

Multiple-Trait MACE with a Variable Number of Traits per Country

P.G. Sullivan and J.W. Wilton

Centre for Genetic Improvement of Livestock, University of Guelph, Ontario, Canada N1G 2W1

1. Introduction

Alternative methods to evaluate sires for multiple traits in multiple countries were reviewed by Sullivan (2000), considering simultaneous evaluation of either one or all traits in all countries. Currently, some but not all countries compute lactation-specific genetic evaluations for dairy production traits. The purpose of the present paper was to consider a multiple-trait MACE model that allows for multiple traits in one country and a single trait in each of the other countries included in international evaluation.

2. Materials and Methods

2.1. Simulation

Data were simulated for two exporting (E1 and E2) and two importing (I1 and I2) countries, as described by Sullivan (2000). Base generation sire populations were selected from truncated normal distributions in all countries, and base generation cow and sire populations were superior by one genetic standard deviation in exporting relative to importing populations. Genetic variances were 1.0 for all lactations in all countries.

The above simulation was also repeated with unselected base generation populations.

2.2. Evaluation Models

Six models were considered:

- Conv:** National sire EBV for lactation traits were converted to foreign country scales and second-country proofs were ignored.
- M:** National sire EBV were combined in an index for each country, and the indexes were combined by MACE.

MTM: National sire EBV were combined in an index for E1, I1 and I2, and combined with the lactation traits for E2 using multiple-trait MACE.

MS: Model **M** was applied with a constraint to force base generation (year = 0) genetic group solutions to average zero instead of the usually implied constraint that all group solutions average zero.

MTMS: Model **MTM** with the constraint that only base generation genetic group solutions average zero.

GAM: A global animal model was applied to all lactation traits from all countries using cow records.

Covariances for each of the evaluation models were based on the parameters used to simulate the data.

The four MACE models were each applied with two different sets of weighting factors:

{model}-n: Number of daughters for the indexes and number of daughters per lactation for the lactation traits.

{model}-edc: Effective daughter contributions (Interbull, 2000) for the indexes, and a deregressed equivalent to edc (see appendix) for the lactation traits.

The multiple-trait MACE models were simpler than those of Schaeffer (2000) and Madsen et al. (2000) because they did not involve residual correlations directly. Residual correlations were ignored when using numbers of daughters as weighting factors, and were accounted for in the deregression step when edc were used. Preliminary work showed that a deregressed number of daughters weighting factor approach was essentially equivalent to the method of Schaeffer (2000). The use of deregressed edc should therefore be superior to either the Schaeffer or Madsen models, given the benefits of

edc as shown by Fikse and Banos (2001) for single-trait MACE.

3. Results and Discussion

Relative model performances were as expected when the base generation populations were unselected (Figure 1). Breeding value prediction error, as measured by root mean squared difference (RMSE) between true and estimated breeding values, was highest for **Conv**, lowest for **GAM** and intermediate for the MACE models. **MTM** and **MTMS** were superior to **M** and **MS**, respectively.

The models ranked differently when base generation populations were selected. The MACE models were inferior to **Conv** and there was little difference between **Conv** and **GAM**, which would raise questions about the need to conduct international evaluations rather than using simple conversions. On the other hand, models **MS** and **MTMS** were notably superior to **Conv**.

The assumptions made about genetic groups are critical to the performance of international evaluation models, since incorrect assumptions can actually make international evaluations inferior to simple conversions.

Differences in RMSE between the models were largely affected by differences in country biases, in particular for importing country bulls on exporting country scales of evaluation. Models **MS** and **MTMS** essentially eliminated these biases when base populations were unselected and dramatically reduced the biases when base populations were selected (Figure 2). Similar benefits would also be expected for a **GAMS** model relative to **GAM**, although this was not investigated.

Model results for bias were very similar for either set of weighting factors (n or edc), following the similarity of results for RMSE (Figures 1a versus 1b). Plots of bias (Figures 2 and 3) were therefore limited to the edc analyses to avoid redundancy.

