PREDICTION OF INTERNATIONAL BREEDING VALUES FOR NON-MEASURED TRAITS: APPLICATION TO CLINICAL MASTITIS

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INTRODUCTION

Direct information often is missing for a breeding goal trait due to difficulties in recording the trait. Examples are stillbirth, fertility and clinical mastitis (**CM**). The latter is only recorded and used in genetic evaluations in Nordic countries. International genetic evaluations provide an opportunity to incorporate CM information from the Nordic countries into selection decisions in countries without direct CM information (Mark *et al*., 2002). However, current evaluations do not facilitate an optimal use of the CM information in countries without CM records. This is because the CM information is converted to milk somatic cell (**SC**) breeding values in such countries. More of the CM information could be captured by directly relating CM in the Nordic countries (as well as SC in each country) with CM in the target country.

The aim of this paper is to investigate the predictive performance of a method to predict international breeding values for non-measured traits and the sensitivity of the method to assumed genetic parameters. Here we focus on applying the method to predict breeding values for CM in countries that have genetic evaluations for a correlated trait.

MATERIALS

National genetic evaluation results for SC from 8 national Holstein populations and CM evaluations from 3 of these populations were considered. The data were a subset of data used in the February 2004 Interbull udder health evaluation, and is described in more detail by Mark and Sullivan (2006). In summary, there were 4338, 635 and 1381 CM sire evaluations from Denmark, Finland and Sweden, respectively. Furthermore, there were 52,073 sire evaluations for SC available for a total of 49,536 bulls with daughters in at least one of the 8 countries.

METHODS

International breeding values were computed with a multiple-trait-multiple-country model (**MT-Mace**) which treats each trait in each country as a different, but correlated trait (Mark and Sullivan, 2006). The vectors of MT-Mace solutions ($\mathbf{u}_i$) for each country-trait (i) were subsequently combined into direct breeding values ($\mathbf{u}_{i+}=BV_{dir}$) for a non-measured trait (i+) as follows: $\mathbf{u}_{i+}=\mathbf{g}'\mathbf{V}^{-1}\mathbf{u}_i$, where **g** is a vector containing the expected correlation between breeding values for the non-measured trait and predicted breeding values for the measured traits included in MT-Mace, and **V** is the (co)variance matrix among the predicted international breeding values from MT-Mace. This formula is a generalisation of the equation derived by Klei (1995, p. 98-99) for a situation in which a bull has daughter information in only one country for a total of two countries. All elements in $\mathbf{g}'\mathbf{V}^{-1}\mathbf{u}_i$ are available when solving the MT-Mace equations, but genetic correlations involving non-measured traits need to be specified.

Genetic parameters. Genetic (co)variances among traits with data were estimated using REML as described by Mark and Sullivan (2006). The estimated correlations were used to determine the correlations between the non-measured trait in country k and the measured traits in country i and k. Thus, the necessary genetic correlations (r_G) involving the non-measured

traits were obtained as follows: $r_G(CM_k,CM_i) = b_{CM}r_G(SC_k,SC_i)$ and $r_G(CM_k,SC_i) = b_{SC}r_G(SC_k,SC_i)$. The constants b_{CM} and b_{SC} were assigned the values 0.95 and 0.65, respectively, based on the structure for genetic correlations among measured traits. The sire variances for non-measured traits were set to one. The impacts of the assumptions about genetic parameters involving non-measured traits were investigated by sensitivity analyses.

Analyses and comparisons. Firstly, an MT-Mace analysis was conducted including SC from 8 countries and CM from 3 of these countries. This international genetic evaluation was identical to the one presented by Mark and Sullivan (2006), and the resulting breeding values were labelled reference breeding values. Next, three analyses were performed to investigate the predictive performance of the method. Here, either all the Danish, Finnish or Swedish CM records, respectively, were set missing while the exact same (co)variance structure from the 11-trait reference evaluation was maintained. Effective independent weighting factors and multivariate deregressed evaluations were used for countries with multiple-trait national evaluations for CM and SC in all analyses. The reference breeding values were compared with the following 3 sets of breeding values from the analyses with a CM trait set missing:

- Direct breeding values for the non-measured trait of interest (BV_{dir})
- Breeding values for SC from the same country as the trait of interest (BV_{sc})
- Breeding values with the highest correlation to the reference breeding values (BV_{max})

The potential loss of genetic progress (ΔG), by using an alternative selection strategy, was:

$$\Delta G = \frac{1}{100\sigma_{sire}}\left(\sum_{i=1}^{100} BV - \sum_{j=1}^{100} BV\right),$$

where BV is the reference CM breeding values, σ_{sire} is the sire standard deviation, i is the ranking based on the reference breeding values, and j is the ranking based on breeding values for either direct, within-country SC or best correlated trait. All traits were standardized so that high breeding values were preferable.

