

International Genetic Evaluations for Female Fertility Traits Using Multi-trait MACE

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Abstract

Several countries participating in international genetic evaluations for female fertility traits do have multi-trait genetic evaluations nationally. The current single-trait MACE procedure cannot take into account the information from within-country correlated traits, therefore a multi-trait MACE procedure was applied to the data. Data were analyzed with both single-trait and multi-trait procedures and international reliabilities were compared. The study showed a 3% increase in the reliability of international evaluations using multi-trait MACE compared to single-trait MACE.

Introduction

A few decades of intense selection for milk production traits have resulted in a decreasing trend in female fertility traits. Accordingly, the attention to female fertility traits has increased both nationally and internationally, which led to the inclusion of international genetic evaluation for female fertility traits into the Interbull service portfolio in 2007. The first international genetic evaluation of bulls from 11 populations was released in February 2007 for the Holstein breed for three trait groups. Since then, international genetic evaluation of fertility traits has been expanded to six breeds and five trait groups and the number of countries submitting data and the number of traits per country has increased gradually.

Female fertility traits are in many countries evaluated using multi-trait models but must be treated by Interbull as single traits, because the single-trait MACE method (Schaeffer, 1994) for international genetic evaluations only allows the inclusion of one trait from each country. Therefore, running several single-trait MACE evaluations, each including one trait from each country, were unavoidable. This way, the benefits of jointly analyzing multiple traits from each country (e.g., traits that usually have high correlations and high percentages of common bulls with each other) cannot be exploited. Implementation of multi-trait

MACE methodology (Schaeffer, 2001) and the methods for multi-trait EDC (Effective Daughter Contribution) calculation and multi-trait de-regression (Sullivan and Wilton, 2001) facilitated multiple trait multiple country genetic evaluations.

The aim of this study was to test the usability of multi-trait MACE for international genetic evaluation of female fertility traits and comparing it with single-trait MACE in term of reliability.

Material

Data from seven countries/populations on ten traits was extracted from the data used in Interbull's test run September 2007. The following countries and traits were used (see Table 1 for data description): days open from Belgium (BEL_{DO}), calving to first insemination and first insemination to conception from Canada (CAN_{CF} and CAN_{FC}), calving to first insemination from Switzerland (CHE_{CF}), calving to first insemination and first to last insemination from Germany-Austria (DEU_{CF} and DEU_{FL}), calving to first insemination and first to last insemination from Denmark-Finland-Sweden (DFS_{CF} and DFS_{FL}), days open from Spain (ESP_{DO}) and daughter pregnancy rate from the United States of America (USA_{DP}).

Methods

ST-MACE model:

$$y_i = \mu_i I + Z_i Q g_i + Z_i s_i + e_i$$

where: y_i is the vector of sire de-regressed national evaluations (the information used for de-regression are the national pedigree, heritabilities, and EDC values), μ_i is the vector of country bases, g_i is the vector of phantom parent groups (phantom group size of 30), s_i is the vector of sire genetic effects and e_i is the vector of random residuals. Z and Q are the matrices relating sires to observations, and sires to phantom parent groups, respectively.

One assumption of this method is that in each analysis, only one trait from each country can be included. To fulfill this assumption, eight different 7-trait analyses were carried out, each including all single trait countries (BEL, CHE, ESP, USA) and different combinations of traits from bi-trait countries (CAN, DEU, DFS). Both genetic correlations and the reliability of international genetic evaluations were estimated in all runs.

A 10×10 genetic correlation matrix was derived from the three reported within-country genetic correlations (0.274, 0.370 and 0.409 for CAN, DEU and DFS, respectively) and the average of those eight 7×7 genetic correlation matrices. A weighted bending procedure (Jorjani *et al.*, 2003) was used for making sure that the derived genetic correlation matrix was positive definite.

MT-MACE model:

$$y_{ij} = \mu_{ij} I + Z_{ij} Q g_{ij} + Z_{ij} s_{ij} + e_{ij}$$

where all terms are as defined before, with i and j related to the country and the trait, respectively, considering residual correlations among traits from each country (-0.047, 0.278 and -0.082 for CAN, DEU and DFS, respectively). The reported within-country genetic correlations were also used for de-regression of the national evaluations. This method enables all country-traits to be analyzed simultaneously. Genetic correlations

and the reliability of international genetic evaluations were estimated.

