NORTH AMERICAN GENETIC EVALUATION OF AYRSHIRE BULLS
WITH A LINEAR MODEL

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SUMMARY

A system was developed to compare bulls across countries. The system was tried on Ayrshire bulls from the United States of America (USA) and Canada (CAN). Best Linear Unbiased Prediction (BLUP) animal model bull proofs for milk from each bull's country of evaluation were used. These proofs were first deregressed and standardized within country of evaluation. They were subsequently pooled across countries and analyzed by a linear model which included country of evaluation, genetic group, and bull effects. Genetic group and bull solutions were combined to form the bull's North American proof (NAP). Genetic differences and genetic trends in bull populations were also estimated.

INTRODUCTION

Extensive exchange of semen between countries has resulted in a growing demand to rank bulls on an international basis and measure genetic differences between populations. One method is to convert proofs from the exporting country to figures that compare with proofs in the importing country, using regression techniques (Interbull, 1986). An alternative is to combine information from different countries and obtain an international BLUP estimate of bull's transmitting ability using a linear model. The latter approach was taken by Rozzi (1987) to compare Holstein-Friesian bulls from USA, CAN, and Italy, and by Jacques and Klemetsdal (1989) for Scandinavian dairy bull comparisons. In both cases bull proofs by various sire models within country were used. Animal model proofs, however, are less biased since they better account for non-random mating of bulls. Implementation of animal model also improved the genetic correlation between proofs from USA and CAN, since all lactations were considered in the latter compared to only first lactation previously used.

This research was undertaken to develop a method to deregress animal model bull proofs within country, and then use the deregressed proofs to estimate bull transmitting abilities on an international base and compare bulls across countries; also to calculate genetic trends and genetic differences between USA and CAN Ayrshire populations.

MATERIAL AND METHODS

Official animal model milk yield proofs from August 1989 on bulls with daughters in at least 10 herds and 70% reliability were provided by Agriculture Canada. A similar edit was applied on a list of July 1989 animal model bull proofs from the United States Department of Agriculture. After removing records with missing bull's birth year, 682 and 482 records were left in the USA and CAN data sets, respectively. Bulls were born between 1950 and 1984. There were 87 bulls proven in both, the USA and CAN, for a total of 1077 bulls.

The linear model for across country evaluation as proposed by Schaeffer (1985), can be expressed in matrix notation as follows:
\[ Y = Xc + ZQg + Zs + e \]

where:
- \( c \) is the country of evaluation fixed effect;
- \( g \) is a genetic group fixed effect;
- \( s \) is the bull within group random effect, \( \text{Var}(s) = A \sigma^2_s \), \( A \) the numerator relationship matrix;
- \( e \) is the random residual \( \text{Var}(e) = R\sigma^2_e \), \( R \) a diagonal matrix with diagonals equal to the number of effective daughters of each sire in each country of evaluation;
- \( X, Z \) are incidence matrices;
- \( Q \) is a matrix that assigns sires to genetic groups.

Heritability used was .29. Genetic groups were defined by the bull's national origin and year of birth. The national origin of each animal was determined using pedigree information and the registration number. If a bull had any pedigree information at all, it was used according to the model:

Bull origin = \( 1/2 \) sire origin + \( 1/4 \) maternal granddam origin + \( 1/4 \) maternal grandsire origin

To accommodate this model, \( Q \) matrix included elements other than 0 and 1. Countries of origin were the USA, CAN, and Great Britain (GBR), since some Ayrshire bulls were either British imports or had imported ancestors.

The dependent variables (\( Y \)) were measures of the bull's average daughter performance (ADP) in each country of evaluation, free of all effects included in the international model. The procedure for deregressing original proofs (\( P \)) to estimate ADP involved the following steps (\( k \) was the ratio of residual to bull variance used in within country evaluation):

1. Let \( B = (Q' A^{-1} k) P \), then
2. \( g = (Q' A^{-1} k Q)^{-1} B \) and
3. \( s = P - Qg \), also
4. \( R^{-1} Qg + (R^{-1} + A^{-1} k) s = R^{-1} (ADP) \), therefore
5. \( ADP = RR^{-1} (ADP) \)

Steps 2 and 3 yield what would have been group and bull solutions if a country had utilised this sire model for its own evaluation. Step 4 results in right hand side values for bulls, within country, under this model.

