

Comparison of National, MACE, and Borderless Genetic Evaluations in Holstein Populations

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Abbreviation key: **INTERBULL**=International Bull Evaluation Service, **MACE**=multiple-trait across country evaluation, **HTM**=Herd test month, **HYS**=Herd year season, **AC**=Age at calving, **MF**=milking frequency, **DIM**=Days in milk, **PI**=Pedigree index, **RRTM**=Random regression test-day model, **AC**=age at calving, **MF**=milking frequency, **LM**=lactation model, **BST**=borderless single trait model, **BMT**=multiple trait across country model, **BCLU**=borderless herd cluster model **NAT**=national evaluation **RMSE**=square root of mean square error.

Introduction

The multiple-trait across country evaluation (MACE) procedure (Schaeffer, 1994) is currently used for international dairy sire evaluation. This procedure utilizes sires EBVs from countries participating in **INTERBULL** and produces international evaluations for bulls in all participating countries. In recent years, semen and embryo exchanges have become common, and management conditions between countries are getting similar. Genetic improvement in dairy cattle is facing globalization. In the past due to computation limitations, it was not practical to perform a borderless evaluation based on animals' test-day records. Better computing facilities and statistical methods make it possible to improve the current genetic evaluation procedures. Finding new tools for a better comparison between animals is one of the major goals for international dairy cattle genetic improvement.

Several methods have been proposed in the past for borderless genetic evaluations. Lohuis and Dekkers (1998) used animal performance records and treated production in different countries as a different trait. Instead of using country boundaries, some researchers

suggested to evaluate animals based on management and environmental differences (Weigel and Rekaya, 2000; Zwald *et al.*, 2001). Other approaches proposed are based on reaction norm (Fikse *et al.*, 2002) and on yield deviations (Canavesi *et al.*, 2001). A review of those methodologies can be found in Weigel (2002).

The objective of this paper was to compare genetic merit under different evaluation methods for milk yield production.

Materials and Methods

Data

Test-day records of first parity cows between 1991 and 1997 from Australia, Belgium, Canada, Czech Republic, Finland, Germany, Hungary, Ireland, Israel, Italy, The Netherlands, New Zealand, South Africa and United States were included. Cows with first test-day record after 90 days post-partum were excluded from the analysis. Sires with less than five daughters were excluded from the analysis. Table 1 shows the frequency of herds and cows in each country.

Table 1. Summary of data in the present study.

Country	No of herds	No of cows
AUS	9651	934931
BEL	3028	75656
CAN	14447	1062664
CSK	14897	208338
DEU	65802	3424192
FIN	14176	137067
HUN	1354	440624
IRL	6453	173215
ISR	1103	223416
ITA	17584	1470053
NLD	26340	1510595
NZL	18450	1559093
USA	42478	4701528
ZAF	1286	135963

AUS = Australia, **BEL** = Belgium, **CAN** = Canada, **DEU** = Germany, **FIN** = Finland, **HUN** = Hungary, **IRL** = Ireland, **ISR** = Israel, **ITA** = Italy, **NLD** = The Netherlands, **NZL** = New Zealand, **USA** = United States, **ZAF** = South Africa

Cow pedigrees were obtained from each country. Pedigree data for bulls were from the official Interbull pedigree file.

Statistical analysis

The comparison involved four approaches:

- National genetic evaluation followed by MACE.
- Single-trait borderless evaluation.
- Multiple-trait across country evaluation.
- Borderless herd-cluster model.

Fixed effects included in all models were: herd **x** year **x** season of calving (**HYS**) or herd **x** year **x** test month (**HTM**), milking frequency (**MF**, 2 levels) and age at calving (**AC**, 5 levels).

National evaluation followed by MACE. A random regression test-day model (**RRTDM**) or a lactation model (**LM**) were used according to the origin evaluation system. Second order Legendre polynomials were used in **RRTDM** for modelling lactation curves. Genetic evaluation models used for each country are given in Table2.

Table 2. National evaluation systems.

RRTDM	LM	
AUS	BEL	ITA
CAN	CSK	USA
DEU	HUN	ZAF
FIN	IRL	
NLD	ISR	
NZL		

The model for **RRTDM** was:

$$y = HTM + MF + AC + \sum_{m=1}^3 \beta \times f + \sum_{m=1}^3 \beta \times a + \sum_{m=1}^3 \beta \times p + e$$

where:

- y** = test-day milk yield
HTM = herd test month
MF = milking frequency
AC = age at calving
 β_{1-3} = Legendre polynomial with $z_{..1}=1$,
 $z_{..2} = \sqrt{3} X$, $z_{..3} = \sqrt{\frac{5}{4}} (3X^2 - 1)$ with
 $X = (-1 + 2DIM)$
f = fixed regression coefficients
a = additive genetic effect
p = permanent environmental effect
e = residuals

Additive, genetic, permanent environment and residual (co)variances for test-day models were assumed known. Estimated (co)variances were obtained from random samples using Gibbs sampling with a single chain of 100,000 samples and the first 10,000 samples discarded as burn-in.