RESULTS AND DISCUSSION

Direct breeding values for assumed non-measured traits were closer to reference CM breeding values compared with SC breeding values for the same country and with CM breeding values for a different country (Table 1). This was especially the case for bulls with the majority of daughters in another country than the given country. Within-country SC is not necessarily the best alternative to direct breeding values for non-measured traits. The best correlated trait was CM in Sweden, SC in Germany-Austria and CM in Denmark when the trait of interest was CM in Denmark, Finland and Sweden, respectively. The relatively low correlations for bulls with most daughters in the given country (Table 1) show that there is no substitute for considering direct data of the trait of interest in the international genetic evaluation.

Table 1. Correlation between reference[A] and direct breeding values[B] (r_{dir}), correlation between reference[A] and within-country SC[C] breeding values and best correlation between reference[A] and correlated breeding values[D] (r_{max}) for Clinical Mastitis in Denmark, Finland and Sweden for either domestic[E], foreign[F] or all bulls

	Denmark			Finland			Sweden		
Bulls	r_{dir}	r_{sc}	r_{max}	r_{dir}	r_{sc}	r_{max}	r_{dir}	r_{sc}	r_{max}
Domestic	0.63	0.62	0.63	0.60	0.61	0.62	0.82	0.76	0.81
Foreign	0.91	0.85	0.90	0.99	0.88	0.95	0.98	0.88	0.95
All	0.87	0.82	0.87	0.98	0.88	0.94	0.98	0.88	0.95

[A-D] See description in "analyses and comparisons"

[E] Bulls with most daughters in the given country

[F] Bulls with most daughters in country other than the given

The differences in breeding values had a noticeable impact on which bulls have the best breeding values and on the potential genetic progress that can be achieved by using the different selection strategies (Table 2). The potential loss of genetic progress from selecting the bulls with the 100 highest breeding values was consistently lower for direct CM breeding values compared with breeding values for any other trait than the given.

Table 2. Number of co-selected bulls in top 100 rankings (CB) and potential loss of genetic progress (ΔG loss) by using either direct, within-country SC or best correlated trait compared with top 100 reference breeding values

	Direct		Within-country SC		Best correlated	
	CB	ΔG loss	CB	ΔG loss	CB	ΔG loss
Denmark	18	0.403	19	0.530	19	0.427
Finland	69	0.059	34	0.310	47	0.150
Sweden	42	0.209	33	0.338	32	0.297

The genetic correlations determine the weight which is given to information measured for different countries and traits. The advantage of having CM information increases as the ratio between b_{CM} and b_{SC} increases. The direct international breeding values for CM were not very sensitive to varying genetic correlations. That is, the correlation between direct breeding values was always higher than 0.994 for the investigated changes in genetic correlations (>0.94 when only top 100 breeding values were considered). The sensitivity to varying genetic correlations was more noticeable for bull rankings (Table 3). Direct breeding values for bulls with daughters in multiple countries were slightly more sensitive to varying genetic correlations than bulls with all daughters in one country. The heritability for the direct trait does not affect the direct breeding values, because there are no observations for the trait of interest. This was confirmed by assuming heritabilities ranging from 0.02 and 0.08 for CM in USA.

Table 3. Percent co-selected bulls[A] and percent bulls with clinical mastitis (CM) records among best 100 breeding values for direct CM breeding values in USA when different genetic correlations are used (b_{CM} and b_{SC} defined in methods section)

	Percent co-selected bulls[A]			Percent bulls with CM records		
	b_{CM}=0.90	b_{CM}=0.95	b_{CM}=1.0	b_{CM}=0.90	b_{CM}=0.95	b_{CM}=1.0
b_{SC}=0.60	98	91	87	66	72	74
b_{SC}=0.65	93	100	93	59	64	69
b_{SC}=0.70	84	90	96	50	56	62

[A] Common bulls between top 100 bulls for variable (b_{CM},b_{SC}) and top 100 bulls for (b_{CM}=0.95,b_{SC}=0.65)

The ratio between reliabilities for CM and SC in the USA was 0.59 on average for all bulls when b_{CM}=0.95 and b_{SC}=0.65, which corresponds to 0.74, 0.74 and 0.71 for similar ratios for reliabilities of reference breeding values in Denmark, Finland and Sweden, respectively. Approximate reliabilities for direct CM breeding values were substantially affected by changes in the assumed genetic correlation structure.

The approach to assign genetic correlations for non-measured traits may be modified to account for the fact that some definitions of SC better describe CM than others. Measures of similarity of productions systems may also be used to develop prediction formulas for prior genetic correlations based on estimated correlations. The Interbull Centre applies a detailed procedure to post-process estimated genetic correlations which could be applied to obtain genetic correlations for non-measured traits as well. The problem of assigning genetic

correlations for non-measured traits may not be much different than obtaining suitable genetic correlations among measured traits in some extreme cases (e.g., Mark *et al*., 2005).

CONCLUSION

A method to predict breeding values for non-measured traits was applied to udder health data from multiple countries. The method can yield direct breeding values which enable more efficient selection for resistance to clinical mastitis in countries without direct mastitis records. The method could also be used to predict breeding values for countries that do not participate with any data in current international genetic evaluations.

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