Developments in Applying MACE to the Conformation Traits

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Abstract

MACE has now successfully been applied to 12 linear conformation traits and overall conformation to provide evaluations on foreign bulls on the Canadian basis. A simple and effective method for estimating sire variances within countries is described here and differences from the a previous approximate EM-REML approach are reported. Higher estimates of genetic correlations between countries have been found for all traits and reported here. In an effort to make MACE results more accessible to the end-user, complete and abridged files have been placed on the Internet for timely and cost-effective delivery. In addition, database software for the PC has been developed that allows simple viewing and ranking of all foreign bull evaluations for production and conformation traits.

Introduction

Applications of Multiple-trait Across Country Evaluations (MACE) have been successfully carried out for production traits since 1993 (Schaeffer and Zhang), and INTERBULL now regularly provides this service on a semiannual basis. In contrast, the application of MACE to conformation traits has only been used in Canada to provide official evaluations on foreign Holstein bulls (Weigel et al., 1995) and is presently under development by INTERBULL. Due to the large number of conformation traits the application of MACE is not straightforward, and differences that exist in trait definition, recording, data handling and genetic evaluation can cause genetic correlations to be considerably lower than for production traits (Weigel et al., 1995). Schaeffer et al. (1996) determined that many factors can affect conversion formulas, such as data editing by year of birth, inclusion of second-country proofs, and biased proofs leading to overestimated genetic trend. In addition, the quality of genetic ties between countries, the inclusion of second-country proofs and the method used to estimate sire variances and covariances are important to accurate ranking of bulls across country (Sigurdsson and Banos, 1995). In a study limited to bulls from Denmark, USA and Canada, Fikse et al. (1995) showed that higher estimates of genetic correlations between countries can be obtained using a bivariate REML procedure if there is careful selection of data sets rich in genetic ties. This paper will document further developments made in the application of MACE to conformation traits in Canada.

Weigel (1995) demonstrated that because conformation traits can be defined differently between countries, MACE is particularly useful because bull evaluations are allowed to rank differently in each country. By contrast, conversion formula, regardless of how they are computed, assume that all bulls rank the same in all countries. Because of this difference, the simple release of conversion formulas is no longer acceptable and should be replaced by the release of the actual MACE evaluations themselves. In countries where there is a great deal of semen importation through a number of agents, the uniform and timely release of MACE results becomes an issue. Steps taken in Canada to lead to the more effective use of MACE results will be outlined below.

Methods

National sire evaluation and pedigree data sets were obtained for all available conformation traits from six countries (CAN, USA, NLD, DEU, FRA, and ITA). Overall conformation and 12 linear traits were matched according to globally harmonized trait definitions as follows, stature, body depth, rump angle, rump width, rear leg set, foot angle, fore udder attachment, rear udder height, central ligament, udder depth, front teat placement and front teat length. In addition, MACE was applied to some general traits using composite traits from foreign countries. The total number of bulls from each country includes all bulls with official evaluations born since 1981 with status codes of 00 (unknown) or 10 (AI bull). Bull evaluations from each country were deregressed as described by Banos et al. (1993), where the MME for de-regression of proofs can be written as:

 $\begin{bmatrix} 1'R^{-1}1 & 1'R^{-1}Z & 0\\ Z'R^{-1}1 & Z'R^{-1}Z \cdot A^{pp}\alpha & A^{po}\alpha\\ 0 & A^{op}\alpha & A^{oo}\alpha \end{bmatrix} \begin{bmatrix} \hat{c}\\ \hat{a}_p\\ \hat{a}_o \end{bmatrix} - \begin{bmatrix} 1'R^{-1}Y\\ Z'R^{-1}Y\\ 0 \end{bmatrix}$

where,

- Y is a vector of de-regressed proofs
- \hat{c} is a vector of country effect (unknown)
- \hat{a}_p is a vector of proofs of bulls from each country (known)
- \hat{a}_o is a vector of proofs of ancestors, phantom parent groups (unknown)
- **A** is the relationship matrix
- R⁻¹ is the diagonal matrix of number of daughters in each country
- **Z** is the incidence matrix.

