Impact of national genetic evaluation models on international comparisons

Ulf Emanuelson, Freddy Fikse and Georgios Banos
Interbull Centre, SLU Box 7023, S-750 07 Uppsala, Sweden

Abstract

Data quality has always a profound effect on the result of statistical analyses, and international genetic comparisons are no exceptions. Main factors affecting data quality in this context are completeness and accuracy of data recording and pedigree information, and methods of estimation of breeding values on the national level. Currently, there is large variation in the procedures applied in national genetic evaluations, both in terms of model specification and computational methods. Thus, breeding values used in the Interbull routine evaluation of Holstein bulls in February 1999 originated from multiple-trait test-day animal models (AM) and lactational AM, as well as single-trait lactational repeatability AM and sire models, represented by two, three, fourteen, and two countries, respectively. Also, heritabilities used in the national evaluations ranged from 0.23 to 0.42.

Differences in national genetic evaluation models may be one source of variation contributing to differences between countries, indicated by genetic correlations of less than unity in international comparisons. Such effects would, however, be difficult to isolate from "true" GxE interactions in the framework of MACE. Nevertheless, changes over time in correlations between countries could be used to study the impact of different models when concurrent changes in national evaluations have occurred. Major changes in national evaluation models during the last couple of years have, depending on the nature of the changes, been seen to both decrease and to increase correlations.

Changes in national models do not only affect correlations with other countries, but also sire variance estimates and selection differentials within and across countries. Changing genetic parameters may have considerable impact on the international ranking of bulls. For example, decreasing correlations of any country with the rest would result in more domestic bulls on the top of the local scale list, but less bulls from this country on the top of foreign scale lists. Such and other changes are used to illustrate the impact of national genetic evaluation changes on international comparisons.

Keywords: sire evaluation, dairy cattle, Interbull

1. Introduction

It is generally accepted that no chain is stronger than its weakest link, and that all possible weak elements need first to be identified in order to be able to improve the end result. This also holds for the international genetic evaluation of dairy sires, where the relevant links in the chain could be said to be the national data recording, the national evaluation system, and the international evaluation system. Key elements in the quality of each of these links, with respect to international comparisons, were identified by the Interbull audit group (Dommerholt et al., 1998). For instance the group recognised correct identification and registration of individual animals as a crucial factor in data recording, while statistical models and genetic parameters were important factors in national evaluations.

The objective of this presentation is to review current national genetic evaluation procedures for dairy cattle, and to discuss the possible impact of differences on international genetic evaluations.

2. National evaluation models

Genetic evaluation procedures can vary between countries in many different aspects, and there is also within-country variation in how different breeds are evaluated. A comprehensive and exhaustive review would therefore be exceedingly large. However, some key features of national evaluation systems contributing data to the routine evaluation of the Holstein breed at the Interbull Centre in February 1999 are presented in Table 1.

Table 1. Statistical models, heritabilities (h^2), and number of lactations used in national breeding value estimations contributing to the Interbull Holstein evaluation in February 1999.

Country	Model[*]	h^2	# lactations
Australia	AM	0.25	All
Austria	AM MT	0.27-0.30	3
Belgium	AM	0.30	3
Canada	AM TD	0.31-0.42	3
Czech Rep.	AM MT	0.23-0.24	3
Denmark	AM	0.30	3
Estonia	AM MT	0.23-0.24	3
Finland	AM	0.30	3
France	AM	0.30	3
Germany	AM TD	0.35-0.37	3
Ireland	AM	0.35	5
Israel	AM	0.25	5
Italy	AM	0.30	All
Netherlands	AM	0.35	3
New Zealand	AM	0.28-0.35	All
Slovenia	SM	0.25	1
Spain	AM	0.25	All
Sweden	SM	0.25	1
Switzerland	AM	0.25-0.38	5
Unit. Kingdom	AM	0.35	5
Unit. States	AM	0.30	5

[*]AM=repeatability animal model; AM MT=multiple-trait animal model; AM TD=multiple-trait test-day animal model; SM=sire model

Differences as those presented in Table 1, are bound to affect national evaluation results. For instance, Sigurdsson and Arnason (1995), using simulated data, showed that a repeatability animal model with three lactations overpredicted the genetic trend, while a true multiple-trait model did not. Differences between single trait sire models and multiple-trait test-day animal models are likely to be even larger. Also, number of lactations included affects the genetic evaluations, but the mode of action is different depending on model and other specifications.

However, not only does the basic statistical model differ between countries, but there is also a large variation in how fixed factors are defined and handled. Thus, 16 of the countries in Table 1 use some kind of pre-correction of data for fixed effects, while the rest does a simultaneous correction. Although many fixed effects are in common between countries, only 16 includes a correction for days open (or similar), a factor that has been under some debate lately. Moreover, there is also variation in how records in progress and heterogeneous variance between herds are handled, both factors that are known to have significant effects on national evaluations.

