

Preliminary Report on International Dairy Sire Evaluation Using Individual Performance Records

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Introduction

International genetic evaluation of dairy sires is currently a two-stage process. Sire EBV are first calculated at the national level based on data of local progeny, then these national EBV are combined into international EBV at the Interbull Centre. However, differences in within-country procedures for data collection and genetic evaluation can affect the results, and traits or production environments must be defined according to country borders. Therefore, the objective of this study was to examine the potential for international dairy sire evaluation based on individual animal performance records using raw data collected in participating Interbull member countries.

Materials and Methods

Data

Test-day milk records were obtained from first parity cows in fifteen Interbull member countries, as shown in Table 1. Cows with

Holstein sires that calved between January 1, 1990 and December 31, 1997 were considered. Table 1 shows the number of cows, herds, and test-day observations (from calving to 305 days postpartum) in each country. In addition, the mean number of cows per herd-year class, peak daily milk yield, and persistency of lactation (defined as milk weight at the test closest to 240 days postpartum divided by milk weight at the test closest to 60 days postpartum) are shown. All figures are in kg (or kg²). Table 1 also shows the median days in milk at last test, as well as the percentage of herds with at least one cow milking past 260 days postpartum and 290 days postpartum. Based on these data, it was determined that 305-day lactation records were not appropriate for all countries. Therefore, test day milk weights were combined into 305-day lactation records for all countries except AUS (290 d), IRL (290 d), NZL (270 d), and ZAF (290 d). Partial lactation records were extended using lactation curves derived from completed lactations in each country by age at calving by herd production level class.

Table 1. Data used in the present study

Country	Cows	Herds	Test Days	Cows per HY	Peak Yield	Persis- tency	Last Test	Herds milking		Lactation Yield
								260 d	290 d	
Australia (AUS)	945,798	9,706	7,016,610	23.7	22.0	.676	271	.92	.83	4805
Austria (AUT)	15,157	2,344	120,327	3.2	25.4	.767	284	.93	.86	6083
Belgium (BEL)	78,925	3,076	682,682	5.7	26.6	.779	284	.96	.93	6534
Canada (CAN)	1,075,516	14,186	8,839,030	13.3	29.4	.783	282	.97	.93	7567
Czech Rep. (CSK)	214,464	6,112	1,858,711	15.8	21.3	.710	280	.91	.73	4980
Germany (DEU)	3,470,932	63,643	29,866,962	12.0	25.5	.770	283	.95	.92	6159
Estonia (EST)	45,788	1,775	380,865	12.2	18.3	.745	280	.92	.84	3778
Finland (FIN)	137,621	14,191	1,247,701	2.4	25.2	.782	283	.93	.87	6220
Hungary (HUN)	442,184	1,354	3,583,013	61.7	26.6	.803	281	.97	.94	5557
Ireland (IRL)	179,312	6,442	1,439,642	8.9	23.7	.649	268	.83	.68	5218
Israel (ISR)	223,609	1,103	1,935,741	31.8	33.9	.902	281	.95	.93	8850
Netherlands (NLD)	1,537,056	26,436	14,203,138	11.3	27.2	.782	284	.97	.95	6788
New Zealand (NZL)	1,560,268	18,454	6,007,037	30.5	17.5	.598	220	.46	.13	3541
United States (USA)	4,800,850	42,865	40,042,303	22.9	32.1	.857	283	.92	.89	8329
South Africa (ZAF)	138,670	1,269	1,099,563	27.8	26.3	.833	279	.94	.86	6420

Models

The following genetic models were applied to first lactation milk yield data in the present study:

- 1) Single-trait model (model **ST**)
 - Assumes genetic correlation = 1 between all countries
- 2) Multiple-trait model by region (model **MR**)
 - Assumes genetic correlation ≤ 1 between geographical regions
 - Assumes genetic correlation = 1 between all countries within a region

<u>Region 1</u>	<u>Region 2</u>
Australia	Canada
Ireland	Israel
New Zealand	USA
South Africa	
<u>Region 3</u>	<u>Region 4</u>
Belgium	Austria
Finland	Czech Republic
Germany	Estonia
Netherlands	Hungary

- 3) Multiple-trait model by country (model **MC**)
 - Assumes a genetic correlation ≤ 1 between all countries

All three models were of the following form:

y = herd-year-season + age at calving + milking frequency + heterosis class + sire + error

