

Effect of Data and Model Selection on Estimated Genetic Correlations Between Countries

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Introduction

A multiple-trait across country evaluation (MACE) analysis requires knowledge of the genetic covariances between countries. Sigurdsson and Banos (Interbull Bull. 11) developed a REML procedure for estimating correlations using common bulls (with progeny in >1 countries) and full-sib groups (with sons in >1 countries). Recently, Klei (pers. comm.) developed a procedure using all bulls that have been progeny tested in each country.

MACE estimated breeding values (EBV) are sensitive to estimated genetic (co)variance parameters, particularly the within-country genetic variances. Correlations between countries can affect relative rankings of local and foreign bulls, and estimated correlations are affected by climate, management level, management type, genetic composition of the cow population, national genetic evaluation procedures and genetic ties between countries.

It is accepted that genetic correlation parameters can influence MACE EBV, but the specific impact of these correlations has not been documented. Furthermore, effects of data selection policies and national genetic evaluation models on estimated genetic correlations are unknown. This is particularly important with many countries working toward implementation of a test day model for national genetic evaluations.

The objectives of this study were to document the effects of genetic correlations and progeny group size on MACE EBV of bulls with differing pedigree indexes and to determine the sensitivity of estimated genetic correlation parameters to changes in data selection policies and national genetic evaluation procedures.

Materials and methods

Three hypothetical bulls were used to demonstrate

the effects of genetic correlations and progeny group size:

	True Breeding Value (BV)		
	<u>Bull</u>	<u>Sire</u>	<u>MGS</u>
Bull 1	2.50 (SD)	0.25	-0.75
Bull 2	2.25	1.00	0.00
Bull 3	2.00	1.75	0.75

Five hypothetical countries were assumed, with the following correlation structure:

	<u>H</u>	<u>A</u>	<u>B</u>	<u>C</u>	<u>D</u>
Home country (H)	1.0	.95	.90	.84	.77
Foreign country A	.95	1.0	.90	.84	.77
Foreign country B	.90	.90	1.0	.84	.77
Foreign country C	.84	.84	.84	1.0	.77
Foreign country D	.77	.77	.77	.77	1.0

The number of progeny per bull varied from 20 to 200 in increments of 20. In Figures 1A-1E, it was assumed that all progeny resided in the home country. In Figures 2A-2C, it was assumed that each bull had 80 total progeny, and a portion of these 80 progeny were located in one of the foreign countries.

In Figures 3A-3C, it was assumed that 80 additional progeny per bull were added, with these additional progeny in the home country and/or in one of the foreign countries. The sire and maternal grandsire of each bull were assumed to have 500 progeny in each of the five countries. Heritability was .30 in all countries.

National evaluation data from the USA (5/97), Canada (CAN; 2/97), The Netherlands (NLD; 2/97), Germany (DEU; 1/97) and Italy (ITA; 3/97) were used in correlation estimation. Test day results for USA were from Cornell University (5/97), and test day results for Germany were from VIT (1/97). Genetic correlations were estimated using common bulls and full-sibs born since 1971, 1976 or 1980 or by using all bulls born since 1976 (Klei method). Lastly, correlations were estimated using Cornell test day data for the USA and VIT test day data for DEU.

Results and discussion

In Fig. 1A-1E, we see that an average bull with high pedigree index often ranks higher than a better bull with low pedigree index. In the home country, 45 progeny are needed before bull 1 (with highest true BV) is recognized as the best bull. Genetic correlations between countries have a large affect on MACE EBV. With a correlation of .90, 65 progeny are required to obtain correct sire rankings, and with a correlation of .77, 170 progeny are required. Bulls rarely have 170 first-crop progeny.

In Figures 2A-2C and 3A-3C, we see that spreading progeny across multiple countries can benefit MACE EBV of bulls with high true BV but with low pedigree index, especially when genetic correlations are low. No detrimental effects on home country EBV were observed.