Country rankings in top bull lists are significantly altered by country biases. For example, **MTM-edc** placed 24% and 54% more I2 bulls in the E2 top 100 list compared with **MTMS-edc**, for unselected and selected base populations respectively.

Use of **MTM(S)** instead of **M(S)** either reduced ($P < .05$) or didn't affect RMSE for the main traits of interest, those being the indexes on scales E1, I1 and I2 and the lactation traits on scale E2 (Table 1). In contrast, the RMSE of the index on scale E2 was not reduced and in some cases increased. This latter result was unexpected given the consistent reductions in RMSE for the lactation traits comprising the E2 index. For **MTM** and **MTMS**, the lactation trait evaluations were combined after international evaluation to derive the E2 index, and for **M** and **MS** each lactation trait evaluation was assumed equal to the international E2 index.

There was no change in RMSE for the E2 index when model assumptions were valid (i.e. unselected base populations with the *S models), otherwise the increases were small, particularly when edc were used as weighting factors. By switching to multiple-trait MACE, new information is provided to improve the indexes in the other countries and the lactation traits in E2, but there is no new information to improve the accuracy of the E2 index. Problems caused by invalid model assumptions may have been amplified for E2 when three traits were included instead of one, resulting in decreased accuracy for the E2 index in those cases.

Biases for the lactation traits (Figure 3) were on average consistent with the biases for the E2 index (Figure 2). There was more variability of bias across the three lactation traits with the multiple-trait MACE models, and a notable, increasing trend in bias across lactations for **MTMS**. Model changes may still be needed to account for culling from first to third lactation in order to minimize variation and trends of bias across lactations.

Table 1. Change in RMSE for all bulls evaluated, across 20 replicates, when switching to multiple-trait MACE. Numbers in parentheses are the corresponding t-value statistics

Trait	Relative to MACE model			
	M-n	M-edc	MS-n	MS-edc
Unselected Base populations				
I1-index	-.010 (-5.5)	-.010 (-5.7)	-.009 (-4.5)	-.008 (-4.4)
I2-index	.002 (1.9)	.001 (1.8)	-.001 (-1.8)	-.002 (-2.1)
E1-index	-.002 (-3.1)	-.002 (-2.7)	-.003 (-4.0)	-.003 (-4.1)
E2-trait1	-.033 (-7.2)	-.034 (-7.3)	-.040 (-8.6)	-.038 (-8.5)
E2-trait2	.000 (0.0)	-.003 (-1.1)	-.006 (-2.9)	-.005 (-2.7)
E2-trait3	-.011 (-2.7)	-.014 (-3.7)	-.014 (-7.6)	-.014 (-7.2)
E2-index	.005 (5.0)	.003 (3.4)	-.001 (-1.1)	.000 (0.0)
Selected Base populations				
I1-index	-.005 (-5.0)	-.005 (-5.3)	-.006 (-4.7)	-.006 (-5.0)
I2-index	.000 (0.0)	.000 (0.0)	.000 (0.0)	.000 (0.0)
E1-index	-.001 (-2.0)	-.001 (-1.9)	-.001 (-0.9)	-.001 (-1.3)
E2-trait1	-.019 (-5.2)	-.022 (-5.9)	-.031 (-7.6)	-.031 (-7.8)
E2-trait2	-.008 (-1.8)	-.014 (-3.2)	-.010 (-3.2)	-.013 (-4.0)
E2-trait3	-.006 (-1.4)	-.013 (-3.3)	-.003 (-0.6)	-.008 (-1.7)
E2-index	.007 (4.6)	.002 (1.1)	.005 (6.5)	.002 (3.3)

4. Conclusions

International evaluations are strongly affected by the assumptions made about genetic groups, and can be less accurate than converted national evaluations if those assumptions are incorrect.

International evaluations with MACE are improved with multiple-trait MACE, for all traits included in the analysis, but not necessarily for functions of those traits (e.g. an index of lactation trait evaluations). This was true for selected and unselected base populations, and for situations when correct or incorrect assumptions were made about genetic groups.

