

Multi-trait, Across Country Evaluation of Dairy Sires

L. R. Schaeffer
Department of Animal and Poultry Science
University of Guelph
and
Wencan Zhang
Semex Canada
Guelph, Ontario, CANADA

August 1993

1 Collaborators

Andy Robinson and Jacques Chesnais, Agriculture Canada
Hans Wilmink, NRS; George Wiggans, USDA
Paola Rozzi, ANAFI; Herman DeBoer, Semex Canada
Murray Hunt, CAAB

2 Introduction

The international comparison of dairy sires is a very important issue to organizations that deal in the import and export of semen and embryos. INTERBULL was founded on the basis of trying to standardize the methodology used in making comparisons between countries in order to reduce the political tensions caused by different comparison practices. Scientists are very aware of the pitfalls in making across country comparisons, many of which can not be overcome by statistical analyses, but the fact is that comparisons will continue to be made whether scientists become involved or not.

The simplest procedure has been the regression of the proofs from the importing country on those from the exporting country. INTERBULL has made recommendations on

the minimum repeatability for bull proofs to be included in these regressions and on the actual methodology. For the most part, there appears to be compliance with these recommendations, but some people believe the recommendations are too broad and leave each country free to interpret them in their own way.

Schaeffer (1985) proposed a linear model for sire proofs which could combine the information from two or more countries to form a single international proof. Rozzi (1987), Banos et al. (1990), and Banos (1992) have used this procedure, with modifications, to compare various populations of dairy cattle. The method assumes no G x E interaction, and a genetic correlation between production in different countries that is unity. Also, the proofs from each country must remove as much bias from the proofs as is technically possible. The main biases are those due to nonrandom mating of imported sires and to preferential treatment of their daughters in the importing country. Another assumption is that the same heritability applies to production in each country. One suggestion to overcome preferential treatment has been to exclude the data on imported bulls from the analysis. Ironically, these are the bulls that are used in the regression approach to provide the conversion formulas.

The objectives of this study were to

1. Evaluate production traits of Holstein dairy bulls from proofs provided by Canada, Italy, the Netherlands, and the United States in a multi-trait linear model approach where production in each country is a separate trait. Thus, each bull would receive one proof for each country for each trait. The new evaluations will be denoted as Multi-trait Across Country Evaluations (MACE).
2. Estimate the genetic correlation between countries for the multiple trait model, and
3. Compare MACEs with official within country proofs.

3 The Model

The model that describes Holstein sire DYDs (daughter yield deviations) for the i^{th} country is

$$y_i = \mu_i 1 + Z_i Q g_i + Z_i s_i + e_i$$

where

y_i is the vector of average daughter yield deviations (DYD) from country i for one particular trait, such as protein yield.

μ_i is the overall average DYD for the i^{th} country, which reflects the definition of the genetic base for that population.

g_i is a vector of phantom parent genetic group effects where groups will be defined on the basis of year of birth and country of origin.

s_i is a vector of random sire genetic effects (transmitting abilities) for the i^{th} country. Note that this vector is of length equal to the number of bulls to be evaluated (including ancestor sires) in all countries combined, even though they might not have a proof in country i .

e_i is a vector of random mean residual effects.

Z_i is the matrix that relates elements of y_i to elements in s_i , and

Q is a matrix that associates sires with their corresponding genetic groups. This matrix is the same for each country.

Suppose that there are t countries involved. Then

$$V \begin{pmatrix} e_1 \\ e_2 \\ \vdots \\ e_t \end{pmatrix} = \begin{pmatrix} D_1\sigma_{e_1}^2 & 0 & \cdots & 0 \\ 0 & D_2\sigma_{e_2}^2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & D_t\sigma_{e_t}^2 \end{pmatrix},$$

and

$$V \begin{pmatrix} s_1 \\ s_2 \\ \vdots \\ s_t \end{pmatrix} = \begin{pmatrix} A\sigma_{s_1}^2 & A\sigma_{s_1s_2} & \cdots & A\sigma_{s_1st} \\ A\sigma_{s_1s_2} & A\sigma_{s_2}^2 & \cdots & A\sigma_{s_2st} \\ \vdots & \vdots & \ddots & \vdots \\ A\sigma_{s_1st} & A\sigma_{s_2st} & \cdots & A\sigma_{st}^2 \end{pmatrix}.$$

A is the additive genetic relationship matrix for all bulls based on sire and MGS relationships, and D_i is a diagonal matrix with diagonal elements equal to one over the number of daughters in a bull's proof. This number should be directly related to the accuracy of a bull's proof and should include information on number of relatives and the amount of information on the bull's parents and all other relatives.