Number of bulls used in estimating correlations was:

Data	USA	CAN	NLD	DEU	ITA
1971	2582	1597	921	928	757
1976	2216	1377	780	797	547
1981	1662	1027	547	529	330
ALL	18473	4954	4244	7883	2862
Test day (USA)	1473	1090	722	749	534
Test day (DEU)	2175	1358	710	584	529

In Figures 4A-4C, we see that time period of data has little effect on estimated genetic correlations. Estimates using bulls born since 1976 were slightly higher than estimates using bulls born since 1981, probably due to more genetic ties between countries, but adding bulls born from 1971 to 1976 gave little additional benefit. Using all bulls born since 1976 (Klei method) caused little change in estimated genetic correlations among these countries, but the impact of using all bulls may have been greater for countries with fewer

genetic ties; USA, CAN, NLD, DEU and ITA already share many common bulls and full-sib groups.

In Figures 5A-5C, we see the impact of a change in national genetic evaluation model. Estimated genetic correlations between USA and CAN, DEU and ITA were lower using the Cornell test day data (probably due to fewer genetic ties), but correlations between USA and NLD were slightly higher. Estimated correlations for milk yield between DEU and other countries were lower using DEU test day data, but estimated correlations for fat yield were generally higher (except with NLD). For protein, DEU test day data gave higher correlations with the USA, and lower correlations with CAN and NLD.

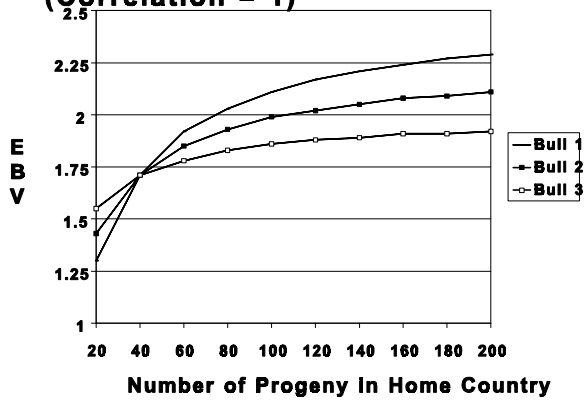
Conclusions

Pedigree index has a substantial effect on MACE EBV, particularly when genetic correlations are low or when progeny group size is small. Spreading progeny across multiple countries can help identify superior bulls with average or low pedigree indexes without decreasing the home country evaluation. Adding historical data can slightly increase estimated genetic correlations between countries, presumably by increasing genetic ties. Changes in national genetic evaluation models, e.g., to a test-day model, can cause substantial differences in the estimated genetic correlation structure between countries.

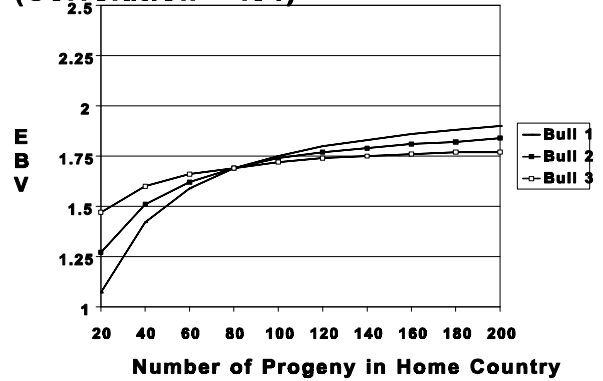
Acknowledgments

Data were generously supplied by ANAFI, CDN, Cornell University, NRS, USDA and VIT, and financial support was provided by the National Association for Animal Breeders and World-Wide Sires, Inc.

