Options to Evaluate Sires for Multiple Traits in Multiple Countries

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1. Introduction

The MACE model described by Schaeffer et al (1996) can be used to evaluate sires for a single trait that is observed in multiple countries. Interbull applies this model repeatedly to evaluate sires for more than one trait. Schaeffer (1999) described an extension of the MACE model for simultaneous evaluation of multiple traits in multiple countries, and has also proposed a method to estimate the required variance components (Schaeffer, 2000).

Interbull uses the single-trait MACE approach to routinely evaluate yields of milk, fat and protein, and a number of conformation traits. Many of these traits are moderately or highly correlated with each other, and may be better suited for simultaneous evaluation using the multiple trait and country approach of Schaeffer (1999). The multiple trait and country approach may also be useful to evaluate trait combinations like mastitis incidence and somatic cell score (SCS), or to accommodate lactation-specific traits for interested countries. With multiple-trait MACE, it is possible to model lactation-specific traits for only the subset of countries providing them, without expanding the system of equations for the other countries.

The purpose of the present paper was to compare single-trait versus multiple-trait MACE approaches for combining multiple lactation-specific evaluations of sires from multiple countries.

2. Materials and Methods

2.1 Simulation

Data were simulated for four separate populations (countries), each recording three lactation-traits subjected to sequential culling within herds. Genetic and residual correlations and heritabilities were typical of first, second and third lactation protein yield and all genetic variances were equal to unity.

Two countries (EXP1 and EXP2) exported and exchanged semen, and two countries (IMP1 and IMP2) imported but did not export semen. Each country managed an AI stud and a traditional progeny-testing program. Proven bulls in each AI stud lineup comprised minimums of 75% local bulls and 16% foreign bulls. Actual bull proportions were dictated by the superiority of the local and imported bulls available each year. Proportions of local bulls were higher in exporting than in importing countries.

Bull superiorities were determined by a linear index of estimated breeding values for the three lactations in each country. The index weights used in each country were:

EXP1➜[.60 .30 .10] EXP2➜[.33, .33, .33]
IMP1➜[.75 .25 .00] IMP2➜[.40, .30, .30]

Young bulls were randomly mated to 50 cows, then shelfed until proven. Mating frequency for proven bulls ranged from 100 to 200 mates per year, depending on the predicted genetic merits of the bulls. Elite bulls (top 50% of proven bulls in each stud) were mated to elite cows (top 2 cows in each herd) to create the next generation of sampling bulls for each country. Close inbreedings were avoided for all matings.

Herd size was fixed at 30 milking cows in all countries. Country EXP1 had 200 herds, while EXP2, IMP1 and IMP2 had 100 herds each. Age distribution within-herds was fixed at 10, 7, 5, 3, 2, 2, and 1 cows aged from 2 to 8 years respectively in each herd. Culling of cows each year was based on phenotypic performance in the most recent lactation.

Base generation cow populations were simulated to average 0 in EXP1 and EXP2 and -1 genetic standard deviation for all traits in IMP1 and IMP2. Base generation bull studs included bulls that were sampled from truncated normal distributions to be above average for the linear index of EBVs specific to each country. Ten production cycles were simulated, with each cycle including calving, lactation, within-country animal-model genetic evaluation, selection and mating. The simulation was replicated 20 times.

2.2 Models

Four possible MACE applications were considered:

SM1: National EBV for the lactation traits were combined into a linear total-merit index ($K'EBV_N$), using country-specific index weights. The merit indexes were then used in a single-trait MACE application, using total number of daughters per sire as weighing factors.

SM2: Lactation-specific EBVs were used in single-trait MACE applications by lactation, using number of daughter lactation records as weighing factors.

MM1: The methods of Schaeffer (1999) were applied, using lactation-specific EBVs from all countries. Weighing factors considered record combinations and residual covariances.

MM2: The model of Schaeffer (1999) was applied, ignoring residual covariances between traits when computing the weighing factors.

A global animal model (GAM) was also applied to all lactations and countries using performance records of cows.

Covariances for all models were the true values used to simulate the data.

For models SM2, MM1, MM2 and GAM, the lactation-specific international evaluations were combined using the linear index weights for each country ($K'EBV_I$). The international merit indexes from each method were compared to true breeding merits ($K'BV$), which were computed using the same country-specific index weights.

3. Results and Discussion

Evaluation methods were compared firstly for their ability to identify the very best genetics globally. The superiority of bulls on the top 10 lists for each country was similar for all methods (Table 1). Models SM2, MM1 and MM2 tended to outperform SM1 and GAM for some of the countries, but the differences were not significant (P>.05).

