

Joint Evaluation of Milking Shorthorn Dairy Cattle for Production Traits

R.A. Barrett¹, F. Miglior^{2,3}, J. Jamrozik¹, G. Jansen¹, L.R. Schaeffer¹

¹*CGIL, University of Guelph, Guelph, ON, Canada*

²*Agriculture and Agri-Food Canada, Dairy and Swine Research and Development Centre, Lennoxville, QC, Canada*

³*Canadian Dairy Network, Guelph, ON, Canada*

Introduction

The potential benefit of international evaluation of dairy cattle for production traits has been well documented in the past several years (Banos and Smith, 1991; Lohuis and Dekkers, 1998). As a result, multiple trait across country evaluations, MACE (Schaeffer, 1994), for several traits are performed by the INTERBULL center for six dairy breeds. However, the Milking Shorthorn dairy breed has not been included for international evaluations. Milking Shorthorns are one of the oldest established dairy breeds in the world, and the breed has been increasing in popularity in several countries. Milking Shorthorns are present in several countries, with sizeable populations and active breed associations in Australia, Canada, Great Britain, New Zealand, and the United States. In Australia, the Illawarra breed is identified as “Milking Shorthorn”, as is the Dairy Shorthorn population in Great Britain.

While MACE is the current method of international evaluation for dairy cattle, it has been suggested that test day models may yield more accurate evaluations, due to (i) inclusion of a complete pedigree of cows and bulls, (ii) evaluations based directly on animal records, and (iii) greater accounting for environmental effects (Swalve, 2000). It has also been noted that use of test day models allows for greater flexibility in coordinating evaluation with national recording methods (Schaeffer *et al.*, 2000).

Therefore, the primary objective of this study was to develop a method of joint evaluation of production traits for the Milking Shorthorn breed using a multiple-country, multiple-lactation test day model for five countries with populations of Milking Shorthorn-type cattle. Secondary objectives included the creation of a consolidated, international pedigree file for Milking Shorthorns

which currently does not exist, determination of genetic ties among countries in the study, estimation of within and across country genetic parameters among traits, and calculation of various production parameters in the different dairy production systems.

Materials and Methods

Test day data and pedigree information was provided by national genetic evaluation centres in five countries (Australia, Canada, Great Britain, New Zealand, and the United States). These five countries represented a wide range of production systems and genetic compositions. The following production and pedigree edits were applied: records from animals without identified sires were deleted, test day records less than 5 days in milk or greater than 305 days in milk were deleted, age at calving in months was restricted to between 18 and 63 months, and cows with records born before 1985 were excluded from the data. Additionally, parity number for records from Australia and Great Britain had to be enforced using age at calving and number of calving dates in the data, due to concerns with data validity. Total size of data across five countries after editing was 1,018,528 records and 68,653 cows with records. Australia had the largest population of cows with records (38,533), and Canada had the smallest (1,235).

Single and multiple-country variance components were estimated using a random regression test day model employing Gibb's sampling. Single country parameter estimation for milk and protein yield was performed on entire single-country data sets, while multiple country estimation for milk was done on the data set generated from the connected herds.

Connectedness was measured by number of common sires and daughters/granddaughters of common sires. A common sire was defined as having at least 5 daughters/granddaughters in two or more countries. Using a compiled list of common daughters/granddaughters, the percentage of each herd comprised of these common cows was calculated, and these percentages were used to select “common herds” by country, according to threshold values set for each country. All records per herd were then aggregated for the 131 selected herds and used for multiple-country parameter estimation. This data set had a total of 156,574 test day records and 11,056 cows with records across five countries.

The model for parameter estimation can be expressed as:

$$\mathbf{y}_m = \mathbf{H}_m \mathbf{h}_m + \mathbf{X}_m \mathbf{b}_m + \mathbf{W}_m \mathbf{p}_m + \mathbf{Z}_m \mathbf{u}_m + \mathbf{e}_m$$

