

Prospects of Performing Multiple-Country Comparison of Dairy Sires for Countries not Participating in Interbull International Genetic Evaluations

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Abstract

The question has been raised if there is a way to perform international genetic evaluations for countries unable to submit national evaluation data to Interbull. In this study a method using correlated recorded traits have been used to predict international genetic merits for Argentina. Different correlation matrices were used, and the results were compared with the results obtained when using Argentinean data in an Interbull evaluation. The result showed that the method worked, but with a potential loss in genetic progress.

Introduction

Besides the countries participating in Interbull international genetic evaluations there are many member countries in the organization. Today these countries for various reasons do not submit data and participate in the evaluations. Although, these countries participate in the international trade of semen and could also have use of international evaluations when selecting bulls. In connection to this discussion the question has been raised if there is any possibilities for Interbull to perform international evaluations for countries not submit own data.

The ranking of bulls differ between countries. This re-ranking is due to genotype by environment interaction, differences in trait definitions and differences in the national analyses (Powell and VanRaden, 2002). The bigger the differences are between countries the bigger the differences are in the performance by the daughters. This is accounted for in estimating international genetic merits by treating national genetic merits as different correlated traits.

In general the correlation for milk production is high, ranging between 0.85 and 0.90 among the countries in the Northern hemisphere, around 0.90 in Oceania and between 0.75 and 0.84 between Northern and Southern hemisphere (Fikse, 2004).

Today in international genetic evaluation correlations between countries are estimated before predicting the genetic merits.

The objective of this study was to predict international genetic merits for a country with no national data available and also to look at the differences between the predicted genetic merits obtained without data with the results obtained from an Interbull evaluation.

Argentina submitted data for this study and was used as representative for countries not participating in Interbull evaluations.

Material and Methods

Data

The data used was predicted genetic merits for milk yield for Holstein, Interbull routine run August 2006, including data from 24 populations and in total 100 642 bulls. Also national breeding values for milk yield from Argentina. The Argentinean data included 909 Holstein bulls.

Analysis with Argentinean data

Estimation of correlations and prediction of international genetic merits for Argentina was

performed in the same way as in common Interbull evaluations, with the methods EM-REML and MACE.

Analysis without Argentinean data

We used two different ways of obtaining the unknown correlation between Argentina and the other participating countries. First assumed correlations, e.g. we used 0.5, 0.6, 0.7 and 0.8 between Argentina and all the other populations. The other way was by using prior correlations. With the prior method genetic correlations are predicted using a multiple regression method. Values that potentially explain variations between countries are variables in model [1] and [2]. The variables are from different sources: climate variables, production system indicators and national evaluation descriptors. Model [2] is a modification of model [1] where variables not directly associated with G x E are excluded. These variables are included in μ' and are fixed at their maximum values

$$\text{Prior: } r^5 = \mu + b_1\text{milk} + b_2\text{grass} + b_3\text{wind} + b_4\text{temp} + b_5h^2 + b_6\text{par} + b_7\text{CB} \quad [1]$$

$$\begin{aligned} \text{Prior +: } r^5 &= \mu' + b_1\text{milk} + b_2\text{grass} + b_3\text{wind} + b_4\text{temp} \\ \mu &= -0.586 \\ \mu' &= \mu + b_5(1) + b_6(1) + b_7(990) \end{aligned} \quad [2]$$

where, **milk** = ratio for milk yield, **grass** = grazing, **wind** = ratio for average wind speed, **temp** = ratio for average temperature, **h²** = ratio for heritability, **par** = ratio for number of parities, **CB** = ratio for number of common bulls.

The values for μ and b are printed in Mark *et al.* (2006b).

When predicting genetic merits for Argentina without national data a model [3] previously used by Mark *et al.* (2006a) was used. This model predicts genetic merit for a non-recorded trait with data from a correlated recorded trait. For this study the result from Interbull routine run August 2006 was used as the recorded trait. The (co)variance matrix came from the same routine run.

$$U_{i+} = gV^{-1}u_i \quad [3]$$

g is the vector containing the correlations, V^{-1} is the (co)variance matrix and u_i is a vector containing the MACE solutions.

When combining the different methods for obtaining correlations and genetic merits both with and without Argentinean data, we got eight different alternatives, see Table 1. The different alternatives were statistically compared using SAS software.

Table 1. The different alternatives used when predicting international genetic merits for Argentina.

	r_G^a	σ_s^b	PGM ^c	Data ^d	N ^e
r_{ref}	REML	REML	MACE	25	100,895
r_{REML}	REML	REML	Model [3]	24	100,642
$r_{0.5}$	0.5	1.0	Model [3]	24	100,642
$r_{0.6}$	0.6	1.0	Model [3]	24	100,642
$r_{0.7}$	0.7	1.0	Model [3]	24	100,642
$r_{0.8}$	0.8	1.0	Model [3]	24	100,642
r_{prior}	Prior ^f	1.0	Model [3]	24	100,642
r_{prior+}	Prior + ^g	1.0	Model [3]	24	100,642

^a Method of estimating correlation or the value of the correlation, ^b Sire standard deviation, ^c The method used for predicting international genetic merit, ^d Number of countries included for prediction of international genetic merit, ^e Number of bulls included in each alternative, ^f Equation [1] was used when estimating correlations, ^g Equation [2] was used when estimating correlations

Result

The results from the estimations of correlations between Argentina and the other countries are shown in Table 2.

