

MERITS OF INTERNATIONAL GENETIC EVALUATIONS USING PERFORMANCE RECORDS

W.F. Fikse

Interbull Centre, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

INTRODUCTION

Genetic improvement and genetic evaluation programs for dairy cattle have been primarily organised within country. Exchange of genetic material between countries increased rapidly during the last decade, a more recent development is the merging of national breeding companies into international AI corporations leading to breeding programs that operate globally. A global breeding plan has also been designed for the Guernsey breed, to warrant the competitiveness of the Guernsey breed compared to other dairy breeds, despite its small numbers.

Banos and Smith (1991) showed that selecting bulls across countries can enhance genetic progress considerably when countries have identical breeding goals. An implicit assumption was that breeding value predictions were similar in all countries. However, genetic correlations between countries can deviate from unity due to differences in the genetic evaluation systems (e.g., Banos *et al.*, 1992 ; Emanuelson *et al.*, 1999). Lohuis and Dekkers (1998) showed that this erodes genetic progress, and suggested that borderless evaluations be done.

The studies by Banos and Smith (1991) and Lohuis and Dekkers (1998) were deterministic simulations that focussed on optimization of the breeding program. However, little is known about the gain in precision of predicted breeding values when international genetic evaluations are borderless. The aim of this study was to investigate gain in precision and accuracy of prediction of genetic merit when individual performance records can be used instead of national breeding values, and when production environment rather than country is the trait of evaluation.

MATERIAL AND METHODS

Three countries and two production environments were simulated. Animals were generated within countries, and observations within production environments. That is, the breeding programs were run within countries, but true breeding values and observations were generated specific to production environments. The simulation was run for eight generations, and repeated five times. Generated data was subsequently used as input to three different methods of international genetic evaluation : 1) multiple-trait evaluation of de-regressed national breeding values (MACE), 2) performance records analyses where countries were treated as separate, though correlated traits (GAMcou), and 3) performance records analyses where production environments were treated as separate, though correlated traits (GAMenv).

The breeding program was a conventional progeny test scheme. Countries A and C were of equal size and comprised 20000 cows per generation. Country B was only half as large. Each generation 200 young bulls were tested in countries A and C (100 in country B), of which the best 20 (10) and

10 (5) were promoted to serve as proven bull and sire of sons, respectively, in the next generation. Cows were replaced by their own progeny. Hundred (50) elite dams were selected as dams of sons, and each dam produced two full brothers. Sires of sons and proven bulls were exchanged between countries from generation four onwards. Level of importation was 50% for country B, and 25% for country A and C.

True breeding values (TBV) for first lactation production in two production environments were generated as the sum of the parent average and a Mendelian sampling deviation. This Mendelian sampling variation was drawn from a multivariate normal distribution and considered the genetic covariance structure among both traits as well as the inbreeding coefficients of the parents. The genetic variances and heritabilities for both traits were 210 and .30, respectively. Genetic correlation between production environments was .90.

Females were given first lactation observations in only one production environment and country. Within each country, two production environments occur. Two different distributions of environments over countries were considered. In the first situation (balanced), 50% of the observations in each country were made in each production environment. In the second situation (unbalanced), 90% of the observations in country A and B, and 10% of the observations in country C were made in the first production environment.

Observations were generated as the sum of a contemporary group effect, the TBV and a residual. Contemporary group size was on average 20 with a SD equal to five, and a minimum size of five. Contemporary group effects were drawn from a normal distribution with mean zero and variance equal to 10% of the total phenotypic variance.

De-regressed national breeding values for bulls (Jairath *et al.*, 1998) were used as input to MACE. National breeding values were predicted with a model including a fixed contemporary group effect and a random animal effect, and variance components estimated with a sire model were used. Variance components for the MACE evaluations were estimated with EM-REML (Sigurdsson *et al.*, 1996). The statistical model for both international evaluations that used performance records contained a fixed contemporary group effect and a random animal effect. Variance components were estimated with a sire model and AI-REML (Jensen *et al.*, 1997).

RESULTS AND DISCUSSION

The bias in estimated genetic correlations between countries for the balanced situation was twice as high for MACE compared to GAMcou (Table 1). The difference in RMSE between both methods was somewhat smaller due to the higher precision of the genetic correlations estimated with MACE. The true genetic correlation between countries was equal to unity by design for the balanced situation, and this may be one reason for the bias. The true genetic correlation between country 1 and 2 in the unbalanced situation was also unity, and bias and RMSE were higher for MACE. The true genetic correlations for the other country pairs were lower, and, interestingly, the bias and RMSE was smaller for MACE compared with GAMcou.