where $\mathbf{y}_m$ is a vector of observations within country and lactation group $\mathbf{m}$, $\mathbf{h}_m$ is a vector of fixed herd-test day effects, $\mathbf{b}_m$ is a vector of fixed age-parity-season of calving effects, $\mathbf{p}_m$ is a vector of random regression coefficients for permanent environmental effects, $\mathbf{u}_m$ is a vector of random regression coefficients for animal genetic effect, $\mathbf{e}_m$ is a vector of residuals, and $\mathbf{H}_m$, $\mathbf{X}_m$, $\mathbf{W}_m$, and $\mathbf{Z}_m$ are incidence matrices assigning observations to effects. Expectations and covariance structure for random effects can be described in matrix notation as:

$$\begin{aligned} \mathbf{E}(\mathbf{y}) &= \mathbf{H}\mathbf{h} + \mathbf{X}\mathbf{b}, \mathbf{E}(\mathbf{p}) = \mathbf{0}, \mathbf{E}(\mathbf{u}) = \mathbf{0}, \mathbf{E}(\mathbf{e}) = \mathbf{0} \\ \mathbf{V}(\mathbf{p}) &= \mathbf{P}, \mathbf{V}(\mathbf{u}) = \mathbf{G}, \text{ and } \mathbf{V}(\mathbf{e}) = \mathbf{E} \end{aligned}$$

where: $\mathbf{P} = \mathbf{I} \mathbf{q} \mathbf{P}_0$, $\mathbf{G} = \mathbf{A} \mathbf{q} \mathbf{G}_0$, $\mathbf{A}$ is an additive relationship matrix, $\mathbf{P}_0$ and $\mathbf{G}_0$ are across lactation covariance matrices for environmental and genetic regression coefficients, respectively, of size 15x15 for single country estimation and 75x75 for multiple country estimation. $\mathbf{E}$ is a residual covariance matrix. Lactation curves were modeled using Legendre polynomials of order four.

Single country parameter estimation ran for 120,000 iterations after a 20,000 iteration burn-in, while multiple-country estimation ran for 20,000 iterations after a 10,000 iteration burn-in.

Breeding values for milk yield were estimated using a multiple-country, multiple-lactation random regression test day model equivalent to the model used for variance component estimation with the inclusion of genetic groups. Mixed model equations were solved iteratively over 1000 rounds on the entire data set (after edits). EBV correlations and genetic trend over time were calculated by averaging EBV across lactations and across country scales, and expressed in standard deviation units.

Results and Discussion

Descriptive statistics of single country data are in Table 1. New Zealand population had by far the largest milk solid percentages, while having the lowest daily milk yield. Canada and United States had the smallest contemporary group sizes for herd-test day groups, daughters per sire and herd size, and this may reflect the similarity between these two countries in terms of production system and genetic base. However, there was considerable variability shown for all countries for these contemporary group descriptors, with many standard deviations up to twice the magnitude of the mean, and with group sizes being much smaller than those reported in other studies using test day data (Jamrozik *et al.*, 2002). Plots of daily milk yield (Figure 1) and protein percentage (Figure 2) by day in milk show similar trends to Table 1, with New Zealand having the only sizeable difference in curve. One result which was expected was the plateau that the New Zealand population experienced in late lactation for both milk yield and protein percentage.

Posterior means for average daily heritabilities and genetic correlations from single-country models for milk and protein yield are shown in Table 2. For milk, Australia had noticeably lower heritabilities for all three lactations than other countries, with Canada and the United States having the highest heritabilities. This contrasts with the results for protein yield, where Canada and Great Britain had the highest heritabilities, and the United States has the lowest. Correlations for Australia, New Zealand and Great Britain were also much lower for protein yield than for milk yield likely due to an increased emphasis on forage-based dairying in these countries.

There were 66 sires with at least five daughters-granddaughters in at least two countries. By country of origin, these can be broken down into 30 sires from United States, 26 from Australia, 5 from New Zealand, 3 sires from Norway, and 2 sires from Canada, of which one is a Red Holstein. Among the common sires, there were three NRF sires and one Red Holstein, as these breeds have been used in genetic expansion programs in both the United States and Australia.

There was also great variability in sire usage, as the United States had progeny from 57 of the 66 common sires, while Great Britain only had representation from 7 common sires.