Equations were solved for Y while holding \hat{a}_{r} constant.

Previously, estimates of within country sire variances were done simultaneously with the

de-regression of proofs, based on a singletrait, approximate EM-REML procedure. However, this approach led to estimates that differed considerably from the variance of raw proof information in some cases, especially when a population is making rapid genetic change or if different sub-populations are present in the data. A more stable approach (Schaeffer et al., 1996) was applied to estimation of sire variances within country after de-regression of proofs is completed, and is described as follows:

Step 1:

Set up equations similar to (1) and solve.

Step 2: Compute:

$$z_{bull} - s_{bull} - .5 (s_{stre}) - .25 (s_{MGS} - s_{MGD})$$
 (2)

and,
$$SSA = \sum z_{bull}^2 c$$
 (3)

where c = 16/(11+x), and x depends on sire and MGS identification. If both sire and MGS are known, x=0; if MGS is unknown, x=1; if sire is unknown, x=4; and if both sire and MGS are unknown, x=5. SSA is the usual quadratic form for REML which is equivalent to $\hat{s}'A^{-1}\hat{s}$. Thus, this is an attempt to estimate the Mendelian sampling variance or one-half the additive genetic variance.

Step 3:

Simulate a new de-regressed proof vector, Y, using a variance of 1 and a residual variance of k_i and random normal deviates for sire and residual effects. This is easily accomplished when animals are ordered oldest to youngest.

Step 4:

Repeat steps 1 and 2 using the simulated proof vector, and compute SSA again (SSA*). The sire variance can be estimated by:

$$\sigma_{ster}^2 \cdot \frac{SSA}{SSA}.$$
 (4)

then, repeat steps 3 and 4 at least 25 times and average the estimates.

The above procedure is simple and does not rely on evaluating likelihoods or computing inverses to mixed model equations, but does require the heritability to be fixed. If heritability is not correct, then the estimate of the sire variance could be biased.

The procedure for estimating correlations between countries was as follows:

- 1. Apply MACE to all country's de-regressed proofs assuming a zero prior for sire covariances between all countries.
- 2. For each pair of countries, find the ancestor sires with sons or grandsons in both countries.
- 3. Calculate the correlation of ancestor sire solutions in the two countries, and also the expected correlation based on number of sons.
- 4. An estimate of the genetic correlation is then the actual correlation divided by the expected correlation. Covariances are obtained using the sire variances estimated as described above.

Unfortunately, the number of common ancestors between countries were limited to between 121 to 222 bulls despite including second-country proofs. In this procedure, care must be taken to ensure that the estimate of **G** is positive definite. If **G** is non-positive definite, the variance covariance matrix has to be modified (i.e. all eigenvalues should be positive). Likewise, if correlations are estimated on a pairwise basis, there is no guarantee that the final matrix will be positive definite.

To calculate sire solutions, MACE procedure was followed as described by Weigel et al. (1995). Only bulls with Interbull codes of 11 or 12 were used (i.e. proofs of imported bulls were excluded). Conversion formulas were estimated by simple regression of proofs for bulls that have a proof in one of the two countries with at least 35 daughters. Reliabilities for conformation were estimated as a function of the inverse of the prediction error variances.

Results and Discussion

As shown in the following tables, present estimates of sire variances were compared to previous results using an approximate EM-REML procedure (Weigel et al., 1995) and also compared to variances of proof information. From theory, one expects the variance of proof values to be smaller than sire variances because proof information is regressed according to the inverse of the reliability associated with each bull. However, if the proof information spans many years and/or if considerable genetic progress has taken place, one would expect the variance of proofs to be expanded and the difference from sire variances to be reduced. From the tables, that the present method (V2) provides estimates that are more consistent and closer to the variation of proof data than the previous method (V1). Some evidence suggested that differently scored subpopulations within a population should be treated separately.