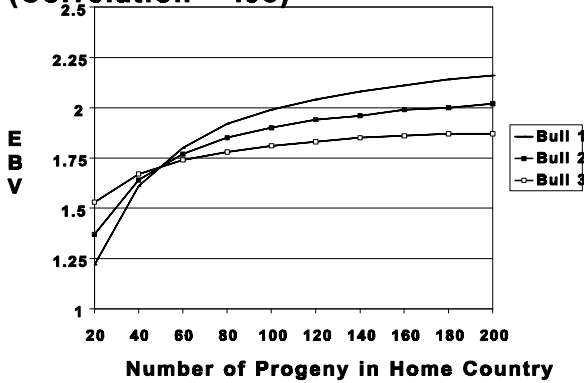
**1A. EBV in Home Country
(Correlation = 1)**



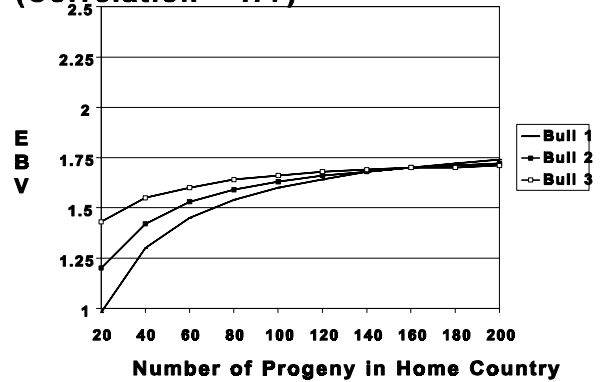
**1D. EBV in Foreign Country C
(Correlation = .84)**



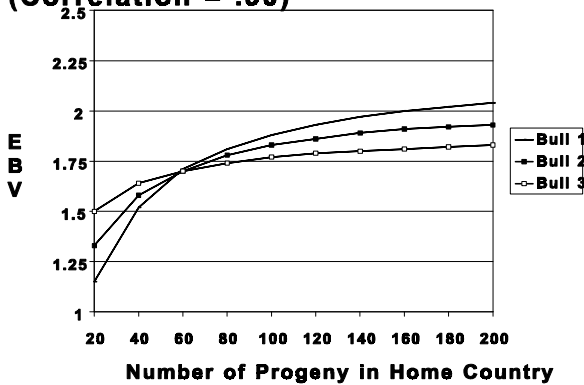
**1B. EBV in Foreign Country A
(Correlation = .95)**



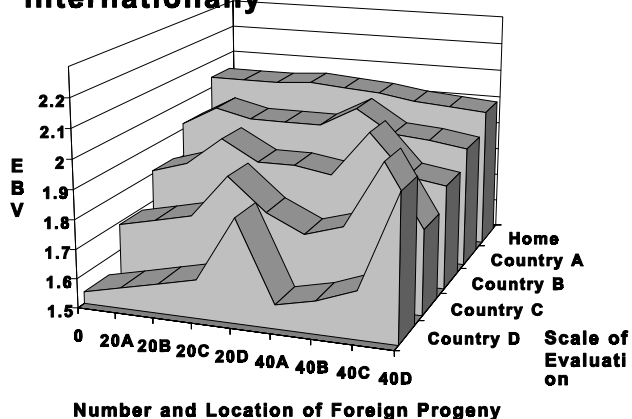
**1E. EBV in Foreign Country D
(Correlation = .77)**



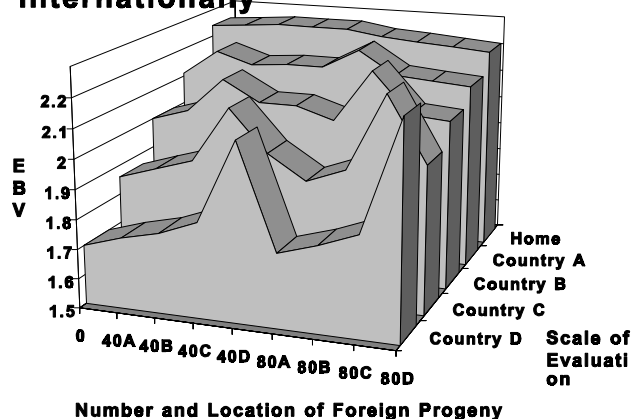
**1C. EBV in Foreign Country B
(Correlation = .90)**