Notice that the residual and sire components could be different for each country, and the covariance between sire proofs in different countries can give a correlation that is less than one. Hence the heritabilities in each country can be utilized. For production traits, this covariance could reflect a G x E interaction.

The DYDs from each country do not need to be converted to one scale of measurement (such as kilograms). Each country can maintain the units used by that country. The DYDs can be BCAs, kilograms, or pounds, whichever measure is used by that country.

This model assumes, as in Schaeffer (1985), that the residual effects within a country are uncorrelated. Also, the genetic evaluation model employed in each country is assumed

to account for nonrandom matings through the additive genetic relationship matrix, and for all other important nongenetic effects for that country.

Phantom parent grouping was used as in Westell et al.(1988) where unknown parents are assigned to a genetic group. Assignment was on the basis of birth year of the progeny and country of first registration. Mixed model equations were constructed such that $Q\hat{g} + \hat{s}$ was estimated directly from the equations, and the phantom parent groups were random effects, so that the same genetic base was forced upon the solutions within each country. Phantom parent grouping accomplishes the same idea as defining the origin of a bull by

$$.5(\text{origin of sire}) + .25(\text{origin of dam}) + .25(\text{origin of MGS})$$

except that the definitions were entirely on a sire-MGS basis, ignoring the dam, because the relationship matrix in the model was computed on the basis of sire and MGS only.

4 Data

DYDs for production traits (milk, fat, and protein yields) were available on bulls from four countries, i.e. Canada(CAN), Italy(ITA), the Netherlands(NLD), and the United States (USA). Only bulls whose proofs for Spring 1993 were based on daughters in at least 10 herds and whose first daughters calved within the last ten years were included in the analyses. Proofs of bulls from country i that were first progeny tested in country j were not included based on the recommendation of Banos(1992). The number of bulls with DYDs from each country and the number of ancestors (sires and MGSs) without DYDs are given in Table D1. Between countries some of the ancestors were common and thus, the total number of ancestors at the bottom of the table does not equal the sum of the number of ancestors in each country.

Table D1:
Summary of Number of Bulls

Country of Origin	Number with DYDs	Number of ancestors
CAN	2494	418
ITA	1607	414
NLD	3269	674
USA	8329	576
Total	15,699	1577

Unknown sires and MGSs were assigned to 43 phantom parent groups based on the country of registration and the earliest year of birth of their sons or grandsons. A description of the phantom groups and the number of bulls in each are given in Table D2. Due to the low number of bulls represented from DNK and NZL, they were pooled together into phantom groups #42 and #43, because they were from similar year groups.

Table D2:
Description of Phantom Groups

Country of Origin	Years of Birth	Sire Groups		MGS Groups	
		Group No.	No. Bulls	Group No.	No. Bulls
CAN	≤'75	1	93	2	93
	'76-'78	3	111	4	134
	'79-'81	5	66	6	79
	'82 ≥	7	37	8	38
ITA	'75-'77	9	67	10	170
	'78-'81	11	13	12	261
	'82 ≥	13	7		
	'82-'84			14	107
	'85 ≥			15	12
NLD	≤'75	16	161	17	161
	'76-'78	18	187	19	187
	'79-'81	20	60	21	60
	'82 ≥	22	14	23	14
USA	≤'75	24	162	25	162
	'76-'78	26	326	27	343
	'79-'81	28	170	29	176
	'82-'84	30	55	31	55
	'85 ≥	32	10	33	10
DEU	≤'81	34	16	35	16
	'82 ≥	36	14	37	14
ISR	'85-'86	38	2	39	2
GBR	'76-'77	40	3	41	3
DNK,NZL	'82-'84	42	4	43	4

There was one bull (NLD) whose sire and MGS were the same animal and therefore, the bull was inbred. The calculation of the inverse of the relationship matrix assumed no inbreeding. Thus, the MGS for this bull was changed to unknown and assigned to phantom group # 19. A CAN bull appeared twice in the ITA DYD file with the same DYDs, but with different sire and MGS. One of the two records was discarded.

