MACE with Sire-mgs and Animal Pedigree

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1. Introduction

At the Interbull technical workshop in Beltsville, USA in March 2003, two papers were presented about problems with phantom groups in the current MACE model (De Jong, 2003; Fikse, 2003). Experiences with MACE at several evaluation centres have shown that international genetic evaluation results are sensitive to treatment and definition of phantom groups (Fikse, 2003). Fikse (2003) mentioned as an illustration of these experiences the disadvantage of currently applied random phantom groups in multiple-trait models that the trend in genetic group effects is more regressed (less steep) for one trait than for another trait. For example, in MACE the trend in US maternal granddam group effects on the Dutch scale is flatter than the trend of the same groups on the US scale. In extreme cases the trend may have a different sign! De Jong (2003) proposed to include full pedigree for all bulls into the MACE system, to reduce the effect of phantom groups on bull proofs. This model would be a model including animal pedigree, but including only observations on bulls (i.e. de-regressed proofs).

The aim of this study is to compare the ability to convert proofs across countries between MACE with sire-mgs pedigree and MACE with animal pedigree.

2. Material and Methods

2.1 Data

Seven countries participated in this study: Canada (CAN), France (FRA), Germany (DEU), Italy (ITA), the Netherlands (NLD), New Zealand (NZL) and the United States (USA). Files with bull proofs for milk, fat and protein production, and identification numbers of parents and maternal grandparents of bulls (010-files) from the participating countries were obtained from the Interbull centre. The participating countries provided these files to Interbull for the May 2004 evaluation. Pedigree files were obtained from the participating countries except for New Zealand. The pedigree files contained male and female ancestors of all bulls in the 010-files. The pedigree file of New Zealand was extracted from the pedigrees in the 010-file. One master pedigree file was created including one unique pedigree record per animal. The number of data and pedigree records are in Table 1.

Table 1. The number of bull proofs and the number of records in the master pedigree file per country.

Country	Bull proofs	Master pedigree file
CAN	7,363	19,011
DEU	24,673	51,997
FRA	18,805	34,954
ITA	7,609	22,321
NLD	14,653	28,602
NZL	9,226	11,912
USA	52,248	119,070
Total	134,577	287,867

Most countries have about twice as many records in the master pedigree file as in the data file (Table 1). New Zealand has relatively fewer records in the master pedigree file due to providing only 2 generations of pedigree.

2.2 Methods

Genetic correlations were estimated with MACE software (Holstein Association, USA). Data selection was carried out in line with Interbull's current MACE system. All bulls with offspring in multiple countries and all bulls with ¾ sibs (same sire and maternal grandsire) in another country were selected. All bulls with at least 10 daughters in 10 herds were included in the estimation of the genetic correlations. Correlations were estimated in subsets, including USA and two other countries per subset. Two methods of MACE were applied in the estimation of genetic correlations and in the genetic evaluation:

1. MACE sire-mgs pedigree (current MACE, **SP**).
2. MACE animal pedigree (**AP**).

For the genetic evaluation, only bulls born after 1985 were included. Domestic proven bulls (type of proof 11 or 12, TOP1) needed to have at least 10 daughters in 10 herds and foreign proven bulls (type of proof 21, TOP2) needed to have at least 75 daughters in 50 herds. The minimum phantom group size for all methods was 30.

2.3 Use of pedigree

Including full pedigree in the AP evaluation was not possible due to large CPU-time requirements. Therefore all bulls with and without proofs in the data set plus 3 generations of their ancestors were included. For the third generation of ancestors a phantom group replaced the dam if that dam had only one offspring. Phantom groups for dams were assigned in the same way as for sires. The percentage of known ancestors was 97% or higher for all countries except NZL. An ancestor was known if the identification number was known and not replaced by a phantom group. The genetic evaluation included 58,592 pedigree records, 55,935 performance records and 196 phantom groups for the SP evaluation and 108,872 pedigree records, 55,819 performance records and 228 phantom groups for the AP evaluation. The AP evaluation included about twice as many pedigree records, reducing the influence of phantom groups.