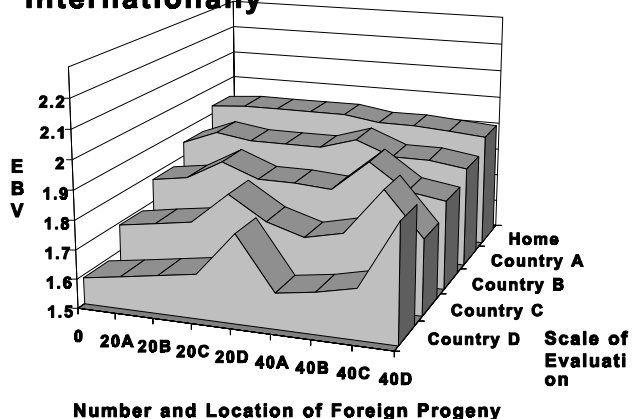
2A. Bull 1: 80 Total Progeny Internationally



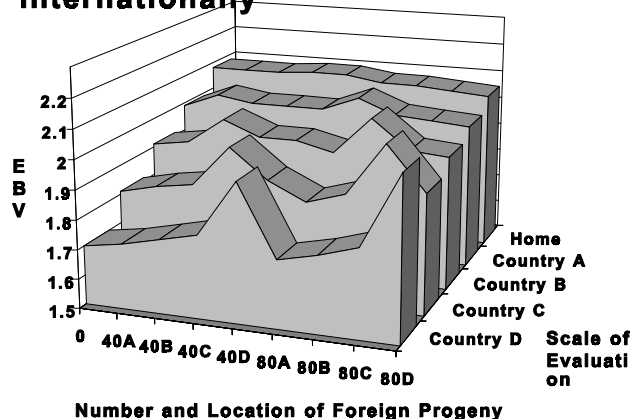
3A. Bull 1: 160 Total Progeny Internationally



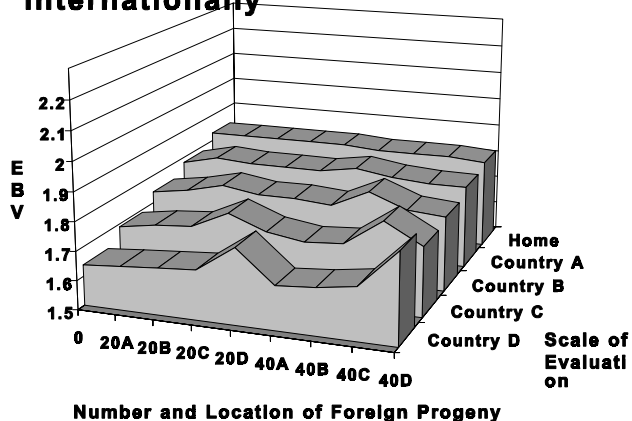
2B. Bull 2: 80 Total Progeny Internationally



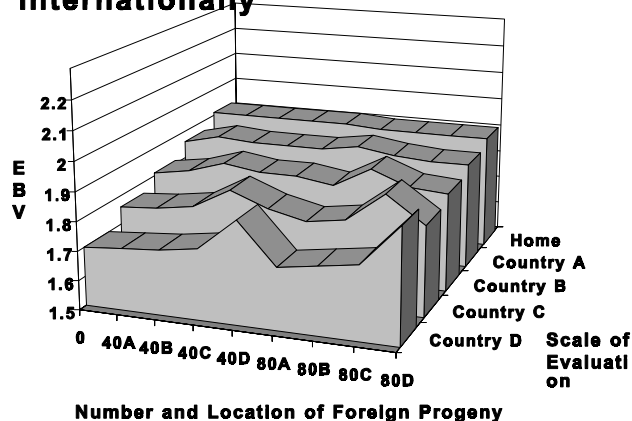
3B. Bull 2: 160 Total Progeny Internationally



2C. Bull 3: 80 Total Progeny Internationally



3C. Bull 3: 160 Total Progeny Internationally



4A. Estimated Milk Correlations (Official Data)