The key difference between the two methodologies (ST-MACE vs. MT-MACE) is the EDC used in the evaluation of the bull. For ST-MACE the country reported EDC_{ST} values (Fikse and Banos, 2001) were used, except for DEU that had been using another method (Liu *et al.*, 2004) to convert bull's block EDC matrix to a scalar one. For MT-MACE, the country reported EDC_{ST} values were converted to EDC_{MT} values using the method proposed by Sullivan and Wilton (2001).

The original version of MT-MACE works with a block R^{-1} matrix in MME (Schaeffer, 2001). As there were difficulties in the calculation of block EDC_{MT} matrices for each bull at the national level to be sent to Interbull Centre, Sullivan and Wilton (2001) came with a method to calculate scalar EDC_{MT} matrices from EDC_{ST} values reported by the countries. It has been claimed that those scalar EDC_{MT} matrices can produce the same PEV as using block EDC_{MT} matrices (Mark and Sullivan, 2006). Those EDC_{MT} values will then be used for de-regression of the national evaluations and re-regression of the de-regressed national evaluations.

Results and Discussion

Values represented in Table 1 show that country-traits differed with respect to the amount of information, sampling from bulls and the distribution of bulls' daughters in herds both among and within countries. These factors together with the heritabilities and the model of national genetic evaluation system will influence the EDC and the reliabilities of bulls. The ratio of EDC/DTR/bull shows the contribution of each daughter in reducing PEV and increasing reliability of the bull.

In all cases, EDC_{MT} values were lower than EDC_{ST} values (Table 2), maybe due to the fact that two daughters each recorded for one trait provide more information to the evaluation of the bull than one daughter recorded for two traits. The lowest ratio of EDC_{MT}/EDC_{ST} was

for DEU_{FL} with the highest standard deviation, which may be explained by its low heritability or a different way of EDC_{ST} calculation (Liu *et al.*, 2004).

Except for DEU, the variances of the de-regressed national evaluations were twice the variances of the national evaluations. The variances of the multi-trait de-regressed national evaluations were slightly higher than the variances of the single-trait de-regressed national evaluations, probably due to the low difference between EDC_{ST} and EDC_{MT} values.

On average, genetic correlations estimated by MT-MACE were 4.7% lower than ST-MACE genetic correlations (Table 3). The main reasons for these differences are the analyses of different number of traits, using different EDC values and the fact that genetic correlations derived by MT-MACE are the genetic correlations in the sense that all country-traits are residually independent.

The reliability gain by MT-MACE over ST-MACE was studied, which was on average 3% across all bulls over all country-traits. The reliability gain by MT-MACE was in accordance with the results of Mark and Sullivan (2006) on udder health traits, in which the reliability gain was 1.58%, with two traits from a country (Denmark) among 11 country-traits, evaluated in a multi-trait national model. Sullivan and Wilton (2001), using a simulated data showed the improvement of the accuracy of international genetic evaluations by MT-MACE.

Conclusion

Increasing the number of traits submitted per country, makes the use of MT-MACE

necessary for international evaluations. This need is even more evident for female fertility traits as there are several measures available. Whereas most of these traits were analyzed in a multi-trait national model, implementation of MT-MACE may be able to increase the consistency between national and international genetic evaluations. Also, countries are more willing to submit their original national evaluations to Interbull Centre and receive international evaluations back instead of combining them into indices.

References

- Fikse, W.F. & Banos, G. 2001. Weighting factors of sire daughter information in international genetic evaluations. *J. Dairy Sci.* 84, 1759-1767.
- Jorjani, H., Klei, L. & Emanuelson, U. 2003. A simple method for weighted bending of genetic (co)variance matrices. *J. Dairy. Sci.* 86, 677-679.
- Liu, Z., Reinhardt, F., Bünger, A. & Reents, R. 2004. Derivation and calculation of approximate reliabilities and daughter yield deviations of a random regression test-day model for genetic evaluation of dairy cattle. *J. Dairy Sci.* 87, 1896-1907.
- Mark, T. & Sullivan, P.G. 2006. Multiple-trait multiple-country genetic evaluations for udder health traits. *J. Dairy Sci.* 89, 4874-4885.
- Schaeffer, L.R. 1994. Multiple-country comparison of dairy sires. *J. Dairy Sci.* 77, 2671-2678.
- Schaeffer, L.R. 2001. Multiple trait international bull comparisons. *Livest. Prod. Sci.* 69, 145-153.
- Sullivan, P.G. & Wilton, J.W. 2001. Multiple-trait MACE with a variable number of traits per country. *Interbull Bulletin* 27, 68-72.