The heritabilities used by each country (for milk, fat, and protein) were .25 for ITA and USA, .30 for NLD, and .33 for CAN.

5 Estimation of Variances

Henderson's Method 1 was used to estimate the sire variances of the DYDs assuming that the heritability estimates used in each country were correct, and that sires were

not related. The estimates of residual variances were then assumed to be constant for the estimation of sire variances and covariances. An extension of the pseudo expectation method was used to estimate the sire covariances between countries within a trait. These were estimated on a pair-wise basis rather than all four countries simultaneously. The starting correlation was assumed to be .60, and this was followed by 7 iterations of the pseudo expectation method.

The estimation of the variances and covariances was complicated by the fact that DYDs were averages and not individual observations. Thus, it was impossible to obtain a total sum of squares on individual observations. This made estimation of the residual variance difficult and necessitated the assumption that the heritabilities which were provided were indeed correct.

The resulting sire variance-covariance matrices were checked to ensure that they were positive definite by computing the eigenvalues. All reported matrices were positive definite.

The appropriate estimation of variances and covariances for this analysis could use more refinement.

5.1 Sensitivity Study

Before variances and covariances were estimated, a sensitivity study using protein yields was undertaken to compare the effect of three different assumed genetic correlations, namely at .50, .75, and .99. Table S1 contains the resulting conversion formulas from the three analyses for protein yield, for converting CAN proofs into those for ITA, NLD, and USA. The conversion formulas were computed using MACE evaluations of bulls that had repeatabilities of .90 or better for all four countries. This was around 2000 bulls. The simple regressions of CAN proofs on the other countries were computed.

Table S1:

Conversion formulas for Protein Yields

Conversion TO	Conversion from CAN	
	a-value	b-value
Correlation=.99		
ITA	19.9	4.06078
NLD	-.5	3.66674
USA	-2.9	4.24551
Correlation=.75		
ITA	17.0	3.57295
NLD	3.1	2.89975
USA	8.5	3.68914
Correlation=.50		
ITA	14.4	3.36595
NLD	2.5	2.67267
USA	11.2	3.21377
Current Official		
ITA	21.1	3.22
NLD	5.0	2.1
USA	-2.3	3.33

The impact of the assumed genetic correlations on the a- and b-values in Table S1 was substantial. To better visualize the effect, Canadian BCA proofs were converted to proofs in the other countries using each of the formulas in Table S1 (shown in Table S2). There were significant differences in the resulting converted proofs.

Table S2:
 Converted Canadian Protein Proofs
 Using Different Conversion Formulas in Table R4.

CAN Protein Proof(BCA)	ITA(kg)	NLD(kg)	USA(lb)
Corr=.99			
+20	101	73	82
+15	81	55	61
+10	61	36	40
Corr=.75			
+20	88	61	82
+15	71	47	64
+10	53	32	45
Corr=.50			
+20	82	56	75
+15	65	43	59
+10	48	29	43
Current Official			
+20	86	47	64
+15	69	36	48
+10	53	26	31

If one assumes the current official conversion formulas are correct, then the genetic correlation between CAN and ITA should be about .75, and between CAN and NLD or CAN and USA should be something lower than .50. Such low correlations are as difficult to accept as the high estimated correlations of .99. There are several conclusions which can be drawn from this sensitivity study of protein yields.

1. The assumed genetic correlations between countries need to be accurately estimated.
2. The actual genetic correlations must be significantly lower than .99 for these four countries, and could be different between specific pairs of countries. That is, for example, between CAN and USA it could be .80 while between ITA and NLD it could be .95.
3. Regardless of the actual genetic correlations, it appears that MACE evaluations will produce very different conversion formulas from the current official formulas.