Genetic correlations between countries for various traits were re-estimated as described above and shown in following tables. In almost all cases the present estimates were higher than previous ones particularly involving the Netherlands and Germany. In some cases, estimates were over 30% higher. This is most likely due to a growing number of common ancestors between countries and more careful data editing techniques. In most cases, estimates were lower than those found by Fikse et al. (1995), but were on par with those found by Weigel (1995) and Klei (1995). Regardless, the method does not seem to adequately estimate correlations among European countries where genetic ties may be mostly through North-American sires. An alternative EM-REML method for estimating sire covariances (Banos and Sigurdsson, 1995) is presently being tested in Canada.

To increase the timely access to MACE evaluations, MACE files and descriptions are now available on the Internet. For those with access to the World-Wide-Web (WWW), a complete description of the MACE evaluations and directions to all files can be found at the following sites:

http://www.aps.uoguelph.ca/cgil/MACE/ MACE.html

ftp://wright.aps.uoguelph.ca/cdn/files/foreign/

Since not all users have Internet connections, and sometime large files can be slow to download, database software for the PC has been developed using "FoxPro" to be released by the Canadian Dairy Network (CDN) that will allow semen importers, AI studs and farmers to view all MACE evaluations for foreign bulls on their own personal computers. This software is now available from CDN via diskette and via the internet. The advantage this software provides is that if a MACE evaluation is not available for a particular bull, the program will allow the user to calculate a converted proof on the Canadian basis.

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Estimated Sire Variances: Centre Ligament

	CAN	FRA	GER	ITA	NLD	USA
h ²	.15	.26	.20	.15	.25	.24
Vp (proof)	24.6	0.67	136	2.25	15.5	1.37
V1 (sire)	25.0	0.77	230	2.74	51.1	1.75
V2 (sire)	23.5	0.86	163	2.66	17.2	1.60
Vp / V1	0.98	0.87	0.59	0.82	0.30	0.78
Vp / V2	1.05	0.78	0.84	0.85	0.90	0.85

V1 = July 95 method V2 = Jan 96 method

Lohuis, et al., 1996

Estimated Sire Variances: Fore Udder

	CAN	FRA	GER	ITA	NLD	USA
h²	.14	.34	.20	.15	.35	.29
Vp (proof)	24.7	0.57	176	1.97	18.3	1.19
V1 (sire)	31.4	n/a	287	2.78	53.8	1.60
V2 (sire)	28.1	0.72	221	2.58	23.1	1.57
Vp / V1	0.79	n/a	0.61	0.71	0.34	0.74
Vp / V2	0.88	0.80	0.80	0.77	0.79	0.76

V1 = July 85 method V2 = Jan 96 method

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Estimated Sire Variances: Conformation (Total Score)

	CAN	FRA	GER	ITA	NLD	USA
h²	.18	.30	.30	.15	.30	.29
Vp (proof)	25.0	0.62	121	0.46	21.4	0.76
V1 (sire)	25.6	0.70	190	0.54	48.5	0.73
V2 (sire)	25.9	0.80	142	0.49	18.7	0.72
Vp / V1	0.98	0.89	0.64	0.85	0.44	1.04
Vp / V2	0.96	0.77	0.85	0.95	0.79	1.06

V1 = July 95 method V2 = Jan 96 method

Lohuis, et al., 1996

Estimated Sire Variances: Body Depth

	CAN	FRA	GER	ITA	NLD	USA
h²	.22	.36	.31	.31	.35	.37
Vp (proof)	25.5	1.06	160	1.59	17.4	0.90
V1 (sire)	n/a	n/a	n/a	n/a	n/a	n/a
V2 (sire)	25.5	1.20	187	1.74	17.2	1.09
Vp / V1	n/a	n/a	n/a	n/a	n/a	n/a
Vp / V2	1.00	0.88	0.86	0.92	1.01	0.83

V1 = July 85 method V2 = Jan 96 method

Lohuis, et al., 1996

Estimated Sire Variances: Udder Depth

	CAN	FRA	GER	ITA	NLD	USA
h²	.27	.35	.31	.29	.45	.28
Vp (proof)	25.0	0.61	138	1.54	18.0	1.44
V1 (sire)	n/a	n/a	n/a	n/a	n/a	n/a
V2 (sire)	35.7	0.85	198	2.21	22.2	2.05
Vp / V1	n/a	n/a	n/a	n/a	r/a	n/a
Vp / V2	0.70	0.72	0.70	0.69	0.81	0.70