Posterior means of genetic correlations from multi-country model for milk yield are shown in Table 3. Due to time constraints, milk yield was analyzed only. Within country, correlations between lactations were noticeably lower than those from single country estimation. Between country correlations were also very low, with the highest value at only .46, and lowest at .08. The highest values of correlations were between the United States and the other four countries, while the lowest values were between Canada and the other four countries. These low correlations with respect to the Canadian population may be due in part to the limited size of that country's contribution to the data. Genetic correlations were substantially lower than correlations found in Holstein in both test day (Jamrozik *et al.*, 2002) and lactation model analyses (Weigel *et al.*, 2001; Interbull, 2004). Posterior standard deviations of genetic correlations were in the range of 0.04 to 0.12, which was approximately double those found in the same studies cited above.

Noting the estimated genetic correlations and the contemporary group sizes in Table 1, it is likely that in reality, genetic correlations between countries for Milking Shorthorns were lower than those found in other dairy breeds. A lack of international sampling of sires and extensive use of other breeds may be largely responsible for these results. However, it may also be very likely that the correlations found in this study might not accurately reflect reality, due to a potentially over-parameterized model in relation to the size and contemporary group structure of the data for this breed.

Using the parameters estimated from the connected data subset, estimation of breeding values was performed and correlations of estimated breeding values (EBV) across lactations and across country scales were estimated. While it was expected that these correlations would be higher than genetic correlations, these values were substantially higher in all instances, with the highest correlations between the United States and Canada, a likely reflection of a common genetic base. EBV correlations ranged between 0.36 between 2nd lactation in Canada and 1st lactation in Great Britain, and 0.82 between 2nd lactation for both United States and Canada. EBV correlations between sires with greater than 10 daughters showed an even greater increase in correlations, as shown in Table 4.

On each country's scale, a listing of Top 100 sires for milk EBV were generated, with EBV averaged across lactations. The largest contributor of sires over all lists was made by Australian sires (48.8 sires), over three times the contribution of the next largest contributor, the United States (14.8 sires). Top 100 lists for American and Australian scales had the biggest similarity (50 sires), and the British and Australian lists had the least similarity (20 sires). Composition of these lists by sire's country of origin is shown in Table 5. There were big differences in composition of lists by country scale, with Australia being the largest contributor of sires to the Australian, Canadian, and United States lists. When averaged across all five lists, Australia had the largest contribution of sires at over three times the level of the next highest contributor (the United States), followed by Great Britain, Canada and New Zealand in decreasing order of contribution.

Figure 3 illustrates the genetic trend of EBV in average standard deviation units for cows over a ten year period from 1989 to 1998. In the cow population, there was a distinct upward trend for each country, with the American population showing the largest improvement. The differences in genetic response may be due to several reasons, including the ratio of A.I. sires to natural sires, selection emphasis for traits other than milk production, and breed of sire.

Conclusion

Results of this study indicate that a multiple-country, multiple lactation test day model may not be the most appropriate method for joint evaluation of Milking Shorthorns, due to potential lack of connections, and over-parameterization of the model in relation to the size and structure of available data. However, international sampling is currently underway, with connections expected increase substantially in the near future. Therefore, future evaluation with a different model and a better connected pedigree may more easily facilitate international evaluation of Milking Shorthorns.

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Table 1. Descriptive means for cows with records in the edited single country data sets.

	AU S	CA N	GB R	NZ L	US A
Daily milk kg	15.3	20.2	17.9	12.5	21.1
Fat %	3.79	3.66	3.93	4.49	3.60
Protein %	3.29	3.34	3.34	3.76	3.27
% first parity	48.4	47.8	43.8	45.1	42.8
Obs/HTD group	12.9	6.8	10.2	11.7	7.5
Herd Size	45.2	19.6	29.1	20.6	16.5
Daughters/Sire	16.0	8.7	15.0	13.0	10.2

Table 2. Average daily heritabilities and genetic correlations between lactations and nations for milk and protein yield.

		Milk			Protein		
		h^2	2	3	h^2	2	3
AUS	1	.33	.69	.66	.41	.62	.49
	2	.37		.89	.45		.69
	3	.40			.45		
CAN	1	.47	.77	.67	.45	.76	.63
	2	.45		.81	.45		.80
	3	.43			.42		
GBR	1	.40	.65	.56	.43	.62	.45
	2	.41		.84	.46		.65
	3	.40			.46		
NZL	1	.38	.79	.72	.41	.59	.42
	2	.43		.84	.44		.62
	3	.43			.44		
USA	1	.42	.87	.81	.37	.84	.76
	2	.43		.92	.41		.91
	3	.43			.42		

Table 3. Posterior means of genetic correlations for milk across lactations and countries (above diagonal) and posterior standard deviations for genetic correlations (below diagonal) for five countries with Milking Shorthorn populations.