6 Results

6.1 Variances and Covariances

The estimates of variances and covariances are given in Tables R1 and R2. Keep in mind that these are estimates from a sire model. Thus, the residual variances may be slightly greater than from an animal model. Recall that the residual variances were from Method 1 estimation and that sire variances and covariances are from pairwise pseudo expectation estimation. For each country, three estimates of the sire variance were obtained (one with each of the other countries), and these were averaged. The estimated sire correlations were used to obtain the sire covariances from the averaged sire variances. Because the residual variances were held constant and the sire variance allowed to change, the resulting heritabilities were slightly different from those provided by each country.

Table R1:
Estimates of Sire Variances
Covariances and Correlations

Countries		Fat	Cor.	Protein	Cor.
CAN	CAN	64.4	1.000	38.9	1.000
CAN	ITA	105.7	.967	71.7	.973
CAN	NLD	93.1	.860	53.4	.906
CAN	USA	224.6	.861	150.1	.948
ITA	ITA	185.4	1.000	139.3	1.000
ITA	NLD	160.1	.871	103.1	.924
ITA	USA	413.8	.935	290.2	.969
NLD	NLD	182.2	1.000	89.3	1.000
NLD	USA	396.1	.903	227.3	.948
USA	USA	1056.4	1.000	644.3	1.000

Table R2:
Estimates of Residual Variances
and Heritabilities

Country	Fat	Heritability	Protein	Heritability
CAN (BCA)	608.2	.383	427.3	.334
ITA (kg)	2585.7	.268	1946.3	.267
NLD (kg)	2062.3	.325	1036.9	.317
USA (lb)	11,716.3	.331	7683.0	.309

6.2 Comparison to Within Country Proofs

The MACE evaluations of bulls were correlated with their within country proofs for those bulls with DYDs. Means and standard deviations were also calculated (Table R3). Please note that the MACE evaluations are expressed as ETAs, but that proofs in ITA and NLD are expressed in terms of EBVs. Thus, the averages for MACE ETAs for ITA and NLD were multiplied by two.

Table R3:
Comparison of MACE ETAs and
Within Country Proofs

Country	Trait	MACE ETA		Proofs		Correlation
		Mean	SD	Mean	SD	
CAN (BCA)	Fat	2.74	7.19	1.22	7.63	.9912
	Protein	0.65	6.63	1.14	7.05	.9933
ITA (kg)	Fat	22.1	27.9	21.5	29.1	.9952
	Protein	21.2	25.6	20.2	26.3	.9957
NLD (kg)	Fat	4.7	27.4	4.7	27.9	.9983
	Protein	4.2	19.8	4.4	20.2	.9980
USA (lbs)	Fat	23.3	26.1	23.4	27.5	.9954
	Protein	16.8	20.8	18.7	21.8	.9833

7 Conversion Formulas

Bulls having a repeatability of .75 or better for their MACE evaluations in all four countries were used to compute conversion formulas. There were 5,202 bulls for fat yields and 12,044 bulls for protein yields. The difference in numbers is due to the lower genetic correlations between countries for fat yields compared to protein yields. However, both numbers are substantially greater than any numbers of bulls that have been used in the past to calculate conversion formulas.

Table R4:
Conversion formulas for Protein Yields

Proof in Country	=	Intercept +	b-value times	Proof in Country
CAN	=	-5.99	.2681	ITA
CAN	=	-1.82	.3443	NLD
CAN	=	-.73	.2466	USA
ITA	=	22.37	3.7141	CAN
ITA	=	15.52	1.2883	NLD
ITA	=	19.59	.9221	USA
NLD	=	5.38	2.8292	CAN
NLD	=	-11.72	.7641	ITA
NLD	=	3.22	.7075	USA
USA	=	3.05	3.9880	CAN
USA	=	-21.04	1.0766	ITA
USA	=	-4.38	1.3927	NLD

Table R5:
Conversion formulas for Fat Yields

Proof in Country	=	Intercept +	b-value times	Proof in Country
CAN	=	-6.59	.2915	ITA
CAN	=	-.59	.2822	NLD
CAN	=	-2.07	.2404	USA
ITA	=	22.67	3.3878	CAN
ITA	=	20.61	.9987	NLD
ITA	=	15.36	.8347	USA
NLD	=	2.17	3.3040	CAN
NLD	=	-19.84	.9714	ITA
NLD	=	-4.99	.8169	USA
USA	=	8.90	3.9338	CAN
USA	=	-17.80	1.1753	ITA
USA	=	6.37	1.1825	NLD

