits in Angus cattle in Australia, which are scored on a 1 to 9 scale, with lack of recording at the extreme categories, a threshold model may be an appropriate method for genetic evaluation. Therefore, various generalized threshold model and the conventional linear models were compared to identify an appropriate method to express breeding values, which allows breeders to easily differentiate Angus cattle with normal SS traits from others.

MATERIALS AND METHODS

Data used for this study were from Angus seedstock herds using the BeefClass Structural Assessment System, which was initiated in 2001. Of the SS traits scored in the above system, the feet and leg

¹ AGBU is a joint venture of NSW Department of Primary Industries and the University of New England

Genetic Evaluation

(FLEG) traits were considered important, and comprised: front feet angle (FA), rear feet angle, front feet claw set, rear feet claw set, rear leg side view and rear leg hind view. The majority of males were scored before two years of age and most of the females were scored between two to three years of age. The estimated heritability for FA from a univariate REML procedure was $0.33(\pm 0.05)$ and was very close to the estimates obtained for other FLEG traits in this study. Therefore, FA was chosen as an example trait in this study to predict and express breeding value for SS traits in Angus. Front feet angle scores on 2054 males and 872 females born in 2000 to 2003 from 126 herds across Australia, with the mean of 6.2 and the standard deviation of 0.7, were used in this study. The distribution of observations across the FA scores is given in Figure 1. The majority (99.7%) of the observations was between the scores of 5 to 8 and no animal was scored with the score of 1 to 3.

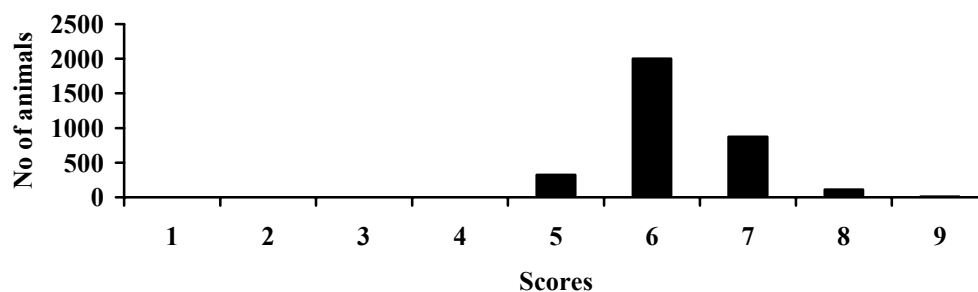


Figure 1. Distribution of scores for front feet angle in Angus males and females below the age of 3 years.

Genetic evaluation. The model fitted for the prediction of breeding values for FA was

$$Y_{ijk} = \mu + CG_i + age_j + a_k + e_{ijk}$$

where Y_{ijk} is the FA score of the k^{th} animal in the i^{th} fixed contemporary group (CG_i) with j^{th} age with a_k is the random animal effect and e_{ijk} is the random residual error. Contemporary group was formed by combining a) herd in which traits were recorded b) date of measurement c) trait management group d) weaning weight management group e) sex and f) 60 days age slicing. Age at scoring was fitted as a linear covariate. Variances estimated from a univariate analysis using ASREML (Gilmour *et al.* 1999) were used as the priors to predict EBVs. Three options were considered for the prediction of EBVs.

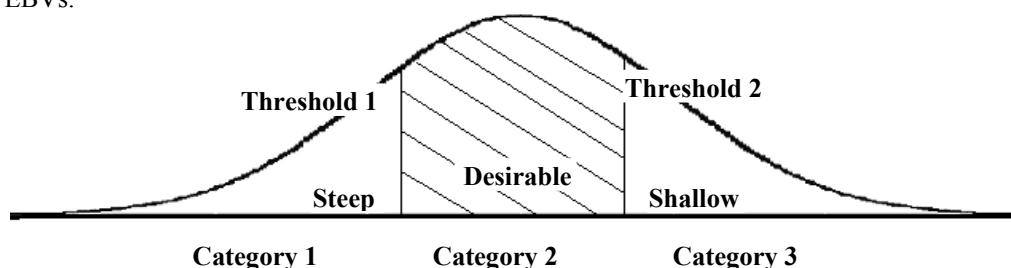


Figure 2. The distribution of front feet angle scores with three categories and two thresholds.

Option 1: A generalized twin-threshold model was used to obtain probabilities within defined categories. Scores of 1 to 9 were grouped into three categories: animals with the scores 1 to 4 were grouped into Category 1 (Steep), a score of 5 was grouped into Category 2 (Desirable) and scores 6 to 9 were grouped into Category 3 (Shallow) as shown in Figure 2. The above grouping was made to differentiate the steep and shallow angles in FA. The genetic solution for FA on the underlying scale was simultaneously adjusted for contemporary group and age effects. The adjusted genetic value was then converted to %STE (for category 1) and %SHA (for category 3) by calculating the area that a random normal variable deviate from the Threshold 1 and Threshold 2, respectively. %DESI (for category 2) was obtained by calculating the area within the %STE and %SHA deviations.