V1 = July 95 method V2 = Jan 96 method

Lohuis, et al., 1996

Estimated Sire Variances: Fore Teat Length

	CAN	FRA	GER	ITA	NLD	USA
h²	.28	.30	.24	.22	.45	.26
Vp (proof)	25.3	0.80	137	2.31	21.0	1.28
V1 (sire)	n/a	n/a	n/a	n/a	n/a	n/a
V2 (sire)	32.7	1.15	195	3.56	26.6	1.94
Vp / V1	n/a	n/a	n/a	n/a	n/a	n/a
Vp / V2	0.77	0.70	0.70	0.65	0.79	0.66

V1 = July 95 method V2 = Jan 96 method

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Estimated Sire Variances: Stature

CAN	FRA	GER	ITA	NLD	USA
.40	.47	.43	.38	.60	.42
25.0	1.44	110	1.47	20.6	1.02
26.6	1.64	177	1.73	48.7	1.21
28.5	1.76	143	1.92	22.9	1.32
0.94	0.88	0.62	0.85	0.42	0.84
0.88	0.82	0.77	0.77	0.90	0.77
	CAN .40 25.0 26.6 28.5 0.94 0.88	CANFRA.40.4725.01.4426.61.6428.51.760.940.880.880.82	CANFRAGER.40.47.4325.01.4411026.61.6417728.51.761430.940.880.620.880.820.77	CANFRAGERITA.40.47.43.3825.01.441101.4726.61.641771.7328.51.761431.920.940.880.620.850.880.820.770.77	CANFRAGERITANLD.40.47.43.38.6025.01.441101.4720.626.61.641771.7348.728.51.761431.9222.90.940.880.620.850.420.880.820.770.770.90

V1 = July 95 method V2 = Jan 96 method

Lohuis, et al., 1996

Estimated Sire Variances: Rump Angle

	CAN	FRA	GER	ITA	NLD	USA
h²	.30	.34	.26	.25	.35	.33
Vp (proof)	25.4	0.68	143	1.88	17.0	1.17
V1 (sire)	29.6	0.79	221	2.48	49.4	1.68
V2 (sire)	28.5	0.82	176	2.59	20.6	1.74
Vp / V1	0.86	0.86	0.64	0.76	0.34	0.70
Vp/V2	0.78	0.83	0.81	0.73	0.82	0.67

Estimated Sire Variances: Rump Width

	CAN	FRA	GER	ITA	NLD	USA
h²	.24	.32	.24	.29	.30	.26
Vp (proof)	25.0	0.93	135	1.41	19.3	0.98
V1 (sire)	27.5	1.10	199	1.68	54.7	1.26
V2 (sire)	25.6	1.11	158	1.72	21.4	1.19
Vp / V1	0.91	0.85	0.67	0.84	0.35	0.78
Vp / V2	0.98	0.84	0.86	0.82	0.90	0.82

V1 = July 95 method V2 = Jan 96 method

Lohuis, et al., 1996

Estimated Sire Variances: Rear Leg Set

	CAN	FRA	GER	ITA	NLD	USA
h²	.16	.07	.13	.16	.35	.21
Vp (proof)	25.3	0.88	128	2.13	16.5	1.35
V1 (sire)	36.8	1.32	276	2.93	52.0	2.30
V2 (sire)	31.5	0.83	166	2.67	22.2	2.01
Vp / V1	0.69	0.67	0.46	0.73	0.32	0.59
Vp / V2	0.80	1.06	0.77	0.80	0.74	0.67

V1 = July 95 method V2 = Jan 96 method

Lohuis, et al., 1996

	CAN	EDA	GED	ITA	NI D	
h ²	.07	.10	.13	18	20	15
Vp (proof)	25.0	0.79*	146	1.68	12.3	1.23
V1 (sire)	35.8	n/a	288	2.52	56.4	2.04
V2 (sire)	22.8	0.46*	175	2.34	19.2	1.57
Vp / V1	0.70	n/a	0.51	0.67	0.22	0.60
Vp/V2	1.10	1.73*	0.83	0.72	0.64	0.79