There is an interesting property associated with these conversion formulas. Using figures from Table R4, for example,

$$\text{NLD} = 5.375 + 2.82916(\text{CAN}),$$

which can be re-arranged to give

$$\text{CAN} = (2.82916)^{-1}(-5.375 + \text{NLD})$$

$$\text{CAN} = -1.8997 + .3535(\text{NLD}).$$

This last equation is very similar to the estimated conversion formula for converting Dutch proofs to Canadian equivalents, namely,

$$\text{CAN} = -1.8212 + .3443(\text{NLD}).$$

Thus, there is some degree of reciprocity between conversion formulas. That means you can convert a Dutch proof to a Canadian equivalent, and then convert it back to a Dutch proof and arrive at the same proof with which you started. However, you can also convert from country 1 to country 2 to country 3 to country 4 and then back to country 1 and end up with the exact same value with which you started. The degree of reciprocity seems to be associated with the genetic correlation between countries. As the correlation increases so does the degree of reciprocity. Thus, the reciprocity is better for protein yields than it is for fat yields in this study. True reciprocity exists only when the genetic correlation between countries is unity.

8 Discussion

This study has shown that a multi-country evaluation model can be applied in practice. The estimation of variance and covariance parameters still needs much work as the results depend on the assumed genetic correlations between countries. The resulting sire ETAs were highly correlated with their country of origin proofs, but were slightly less variable. Bulls could rank slightly differently in each country based on their MACE ETAs.

The multi-trait mixed model equations were solved by 400 Gauss Seidel iterations. The connections among countries were based entirely on additive genetic relationships, and many of the relationships were from North America going to Europe, but none that went in the other direction. The relationship connections among the four countries in this study were adequate, but were weak. The relationship connections among countries should be quantified in some manner prior to combining their DYDs into a MACE evaluation. If the degree of relationship is too weak, then an analysis should probably not be attempted. However, the relationship ties among the countries in the present study should only improve in the future, and so constant monitoring of connections should take place.

9 References

- Banos, G., L. R. Schaeffer and E. B. Burnside. 1990.
North American genetic evaluation of Ayrshire bulls
with a linear model. 4th World Congress - Edinburgh.
- Banos, G. 1992. Report on COPA/INTERBULL joint project.

INTERBULL open meeting, June 7-8, 1992, Neustift, Austria.

Rozzi, P. 1987. Ph.D. Thesis. University of Guelph. Canada.

Schaeffer, L. R. 1985. Model for international evaluation of dairy sires. *Livest. Prod. Sci.* 12:105-115.

Van Raden, P. M. and G. R. Wiggans. 1991.
Derivation, calculation, and use of national animal model information. *J. Dairy Sci.* 74:2737-2746,

Westell, R. A., R. L. Quaas, and L. D. Van Vleck. 1988.
Genetic groups in an animal model.
J. Dairy Sci. 71:1310-1318.

10 Example Calculations

Consider data on bulls from three countries (C1, C2, and C3) whose proofs are expressed in different units, say meters, cm, and inches(in), respectively. Bull identification was standardized across countries so that each bull was uniquely identified. The average daughter yield deviations (DYDs), and progeny numbers are given in Table X1. A few bulls had proofs in more than one country. (Note: To avoid bias due to preferential treatment, only proofs of bulls from the country in which they were first progeny tested should be used. However, this small example illustrates that the methodology can handle proofs in more than one country if these are found to be free of bias.) DYDs are assumed to be computed in the same manner in each country and should be free of estimated fixed effects in the evaluation model.