2.4 Genetic ties

The number of common bulls per two countries and the number of common dams are in Table 2. The common dams include dams that have male offspring being full-sibs or half-sibs with data in different countries. Dams of common bulls were not regarded as common dams.

Table 2. Number of common bulls (below diagonal) and common dams (above diagonal) in two countries.

	CAN	DEU	FRA	ITA	NLD	NZL	USA
CAN		226	450	63	116	12	478
DEU	543		468	79	274	109	299
FRA	638	765		184	382	159	1096
ITA	504	796	735		110	61	111
NLD	578	1178	848	686		33	179
NZL	509	342	348	319	512		75
USA	1363	966	1241	925	1211	622	

The minimum number of common bulls between two countries was 319 and the maximum was 1363. The minimum number of common dams was 12 and the maximum was 1096. These numbers show that many additional genetic relationships between animals are taken into account when female animals are added to the MACE evaluation. From the 55,819 bulls in the AP evaluation, 29% was the only male offspring with a proof of a dam and 71% had a full-sib or half-sib with a proof in the genetic evaluation.

2.5 Validation

The two MACE methods were compared by two validations:

1. Bulls with TOP1 proofs in multiple countries.
2. Bulls with TOP2 proofs in multiple countries.

Validation 1: For bulls with TOP1 proofs in multiple countries the two countries with the most daughters were determined. Within this validation two genetic evaluations were carried out. In the first evaluation data of one randomly chosen country was discarded and in the second evaluation data of the other country was discarded. In this way, every bull had in two countries a proof with daughters (realised proof) and without daughters (converted proof) and these two proofs were compared afterwards. In the SP and the AP evaluation there were 1927 and 1921 bulls born after 1985 with TOP1 in multiple countries, respectively.

Validation 2: All TOP2 proofs of bulls born after 1992 with at least one TOP1 proof and one TOP2 proof were removed. After the evaluation, the converted proof was compared to the realised proof. TOP2 proofs of bulls born before 1993 were kept in the data set so that there were still enough genetic links between countries and that most bulls used for the validation still had a sire with a TOP2 proof. In total 421 TOP2 proofs of 222 bulls born after 1992 were discarded, both in the SP and the AP evaluation.

Both validation methods aim to calculate the predictive ability of SP and AP. The predictive ability of both models was investigated by the mean and the standard deviation of the differences between the converted and the realised proof per country.

3. Results

3.1 Genetic correlations in Interbull, AS and AP

Genetic correlations for protein were estimated with SP to check whether the results were consistent with genetic correlations estimated by Interbull (November 2004 correlations instead of May 2004, due to changing the method of estimation by Interbull, Italy changed their national genetic evaluation model to a test-day model meanwhile). The genetic correlations estimated with SP were on average 0.009 higher. The absolute differences between Interbull and SP correlations were 0.02 or smaller between all countries except the correlations of New Zealand with Germany (0.06 higher with SP) and France (0.03 higher with SP). The change in correlations with New Zealand might be due to the effect of other countries (e.g. Australia) on the correlations estimated by Interbull. The differences in sire standard deviations estimated per country between Interbull and SP were 0.4% or smaller. Table 3 gives the genetic correlations for protein estimated with AP. The average correlation for protein estimated with AP was 0.79, the minimum correlation was 0.52 and the maximum correlation was 0.94.

Table 3. Genetic correlations estimated with AP for protein (sire standard deviations on diagonal, differences with SP correlations above diagonal).

	CAN	DEU	FRA	ITA	NLD	NZL	USA
CAN	**11.77**	-0.03	-0.03	-0.02	-0.01	-0.01	0.00
DEU	0.86	**8.56**	0.00	-0.04	-0.01	0.00	-0.02
FRA	0.88	0.82	**9.80**	-0.04	0.00	-0.01	-0.01
ITA	0.91	0.79	0.84	**8.38**	-0.06	-0.03	0.00
NLD	0.89	0.88	0.88	0.81	**8.98**	-0.01	-0.02
NZL	0.58	0.52	0.68	0.56	0.62	**4.75**	-0.01
USA	0.93	0.83	0.87	0.94	0.85	0.57	**19.23**
AV[1]	0.84	0.78	0.83	0.81	0.82	0.59	0.83

[1] Average correlation with other countries.