Estimated Sire Variances: Fore Teat Placement

	CAN	FRA	GER	ITA	NLD	USA
h²	.24	.30	.27	.22	.45	.26
Vp (proof)	25.1	.89	141	1.69	16.7	1.46
V1 (sire)	28.0	1.00	242	2.17	48.0	1.77
V2 (sire)	28.4	1.16	187	2.14	19.5	1.67
Vp/V1	0.90	0.89	0.58	0.78	0.35	0.82
Vp / V2	0.88	0.77	0.75	0.79	0.86	0.87

V2 = Jan 96 method

Lohuis, et al., 1996

Ja	n 96 (/	Aug 9	5)	uature	5	
[h²]	CAN	USA	NLD	DEU	FRA	ITA
CAN	[.40]	.36 (.37)	.80 (A3)	.71 (.80)	(86.) 20.	
USA	.96 Filtae .90 Weig	[42]	.00 (.84)	.76 (.70)	.70 (.72)	.79 (.78
NLD		.85 F.Jan .89 Weig	म्प	.70 (.72)	.17 (.83)	.42 (.45
DEŲ		.75 Weig		- নেগ	.81 (.86)	
FRA					1742	-12 (.12
ITA	h	.30 Weig				[,40
AVG	.64 (.83)	.74 (.72)	.58 (.54)	.88 (.84)	(20.) 20.	.81 (.89)

Correlations [h²]: Rump Angle Jan 96 (Aug 95)

[h²]	CAN	USA	NLD	DEU	FRA	ITA
CAN	L'201	(84.) 06.	.72 (.86)	.30 (.84)	.72 (.69)	.73 (.74)
USA	.12 Filcae .10 Weig	ाय्य	.85 (.88)	JIT (,77)	.76 (.74)	. JFT (.JHT)
NLD		.19 Weig	[उडा	.86 (.74)	.46 (.87)	JEZ (,72)
DEU		JEZ Weig		[.26]	.71 (.74)	.79 (.74)
FRA					[24]	- 77 (77)
ITA		.H Weig				[26]
AVG	.77 (.70)	.36 (.79)	.77 (.66)	.50 (.73)	.72 (.70)	.30 (.77)
	Films + Films - Weig = Weigel Alai = Kiel B.,	nt ni., 1996 I K.A., 1996 1996			Lohuis, et	al., 1996

Jan	96 (A	ug 95)	1			
[h ²]	CAN	USA	NLD	DEU	FRA	п
CAN	[-24]	.96 (.96)	.44 (.43)	JI2 (JP1)	(CAL) PB.	.) CL
USA	.87 Filcle .81 Weig	[.26]	.66 (.65)	(25.) 08.		.) H .
NLD		.29 KJel .76 Weig	[.30]	(23.) 28.	.36 (.30)	.) W.
DEU		.77 Weig			.48 (.81)	-74 (.7
FRA					[32]	.) DR.
ITA		.#1 Weig				
AVG.	.77 (.76)	.79 (.79)	.63 (.61)	.77 (.71)	.82 (.81)	.77 (.7

Ja	n 96 (/	Aug 9	5)	ear L	ey set	1
h²]	CAN	USA	NLD	DEU	FRA	ITA
AN	[Int]	.70 (.70)	.46 (.39)	.45 (.56)	(181) 18	
SA	.34 Filtae .76 Weig	ूट्रग्	(84.) 88.	.73 (.69)	.84 (.82)	.84 (.88)
LD		.75 Weig	fart	A3 (A8)	.80 (.41)	.87 (.82)
€Ų		.75 Weig		[.13]	.64 (.66)	.80 (.87)
RA					[.07]	72 (.71)
A	}	JA Weig				, 10
VG	.61 (.68)	.70 (.67)	.54 (.49)	.81 (.86)	.60 (.55)	