The results of this study were derived with knowledge of the true genetic covariances, and were hence unaffected by potential differences in ability to accurately estimate those covariances. Efforts in covariance component estimation should be targeted to the preferred model, however, rather than limiting model choices due to potential difficulties with covariance component estimation.

The weighting factors derived for **MTM-edc** were designed to allow each trait within a country to be treated as a separate country for the MACE analysis. This approach simplifies the implemen-

tation of multiple-trait MACE, since existing MACE and covariance estimation programs currently used by Interbull for single-trait MACE could also be used for multiple-trait MACE. The approach also makes it easy to implement the edc weighting factor approach in a multiple-trait-by-country context, offering advantages over alternative multiple-trait MACE methods that are based on numbers of daughters.

References

- Fikse, W.F. & Banos, G. 2001. Weighting factors of sire daughter information in international genetic evaluations. *J. Dairy Sci.* 84, 1759-1767.
- Interbull. 2000. New weighting factors for the international genetic evaluations; revised July, 2000. *Mimeo.*
- Madsen, P., Jensen, J. & Mark, T. 2000. Reduced rank estimation of (co)-variance components for international evaluation using AI-REML. *Interbull Bulletin* 25, 46-50.
- Schaeffer, L.R. 2000. Multiple trait international bull comparisons. *Mimeo. U. of Guelph, Canada.*
- Sullivan, P.G. 2000. Options to evaluate sires for multiple traits in multiple countries. *Interbull Bulletin* 25, 13-17.

Figure 1a. RMSE for average index of all bulls across all scales, using number of daughters in MACE

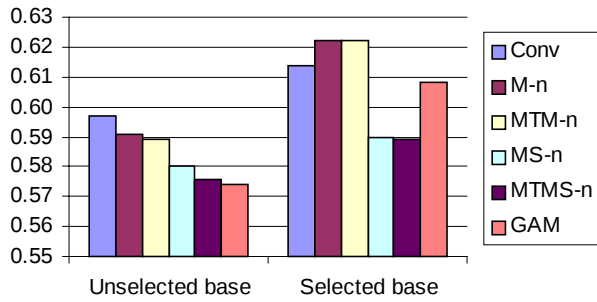


Figure 1b. RMSE for average index of all bulls across all scales, using edc in MACE

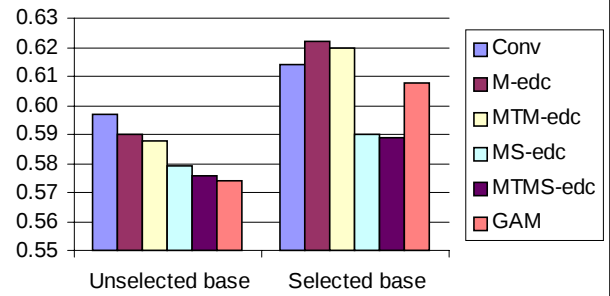


Figure 2a. Index bias for Importing country bulls on Exporting country scales, with unselected base

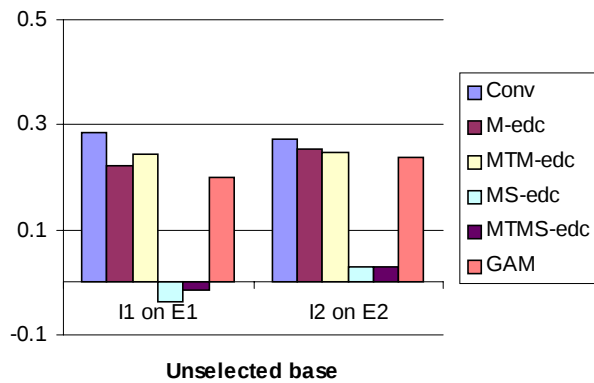


Figure 2b. Index bias for Importing country bulls on Exporting country scales, with selected base