Table 1. True values (K'BV) for top 10 evaluated bulls

	Country of Evaluation			
Evaluation Method	EXP1	EXP2	IMP1	IMP2
SM1	3.33	3.02	3.06	2.92
SM2	3.32	3.08	3.10	2.93
MM1	3.33	3.07	3.09	2.94
MM2	3.33	3.08	3.10	2.93
GAM	3.31	3.05	3.04	2.88
Range of SE	.06-.07	.06-.07	.06-.07	.07-.08

Table 2. Difference (foreign-local) in top 3 bulls bias (K'EBV-K'BV), in exporting countries

	IMP1 evaluated in:		IMP2 evaluated in:	
Evaluation Method	EXP1	EXP2	EXP1	EXP2
SM1	.61	1.07	.62	.82
SM2	.59	.97	.62	.83
MM1	.55	.94	.58	.82
MM2	.55	.95	.58	.82
GAM	.72	1.05	.80	.95
Range of SE	.10-.11	.11-.12	.09-.10	.08-.10

Fairness of country rankings, based on top bull evaluations, was the second consideration for ranking the methods. Country rankings for top bulls have a potentially large impact on international semen sales. For all of the methods considered, there was a bias of country comparisons favouring importing country bulls. This showed up as both an advantage for importing country bulls evaluated in EXP1 and EXP2 (Table 2) and a disadvantage for exporting country bulls evaluated in IMP1 and IMP2 (Table 3). The country biases were generally similar for all methods, but in some cases were greater for SM1 and GAM relative to the three MACE approaches that computed lactation-specific EBVs for each country.

The biases contributed to imperfect ranking of country means for top bulls, as seen in Table 4. Correlations between true and predicted average merit of the top 3 bulls from each country were consistently highest for SM2, MM1 and MM2, and lower in some countries for SM1 and GAM.

Method SM1 was the simplest, and was expected to have less desirable performance than the other methods, as was observed. The GAM, on the other hand, did not perform as well as expected, relative to the MACE methods. The MACE methods using lactation-specific EBVs seemed to give less bias in comparisons of top bulls from importing versus exporting countries. Possible explanations relate to selection bias concerns and convergence of GAM solutions.

Table 3. Difference (foreign-local) in top 3 bulls bias (K'EBV-K'BV), in importing countries

	EXP1 evaluated in:		EXP2 evaluated in:	
Evaluation Method	IMP1	IMP2	IMP1	IMP2
SM1	-.19	-.15	-.37	-.30
SM2	-.18	-.21	-.31	-.27
MM1	-.18	-.25	-.35	-.30
MM2	-.17	-.24	-.34	-.29
GAM	-.48	-.64	-.59	-.70
Range of SE	.10-.12	.07-.10	.10-.10	.10-.11

Table 4. Country correlations for top 3 bulls, true (K'BV) versus estimated merit (K'EBV)

	Country of Evaluation			
Evaluation Method	EXP1	EXP2	IMP1	IMP2
SM1	.89	.83	.80	.72
SM2	.89	.88	.84	.84
MM1	.89	.89	.84	.82
MM2	.89	.89	.84	.82
GAM	.86	.89	.79	.66
Range of SE	.02-.03	.02-.04	.03-.04	.04-.07

Important assumptions for all of the models were that base generation populations were unselected, and that all performance data used for selection were available for the genetic evaluation. The simulation included selected base generation bull populations with truncated normal distributions of breeding values. There was also an average difference in the base population genetic levels of EXP1 and EXP2 relative to IMP1 and IMP2. Genetic groups were applied in all within-country and international evaluation models to account for selection bias related to these factors, but there may still have been biases that genetic grouping was not able to account for. Perhaps these biases had a greater impact on GAM than on MACE results.

There may also have been differences in convergence of solutions, which for all models were derived by Gauss-Seidel iteration. The GAM solutions were assumed to have converged when the variance of animal solution changes divided by the variance of animal solutions was less than 10^{-8}. The MACE solutions were computed to a much greater degree of convergence because additional iterations were required to reach convergence of country mean solutions, and because these methods could easily be run longer, being thousands of times faster than GAM.

Method SM1 is the model currently used by Interbull. One of the problems with SM1 is that it does not produce international sire evaluations

for lactation-specific traits, which may be of interest in some countries. Models SM2, MM1 and MM2 each produce lactation specific sire evaluations and were equal or better than SM1 for identifying the very best bulls globally and for fairness of country comparisons in each country of evaluation.

All of the MACE models were comparable or better than the GAM, were much simpler to apply, and would allow for simultaneous evaluation of a greater number of traits per country given fixed computer or time limitations.

Variance component estimation was not addressed in the present study, but would be a critical consideration in the application of any of these methods.

References

Schaeffer, L.R., Reents, R. & Jamrozik, J. 1996. Factors influencing international comparisons of dairy sires.

Schaeffer, L.R. 1999. Across country evaluation of beef bulls. Beef Improvement Federation Genetic Prediction Workshop, Kansas City.

Schaeffer, L.R. 2000. Multiple trait international bull comparisons. Mimeo.