Jar	rrelati n 96 (/	ions [l Aug 98	າ⁻]: Fo 5)	oot Ar	ngle	
[h²]	CAN	USA	NLD	DEU	FRA	ITA
CAN	[.07]	.92 (.93)	.87 (.88)	.73 (.88)	.#0 (n/a)	.60 (.60
USA	.84 Filtee .72 Weig	[,10]	.741.711	. 45 (.64)	.73 (N/A)	
NLD		.53 Weig	ा.उग	.44 (.42)	A6 (n/a)	
DEU		.42 Weig		[.13]	.84 (n/a)	.40 (.30
FRA					[,10]	.43 (n/a)
ITA		.74 Weig				[.18]
AVG.	.72 (.69)	.77 (.76)		.87 (.80)	.44 (n/a)	

Ja	orrelat in 96 (/	ions (Aug 9	h*]: 1 5)	feat P	lacem	ent
2]	CAN	USA	NLD	DEU	FRA	ITA
NN.	[34]	.91 (.83)	.36 (.76)	.78 (.70)	.87 (.85)	.72 (.76)
3A	.96 Fikae .86 Weig	1.201	.83 (.78)	- 34 (.74)	.77 (.78)	.#2 (.#4)
D.		JT Klei JO Weig	[कटा	.76 (.76)	.00 (.06)	.61 (.64)
U		.co Weig		1271	.74 (.73)	.89 (.87)
A					[30]	.88 (.87)
		.77 Weig			···	.22
G.	(ORC.) ZIL	JE (JE)	.77 (.73)	.74 (.70)	.76 (.73)	.70 (.70)
	Fitme - Fitme Visig - Visign Kint - Siet B.	nt nl., 1996 / K.A., 1996 1996	ł		Lohuls, e	t ni., 1996

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[h²]	CAN	USA	NLD	DEŲ	FRA	IT/
CAN	[गग	.96 (.96)	.82 (.73)	.73 (.84)	.78 (.74)	-71 (A
USA	.33 Filme .77 Weig	म्प्रम्	JIT (JH)	(88.) 88.	.60 (.66)	.79 (.71
NLD			[.28]	.73 (.88)	.84 (.83)	. 80 (.8 .
DEU		.Je weig		[.20]		.74 (.83
FRA					[.26]	.61 (.87
ITA		JIC Weig				<u>t u</u>
AVG.		.42 (.74)	.78 (.89)	.72 (.84)		.71 (.84

[h ²]	CAN	USA	NLD	DEU	FRA	П
CAN	[म्प	.87 (.83)	.88 (.87)	(BL) BL		
USA	"Sel Flicae "Sti Weig	الحدا	.80 (.77)		.30 (nia)	
NLD		JE Kjel .77 Weig	rael	.az (.at)	.28 (NA)	.70 (.66
DEU	<u> </u>	.45 Weig		[02.]	241 (n/a)	.78 (.89
FRA					ाम्य	
ITA		JS Weig				Į.18
AVG.			.76 (.70)	.74(.71)	.46 (n/a)	73 (.71

Jan	96 (A	ug 95]. C()	JIIIOI	mauc	711
[h²]	CAN	USA	NLD	DEU	FRA	IT
CAN	ि दिम्ब	.92 (.91)	.64 (.56)		-06 (.68)	A9 (.5
USA	.78 Weig	[rei]	- JIZ (.77)	.346 (.845)	.67 (.66)	.80 (.71
NLD		.85 Kiel .79 Weig	[.30]	.74 (.68)	AB (AB)	.76 (.77
DEU		.62 Weig		لمدر	A0 (A1)	.72 (.5
FRA					[.30]	.40 (.41
ITA		.79 Weig				្រា
AVG.	.66 (.64)	.81 (.78)	.70 (.65)	.69 (.66)	.82 (.82)	.63 (.60

[h²]	CAN	USA	NLD	DEU	FRA	ITA
CAN	[.22]	.95	.73	.78		.89
JSA	.87 Weig	[.37]	.79	.79	.71	.93
NLD		.81 Weig	[.35]	.85	.35	28.
)EU		.74 Weig		1311	.45	.40
RA					[36]	.69
TA		.90 Weig		<u> </u>		[.31]
VG	.79	.83	.72	.73	.56	.84