Genetic and residual variances were allowed to differ between countries (i.e., heterogeneous sire and residual variances by country in model ST and heterogeneous variances by country within region in model MR). Because herd sizes were extremely small in several countries, herd-year-season classes were developed using fuzzy logic. Three-month herd-year-season classes were formed, and each cow was assigned a membership value (between 0 and 1) in the herd-year-season class corresponding to her calving date, as well as the previous and subsequent herd-year-season classes. For example, a cow calving exactly in the middle of the interval could have a membership value of 1, but a cow

calving at the beginning (end) of the interval would have a value < 1 and a nonzero membership in the previous (subsequent) class. If the number of animals within a herd-year-season class was < 5 , membership was further extended to adjacent classes, such that each cow could have nonzero membership in up to five herd-year-season classes. Heterosis classes were defined according to the most common breed compositions found within three-generation pedigrees (e.g., 100% HOL, 50% HOL + 50% JER, 50% HOL + 25% JER + 25% BSW). All three models were implemented in a Bayesian context, with normal priors for location parameters and breeding values and scaled inverted Wishart priors for variance components. Gibb's sampling was used, with 100,000 samples taken following a burn-in period of 10,000 samples. For each model, the Bayesian deviance information criteria (**DIC**) was calculated. The DIC statistic is of the following form:

$$\text{DIC} = E_{\theta|y}[(y - Xb - Zu)' R^{-1} (y - Xb - Zu) + N \log |R_0| + \text{constant}] + 2 p_D$$

where the first three terms measure goodness of fit, and the latter term measures model complexity (i.e., p_D = the effective number of parameters). The ratio of DIC statistics was calculated for each pair of models. Because lower values of DIC indicate better fit and/or more parsimony, values of the DIC ratio less than one indicate superiority of the model represented in the numerator and values greater than one indicate superiority of the model represented in the denominator.

Results

A summary of the data is shown in Table 1. Herd size varied dramatically, from fewer than three first parity cows per herd-year in Finland, to more than 60 per herd-year in Hungary. Peak yield was highest in Israel, followed by the USA and Canada, and peak yield was lowest in New Zealand and Estonia. Persistency of lactation was highest in Israel and the USA, with first parity cows in Israel maintaining more than 90% of peak yield at 240 days postpartum.

Persistency of lactation was lowest in countries that relied exclusively on rotational grazing, such as New Zealand, Ireland, and Australia, because feed quality and availability deteriorated as the lactation progressed. As a result, lactation yield in Israel, USA, and Canada was more than double that of New Zealand and Estonia.

Table 2 shows estimated sire standard deviations, residual standard deviations, and heritabilities for each of the three models shown

in Table 2. As expected based on mean lactation yields, sire and residual standard deviations were substantially higher in Israel, USA, Canada, Netherlands, and Germany than in New Zealand, Estonia, Ireland, Australia, and the Czech Republic. Heritability parameters were similar across countries (.27 to .36) and were generally similar to values used by national genetic evaluation centers in the participating countries. Parameter estimates were nearly identical for all three models.

Table 2. Estimated sire SD, residual SD, and heritability for the single-trait (ST), multiple-trait by region (MR), and multiple-trait by country (MC) models

Country	Sire SD			Residual SD			Heritability		
	ST	MR	MC	ST	MR	MC	ST	MR	MC
AUS	235	237	242	641	680	705	.35	.33	.32
AUT	274	271	270	857	835	807	.29	.30	.31
BEL	312	312	313	869	902	891	.34	.32	.33
CAN	330	332	332	962	962	945	.32	.32	.33
CSK	246	247	248	769	747	776	.29	.30	.29
DEU	325	329	327	906	894	891	.34	.35	.35
EST	179	179	182	552	560	582	.30	.29	.28
FIN	277	276	276	828	827	804	.31	.31	.32
HUN	284	282	282	935	914	928	.27	.28	.27
IRL	209	207	205	637	643	658	.30	.29	.28
ISR	345	333	331	984	986	988	.33	.31	.31
NLD	329	329	328	898	943	915	.35	.33	.34
NZL	175	176	173	487	482	462	.34	.35	.36
USA	339	339	340	1088	1058	1063	.28	.29	.29
ZAF	311	307	310	885	871	863	.33	.33	.34

Table 3 shows the estimated genetic correlations between countries obtained using the multiple-trait by country model. On average, estimates were slightly lower than the correlation parameters currently used by the Interbull Centre. However, variation in estimated correlations between country pairs was significantly greater, ranging from .69 between Estonia and Hungary to .96 between Netherlands and Belgium. Two clear differences were observed between Interbull parameters and estimates from the present study. First, estimated genetic correlations between Ireland and Australia (.93) and Ireland and New Zealand (.95) were significantly higher than in previous studies. One would expect lactation performance to be a similar trait in these

countries, because all rely heavily on rotational grazing. However, correlations of this magnitude have not been observed in the past, perhaps because they were obscured by differences in national genetic evaluation procedures between countries. Second, estimated genetic correlations between some newer Interbull member countries, such as Estonia (.69 to .79) and Hungary (.69 to .81) with other countries were significantly lower than parameters used by the Interbull Centre. The reason for these lower estimates is unknown, and further investigation is necessary. Posterior standard deviations of the estimated genetic correlations ranged from .01 (e.g., between various combinations of BEL, CAN, DEU, IRL, NLD, and USA) to .10 (between AUT and EST).