Table X1:
Example Across Country Data

Bull ID	Sire ID	MGS ID	Country of proof	Number of daughters	DYD
24	11	23	1	2468	5
24	11	23	3	27	0
24	11	23	2	10827	98
25	13	23	2	111	1106
26	14	18	3	97	220
26	14	18	2	1665	1230
27	15	18	3	114	-140
29	10	26	1	96	12
30	11	20	1	140	8
31	12	24	1	57	-2
32	10	20	1	109	11
33	11	21	1	91	5
34	28	25	1	94	22
35	12	21	1	85	1
35	12	21	2	143	-84
36	13	22	2	67	896
37	13	22	2	103	956
38	31	29	3	87	20
39	16	19	3	244	50
40	16	35	3	157	-10
41	17	24	3	92	-70
42	15	19	3	90	-100
43	17	19	3	113	-40
44	35	24	3	59	0

A pedigree file should be constructed so that sires and MGS appear in the file before their sons and grandsons (bulls given in order of their birthdates). This is necessary for the estimation of variance components to be described later. The sires and MGS of bulls, not having a proof themselves are listed in Table X2. Nine phantom parent groups were formed (arbitrarily for this example), and assigned to the animals in Table X2. Except for Bull #28, the sire and MGS of the bulls in Table X2 were all unknown. The MGS of Bull #28 was #26.

A coded pedigree file is formed to facilitate Gauss-Seidel iteration on data. The coded file is shown in Table X3. When the code is 0, this indicates that column IS is the sire of the bull, IT is the MGS of the bull, and IA is the bull identification.

Table X2:
Phantom Group Assignments
For Bulls with Unknown
Sire or MGS

Bull ID	Sire Phantom Group	MGS Phantom Group
10	1	2
11	1	2
12	1	2
13	3	4
14	3	4
15	5	6
16	5	6
17	5	6
18	5	9
19	6	9
20	2	7
21	2	7
22	4	8
23	4	8
28	1	26

NMIS is 0 if both sire and MGS are known. NMIS is 4 if the sire is unknown; is 1 if the MGS is unknown; and is 5 if both sire and MGS are unknown. This number is added to 11 and divided into 16 to give the constant that is used in forming the inverse elements of the relationship matrix.

When the code is 1, then IA is the sire of IS and IT is the MGS of IS, and NMIS is the number of missing parents appropriate to animal IS. When the code is 2, then IA is the MGS of IS and IT is the sire of IS, and NMIS is the number of missing parents appropriate to animal IS.

The adjustments during iterations due to A^{-1} to the right hand sides of the MME (mixed model equations) are, for code =0:

$$c(i) = 16\lambda_{IAS}(IA, i) - 8\lambda_{IAS}(IS, i) - 4\lambda_{IAS}(IT, i)$$

for $i = 1$ to nc , where nc is the number of countries in the analysis, $s(k, i)$ is the current solution for the k^{th} bull in the i^{th} country and $\lambda_{IA} = (11 + NMIS)^{-1}$.

Table X3:
Coded Pedigree File
For Example Data

IA	Code	IS	IT	NMIS	IA	Code	IS	IT	NMIS	IA	Code	IS	IT	NMIS
1	0	0	0	0	10	0	1	2	5	22	0	4	8	5
1	1	28	26	4	10	1	32	20	0	22	2	37	13	0
1	1	11	2	5	10	1	29	26	0	22	2	36	13	0
1	1	12	2	5	11	0	1	2	5	23	0	4	8	5
1	1	10	2	5	11	1	24	23	0	23	2	25	13	0
2	0	0	0	0	11	1	30	20	0	23	2	24	11	0
2	1	20	7	5	11	1	33	21	0	24	0	11	23	0
2	1	21	7	5	12	0	1	2	5	24	2	44	35	0
2	2	12	1	5	12	1	35	21	0	24	2	31	12	0
2	2	11	1	5	12	1	31	24	0	24	2	41	17	0
2	2	10	1	5	13	0	3	4	5	25	0	13	23	0
3	0	0	0	0	13	1	25	23	0	25	2	34	28	0
3	1	13	4	5	13	1	37	22	0	26	0	14	18	0
3	1	14	4	5	13	1	36	22	0	26	2	29	10	0
4	0	0	0	0	14	0	3	4	5	26	2	28	1	4
4	1	23	8	5	14	1	26	18	0	27	0	15	18	0
4	1	22	8	5	15	0	5	6	5	28	0	1	26	4
4	2	14	3	5	15	1	42	19	0	28	1	34	25	0
4	2	13	3	5	15	1	27	18	0	29	0	10	26	0
5	0	0	0	0	16	0	5	6	5	29	2	38	31	0
5	1	18	9	5	16	1	40	35	0	30	0	11	20	0
5	1	16	6	5	16	1	39	19	0	31	0	12	24	0
5	1	15	6	5	17	0	5	6	5	31	1	38	29	0
5	1	17	6	5	17	1	41	24	0	32	0	10	20	0
6	0	0	0	0	17	1	43	19	0	33	0	11	21	0
6	1	19	9	5	18	0	5	9	5	34	0	28	25	0
6	2	16	5	5	18	2	27	15	0	35	0	12	21	0
6	2	17	5	5	18	2	26	14	0	35	1	44	24	0
6	2	15	5	5	19	0	6	9	5	35	2	40	16	0
7	0	0	0	0	19	2	43	17	0	36	0	13	22	0
7	2	20	2	5	19	2	39	16	0	37	0	13	22	0
7	2	21	2	5	19	2	42	15	0	38	0	31	29	0
8	0	0	0	0	20	0	2	7	5	39	0	16	19	0
8	2	22	4	5	20	2	30	11	0	40	0	16	35	0
8	2	23	4	5	20	2	32	10	0	41	0	17	24	0
9	0	0	0	0	21	0	2	7	5	42	0	15	19	0
9	2	18	5	5	21	2	33	11	0	43	0	17	19	0
9	2	19	6	5	21	2	35	12	0	44	0	35	24	0