BLUE and BLUP solutions were obtained by solving the mixed model equations. EBV for total yield (305d) were calculated based on Jamrozik *et al.* (2001).

The model for **LM** was as

$$y = HYS + MF + AC + a + e$$

where:

Y	= 305d lactation yield (calculated based on Weigel <i>et al.</i> , 2001).
HYS	= herd year season
MF	= milking frequency
AC	= age at calving
A	= additive genetic effect
e	= residuals

The breeding values obtained were de-regressed within country (Jaiarath *et al.*, 1998). Sire variances were estimated within country with an EM-REML algorithm. Genetic correlations were taken by routine Interbull evaluations of year 2000. Genetic groups for unknown parents were defined according to country of origin and year of birth.

Single trait borderless evaluation (BST). The second approach assumes the lactation records from different countries as the same trait, and a single trait borderless evaluation was applied. The model used for this analysis was:

$$y = HYS + MF + AC + a + e$$

where **y** was the vector of 305d lactation yields and all the effects were defined the same as in the **LM** model.

Multiple-trait across country evaluation (BMT). Performance records from different countries were treated as different traits. All variance components were estimated from a sub-sample of 500,000 animals. Sampling of the herds was made according to Weigel and Zwald (2002).

The model used was the following:

$$y = HYS_i + MF_i + AC_i + a_i + e_i$$

where **i**=1..14 = countries.

Borderless herd-cluster model (BCLU). Herds were clustered according to different production environment. Clustering of the herds was performed according to Zwald *et al.* (2002). Variance components were estimated from a sub-sample of 500,000 animals. Each cluster was treated as a different trait, and a 'multi-trait' model was employed as

$$y = HYS_j + MF_j + AC_j + a_j + e_j$$

where **j**=1..4 = clusters.

Two datasets were used for comparison between evaluation methods. The first dataset (**DS1**) included records from 1990 to 1995. The second datasets (**DS2**) from 1990 to 1997. Pedigree index (**PI**) of all the sires with first proof in 1996-1997 was calculated based on parents EBV from 1990-1995 data. The four methods were compared based on square root of mean square error (**RMSE**) of the mean of the differences of EBV obtained with **DS2** versus **PI** obtained with **DS1**. For the **BCLU** model, breeding values for each specific country were obtained by weighting breeding values for each cluster by the proportion of herds belonging to this cluster as found in Fikse (2001).

Discussion

Heritabilities for the different models are reported in Table 3. National heritabilities for test day models were calculated as the average of the heritabilities throughout the lactation. Values ranged from 0.24 for Finland and Hungary to 0.36 for Ireland for national evaluations. Results found with multiple trait and cluster models were consistent with those found by Weigel *et al.* (2001) and Zwald *et al.* (2001). Heritability found with national models (**NAT**) and **BMT** were in the most cases similar, being the largest difference 0.06 for BEL and 0.05 for CAN DEU and NZL. Correlations values found with **BMT** were similar to those used by Interbull for routine international sires evaluations (Table 4). In Table 5 are reported correlation values found with **BCLU** model. Cluster 4 shows lower genetic correlations. **RMSE** for males are

reported in Table 6. Breeding values predicted with **BCLU** and **MACE** were the ones with lower **RMSE** compared with **MT** model even if the values were close. **ST** showed the highest **RMSE**. Females breeding values were analyzed with a regression of contemporary group on parent average. Results on females (not shown) were similar for all the models except for **ST** where magnitude of regression was smaller. Table 7 reports the number of males in the top 25 for pedigree index in common with the top 25 for EBV of bulls that had first proof in years 1996-1997. Results for **MACE** **BMT** and **BCLU** were similar.

Australia and New Zealand showed the highest number of common bulls with **BCLU** and **BMT**. Even in this case **BST** showed a small number of bulls in common. Pearson correlations and rank correlation (in parentheses) for the four models for the period 1990-1995 and 1990-1997 are showed in Tables 8 and 9. **BMT** and **BCLU** showed the highest correlation. Correlations between **MACE** and **BMT** and **BCLU** were lower. Lowest correlations were between **BMT** and **BST**.

Table 3. Heritabilities for the different models.

Model ¹	AUS	BEL	CA N	CSK	DE U	FIN	HU N	IRL	ISR	ITA	NL D	NZL	USA	ZAF
NAT	0.30	0.33	0.28	0.34	0.27	0.24	0.24	0.36	0.34	0.33	0.27	0.28	0.32	0.30
BST							0.33							
BMT	0.33	0.27	0.33	0.33	0.33	0.23	0.25	0.35	0.31	0.32	0.32	0.32	0.30	0.33
BCLU		Cluster1 0.33			Cluster2 0.35			Cluster3 0.31				Cluster4 0.29		

¹NAT= national evaluation. BST=borderless single trait model MT=borderless multiple trait across country model. BCLU=Borderless herd Cluster model

Table 4. Correlations for multiple-trait across country model.