The impact of differences in national procedures on genetic evaluations was demonstrated by Banos et al. (1992). They showed a correlation between genetic evaluations of sires based on US and Canadian evaluation procedures of only between 0.84 and 0.87, although the same set of individual cow records were used and conceptually very similar methods. Also, the impact of miss-specified national models was clearly shown when a set of tests of genetic trend (Boichard et al., 1995) were applied and revealed problems with over- as well as underestimation's in several countries.

Although it is clearly demonstrated that differences in national methods do affect breeding value estimations, it is not an easy task to identify the most appropriate method to be applied in a specific national evaluation. However, a procedure to assess the validity of genetic evaluation methods using simulated data has been proposed (Dommerholt et al., 1998) and further work in this area is planned.

3. International evaluations

It is obvious that international comparisons must be affected by national evaluation methods, since the international evaluations are based on (de-regressed) national genetic evaluations. The code of practise for Interbull evaluations therefore

requires that major changes in national evaluation methods should always be first reviewed in a test run, prior to the inclusion of such data in a routine evaluation. However, there is no unanimous definition of what constitutes a "major change" and experience has shown that even changes that were considered minor by the country in question has resulted in substantial changes in the international evaluations.

During the last years there have been several changes in national evaluation models that indeed must be regarded as "major". For instance, during 1998 Denmark changed from a sire model to a repeatability animal model, while Germany and Canada introduced multiple-trait test-day models for national genetic evaluations. Such changes can be used to illustrate the effects of national changes on international evaluations and these three particular events will be used here as "case studies". To that end, data from the Interbull routine run in February, 1998, and the test run in March, 1998, will be used for Denmark and Germany, while for Canada the routine run in August, 1998, will be compared to the test run in September, 1998.

3.1. Impact on parameters

Sire standard deviations (SD) for milk production in Holsteins were in Denmark 270 and 253 kg, in Germany 277 and 291 kg, and in Canada 425 and 421 kg before and after the change in national models, respectively. Changes in genetic correlations between countries are shown in Table 2.

Although most changes in genetic correlations are small they generally follow distinct, and anticipated, patterns. Thus, correlations increased between Denmark and other countries using animal models, while the only decreasing correlation was found between Denmark and Sweden, i.e. a country that is using a sire model. On the other hand, German correlations decreased with almost all countries, and this could also be anticipated since a trait based on test-day information is conceptually rather different from lactation information. Also, correlations between Canada and other countries followed a pattern similar to Germany, although there were more exceptions in this case. For instance the genetic correlation between Canada and Germany

increased when Canada also introduced a test-day model.

Table 2. Genetic correlations between countries for milk yield before (b) and after (a) "major" changes in national breeding value estimation models for Holstein

Country	Denmark b	Denmark a	Germany b	Germany a	Canada b	Canada a
Australia	0.81	0.81	0.80	0.79	0.84	0.81[*]
Austria	0.89	0.89	0.92	0.88	0.87	0.85[*]
Belgium	0.91	0.92	0.90	0.87	0.88	0.94[*]
Canada	0.91	0.93	0.92	0.89	-	-
Czech Rep.	0.90	0.90	0.91	0.87	0.89	0.87
Denmark	-	-	0.92	0.90[*]	0.93	0.94
Estonia	0.86	0.87	0.89	0.87	0.86	0.86
Finland	0.94	0.94	0.90	0.87	0.93	0.91
France	0.91	0.93	0.92	0.90	0.95	0.93
Germany	0.92	0.90[*]	-	-	0.89	0.90
Ireland	0.92	0.93	0.89	0.87	0.92	0.90
Israel	0.87	0.88	0.85	0.85	0.86	0.85
Italy[*]	0.90	0.90[*]	0.91	0.87[*]	0.93	0.94[*]
Netherlands	0.94	0.95	0.95	0.91	0.94	0.94
New Zealand	0.76	0.77	0.77	0.77	0.80	0.82
Slovenia	0.88	0.88	0.89	0.86	0.88	0.87
Spain	0.91	0.92	0.90	0.88	0.92	0.93
Sweden	0.94	0.92	0.90	0.86	0.91	0.90
Switzerland	0.90	0.91	0.90	0.87	0.90	0.89
Unit. Kingdom	0.93	0.95	0.90	0.88	0.94	0.93
Unit. States	0.91	0.93	0.91	0.88	0.96	0.95

[*] other concurrent changes in national models

It should be noted, however, that these differences are not affected by change in model only. In most cases, a major change in the statistical model also imposes new restrictions on the data used in the evaluations, and such changes also contribute to differences observed, even if the same sires are included.