If animal IA has progeny, then accumulate in c, for code=1:

$$c(i) = c(i) - 8\lambda_{ISS}(IS, i) + 4\lambda_{ISS}(IA, i) + 2\lambda_{ISS}(IT, i)$$

and for code = 2:

$$c(i) = c(i) - 4\lambda_{ISS}(IS, i) + 2\lambda_{ISS}(IT, i) + \lambda_{ISS}(IA, i).$$

For phantom groups when code = 0,

$$c(i) = c(i) + s(IA, i).$$

After all pedigree elements have been processed for animal IA, then subtract $G^{-1}c$ from the right hand sides of bull IA.

The values in G are one quarter of the additive genetic variances and covariances between countries. For the example, let the *a priori* values be

$$G = \begin{pmatrix} 4.98 & 302.50 & 59.40 \\ 302.50 & 20,356.60 & 3795.93 \\ 59.40 & 3795.93 & 783.89 \end{pmatrix},$$

where the genetic correlation between countries was assumed to be .95. The *a priori* residual variances were

$$R = \begin{pmatrix} 55.357 & 0 & 0 \\ 0 & 305,349.5 & 0 \\ 0 & 0 & 9668.0 \end{pmatrix}$$

which give heritabilities of .33, .25, and .30, respectively, for the three countries.

The right hand sides (RHS) for a bull, after computing the relationship matrix adjustments, are incremented for their DYDs in each country, if any. That is, add

$$r^{ii} * n_{IA} * (DYD_i - \hat{\mu}_i - s(IA, i))$$

to the i^{th} RHS for sire IA, where $\hat{\mu}_i$ is the current estimate of the overall mean for country i , n_{IA} is the number of progeny of bull IA in country i , and r^{ii} is one over the residual variance for country i .

After all of the DYD accumulations are made for bull IA, then new solutions for that bull are computed by premultiplying the adjusted RHS by the inverse of an nc by nc diagonal block of the MME coefficient matrix for that bull, which can be generally represented as D_{IA} , where

$$D_{IA} = \left[\begin{pmatrix} r^{11}n_1 & 0 & 0 \\ 0 & r^{22}n_2 & 0 \\ 0 & 0 & r^{33}n_3 \end{pmatrix} + a^{IA} * G^{-1} \right]^{-1}$$

and a^{IA} is the diagonal of A^{-1} for bull IA. All of the D_{IA} are computed once prior to the iteration program, and then retrieved from a file as they are needed rather than re-computing them in each iteration.

