

# Studies in MACE Correlations for Type

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## Introduction

MACE evaluations for type traits have been computed and delivered to Canadian breeders since 1995. Due to similar industry demands, a parallel service has now also evolved in the United States. Throughout the development of these systems, questions have been raised about the genetic parameters, and specifically the genetic correlations to use for the evaluations. Different studies have given very different genetic correlation estimates and a large number of estimates have been lower than expected, based on simple correlations of proofs (Grignola and Rozzi, 1996; Rozzi, 1997). The importance of these questions has increased with the parallel application of more than one MACE system in North America, because of potentially large differences in the parameters used by each system.

The Canadian system (CMACE) has been using genetic parameters estimated by the procedures of Schaeffer et al. (1996). The current United States system (UMACE) uses parameters estimated by REML procedures developed by Klei (1997). The REML procedures in UMACE are different than the REML procedures used by INTERBULL (Sigurdsson and Banos, 1995) for production traits, and generally give higher estimated genetic correlations for type traits. The UMACE correlations have also been more similar to proof correlations.

The purpose of this study was to examine the estimation procedures, data used and resulting genetic correlation estimates from CMACE and UMACE, and to make recommendations regarding genetic parameters for use in future MACE evaluations for type traits.

## Materials and Methods

Genetic correlation estimates were available from recent CMACE (Aug/97) and UMACE (Nov/97) runs. There were six countries and several traits in

common between the CMACE and UMACE runs, and all were included in our research analyses. For brevity in the report, however, the presentation is limited to three of these countries (Canada (CAN), the United States (USA) and the Netherlands (NLD)). Additionally, only final score plus two high and two low correlation traits, based on UMACE correlation estimates, are presented.

Several differences were noted between the procedures used to estimate genetic correlations in CMACE and UMACE. We will focus on two of these differences. The first difference was that CMACE correlations were estimated from genetic evaluations obtained using an iterative Jacobi (JC) process, whereas the UMACE correlations were estimated from genetic evaluations obtained by direct matrix inversion. The second difference was that the genetic evaluations of ancestors of proven bulls were used for CMACE correlation estimates, compared to the use of genetic evaluations of proven bulls and their ancestors in UMACE.

The iterative process used by CMACE was studied to determine its impact on ancestor (genetic evaluation) correlations, because ancestor correlations formed the basis of the genetic correlation estimates in CMACE. The number of JC iterations was increased, and as an alternative a Gauss-Seidel (GS) iterative process was applied for comparison. These changes were made in each of two separate programs. The first was the deregression program common to both CMACE and UMACE. The second program, specific to CMACE, was used to obtain ancestor evaluations, and subsequently estimate genetic correlations from those evaluations.

Ancestor evaluations could also be obtained directly from the deregression program, removing the need for the second program in CMACE. The problem with this approach was that the deregression program is run within country and uses pedigree files specific to each country. The second (correlation) program reevaluates the ancestors under the same model used for the deregression, but

using a common international pedigree file for all countries.

To study the effect of different genetic evaluation subsets, being used by CMACE and UMACE to estimate genetic correlations, correlations were examined for evaluations of proven bulls and compared to correlations for ancestors of proven bulls. Presumably, correlations between unbiased genetic evaluations with accuracies of 1.0 in both countries would provide unbiased estimates of the true genetic correlations. Proven bulls and ancestors of proven bulls that had accuracies close to 1.0 in both countries were therefore selected to calculate and compare correlations of genetic evaluations.

## Results and Discussion

The effect of iterative procedures, on correlations of ancestor evaluations from the deregression program, can be seen in Table 1. Ancestor correlations between NLD and the other countries increased dramatically when the number of JC iterations was increased, with notable changes continuing to occur between 5000 and 20,000 iterations. By contrast, between CAN and USA, 1500 JC iterations seemed sufficient for the correlations to stabilize. NLD was the most affected by poor JC convergence among the six countries studied.

Table 1. Correlations of ancestor evaluations from the deregression program, with different convergence.

Trait	Jacobi iterations			Gauss-Seidel iterations		International pedigree <sup>1</sup>
	1500	5000	20,000	1000	10,000	
Countries						
Stature						
CAN-USA	.73	.73	.73	.72	.73	.75
CAN-NLD	.20	.43	.67	.68	.68	.69
USA-NLD	.22	.44	.63	.63	.63	.67
Udder depth						
CAN-USA	.62	.63	.63	.62	.63	.62
CAN-NLD	.21	.43	.56	.56	.56	.61
USA-NLD	.33	.61	.73	.73	.73	.75
Rump width						
CAN-USA	.74	.74	.74	.74	.74	.76
CAN-NLD	.31	.65	.66	.66	.66	.67
USA-NLD	.40	.63	.63	.63	.63	.63
Foot angle						
CAN-USA	.66	.66	.66	.65	.66	.66
CAN-NLD	.40	.56	.55	.56	.55	.56
USA-NLD	.34	.58	.59	.59	.59	.58
Final score						
CAN-USA	.72	.72	.72	.71	.72	.73
CAN-NLD	.37	.51	.50	.49	.50	.55
USA-NLD	.40	.65	.66	.66	.66	.70

<sup>1</sup>genetic evaluations obtained from 5000 Jacobi iterations in the deregression program followed by 1000 Gauss-Seidel iterations in the CMACE correlation program.