This estimate of ADP is deregressed to the extent of daughter and male relatives information, i.e. it still contains the effect of the dam of the bull from the animal model, but as dependent variable yields the original proof if the international model is applied within each country. Estimates of ADP were standardized within country to account for differences in units among countries and then pooled across countries to form \( Y \). The linear model was applied to 1077 bulls, 21 genetic groups (seven 5-year periods and 3 countries of origin), and 2 countries of evaluation. The model assumed uncorrelated residuals within country of evaluation and ignored genotype by country interaction.

RESULTS AND DISCUSSION

North American proofs (NAP) were estimated as \( Q \hat{g} + \hat{s} \). Difference between country solutions, \( \hat{\delta} \), was .0552 in favour of the Canadian evaluation system. This value is equivalent to 38.06 USA lbs or 0.53 CAN Breed Class Averages (BCA), and reflects the difference between reference bases of the two countries. Because the base for records age adjustments was specific to each country, conversion of these values to an international unit, for example kilograms, would not be accurate. Countries interested in international comparisons should agree to a common age for record adjustment.

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Average NAP by national origin and time of birth are in Figure 1. Year of birth is the mid-year in a 5 year period. These values illustrate genetic differences between bulls originating from different populations, irrespectively of country of proof. Average genetic trends are in Table 1.

Table 1 Average genetic trends in bull populations per 5 year period by country of origin.

<table>
<thead>
<tr>
<th>Population</th>
<th>Standard Units</th>
<th>USA lbs</th>
<th>CAN BCA</th>
<th>Progress in Last Period</th>
</tr>
</thead>
<tbody>
<tr>
<td>CAN</td>
<td>.3122</td>
<td>215.16</td>
<td>3.01</td>
<td>.5587</td>
</tr>
<tr>
<td>USA</td>
<td>.2654</td>
<td>182.90</td>
<td>2.56</td>
<td>.5869</td>
</tr>
<tr>
<td>GBR</td>
<td>.2777</td>
<td>191.38</td>
<td>2.68</td>
<td>.0172</td>
</tr>
</tbody>
</table>

GBR values refer only to contributions from this country to USA and CAN populations, and do not reflect the genetic progress achieved in the entire GBR bull population.

Average NAP by country of evaluation and time of birth are in Figure 2. These values estimate genetic differences between bulls used in different counties, regardless of their origin. Average genetic trends are in Table 2.

Table 2 Average genetic trends in bull populations per 5 year period by country of evaluation.

<table>
<thead>
<tr>
<th>Population</th>
<th>Standard Units</th>
<th>USA lbs</th>
<th>CAN BCA</th>
<th>Progress in Last Period</th>
</tr>
</thead>
<tbody>
<tr>
<td>CAN</td>
<td>.3132</td>
<td>215.84</td>
<td>3.02</td>
<td>.6812</td>
</tr>
<tr>
<td>USA</td>
<td>.2749</td>
<td>189.45</td>
<td>2.56</td>
<td>.4830</td>
</tr>
</tbody>
</table>

The overall average NAP of bulls evaluated in CAN was 46.22 USA lbs or 0.65 CAN BCAs higher than the average NAP of bulls evaluated in USA.

To account for the differential use of bulls as service sires, a weighted NAP average by the number of daughters was calculated, within country of evaluation and time of birth. Pertinent values are in Figure 3 and represent genetic differences between cows used in each country's progeny testing scheme. Average genetic trends are in Table 3.

Table 3 Average genetic trends in cow populations per 5 year period by country of evaluation.

<table>
<thead>
<tr>
<th>Population</th>
<th>Standard Units</th>
<th>USA lbs</th>
<th>CAN BCA</th>
<th>Progress in Last Period</th>
</tr>
</thead>
<tbody>
<tr>
<td>CAN</td>
<td>.2409</td>
<td>166.02</td>
<td>2.33</td>
<td>.3426</td>
</tr>
<tr>
<td>USA</td>
<td>.1872</td>
<td>129.01</td>
<td>1.81</td>
<td>.2992</td>
</tr>
</tbody>
</table>

Within country, original proofs and NAP + had correlations of .98, for both, the USA and CAN. Changes in rankings occurred only for certain bulls imported from the other country, that were evaluated with lower accuracy in the importing country. Use of the linear model effectively combined information from both countries to estimate NAP.

ACKNOWLEDGEMENTS

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REFERENCES

Figure 1: Average North American proof by national origin and year of birth

Figure 2: Average North American proof by country of use and year of birth

Figure 3: Average NAP weighted by number of daughters, by country of use and year of birth