Option 2: EBVs were predicted using a conventional linear animal model (LAM) using the FA scores of 1 to 9.

Option 3. Linear scores were assigned to FA scores according to Snell's procedures (1964) to clearly differentiate the animals with desirable scores. Values of 20, 40, 60, 80, 100, 80, 60, 40 and 20 were assigned to the FA scores of 1, 2, 3, 4, 5, 6, 7, 8 and 9, respectively. A linear animal model evaluation (SLAM) was used to predict breeding values using the re-assigned values.

RESULTS AND DISCUSSION

Distributions of EBVs expressed as %STE, %SHA and %DESI from Option 1, from LAM in Option 2 and from SLAM in Option 3 among sires with more than 20 progeny (high-acc-sires) and young males born in 2003 (young males) are given in Table 1. Estimated breeding vales expressed as %STE among high-acc-sires ranged between -0.01% and 0.13% and expressed as %SHA ranged between -27% and 9.5%, with 50% of the sires expressing negative probability for %STE. The correlation between EBVs expressed as %DESI and %STE, %SHA, LAM and SLAM in high-acc-sires were 0.9, -1.0, -0.8 and 0.8, respectively, indicating that the EBVs expressed as %STE, %SHA and %DESI from a generalized linear model were highly correlated with each other. There may be a slight re-ranking of sires across EBVs from %DESI and LAM or SLAM. The average EBVs obtained from all three options for young males were very similar from those of the high-acc-sires, but the EBVs of the young males showed less spread for all options relative to those of high-acc-sires. Lack of observations in scores 1 to 3, gave lesser spread for %STE than %SHA for both high-acc-sires and young males. The correlation coefficient of 0.6 between %DESI and the EBVs predicted from SLAM in young males indicated that there is significant re-ranking across these two evaluations. Expressing EBVs as %DESI appeared to be an appropriate way for young males. Therefore, generalized threshold model was more appropriate for the prediction of EBVs in young males and high-acc-sires.

Table 1. Distribution of EBVs for FA among among sires (n=32) with more than 20 progeny (High-acc-sires) and young males (n=540) born in 2003 (Young-males).

EBV Expressed as	From Option	High-acc-sires		Young-males	
		Mean	Standard deviation	Mean	Standard deviation
%STE	1	0.01	0.03	0.01	0.01
%SHA	1	-2.06	9.53	-0.92	3.04
%DESI	1	14.55	9.50	13.42	3.03
LAM	2	-0.04	0.25	-0.04	0.14
SLAM	3	0.78	5.02	0.71	2.90

Desirable method to predict EBVs. The advantage of using a linear animal model evaluation to predict EBVs in LAM or SLAM is that this requires less intensive computing than Option 1. However, EBVs predicted from LAM will not clearly identify the sires which have progeny in the desirable category. In a scoring system with 1 to 9 scores, animals with higher EBVs will have shallow angle and animals with lower EBVs will have steep angle. Therefore, breeders will have difficulty in choosing animals with the most desirable EBV. The EBVs predicted from SLAM are expected to give a clearer direction to breeders in selecting the sires to improve the locomotive capacity. The correlation coefficients of 0.6 and 0.8 between the EBVs derived from %DESI and SLAM in young males and high-acc-sires, respectively, showed that the sires were re-ranked across the two evaluations, particularly for young males. Using Snell scoring procedures to convert the scales by assigning values in SLAM may not yield a normal distribution and may not be appropriate for FA in this study, which lacked observations for extreme scores. Moreover, the differences between the EBVs from SLAM and %DESI is expected to widen when the heritability estimated on the underlying scale is used to predict %DESI in a generalized twin threshold model evaluation.

Under the generalized twin threshold model, expression of %STE in Option 1 depended on the expression of %SHA, with a correlation of -0.88 between the two probabilities. The nature of the two abnormalities is such that the increase in the appearance of one category tends to reduce the appearance of the other category. Therefore, expressing EBVs either in %STE or in %SHA alone may not help to identify the bulls with higher proportion of progeny in the desirable category. Furthermore, presently the outcome of crossing a bull with high %STE to a female with low %SHA or vice versa is not clear. Therefore, expressing EBVs by combining %STE and %SHA provides limited information to beef breeders, while demanding two sets of EBVs for each trait. On the other hand, the EBVs expressed as %DESI had correlation coefficients of 0.9 and -1 with %STE and %SHA, indicating that the EBVs expressed as %DESI will account for both %STE and %SHA, while clearly differentiating between desirable FA and the two angles. Therefore, it is clear from this study that the EBVs expressed in %DESI, after accounting for steep and shallow angles, identify the bulls with a higher proportion of progeny with optimum FA and gives clearer direction to beef breeders.

CONCLUSION

Expressing EBVs as %DESI appears to be an appropriate method to differentiate animals with sound FA from those with abnormal angle. This procedure will be implemented in the BREEDPLAN evaluation once more than 5000 records have been recorded.

ACKNOWLEDGEMENT

The authors would like to thank the Meat and Livestock Australia (MLA) for their financial support through BFGEN 100b and the Angus Society of Australia for providing data for this study.

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