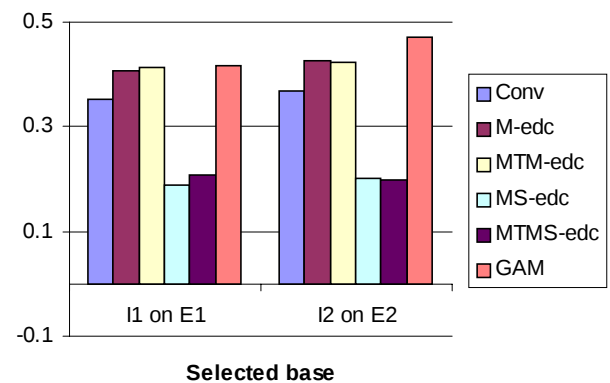


Figure 3a. Trait biases for I2 bulls on E2 Scale, with unselected base

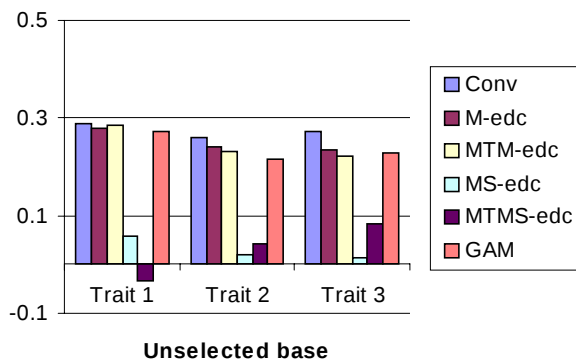
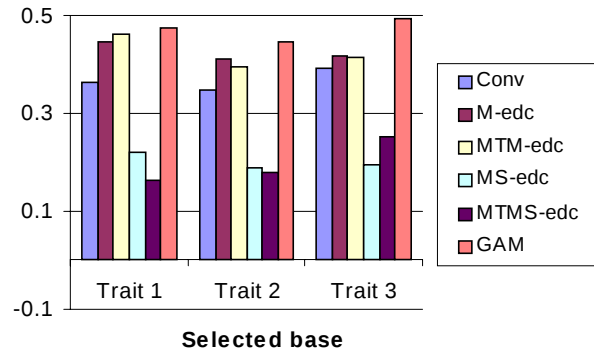


Figure 3b. Trait biases for I2 bulls on E2 Scale, with selected base



APPENDIX

Effective daughter contributions (edc) for each lactation trait are appropriate weighting factors if genetic correlations between lactations are ignored for international evaluation. The edc must be deregressed, however, if genetic correlations between lactations are to be used, as in multiple-trait MACE. The deregression prevents over-weighting the information from countries that contribute lactation-specific evaluations relative to those providing a single evaluation averaged across lactations. Residual correlations can be ignored in the multiple-trait MACE model because they are already accounted for in the edc:

The objective is to find weighting factors (m_t) for a multiple-trait model, assuming zero residual correlations and non-zero genetic correlations, that yield equivalent prediction error variances to those from single-trait models using edc.

For trait (e.g. lactation) 't' of T traits in a given country, let $r_t = R_{tt}$, $g_t = G_{tt}$, $n_t = \text{edc}_t$, $m_t = n_t(\text{deregressed})$, $B = (\text{diag}(m_t/r_t) + G^{-1})^{-1}$, $b_t = B_{tt}$.

RTF: m_t such that $b_t = (n_t/r_t + 1/g_t)^{-1}$

$$\Rightarrow b_t = r_t g_t / (n_t g_t + r_t)$$

$$\Rightarrow n_t = r_t (g_t - b_t) / (g_t b_t)$$

This can be solved by iteration, one animal at a time, as follows:

1. $i = 0$
2. $m_t^{(i)} = n_t$, $t=1, T$
3. Compute $B^{(i)}$
4. $\text{err}_t^{(i)} = n_t - r_t (g_t - b_t^{(i)}) / (g_t b_t^{(i)})$, $t=1, T$
5. $m_t^{(i+1)} = m_t^{(i)} + \text{err}_t^{(i)} * \text{relax}$, $t=1, T$
6. $i = i+1$
7. Until $(\max(\text{err}_t^{(i-1)}) < \text{threshold})$ goto 3

Convergence was generally reached with fewer than 20 iterations in the present study, with $\text{relax}=.5$ and $\text{threshold}=.001$.