The genetic correlations estimated with AP were on average 0.017 lower compared to the SP correlations. Difference in genetic correlations between AP and SP (AP-SP) ranged from 0.00 to -0.06, largest differences were observed for Italy. Due to including more pedigree information in AP than in SP it was expected that the genetic effects of bulls could be estimated more accurately resulting in higher genetic correlations. This positive effect was not found in this study. The differences in sire standard deviations between SP and AP (AP-SP) ranged from 1.2% increase for the Netherlands to 5.2% increase for Italy.

3.2 Comparison of SP and AP converted proofs

All results, including the sire standard deviations of both validation methods, presented in the Tables 4 to 8 are on the transmitting ability (ETA) scale to make results more comparable across countries. Results of the comparison between SP and AP converted proofs are in Table 4. The average difference per country for converted proofs between SP and AP was small. The standard deviations of the differences were also small, but differences were large for some bulls. The standardised standard deviation was almost equal for all countries.

Table 4. Average (AV), standard deviation (STD), minimum (MIN) and maximum (MAX) of the differences (AP-SP) in ETA for converted protein proofs per country.

Country	n	σ_S[1]	AV[2]	STD[2]	MIN[2]	MAX[2]
CAN	50,266	11.52	3%	11%	-112%	95%
DEU	43,770	8.38	6%	13%	-158%	88%
FRA	47,372	9.56	4%	12%	-59%	77%
ITA	51,102	7.96	-3%	12%	-69%	127%
NLD	48,561	8.86	-1%	12%	-117%	69%
NZL	52,761	4.48	0%	14%	-87%	80%
USA	36,880	18.42	-4%	13%	-74%	125%

[1] σ_S is sire standard deviation of the country in SP evaluation.
[2] Expressed as percentage of σ_S.

3.3 Results of validation 1 for SP and AP

Results of validation 1 for SP and AP are in Table 5 and 6, respectively.

Table 5. Average (AV), standard deviation (STD), minimum (MIN) and maximum (MAX) of the realised - converted ETA for protein of bulls with TOP1 proofs in multiple countries.

Country	n	σ_S[1]	AV[3]	STD[3]	MIN[3]	MAX[3]
CAN	489	11.52	4%	48%	-155%	158%
DEU	477	8.38	10%	48%	-149%	236%
FRA	534	9.56	-1%	50%	-146%	186%
ITA	134	7.96	-3%	47%	-93%	152%
NLD	723	8.86	2%	48%	-203%	177%
NZL	383	4.48	0%	63%	-214%	214%
USA	1114	18.42	-4%	43%	-180%	141%
Average[2]			3.6%	48.3%		

[1] σ_S is sire standard deviation of the country in SP evaluation.
[2] Average of absolute values weighted by the number of records.
[3] Expressed as percentage of σ_S.

Table 6. Average (AV), standard deviation (STD), minimum (MIN) and maximum (MAX) of realised - converted ETA for protein of bulls with TOP1 proofs in multiple countries.

Country	n	σ_S[1]	AV[3]	STD[3]	MIN[3]	MAX[3]
CAN	485	11.77	1%	45%	-146%	146%
DEU	475	8.56	5%	47%	-168%	214%
FRA	534	9.8	-3%	48%	-154%	178%
ITA	134	8.38	1%	45%	-84%	135%
NLD	721	8.98	3%	48%	-164%	176%
NZL	383	4.75	-2%	58%	-162%	189%
USA	1110	19.23	-2%	41%	-177%	147%
Average[2]			2.4%	46.5%		

[1] σ_S is sire standard deviation of the country in AP evaluation.
[2] Average of absolute values weighted by the number of records.
[3] Expressed as percentage of σ_S.

