

MIXED MODEL EVALUATION OF ARGENTINE
REGISTERED ANGUS HERDS

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SUMMARY

Weaning weight (WW) records of 2,160 registered Angus calves were used to compare different models of evaluation, to estimate genetic trend and to estimate the relationship between the US base for WW and the base in the two herds under study. Calves were the progeny of 55 bulls and were born during 1973 to 1984. The models analysed considered sires unrelated vs. sires related and sires nested within genetic groups vs. ignoring groups. Mixed model and REML procedures were used to obtain group and sire solutions and the variance components, respectively. The range on Expected Progeny Differences (EPDs) was between 17.7 and 19.1 kg. (2.8 to 3.1 σ). It was observed a positive genetic trend for the north american bulls and the home bred sires showed higher solutions with the increase in north american blood. Correlations among the four methods were between 0.646 to 0.969. Inclusion of the relationship matrix resulted in decreased Standard Error of Prediction (SEP) by 3.7 to 22.9% depending on group. The relationship between the US base and the base in these herds was measured by the equation $EPD_{local} = -5.37 + 0.85 EPD_{USA}$.

INTRODUCTION

The Breeding plans in registered Angus herds in Argentina have included both artificial insemination (AI) with imported semen mostly from the USA and Canada and within herd selection. The consequences of these programs in terms of genetic improvement are not known.

Best Linear Unbiased Predictions (BLUP) procedures of Henderson (1973) are increasingly being used for National Sire Evaluation of beef cattle (Willham, 1979). In dealing with this methodology grouping strategies of sires is critical when most of the animals in the pedigree are not used in the computation of the additive

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relationship matrix A (Sorensen and Kennedy, 1984). Therefore the objectives of this preliminary research are:

- 1- To compare different models of sire evaluation in which sires are grouped or not and A is included or not.
- 2- To estimate genetic trend through direct effects of sire on WW.
- 3- To study the relationship between the US Angus base and the base in these herds.

MATERIAL AND METHODS

The cattle

Data were taken from two herds of registered Angus of the same company during 1973 to 1984. The management of the herds is typical of the purebred operations in central Argentina. It is a temperate area with no snow in winter. Calves are not creep feed until the age at weighting at 182 ± 24 days in this study.

Imports of semen from the US and Canada have taken place before 1973. The data file used included 2,160 calves sired by 55 Angus bulls with 10 of them having progeny in both herds.

Since calves are sometimes managed in small contemporary groups the file was previously edited to keep the groups to a size of at least 5 calves sired by at least two sires.

The models

All models were variations of the mixed model:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$$

where \mathbf{y} , \mathbf{b} , \mathbf{u} and \mathbf{e} are vectors of records (WWs), fixed effects (sex of calf, age of dam, herd, sire genetic group and the regression of WW on age at weaning and contemporary group mean), random effects (sire within group) and residuals, respectively. First moments where $E(\mathbf{y}) = \mathbf{Xb}$, $E(\mathbf{u}) = 0$, $E(\mathbf{e}) = 0$. Second moments were assumed to be $V(\mathbf{u}) = \mathbf{Gc}_s^2$, $V(\mathbf{e}) = \mathbf{Rc}^2$ and $V(\mathbf{y}) = \mathbf{ZGZ}' + \mathbf{R}$. The $V(\mathbf{e})$, \mathbf{R} was considered diagonal since it was detected an heteroscedastic ($P < 0.01$) c^2 due to herd (528.12 vs. 337.34 kg^2).

Sire evaluation alternatives considered

Grouping criteria were origin of bulls, percentage of north american genes and/or bull year of birth. Thus, 7 groups were formed:

- 1N - North american (USA or Canada) bulls born between 1967 to 1972
- 2N - Same as in 1N but born in 1973 or 1974.
- 3N - Same as in 1N but born in 1975 or 1976.
- 4N - Same as in 1N but born from 1977 to 1979.
- 1A - Bulls born in Argentina sired by an N bull.
- 2A - Same as in 1A but with the maternal grand sire being N too.
- NM - Natural mating (unidentified sire).

The A matrix was formed by looking at the pedigrees until the fourth generation.

The models compared were the same 4 as the ones evaluated by Pollak *et al* (1977): the combination of grouping or not and including A or not.

The resulting equations for BLUP were:

$$\begin{bmatrix} X^1 R^{-1} X & X^1 R^{-1} Z \\ Z^1 R^{-1} X & Z^1 R^{-1} Z + G^{-1} \end{bmatrix} \begin{bmatrix} \mathbf{b} \\ \mathbf{u} \end{bmatrix} = \begin{bmatrix} X^1 R^{-1} y \\ Z^1 R^{-1} y \end{bmatrix} \quad (1)$$

\mathbf{a} is the ratio c^2/c_s^2 .