Table 1. Heritabilities (h^2), number of bulls (Bulls), number of daughters per bull (DTR/bull), number of sampling herds per bull (Herd/bull), EDC per bull (EDC/bull), EDC per daughter per bull (EDC/DTR/bull), and the reliability of the proofs (Rel.) submitted by the countries.

Trait*	h^2	Bulls	DTR/bull	Herd/bull	EDC/bull	EDC/DTR/bull	Rel.
BEL _{DO}	0.040	1542	128 ± 258	65 ± 83	297 ± 651	2.23 ± 0.48	55.5 ± 21.6
CAN _{CF}	0.072	4108	252 ± 1606	141 ± 497	605 ± 3904	2.50 ± 1.16	77.7 ± 10.3
CAN _{FC}	0.077	3597	198 ± 1293	116 ± 434	705 ± 4125	4.15 ± 6.32	80.3 ± 8.1
CHE _{CF}	0.059	1135	152 ± 280	119 ± 180	297 ± 582	1.83 ± 0.36	76.2 ± 14.4
DEU _{CF}	0.039	16764	350 ± 1793	152 ± 494	474 ± 2480	1.33 ± 0.17	67.2 ± 13.3
DEU _{FL}	0.010	15166	276 ± 1420	126 ± 423	491 ± 2125	2.52 ± 0.60	52.7 ± 13.7
DFS _{CF}	0.040	12312	296 ± 1708	162 ± 425	629 ± 3588	2.17 ± 0.32	71.5 ± 12.2
DFS _{FL}	0.020	12325	295 ± 1700	162 ± 423	683 ± 3554	2.64 ± 0.38	63.6 ± 13.0
ESP _{DO}	0.045	3614	225 ± 653	122 ± 255	387 ± 1102	1.68 ± 0.35	68.3 ± 17.6
USA _{DP}	0.040	35125	413 ± 1886	169 ± 554	544 ± 2265	1.56 ± 0.28	64.6 ± 13.5

* Refer to the Material's text for country-trait abbreviations

Table 2. The ratio of multi-trait to single-trait effective daughter contributions (EDC_{MT}/EDC_{ST}) and the ratios of the variances of single-trait (V_{ST-DRP}) and multi-trait de-regressed proofs (V_{MT-DRP}) to the sire national proofs (V_{NP}) for bi-trait countries.

Trait	EDC_{MT}/EDC_{ST}	V_{ST-DRP}/V_{NP}	V_{MT-DRP}/V_{NP}
CAN _{CF}	0.982 ± 0.010	2.11	2.14
CAN _{FC}	0.983 ± 0.008	1.89	1.92
DEU _{CF}	0.974 ± 0.010	4.20	4.35
DEU _{FL}	0.817 ± 0.069	8.42	12.41
DFS _{CF}	0.955 ± 0.016	1.90	1.92
DFS _{FL}	0.903 ± 0.037	2.06	2.13

Table 3. Estimated genetic correlations by ST-MACE (below diagonal) and MT-MACE (upper diagonal) methods.

Trait	BEL _{DO}	CAN _{CF}	CAN _{FC}	CHE _{CF}	DEU _{CF}	DEU _{FL}	DFS _{CF}	DFS _{FL}	ESP _{DO}	USA _{DP}
BEL _{DO}	1.000	0.731	0.636	0.726	0.713	0.589	0.695	0.759	0.935	0.856
CAN _{CF}	0.711	1.000	0.307	0.918	0.906	0.188	0.935	0.515	0.743	0.702
CAN _{FC}	0.626	0.275	1.000	0.175	0.201	0.795	0.219	0.796	0.654	0.724
CHE _{CF}	0.726	0.890	0.241	1.000	0.927	0.165	0.940	0.470	0.722	0.665
DEU _{CF}	0.738	0.895	0.320	0.895	1.000	0.083	0.899	0.422	0.684	0.653
DEU _{FL}	0.762	0.512	0.803	0.479	0.371	1.000	0.233	0.880	0.660	0.756
DFS _{CF}	0.720	0.875	0.325	0.865	0.862	0.504	1.000	0.528	0.682	0.679
DFS _{FL}	0.772	0.594	0.761	0.560	0.553	0.857	0.411	1.000	0.795	0.873
ESP _{DO}	0.927	0.740	0.662	0.726	0.729	0.816	0.718	0.828	1.000	0.936
USA _{DP}	0.847	0.734	0.736	0.697	0.712	0.882	0.723	0.882	0.925	1.000