	BEL	CAN	CSK	DEU	FIN	HUN	IRL	ISR	ITA	NLD	NZL	USA	ZAF
AUS	0.85	0.83	0.86	0.85	0.87	0.76	0.92	0.79	0.82	0.82	0.98	0.84	0.83
BEL		0.94	0.86	0.90	0.85	0.80	0.82	0.90	0.91	0.92	0.84	0.96	0.86
CAN			0.83	0.92	0.87	0.86	0.84	0.86	0.94	0.96	0.88	0.94	0.86
CSK				0.87	0.80	0.78	0.81	0.81	0.82	0.89	0.82	0.85	0.90
DEU					0.82	0.78	0.83	0.85	0.92	0.92	0.90	0.93	0.85
FIN						0.79	0.88	0.86	0.85	0.83	0.84	0.88	0.80
HUN							0.76	0.82	0.83	0.84	0.77	0.84	0.80
IRL								0.84	0.83	0.85	0.93	0.84	0.80
ISR									0.84	0.83	0.83	0.89	0.79
ITA										0.92	0.86	0.94	0.84
NLD											0.88	0.93	0.86
NZL												0.90	0.91
USA													0.90

Table 5. Correlations for borderless herd cluster model.

	Cluster2	Cluster3	Cluster4
Cluster1	0.92	0.91	0.86
Cluster2		0.89	0.88
Cluster3			0.87

Table 6. Square root of the mean square error (**RMSE**) of males' breeding values the different models.

Model ¹	AUS	BEL	CAN	CSK	DEU	FIN	HUN	IRL	ISR	ITA	NLD	NZL	USA	ZAF
MACE	6.9	7.1	6.8	7.2	6.7	6.6	6.8	7.3	6.6	6.4	6.4	6.9	6.3	6.4
BMT	6.4	7.2	6.9	7.0	6.8	6.8	6.9	7.0	6.8	6.4	6.6	6.4	6.4	6.8
BCLU	6.3	7.0	6.7	6.9	6.5	6.6	6.7	7.0	6.8	6.3	6.6	6.3	6.4	6.8
BST	10.3													

¹MACE= multiple across country evaluation BST=borderless single trait model BMT=multiple trait across country model. BCLU= borderless herd cluster model.

Table 7. Number of males in the top 25 for PI in common with the top 25 for evaluation for years 1996-1997.

Model ¹	AUS	BEL	CAN	CSK	DEU	FIN	HUN	IRL	ISR	ITA	NLD	NZL	USA	ZAF
MACE	16	16	17	13	17	13	15	16	15	16	15	15	17	15
BMT	15	15	17	14	16	12	15	16	17	15	17	15	17	16
BCLU	18	16	16	13	15	14	14	16	16	16	16	18	18	14
BST	11													

¹MACE= multiple across country evaluation BST=borderless single trait model BMT=multiple trait across country model. BCLU= borderless herd cluster model.

Table 8. Pearson and Rank (parenthesis) correlations between models for **PI**1990-1995.

	BST	BMT	BCLU
MACE	0.76(0.77)	0.84(0.86)	0.83(0.85)
BST		0.76(0.77)	0.76(0.78)
BMT			0.90(0.92)

Table 9. Pearson and Rank (parenthesis) correlations between models for **EBV**1990-1997.

	BST	BMT	BCLU
MACE	0.78(0.78)	0.83(0.84)	0.84(0.85)
BST		0.75(0.78)	0.76(0.77)
BMT			0.90(0.92)

Conclusions

The MACE international evaluation method is currently used and has been improved for several years. The empirical approach used herein compared the ranking of bulls obtained with the official INTERBULL methodology with the borderless approach, one of the possible alternatives to the MACE methodology.

Assuming that the milk production system is the same across all countries, which is the easiest way for a borderless evaluation, appears to be too simplistic. The phenotypic information entering the system has a larger impact on bulls' EBV with respect to MACE or to the other genetic evaluation methodologies here considered.

Considering each country as a trait or clustering the herds based on their management system produces results similar to MACE methodology. With those approaches the variation in ranking of bulls with new information entering the system appears to be similar to the ranking obtained with MACE. In addition, correlations between MACE genetic evaluations and EBVs obtained with other systems indicate that bulls' genetic merit obtained with **BMT** and **BCLU** are similar to MACE, with correlation values larger than 0.8.

Further investigation on borderless evaluation should include the **BMT** and **BCLU** approach, extending the analysis to later parity information.

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