3.2. Impact on ranking

The described changes in genetic parameters will also have an impact on ranking of bulls. In general, an increased correlation would make foreign bulls more competitive on the national scale, and domestic bulls will be more competitive on the foreign scale.

An examination of the ranking of Danish bulls before and after the change in evaluation model (Table 3) showed that they ranked better on the scale in Denmark and on an average of a group of European countries, also using repeatability animal models. However, they did also rank better on the Swedish scale despite the lower correlation, probably explained by the lower sire SD in Denmark. It should be noted that only bulls with an increase in number of daughters between evaluations of less than 10% were included in this comparison in order to limit the effect of new data.

Table 3. Ranking of Danish Holstein bulls for milk production on different scales before (b) and after (a) change in Danish breeding value estimation model.

	Country of scale					
	Denmark		Sweden		Group[*]	
	b	a	b	a	b	a
Rank of top Danish bull	14	5	35	8	49	17
Rank of top 1% Danish bull	905	642	1187	751	1362	729
# Danish bulls in top 50	2	1	2	2	1	1
# Danish bulls in top 100	3	3	3	4	2	2
# Danish bulls in top 500	14	23	9	16	7	16

[*] an average of 3 European countries with repeatability animal models

The ranking of bulls from Denmark, Sweden and the group of European countries on the Danish scale is described in Table 4. Danish bulls performed better throughout the range after the change. The average (median) Swedish bull also ranked better on the Danish scale after the change, while the top 5-10% Swedish bulls ranked lower. This pattern was also observed for the group of European countries, although somewhat less pronounced. This did not reflect the increased genetic correlations between Denmark and the group of countries, but was consistent with the decrease in standard deviations of Danish bulls.

Table 4. Distribution of breeding values for milk production of Holstein bulls from different countries on Danish scale (relative breeding values) before (b) and after (a) change in Danish breeding value estimation model.

	Country of bull					
	Denmark		Sweden		Group[*]	
Percentile	b	a	b	a	b	a
50%	93.8	94.6	86.3	87.9	92.8	93.5
75%	99.6	100.3	94.3	94.4	99.6	99.9
90%	104.3	104.9	100.3	100.1	104.8	104.8
95%	107.1	107.7	103.4	102.5	107.8	107.6
99%	111.7	112.3	108.8	108.2	112.8	112.2
100%	121.0	122.2	115.0	113.9	123.8	122.7

[*] an average of 3 European countries with repeatability animal models

4. Future changes

The rapid development in computing power and of statistical methods will undoubtedly lead to further modifications and improvements in national genetic evaluation methods. The most obvious, in the near future, is probably that more countries will change to test-day models, and that the remaining countries with sire models will change to animal models. However, the evolution of new methods will not necessarily increase the similarities between national procedures, and thus it will possibly continue to compromise international evaluations based on national evaluation results.

This scenario gives additional incentives to look for alternatives to MACE (Multiple Across Country Evaluation), e.g. using individual lactation records of cows rather than breeding values of sires. Such a procedure would certainly alleviate some problems that are due to differences in statistical methods, but is still likely to suffer from differences in data recording and manipulation. The need for better harmonisation of national

methods would then become even more urgent. Currently, there are ongoing efforts to investigate the possibilities, and limitations, of using individual cow records in international comparisons (Anon., 1998).

5. Concluding remarks

There is a considerable variation between countries in the procedures used for genetic evaluation of dairy cattle. This variation has been shown to affect both national and international evaluations. Increased harmonisation of national methods is therefore desirable since it would enhance the value of international comparisons with MACE.

It is also important to continue the work initiated and outlined by the Interbull Audit group to assess and validate national genetic evaluation models and their suitability for specific data structures.

Finally, further research is needed to improve the current MACE methodology, while alternatively investigating the use of individual cow records.

References

Anonymous, 1998. Minutes of the Interbull workshop, Cremona, Italy, October 11-12, 1998.

Banos, G., Wiggans, G.R. and Robinson, J.A.B., 1992. Comparison of methods to rank bulls across countries. J. Dairy Sci., 75: 2560-2568.

Boichard, D., Bonaiti, B., Barbat, A. and Mattalia, S., 1995. Three methods to validate the estimation of genetic trend for dairy cattle. J. Dairy Sci., 78: 431-437.

Dommerholt, J., Wiggans, G.R., Banos, G. and Thompson, R., 1998. Quality assurance systems for international breeding value estimation. Report of the Audit-Expert group of Interbull.

Sigurdsson, A. and Arnason, T., 1995. Predicting genetic trend by uni- and multitrait models. Acta Agric. Scand. Sect. A, Animal Sci., 45: 1-10.