MT-MACE for Female Fertility and Milk Yield

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Abstract

Many countries have implemented multi-trait national genetic evaluations and female fertility traits are also considered in those evaluations. Some countries do consider simultaneous evaluation of production traits and female fertility. International genetic evaluations should follow the trends in the national genetic evaluation strategies. In this study, two female fertility traits from Great Britain, Italy and the Netherlands were used, as well as milk yield data from those countries together with USA. Two separate MT-MACE analyses were performed, one including only female fertility traits and the other one including both female fertility traits and milk yield. The estimated genetic correlations and the predicted genetic merits were consistent between the two analyses. The reliability of the national genetic merits was improved using MT-MACE international evaluations. Also, the reliability of the predicted genetic merits was improved from MT-MACE for female fertility to MT-MACE for female fertility and milk yield.

Introduction

The number of countries applying multi-trait national evaluations is increasing. Most of these countries have multi-trait analyses for traits with the same nature. However, some countries have already started multi-trait analyses of traits with different natures, especially the traits that are strongly associated with each other, like female fertility and milk yield. The trends in the national genetic evaluation systems require a methodology transition in international genetic evaluations from ST-MACE to MT-MACE.

There are three MT-MACE methods available. The first method was introduced by Schaeffer (2001), where a matrix with residual covariances between predicted genetic merits for all traits is built for each bull based on the number of daughters in different combinations of traits and the inverses of the residual variance-covariance matrices. These form the building blocks to create an inverse of the residual variance-covariance matrix for the MME.

The other available method is a block Effective Daughter Contribution (EDC) based method (Liu *et al.*, 2004). This method is developed for deriving multi-trait block EDC matrices for each bull to be used in multi-trait per country international genetic evaluations.

The method uses different sources of information including own performance records, progeny and parental contributions.

The third method has developed by Sullivan *et al.* (2005). The aim of this method is to derive multi-trait scalar EDC values. Applying this method, within country-traits become residually independent making it possible to handle them with ST-MACE (Schaeffer, 1994). Sullivan *et al.* (2005) showed with a simulated data that the errors of prediction in this method are very close to the method of Schaeffer (2001).

Various female fertility measures are available in each country and analyzing those measures together in international evaluations is of advantage. Nilforooshan *et al.* (2009) applied MT-MACE (Sullivan *et al.*, 2005) for several female fertility traits from several countries. In the current study, the aim was to study the inclusion of milk yield data in an MT-MACE analysis of female fertility traits to reduce a possible bias in the genetic trends of female fertility traits.

Materials and Methods

The data from four Holstein populations submitted to Interbull for the test evaluation in

May 2009 were used in this study. Milk yield (MY) from the US as well as MY and two female fertility traits from Great Britain (Non Return Rate 56 (NR) and calving interval (CI)), Italy (CI and calving to first insemination (CF)) and the Netherlands (CI and CF) were included. The reason of choosing Great Britain, Italy and the Netherlands was that these countries have multi-trait national models for female fertility traits including milk yield. Table 1 shows the number of bulls with proofs in each trait submitted from the countries and the heritability of the traits.

Table 1. Number of bulls and heritability of the submitted traits.

Trait	Ν	Heritability
GBR _{NR}	6975	0.019
GBR _{CI}	6975	0.033
GBR _{MY}	10534	0.548
ITA _{CI}	8064	0.057
ITA _{CF}	8064	0.038
ITA _{MY}	8032	0.309
NLD _{CF}	12619	0.222
NLD _{CI}	12735	0.145
NLD _{MY}	13351	0.570
USA _{MY}	40344	0.300

The MT-MACE model used to analyze the data was as follows:

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

where: *y* is the vector of bulls' de-regressed national evaluations, μ_{ij} is the vector of the mean of trait *j* in country *i*, *g* is the vector of random phantom parent groups, *s* is the vector of bulls' additive genetic effects and *e* is the vector of random residuals; all terms are corresponding to country *i* and trait *j*. *Z* and *Q* are the matrices relating bulls to observations and bulls to phantom parent groups, respectively.

The MT-MACE approach of Sullivan *et al.* (2005) was adopted for analyzing the data. This method converts single-trait EDC values to multi-trait EDC values, using the heritabilities of the traits (Table 1) and country reported genetic and residual correlations (Table 2).

Two different MT-MACE analyses were performed, one including two fertility traits from Great Britain, Italy and the Netherlands, and the other one including the traits in the first analysis together with milk yield data from those countries and the United States of America. An EM-REML algorithm was used for the estimation genetic correlations. Genetic merits and reliabilities were predicted followed by the estimation of genetic correlations. The correlations among predicted genetic merits reliability gains from national and to international evaluations were studied for the two MT-MACE analyses.

Results and Discussion

MT-MACE fertility evaluation

Most of the estimated genetic correlations were high and positive, except for the genetic correlations of GBR_{NR}, which was low and positive with ITA_{CF} and were negative with the other country-traits (Table 3: upper diagonal). The differences between the estimated within country genetic correlations and the reported genetic correlations (0.243, 0.045 and 0.027 for Great Britain, Italy and the Netherlands, respectively) were mainly due to: a) analyzing the traits in a different trait combination including the traits from other countries, b) an international sire model based on de-regressed proofs of the bulls versus a national animal model based on the performance records of the bulls' daughters and c) using an international pedigree instead of a national pedigree. Making country-traits residually independent is also another reason for changes in the estimated genetic correlations (Nilforooshan et al., 2009).