Correlations stabilized much more quickly with GS. Ancestor correlations after 1000 GS iterations were essentially the same for all traits and country combinations, when compared to correlations after 10,000 GS iterations, or 20,000 JC iterations. The ancestor evaluations used for Table 1 were from the deregression program, which is run within country. The pedigrees of some animals can be more complete, or otherwise different in some countries than in others. Ancestor evaluations from the deregression program have therefore not been used to estimate genetic correlations in CMACE. CMACE genetic correlations were somewhat less affected by convergence because of this. For example, if evaluations from the deregression program, instead of the correlation program, had been used to estimate genetic correlations, the CMACE genetic correlation for stature between CAN and NLD would have been .24 instead of .60. With better convergence, the CMACE correlations

increased to .82 or .83 using evaluations from the deregression or the correlation programs respectively. These compared to .93 from UMACE (Table 2).

The Aug/97 CMACE ran 1500 JC iterations in the deregression program and 1000 JC iterations in the correlation program. Convergence was improved in CMACE2 by increasing to 5000 JC iterations in the deregression program and running 1500 GS iterations in the correlation program. The most notable change from CMACE to CMACE2 was the 38% increase in the correlation for stature between CAN and NLD (Table 2). This change removed 70% of the difference between genetic correlations from CMACE and UMACE for that particular trait and country combination. In general, discrepancies between CMACE and UMACE were reduced with CMACE2, as expected.

Table 2. Correlations of high accuracy<sup>1</sup> genetic evaluations, and estimated genetic correlations.

Trait	Evaluation correlations		Genetic correlations estimated by		
	Ancestors	Proven bulls	CMACE	CMACE2	UMACE
Stature					
CAN-USA	.87	.96	.92	.92	.98
CAN-NLD	.72	.87	.60	.83	.93
USA-NLD	.74	.93	.67	.76	.92
Udder depth					
CAN-USA	.75	.92	.79	.79	.94
CAN-NLD	.73	.86	.68	.77	.90
USA-NLD	.87	.95	.77	.87	.96
Rump width					
CAN-USA	.82	.86	.97	.97	.86
CAN-NLD	.82	.86	.74	.87	.82
USA-NLD	.72	.80	.78	.75	.77
Foot angle					
CAN-USA	.87	.85	.94	.94	.91
CAN-NLD	.76	.85	.57	.76	.78
USA-NLD	.67	.70	.56	.70	.74
Final score					
CAN-USA	.79	.84	.96	.97	.87
CAN-NLD	.47	.58	.65	.71	.70
USA-NLD	.73	.81	.77	.84	.79

<sup>1</sup>high accuracy genetic evaluations for country combination 'ab' had  $r_{T_{Ia}} * r_{T_{Ib}} > .98$ .  $r_{TI}$  was estimated as  $n/(n+k)$ , with n being the number of daughters plus .5 times the number of granddaughters plus .25 times the number of great granddaughters, and k was the residual to sire variance ratio.

A second difference between CMACE and UMACE was the subset of evaluations used to estimate genetic correlations. CMACE did not use evaluations of all proven bulls directly, whereas UMACE did. The UMACE correlations were generally higher than the CMACE2 correlations. Similarly, correlations of highly accurate evaluations were generally higher for proven bulls than for ancestors (Table 2). This may explain some of the remaining differences between genetic correlations estimated from UMACE and CMACE2. A simple procedure to estimate correlations may compare more favourably to the REML approach used by UMACE if the procedure were to include more directly the information available from the evaluations of proven bulls.

In the interest of uniformity between CMACE and UMACE, CMACE has been updated to estimate correlations using the REML programs of UMACE.

These programs require weeks of run time for the data currently available for CMACE. The feasibility of running these programs is a potential concern if more countries become interested in participating in MACE for type. Research to develop alternative and simplified covariance estimation procedures is ongoing.

The major effects of convergence on ancestor correlations raised concerns about the validity of CMACE genetic evaluations, which have also

relied on a JC iterative process. The third and final CMACE program used to solve mixed model equations was therefore modified to use GS. The solution programs from UMACE were also run for comparison purposes. As with the correlation programs, the UMACE solution programs use direct matrix inversion to solve the required mixed model equations. The data and pedigree files were identical for the JC and GS systems, but not for the direct inversion system. Differences in data processing logic between CMACE and UMACE made it difficult to resolve all of the differences. The data differences that remained, however, were believed to be minimal and relatively unimportant.

Results from comparing JC and GS (CMACE) relative to direct inversion (UMACE) are in Table 3. Some large discrepancies were found between JC and direct inversion results. These discrepancies all but disappeared with GS. The small differences that remained between GS and direct inversion were attributed to the pedigree and data differences known to exist because of the different CMACE and UMACE programs that were used. Udder depth had more known data differences than the other traits, and this showed up in the results of Table 3. Even with the data differences, correlations between GS and direct inversion solutions were .995 and higher.

Table 3. Correspondence between iterative and direct MACE solutions, on the Canadian scale.

Trait	Correlation		SD difference		Maximum  difference	
	JC 1500	GS 1500	JC 1500	GS 1500	JC 1500	GS 1500
Stature	.942	.998	1.66	0.31	20.5	3.9
Udder depth	.936	.995	1.75	0.47	21.0	9.6
Rump width	.950	.999	1.39	0.21	16.6	3.7
Foot angle	.932	.997	1.68	0.35	19.8	4.9
Final score	.961	.998	1.35	0.34	19.2	5.1

## Conclusions

Discrepancies between CMACE and UMACE genetic correlation estimates were partially attributed to convergence problems in CMACE. These convergence issues were easily addressed by

switching from a Jacobi to a Gauss-Seidel iterative process for solving the required mixed model equations. This change also improved the direct estimation of CMACE genetic evaluations, in addition to the improvement resulting from more accurate genetic parameters.

Correlations for high accuracy genetic evaluations were generally higher for proven bulls than for ancestors of proven bulls, as were correlation estimates from UMACE relative to CMACE. It may be feasible to derive simple procedures that mimic REML for estimating genetic correlations. Further research is required to advance the development of simplified procedures.

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