After all sires have been processed, then new country means are estimated by accumulating

$$RHS_i = RHS_i + r^{ii}n_{IA}(DYD_i - \hat{\mu}_i - s(IA, i)),$$

and

$$X_i = X_i + r^{ii}n_{IA}.$$

The new solution at iteration m is

$$\hat{\mu}_i^m = \hat{\mu}_i^{m-1} + RHS_i/X_i.$$

Convergence of the system of solutions is improved at each iteration by forcing

$$\mathbf{1}'\mathbf{A}^{-1}\hat{\mathbf{s}}$$

to be zero after each iteration. This also allows the calculation of $\hat{\mathbf{s}}'\mathbf{A}^{-1}\hat{\mathbf{s}}$ for variance component estimation. Two hundred iterations were performed on the example data.

Approximate accuracies, θ_k , for the k^{th} bull were computed as

$$\theta_{ki} = (g_{ii} - d_{ii})/g_{ii}$$

for $i = 1$ to nc and where g_{ii} is a diagonal element of \mathbf{G} and d_{ii} is a diagonal element of \mathbf{D}_k for the k^{th} bull. This is a very simple approximation that could be refined in the future.

The solutions and accuracies are given in Table X4.

Table X4:
Solutions and Accuracies

Bull ID	Solutions			Accuracies		
	Country 1	Country 2	Country 3	Country 1	Country 2	Country 3
Mean	9.2	403	33.3	.99	.99	.99
1	-1.5	-105	-18.1	.50	.50	.50
2	-2.3	-144	-26.7	.41	.41	.41
3	6.0	387	76.1	.33	.33	.33
4	3.9	252	49.7	.38	.38	.38
5	-4.4	-282	-58.3	.50	.50	.50
6	-2.9	-182	-37.6	.30	.30	.30
7	-.2	-13	-2.4	.11	.11	.11
8	.5	29	5.8	.11	.11	.11
9	-.1	-5	-1.2	.11	.11	.11
10	-.2	-21	-2.2	.42	.42	.42
11	-3.9	-268	-47.3	.52	.52	.52
12	-7.3	-451	-85.6	.42	.42	.42
13	9.8	644	123.4	.52	.52	.52
14	10.0	643	129.8	.27	.27	.27
15	-10.3	-659	-136.1	.42	.42	.42
16	-1.6	-102	-21.2	.42	.42	.42
17	-6.3	-402	-83.2	.42	.42	.42
18	-1.6	-101	-21.2	.15	.15	.15
19	-2.4	-155	-32.0	.21	.21	.21
20	-.3	-21	-3.3	.15	.15	.15
21	-2.9	-179	-34.0	.15	.15	.15
22	3.3	218	42.2	.15	.15	.15
23	2.7	165	33.7	.15	.15	.15

Table X4. (continued):

24	-4.2	-304	-51.5	.99	.99	.96
25	10.2	662	126.8	.84	.89	.84
26	12.9	827	168.6	.94	.99	.96
27	-12.1	-773	-159.7	.85	.85	.91
28	6.5	401	81.5	.30	.30	.30
29	2.9	185	39.2	.90	.85	.85
30	-1.3	-95	-15.8	.93	.87	.87
31	-9.5	-593	-112.2	.86	.82	.82
32	1.5	89	18.6	.91	.85	.85
33	-4.0	-259	-47.8	.90	.84	.84
34	11.8	728	143.5	.90	.84	.84
35	-7.7	-476	-90.8	.93	.94	.91
36	7.1	465	88.7	.78	.83	.78
37	7.9	523	99.5	.82	.88	.82
38	-2.0	-118	-19.0	.83	.83	.88
39	1.1	69	14.3	.89	.89	.95
40	-3.4	-214	-42.3	.87	.87	.93
41	-7.3	-475	-95.3	.83	.83	.89
42	-9.4	-599	-123.8	.83	.83	.89
43	-5.3	-339	-70.1	.85	.85	.91
44	-3.4	-221	-39.1	.79	.79	.84

The sire solutions to these equations are forced to the same genetic base within each country. To obtain their current within country proof, the sire solution must be added to the overall country mean estimates. However, these solutions could be labeled as international evaluations with a particular genetic base in order to distinguish them from their within country proofs. Notice also, that bulls may not necessarily rank in the same order in each country, depending on the genetic correlation between two countries. The correlation between sire solutions from this analysis was greater than .99, even though the *a priori* correlation was assumed to be .95.