Table 2. Estimated correlations between Argentina and the other participating countries.

Country ^a	r_{bend}^c	r_{prior}	$r_{\text{prior}+}$
CAN	0.656	0.612	0.828
DEU	0.578	0.621	0.843
DFS	0.648	0.702	0.811
FRA	0.713	0.678	0.856
ITA	0.652	0.627	0.849
NLD	0.683	0.661	0.847
USA	0.649	0.635	0.833
CHE	0.701	0.681	0.840
GBR	0.643	0.809	0.854
NZL	0.643	0.766	0.916
AUS	0.704	0.649	0.875
BEL	0.687	0.752	0.839
IRL	0.706	0.701	0.883
ESP	0.698	0.593	0.854
CZE	0.650	0.725	0.822
SVN	0.748	0.725	0.861
EST	0.470	0.698	0.832
ISR	0.609	0.658	0.832
CHR	0.720	0.654	0.844
FRR	0.680	0.706	0.859
HUN	0.646	0.684	0.840
POL	0.662	0.716	0.865
ZAF	0.684	0.702	0.865
JPN	0.663	0.665	0.850

The mean predicted genetic merit (PGM) is seen in Table 3, the large difference in size between alternatives r_{ref} , r_{REML} and the others is due to differences in the sire variance used, for r_{ref} , r_{REML} the sire variance from REML was used and for the others the sire variance was set to one.

Table 3. The mean predictive genetic merit (PGM), standard deviation (SD), minimum (Min) and maximum (Max) values for the different alternatives.

Alternative	N	PGM (Mean)	SD	Min	Max
r_{ref}	100,895	30.36	145.08	-607.04	561.86
r_{REML}	100,642	212.13	144.88	-432.84	761.61
r_{prior}	100,642	1.31	0.98	-2.32	5.26
$r_{\text{prior}+}$	100,642	1.56	1.18	-3.34	5.93
$r_{0.5}$	100,642	0.89	0.69	-2.08	3.44
$r_{0.6}$	100,642	1.07	0.83	-2.50	4.13
$r_{0.7}$	100,642	1.24	0.97	-2.91	4.82
$r_{0.8}$	100,642	1.42	1.11	-3.33	5.51

Correlations between PGM obtained from the different alternatives are in. Correlations between the four alternatives with assumed genetic correlations (0.5, 0.6, 0.7, 0.8) are close to one.

Table 4. Pearson correlations of Argentina PGM between different alternatives.

Alternative	r_{ref}	r_{REML}	r_{prior}	$r_{\text{prior}+}$	$r_{0.5}$	$r_{0.6}$	$r_{0.7}$	$r_{0.8}$
r_{ref}	1	0.973	0.925	0.944	0.926	0.926	0.926	0.926
r_{REML}		1	0.946	0.962	0.952	0.952	0.952	0.952
r_{prior}			1	0.987	0.969	0.969	0.969	0.969
$r_{\text{prior}+}$				1	0.992	0.992	0.992	0.992
$r_{0.5}$					1	1*	1*	1*
$r_{0.6}$						1	1*	1*
$r_{0.7}$							1	1*
$r_{0.8}$								1

1* > 0.99998

Potential loss in genetic progress was the least when using prior+ correlations and the most when using prior correlations, for the alternatives with correlations estimated without data from Argentina.

Table 5. Mean Argentina estimated breeding values for milk.

Alternative	PGM _{IG}	Potential loss of genetic progress (%)
r_{ref}	451.54	-
r_{REML}	438.79	2.82
r_{prior}	397.99	11.9
$r_{\text{prior}+}$	417.10	7.6
$r_{0.5}$	402.13	10.9
$r_{0.6}$	402.69	10.8
$r_{0.7}$	402.69	10.8
$r_{0.8}$	403.06	10.7

Discussion

This study showed that it is possible to technically perform evaluations for countries that do not submit any data.

The correlation matrix that gave the best result of the ones without data from Argentina was prior +. But the big difference between the two prior alternatives might indicate that the method is not very reliable.

The assumed correlations gave a larger loss in genetic progress than prior+ correlations, but only by around one percent. Between the assumed correlations there were very small differences, which indicate that the magnitude of the correlations is less important than the dimensions amongst them.

When using the model [3] with the correlation matrix obtained from REML, the loss in genetic progress was 2.82%, this result show that with a suitable correlation matrix the method to use correlated recorded traits to get values for an unrecorded trait is working.

Argentina had about 40 % of there bulls in common with the other evaluated countries. This fact might have influenced the result due to the fact that the amount of common bulls is very important in the international evaluation.

When Mark (2006a) used model [3] it was on udder health traits, a trait with lower heritability than milk yield. That is an

indication that this method could work on other traits than milk yield.

This study has only looked at one country, Argentina. It would also be interesting to see how the method works for countries with a larger difference in environment such as India or Kenya. Also to see how reliable the method is if used on a country already in the evaluations such as the Netherlands.

References

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