The average difference, averaged across countries, was lower for AP than for SP. The maximum absolute difference in AP was smaller (5%, DEU) than in SP (10%, DEU). Furthermore, the standard deviation of differences for AP was lower for all countries.

3.4 Results of validation 2 for SP and AP

The results for validation 2 for SP are in Table 7. The average differences per country were close to zero except for CAN and FRA. The standard deviation of the differences of all countries were comparable, except for DEU and NZL. The larger standard deviation of the differences for DEU was not found in validation 1.

Table 7. Average (AV), standard deviation (STD), minimum (MIN) and maximum (MAX) of the realised - converted ETA for protein of bulls with TOP2 proofs in multiple countries.

Country	n	σ_S[1]	AV[3]	STD[3]	MIN[3]	MAX[3]
CAN	43	11.52	10%	31%	-80%	68%
DEU	113	8.38	-2%	53%	-135%	191%
FRA	47	9.56	15%	36%	-52%	98%
ITA	80	7.96	3%	36%	-98%	97%
NLD	65	8.86	-2%	37%	-81%	104%
NZL	27	4.48	0%	62%	-98%	161%
USA	46	18.42	-3%	34%	-100%	66%
Average[2]			4.4%	41.9%		

[1] σ_S is sire standard deviation of the country in SP evaluation.
[2] Average of absolute values weighted by the number of records.
[3] Expressed as percentage of σ_S.

The results for validation 2 for AP are in Table 8. The average differences per country were close to zero except for DEU (-9%) and FRA (9%). The standard deviations of the differences of all countries were comparable, except for DEU and NZL, which was consistent with SP.

Table 8. Average (AV), standard deviation (STD), minimum (MIN) and maximum (MAX) of the realised - converted ETA for protein of bulls with TOP2 proofs in multiple countries.

Country	n	σ_S[1]	AV[3]	STD[3]	MIN[3]	MAX[3]
CAN	43	11.77	3%	30%	-81%	64%
DEU	113	8.56	9%	55%	-153%	183%
FRA	47	9.8	9%	36%	-59%	101%
ITA	80	8.38	2%	35%	-86%	111%
NLD	65	8.98	2%	40%	-95%	106%
NZL	27	4.75	2%	60%	-120%	158%
USA	46	19.23	0%	31%	-93%	81%
Average[2]			4.8%	42.0%		

[1] σ_S is sire standard deviation of the country in AP evaluation.
[2] Average of absolute values weighted by the number of records.
[3] Expressed as percentage of σ_S.

The average difference, averaged across countries, is slightly higher than for SP. The standard deviation of differences was lower than SP for CAN, ITA, NZL and USA, but higher for DEU and NLD. The maximum absolute difference in AP was smaller (9%, DEU and FRA) than in SP (15%, FRA).

4. Discussion

Differences between SP and AP were large for individual bulls. More research will be carried out to investigate the differences for certain groups of bulls e.g. MGD group in SP, year of birth or country of test.

Differences between SP and AP for TOP2 bulls were very small, but slightly in favour of SP. Differences between SP and AP for TOP1 bulls were larger and in favour of AP. Overall it can be concluded that the differences in predictive ability between SP and AP were small but in favour of AP.

AP with four generations of pedigree was feasible in this study, but results (not included in this paper) showed small differences compared to AP with three generations of pedigree. It is expected that including full pedigree does not result in large differences compared to the current AP results.

The CPU time increased from SP to AP with a factor 28 for the estimation of genetic correlations and a factor 9 for the genetic evaluation with 7 countries included. Therefore it is recommended to investigate the possibilities to reduce the CPU time needed for AP.

5. Conclusions

Standard deviations of the differences between SP and AP per country were small, but differences were large for some bulls.

Genetic correlations estimated with AP were slightly (0.017) lower compared to SP.

Predictive ability of AP was slightly better compared to SP in terms of average and standard deviation of differences of converted vs. realised proofs, especially for TOP1 bulls.

6. Acknowledgements

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7. References

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