		Canada	Netherlands	Germany	Italy
USA	1971	.97	.93	.91	.97
	1976	.97	.92	.91	.97
	1981	.96	.91	.90	.96
	ALL	.97	.92	.91	.96
Canada	1971		.95	.93	.95
	1976		.95	.93	.96
	1981		.94	.93	.96
	ALL		.96	.93	.95
Netherlands	1971			.95	.93
	1976			.95	.93
	1981			.95	.92
	ALL			.95	.93
Germany	1971				.91
	1976				.93
	1981				.92
	ALL				.93

5A. Estimated Correlations for Milk Yield

Common Bulls + Full Sibs Born Since 1976					
	Canada	Netherlands	Germany	Italy	
USA	LACT	.97	.92	.91	.97
	TD _{USA}	.94	.93	.89	.94
	TD _{DEU}	.97	.92	.89	.97
Canada	LACT	.95	.93	.96	
	TD _{USA}	.95	.93	.96	
	TD _{DEU}	.95	.88	.96	
Netherlands	LACT		.95	.93	
	TD _{USA}		.96	.94	
	TD _{DEU}		.89	.93	
Germany	LACT			.93	
	TD _{USA}			.93	
	TD _{DEU}			.88	

LACT = Lactation model; TD_{USA} = Cornell Test-day model; TD_{DEU} = German Test-day model

4B. Estimated Fat Correlations (Official Data)

		Canada	Netherlands	Germany	Italy
USA	1971	.96	.92	.88	.96
	1976	.97	.91	.89	.96
	1981	.96	.91	.89	.95
	ALL	.96	.88	.89	.96
Canada	1971		.93	.91	.94
	1976		.93	.91	.95
	1981		.92	.91	.95
	ALL		.91	.91	.95
Netherlands	1971			.94	.91
	1976			.94	.91
	1981			.94	.90
	ALL			.96	.89
Germany	1971				.88
	1976				.89
	1981				.88
	ALL				.89

5B. Estimated Correlations for Fat Yield

Common Bulls + Full Sibs Born Since 1976					
	Canada	Netherlands	Germany	Italy	
USA	LACT	.97	.91	.89	.96
	TD _{USA}	.93	.91	.88	.95
	TD _{DEU}	.97	.92	.94	.96
Canada	LACT		.93	.91	.95
	TD _{USA}		.93	.92	.95
	TD _{DEU}		.93	.93	.95
Netherlands	LACT			.94	.91
	TD _{USA}			.94	.92
	TD _{DEU}			.92	.92
Germany	LACT				.89
	TD _{USA}				.90
	TD _{DEU}				.91

LACT = Lactation model; TD_{USA} = Cornell Test-day model; TD_{DEU} = German Test-day model

4C. Estimated Protein Correlations (Official Data)

		Canada	Netherlands	Germany	Italy
USA	1971	.96	.92	.88	.96
	1976	.96	.91	.88	.95
	1981	.95	.89	.87	.95
	ALL	.96	.90	.88	.95
Canada	1971		.93	.92	.94
	1976		.93	.92	.95
	1981		.92	.91	.94
	ALL		.93	.91	.94
Netherlands	1971			.93	.92
	1976			.93	.92
	1981			.93	.91
	ALL			.94	.91
Germany	1971				.89
	1976				.90
	1981				.88
	ALL				.91

5C. Estimated Correlations for Protein Yield

Common Bulls + Full Sibs Born Since 1976					
	Canada	Netherlands	Germany	Italy	
USA	LACT	.96	.91	.88	.95
	TD _{USA}	.93	.92	.87	.93
	TD _{DEU}	.96	.91	.90	.95
Canada	LACT		.93	.92	.95
	TD _{USA}		.93	.92	.95
	TD _{DEU}		.93	.88	.95
Netherlands	LACT			.93	.92
	TD _{USA}			.94	.93
	TD _{DEU}			.90	.92
Germany	LACT				.90
	TD _{USA}				.91
	TD _{DEU}				.90

LACT = Lactation model; TD_{USA} = Cornell Test-day model; TD_{DEU} = German Test-day model