Direct inversion was used for both the system (1) and the A matrix.

Variance components were estimated by Restricted Maximum Likelihood (REML) procedures as outlined by Harville (1977) based on iterating the model with and without A not including groups.

RESULTS AND DISCUSSION

The estimates of h^2 were almost equal (0.3025 vs. 0.3018) assuming $G = A$ or $G = I$, respectively. The range in EPDs is shown on table 1 for the four models. Again the values are closely similar. For the Angus breed in Australia Morris and Gibson (1984) reported a value of 18.4 kg. (2.5 c) and in Canada Schaeffer and Wilton found 42 kg. (3 c).

Table 1: Range in EPDs (kg.) for different models (1)

Model		kg.	Range in EPDs c
G	Grouping		
I	NO	17.7	2.8
A	NO	18.8	3.0
I	YES	19.1	3.1
A	YES	18.8	3.0

(1) Sire component = 38.8 kg².

Group solutions for the models assuming sires unrelated ($G = I$) or related ($G = A$) are shown in table 2. The genetic differences between populations (NM, 1A or 2A vs. the imported semen groups) are clearly seen. The positive genetic trend in the imported semen is in agreement with the one reported in the Angus National Sire Evaluation program in the U.S. (Berger *et al*, 1983). The influence of the northamerican genes could be observed while comparing the 1A vs. 2A groups, the latter having a higher value. There were not enough home bred sires in this data set to create more groups based on bull's year of birth. The A matrix had approximately 2% of nonzero elements (not counting the diagonals). As in Pollak *et al* (1977) the groups with less relationships (2N, 4N y 2A) with others had the smaller change in the solutions while the groups 1N, 3N and 2A maintained a similar difference between $G = I$ and $G = A$.

Table 2: Comparisons of sire group solutions from models in which sires were assumed unrelated (G = I) or related (G = A) and increase in SEP due to not including A.

Group	Number of sires	Number of observations	Increase in SEP (%)	Group solutions (kg)	
				G = I	G = A
1N	7	298	11.5	3.75	4.85
2N	19	357	14.6	7.26	7.27
3N	10	430	3.7	10.27	8.97
4N	7	354	3.8	14.57	14.66
1A	6	113	10.2	3.97	4.77
2A	6	158	22.9	5.46	5.62
NM	2	450	-	0.00	0.00

Table 3 shows the correlations among sire solutions for the different models.

Table 3: Correlations among Sire EPDs

	Sires not grouped		Sires grouped	
	G = I	G = A	G = I	G = A
Sires not grouped				
G = I	-	0.969	0.657	0.857
G = A	-	-	0.646	0.884
Sires grouped				
G = I	-	-	-	0.743

Even though correlations are higher than 0.64, they are not as high as the ones obtained by Pollak *et al* (1977) who added sire plus group solutions. However, grouping bulls and including A was better correlated with the no grouping alternatives (0.85 and 0.88) than with the model with groups and G = I (0.74).

Sorensen and Kennedy (1984) have indicated that a condition for the mixed model analysis to partition phenotypic trend correctly is that the relationship matrix is complete. Since this study was carried out with only 2% of the A elements filled a bias is introduced. Therefore, including A and grouping in the model seemed to decrease the bias associated with selection in the present analysis.

Table 2 also shows the increase in the SEPs (on a group basis) due to consider sires unrelated for both models with groups. As expected, including relationships decreased SEPs. Pollak *et al* (1977) also reported an increase in accuracy of prediction due to the inclusion of the A matrix going from 1.5 to 10.5%.

Using EPDs from the 1983 Angus Sire summary it was calculated a correlation of 0.87 between the EPDs in US and in these two herds.

A weighted regression analysis using the inverse of the SEPs gave this relationship between the EPDs in the two countries: EPD local = -5.37 kg. + 0.85 EPD USA.

Discussion

The grouping strategy in this study seemed to be useful to account for genetic trend. More than half of the sires had a higher value for their solutions than the values of their SEPs. In no case a bull had a SEP greater than the BLUE of the difference between herds. The design matrix in the study had a totally connected cell pattern (Searle, 1971).

Including the A matrix resulted in decreased variance of error of prediction specially for sires with few observations.

As Pollak et al (1981) concluded the present study also suggests that including relationships does not negate the need for including sire groups. EPDs accuracy, on the contrary, seems to improve when combining both sources of information using field data.

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