	AUS			CAN			GBR			NZL			USA		
	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3
AUS	1	66	68	19	25	18	20	28	24	28	24	22	37	39	33
	2	3	71	13	22	15	19	27	23	28	25	23	39	41	34
	3	3	3	18	28	18	24	28	25	28	25	22	39	41	34
CAN	1	8	9	10	62	57	14	16	22	19	21	21	30	30	28
	2	9	9	10	5	69	10	8	11	19	19	21	41	46	44
	3	10	9	10	6	4	15	14	13	22	24	22	33	36	32
GBR	1	10	10	10	7	8	8	51	48	25	18	20	27	26	28
	2	10	10	9	8	8	9	5	52	30	28	30	31	28	34
	3	9	10	9	8	9	10	6	6	28	24	21	21	18	21
NZL	1	8	8	8	9	8	9	10	8	10	72	63	43	43	36
	2	9	9	8	9	8	10	11	9	10	3	75	43	42	35
	3	9	9	8	8	9	10	12	9	11	4	3	43	42	35
USA	1	7	7	7	7	6	7	7	8	8	7	8	8	81	72
	2	8	8	8	7	8	7	7	8	9	7	8	8	2	83
	3	8	8	8	8	7	8	8	8	9	7	8	8	3	2

Table 4. Across-country correlations of milk EBV for sires with 10 or more daughters with records, averaged across lactations.

	AUS	CAN	NZL	GBR	USA
AUS		.65	.77	.75	.60
CAN			.76	.63	.83
NZL				.81	.79
GBR					.60

Table 5. Country of origin composition of Top 100 EBV Sires on each country scale.

Country of origin	Mean total contribution	Country scales				
		AUS	CAN	GBR	NZL	USA
AUS	48.8	76	76	14	26	52
CAN	11.8	11	11	17	11	9
GBR	12.8	1	1	44	6	12
NZL	9.8	1	0	4	37	7
USA	14.8	6	10	20	19	19
Others	2.0	5	2	1	1	1

Figure 1. Milk in kilograms by day in milk in five Milking Shorthorn populations.

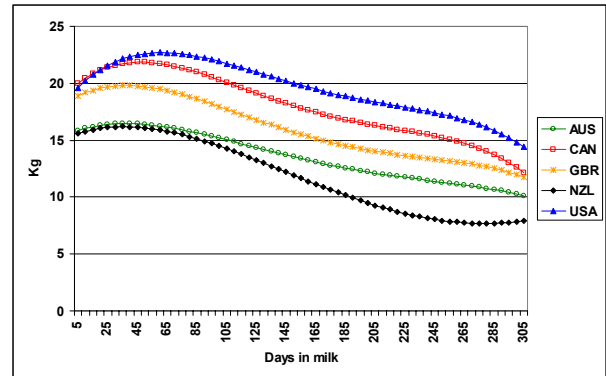


Figure 2. Protein percentage by day in milk in five Milking Shorthorn populations.

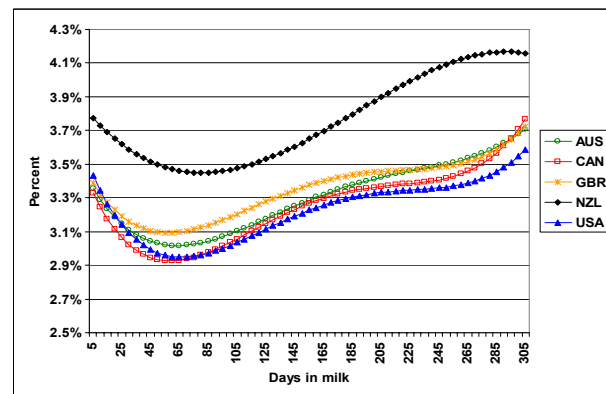


Figure 3. Genetic trend over 10 year period for Milking Shorthorn cows, in standard deviation units.