Table 1. Bias and square root of the mean square error (RMSE) for genetic correlations among countries, for a balanced and unbalanced distribution of two production environments over three countries

	Method	Balanced			Unbalanced		
		$rG_{A,B}$	$rG_{A,C}$	$rG_{B,C}$	$rG_{A,B}$	$rG_{A,C}$	$rG_{B,C}$
Bias	MACE	-0.041	-0.032	-0.049	-0.053	0.018	-0.001
	GAMcou	-0.022	-0.015	-0.018	-0.031	-0.023	-0.010
RMSE	MACE	0.041	0.032	0.049	0.053	0.018	0.007
	GAMcou	0.027	0.021	0.024	0.033	0.025	0.051

International genetic evaluations with GAMenv yielded lowest RMSE, whether the predicted breeding values were expressed on country scales (Table 2) or production environment scales (Table 3). Predicted breeding values were empirically unbiased, and differences in RMSE were mainly due to differences in precision.

Table 2. Square root of the mean squared error (RMSE) for predicted breeding values for three countries, for a balanced and unbalanced distribution of two production environments over three countries

Country	Balanced			Unbalanced		
	MACE	GAMcou	GAMenv ^A	MACE	GAMcou	GAMenv ^A
A	6.1	5.1	5.2	6.5	6.1	5.6
B	5.6	5.4	5.2	7.4	6.1	5.6
C	6.2	5.5	5.2	6.7	6.3	6.2

^A Predicted breeding value on a country's scale was computed based on the predicted breeding values for production environment weighted by the proportion of records in each environment.

Considering production environments yielded only small improvements for the balanced situation, but significant improvements for the unbalanced one (Table 2). It was even more important to consider production environment as trait of evaluation when selection decisions are made within production environment (Table 3). The advantage of having access to performance records is somewhat lower when country is the trait of evaluation, but depends on the distribution of production environments over countries.

Weigel and Rekaya (2001) and Zwald *et al.* (2001) both found smaller number of production environments than the number of countries with data, and production environments were not distributed equally over countries.

Table 3. Square root of the mean squared error (RMSE) for breeding values for two production environments, for a balanced and unbalanced distribution of two production environments over three countries

Production environment	Balanced			Unbalanced		
	MACE ^A	GAMcou ^A	GAMenv	MACE ^A	GAMcou ^A	GAMenv
1	5.9	5.9	5.5	6.7	6.3	5.8
2	6.1	6.2	6.2	6.9	6.6	6.5

^A Predicted breeding value for a production environment was computed from the predicted breeding values for countries weighted by the proportion of records in each country

For the unbalanced situation in this study international evaluations improved when production environments were considered and performance records were used. Genetic correlations between production environments well below the value of .90 used in this study have been reported (.59 by Zwald *et al.*, 2001). For such levels of genetic correlations the differences between the three methods is expected to be larger in favour of GAMenv since this evaluation model better resembles the true situation. The statistical models for national and international evaluations were the same in this study. However, national evaluation models vary widely between countries in practise, and Lohuis and Dekkers (1998) showed that standardisation of data collection and genetic evaluation models could lead to increased genetic gains. If also production environment is chosen as trait of evaluation more genetic progress can be expected.

CONCLUSION

When selection decisions are based on predicted breeding values expressed on country scales irrespective of production environments, access to performance records will improve the international comparisons between sires. Several production systems may exist in practise, and if selection is practised within environment then international evaluations should be based on production environments to obtain optimal genetic gain.

REFERENCES

- Banos, G. and Smith, C. (1991) *J. Anim. Breed. Genet.* **108** : 174-181.
 Banos, G., Wiggans, G.R. and Robinson, J.A.B. (1992) *J. Dairy Sci.* **75** : 2560-2568.
 Emanuelson U., Fikse, W.F. and Banos, G. (1999) *Interbull Bulletin* **20** : 115-119.
 Jairath, L., Dekkers, J.C.M., Schaeffer, L.R., Liu, Z., Burnside, E.B. and Kolstad, B. (1998) *J. Dairy Sci.* **81** : 550-562.
 Jensen, J., Mantysaari, E.A., Madsen, P. and Thompson, R. (1997) *J. Indian Soc. Agr. Stat.* **49** : 215-236.
 Lohuis, M.M. and Dekkers, J.C.M. (1998) *Proc 6th WCGALP* **26** : 169-172.
 Sigurdsson, A., Banos, G. and Philipsson, J. (1996) *Acta Agric. Scand.* **46** : 129-136.
 Weigel, K.A. and Rekaya, R. (2000) *J. Dairy Sci.* **83** : 815-821.
 Zwald, N., Weigel, K.A. and Rekaya, R. (2001) *Interbull Bulletin* **27** : 13-18.