Table 3. Estimated genetic correlation parameters (above diagonal) and posterior standard deviations (below diagonal) from the multiple-trait (by country) model

	AUS	AUT	BEL	CAN	CSK	DEU	EST	FIN	HUN	IRL	ISR	NLD	NZL	USA	ZAF
AUS		.79	.83	.82	.84	.83	.76	.81	.71	.93	.76	.80	.93	.84	.83
AUT	.02		.78	.87	.75	.89	.77	.84	.78	.78	.83	.88	.83	.89	.80
BEL	.02	.02		.93	.83	.91	.76	.85	.76	.88	.84	.96	.84	.94	.82
CAN	.03	.04	.01		.84	.93	.70	.83	.78	.87	.87	.93	.81	.94	.92
CSK	.03	.03	.02	.02		.83	.79	.78	.78	.81	.77	.81	.83	.84	.81
DEU	.03	.01	.01	.02	.03		.71	.82	.75	.87	.84	.92	.84	.91	.90
EST	.07	.10	.04	.07	.06	.07		.74	.69	.75	.71	.76	.73	.74	.74
FIN	.08	.04	.05	.06	.06	.06	.09		.71	.84	.74	.85	.82	.86	.79
HUN	.05	.05	.05	.03	.04	.05	.07	.07		.74	.76	.79	.72	.81	.78
IRL	.02	.03	.01	.01	.03	.02	.06	.06	.05		.80	.83	.95	.87	.83
ISR	.03	.05	.03	.03	.03	.05	.07	.04	.04	.03		.89	.77	.92	.78
NLD	.03	.02	.01	.02	.02	.02	.07	.05	.03	.01	.05		.81	.94	.87
NZL	.02	.03	.02	.02	.03	.03	.08	.07	.05	.02	.03	.03		.83	.89
USA	.03	.03	.01	.01	.02	.02	.06	.04	.03	.02	.02	.01	.02		.87
ZAF	.03	.04	.02	.03	.02	.03	.07	.07	.05	.02	.05	.02	.03	.02	

Estimated genetic correlation parameters from the multiple-trait by region model are shown in Table 4. Genetic correlations were highest between Region 2 (CAN, ISR, USA) and Region 3 (BEL, FIN, DEU, NLD) and between Region 3 and Region 4 (AUT, CSK, EST, HUN). On the other hand, estimated genetic correlations were lowest between Region 1

(AUS, IRL, NZL, ZAF) and region 4 (AUT, CSK, EST, HUN) and between Region 1 and Region 3 (BEL, FIN, DEU, NLD). Posterior standard deviations of the estimated genetic correlations were substantially smaller than in the multiple-trait by country model, with values ranging from .01 to .03 for all pairs of regions.

Table 4. Estimated genetic correlation parameters (above diagonal) and posterior standard deviations (below diagonal) from the multiple-trait by region model

	Region 1	Region 2	Region 3	Region 4
Region 1 (AUS, IRL, NZL, ZAF)		.86	.84	.83
Region 2 (CAN, ISR, USA)	.02		.92	.88
Region 3 (BEL, FIN, DEU, NLD)	.03	.01		.90
Region 4 (AUT, CSK, EST, HUN)	.03	.02	.02	

The DIC test statistics for testing goodness of fit and model parsimony are shown in Table 5. Based on the ratio of DIC statistics, the single-trait model was deemed inferior to both the multiple-trait by region model (1.03) and the multiple-trait by country model (1.12). In

addition, the multiple-trait by country model was slightly preferred to the multiple-trait by region model (1.04). This indicates that, in each case, the model with a greater number of parameters (traits) was favored.

Table 5. Ratios of DIC test statistics for all pairs of models considered in the present study (favored model in bold)

Model Comparison	Ratio of DIC Statistics
Single-trait vs. Multiple-trait by region (ST / MR)	1.03
Single-trait vs. Multiple-trait by country (ST / MC)	1.12
Multiple-trait by region vs. Multiple-trait by country (MR / MC)	1.04

Conclusions

The present study considers the relative merit of three alternative models for international dairy sire evaluation based on individual animal performance records. Estimated genetic correlation parameters were generally similar to parameters used by the Interbull Centre, but estimates were significantly higher for some pairs of countries (e.g., IRL with AUS and NZL) and significantly lower for others (e.g., HUN and EST with all other countries). Based on the DIC test statistics presented herein, the multiple-trait by country model was slightly favored relative to the multiple-trait by region model, which was in turn favored relative to the single-trait model.

Further work is necessary to refine these models and to identify the specific factors that cause lactation performance to differ between herds and production systems. Such information will allow further development of border-less genetic evaluation models, such as the multiple-trait herd cluster model, and comparison of these models with the models considered in the present study.

Acknowledgments

The authors gratefully acknowledge the assistance of scientists at the national genetic evaluation centers of all countries represented in this study.