The correlations between national and international predicted genetic merits were very high; indicating that nationally predicted genetic merits of bulls do not change considerably by MT-MACE in international genetic evaluations. The reliability of genetic merits improved considerably by MT-MACE evaluation for female fertility traits (Table 4).

MT-MACE fertility & milk yield evaluation

The differences between the estimated genetic correlations in the two analyses (with and without MY were low (Table 3). Inclusion of milk yield data from USA was expected to adjust for the selection on milk yield in USA on the evaluation of the other country-traits.

The correlations among national and international genetic merits were high and consistent across comparisons (Table 4). The reliabilities were improved both from national evaluations and MT-MACE for female fertility to MT-MACE for female fertility and milk yield (Table 4). On average, the reliability gain from the national evaluation was a bit less in MT-MACE for female fertility and milk yield compared to MT-MACE for female fertility, probably more realistic reliabilities corrected for the genetic trends in milk yield. Even though the genetic correlations among female fertility traits decreased from the first to the second analysis, the reliability of the predicted fertility genetic merits still had a slight increase from the first to the second analysis.

Conclusion

There are several measures available for female fertility, all unfavorably correlated with milk yield. Considering several traits per country in international evaluations is expected to adjust the evaluations for within and across country genetic trends. It can also be important to adjust female fertility genetic evaluations for the genetic trends of milk yield. This study showed that different MT-MACE analyses give consistent results to each other. Reliabilities increased considerably from national evaluations to MT-MACE evaluations. A further reliability increase is expectable by considering more countries and more traits per country.

References

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Table 2. Country reported genetic correlations (upper diagonal) and residual correlations among within country traits (lower diagonal).

Trait	GBR _{NR}	GBR _{CI}	GBR _{MY}	ITA _{CI}	ITA _{CF}	ITA _{MY}	NLD _{CF}	NLD _{CI}	NLD _{MY}	USA _{MY}
GBR _{NR}	1.000	-0.449	-0.254	0	0	0	0	0	0	0
GBR _{CI}	-0.341	1.000	0.270	0	0	0	0	0	0	0
GBR _{MY}	-0.016	0.036	1.000	0	0	0	0	0	0	0
ITA _{CI}	0	0	0	1.000	0.583	0.273	0	0	0	0
ITA _{CF}	0	0	0	0.358	1.000	0.239	0	0	0	0
ITA _{MY}	0	0	0	0.016	-0.011	1.000	0	0	0	0
NLD _{CF}	0	0	0	0	0	0	1.000	0.830	0.358	0
NLD _{CI}	0	0	0	0	0	0	0.460	1.000	0.530	0
NLD _{MY}	0	0	0	0	0	0	0.358	0.530	1.000	0
USA _{MY}	0	0	0	0	0	0	0	0	0	1.000

diagonal) and among remaie resulting traits and milk yield in the second analysis (lower diagonal).									
Trait	GBR _{NR}	GBR _{CI}	GBR _{MY}	ITA _{CI}	ITA _{CF}	ITA_{MY}	NLD _{CF}	NLD _{CI}	NLD _{MY}
GBR _{NR}		-0.206		-0.477	0.176		-0.433	-0.028	
GBR _{CI}	-0.249			0.868	0.749		0.805	0.838	
GBR _{MY}	-0.159	-0.066							
ITA _{CI}	-0.558	0.851	-0.120		0.628		0.882	0.752	
ITA _{CF}	0.143	0.723	-0.333	0.549			0.585	0.825	
ITA _{MY}	-0.158	-0.073	0.865	-0.126	-0.318				
NLD _{CF}	-0.476	0.775	-0.290	0.862	0.554	-0.271		0.857	
NLD _{CI}	-0.113	0.865	-0.221	0.732	0.802	-0.231	0.831		
NLD _{MY}	-0.156	0.028	0.878	-0.069	-0.219	0.867	-0.260	-0.136	
USA _{MY}	-0.113	-0.057	0.521	-0.136	-0.122	0.595	-0.171	-0.134	0.499

Table 3. Estimated genetic correlations among female fertility traits in the first analysis (upper diagonal) and among female fertility traits and milk yield in the second analysis (lower diagonal).

Table 4. PGM correlations and reliability gains from national evaluation to MT-MACE for female fertility (1,2), to MT-MACE for female fertility and milk yield (1,3) and from MT-MACE for female fertility to MT-MACE for female fertility and milk yield (2,3).

	PGM	1 correlation		Reliability gain				
Trait	1,2	1,3	2,3	1,2	1,3	2,3		
GBR _{NR}	0.956	0.955	0.969	8.09	8.03	3.17		
GBR _{CI}	0.952	0.944	0.978	8.73	8.16	1.71		
ITA _{CI}	0.991	0.985	0.989	8.25	7.54	-0.64		
ITA _{CF}	0.989	0.986	0.992	11.41	12.30	0.05		
NLD _{CF}	0.999	0.997	0.990	1.36	1.39	0.96		
NLD _{CI}	0.999	0.995	0.994	0.83	0.08	0.14		