

Use of National Reliability Figures to Re-Engineer Effective Number of Records for Application in International Genetic Evaluations

Freddy Fikse¹ and Pete Sullivan²

¹*Interbull Centre, Sweden*

²*CGIL, University of Guelph, Canada*

Introduction

Analysis of national breeding values facilitates comparison of performance of bulls' daughters across countries. Today, Mace (Schaeffer, 1994) is being applied by Interbull for international genetic evaluation for production and conformation traits on a routine basis. To account for differences in precision, information coming from various countries is weighted by total number of daughters (n_d). However, this figure does not reflect all differences in precision, and it has been suggested to use other weighting factors instead.

Fikse and Banos (1997) considered using domestic reliabilities for this purpose but reliabilities were not adjusted for contributions from relatives other than daughters. Sullivan *et al.* (1998) devised a method to re-engineer effective number of records, n_e , that does account for these contributions, and thus is a potential weighting factor for international evaluations. In addition, using n_e instead of n_d for the computation of international reliabilities yielded reliabilities that better matched the original national reliabilities.

The aims of this study were to investigate the use of n_e in international genetic evaluations, and study the sensitivity of the procedure to irregularities in national reliabilities.

Material and Methods

Simulation

Two populations of equal size and structure were simulated, as described by Fikse and Banos (1999). In each generation, 300 young bulls and 30 proven bulls sired 36,000 cows. Progeny group size for young bulls was sampled from a normal distribution with mean 80 and variance 25, and each proven bull received an additional 400 progeny. The 300 young bulls resulted from random matings between 10 sires of sires and 150 dams of sires selected among candidates born in the previous generation. After generation 3, sires of sires and sires of cows were exchanged at a fixed rate of 50%.

True breeding values were sampled from a bivariate normal distribution, assuming a genetic correlation between countries of .90. True breeding values were simulated as half the sum of the parents true breeding value plus an Mendelian sampling term adjusted for the inbreeding of the parents.

For each cow, three phenotypic records were generated as the sum of contemporary group, true breeding value and permanent environmental effects, assuming a heritability and repeatability of .30 and .50, respectively. Contemporary group size was on average 20,

with a C.V. of 5%, and a minimum size of five.

At the end of each generation single trait, within population breeding values were estimated for selection of parents of the next generation. First lactation records only were used to estimate the breeding values. Effects in the model were fixed contemporary and genetic group effects, and a random animal effect.

National breeding value estimation and reliability approximation

Following the simulation breeding values were estimated within each country, using records on all three lactations. The model included fixed contemporary group and phantom parent group effects, and random animal and permanent environmental effects.

National reliabilities were computed with the procedure by Meyer (1987), in which the diagonal of the inverse of the coefficient matrix is approximated by the inverse of the diagonal element after absorbing the equations pertinent to sire, dam, progeny and contemporary group. Meyer's (1987) procedure was developed for a single trait animal model with one record per animal. To accommodate multiple correlated records ($n=3$), the equivalent number of independent observations per animal (1.91) was computed as: $DE_{yield} = k_d \times REL_{yield} / (1 - REL_{yield})$, with $REL_{yield} = n h^2 / (1 + (n - 1) r)$ (VanRaden and Wiggans, 1991).

Re-engineered effective number of daughters

We applied the method proposed by Sullivan *et al.*

(1998), to re-engineer effective numbers of record (n_e) from national reliabilities, such that Mace reliabilities are equal to national reliabilities when all genetic correlations

between countries are equal to zero. The relationship between n_e and actual number of daughters, n_d , for bulls with domestic reliability between 80% and 98% was used to obtain n_e for bulls with the maximum reliability of 99%.

Four alternative national reliabilities were considered to re-engineer effective number of records. This included the reliability calculated as described above, yielding $n_{e,cn}$, and three variations: $n_{e,bias}$ obtained after a bias B was subtracted from the original reliability; $n_{e,var}$ after variation in national reliability was increased by adding a random deviate $\sim N(0, \sqrt{B})$; and $n_{e,low h^2}$ from reliabilities computed with a heritability of .20 instead of .30. B was chosen to be 5%, corresponding to values found by Meyer (1987) and Harris and Johnson (1998^b).

International genetic evaluation

Sire breeding values were first de-regressed within country following the procedure described by Sigurdsson and Banos (1995), modified by Rozzi and Schaeffer (1996) to include the effect of mean. The approximate REML procedure of Sigurdsson *et al.* (1996) was used to estimate sire variances within each population.

International breeding values were calculated with the Mace model (Schaeffer, 1994), applying iteration on data. Estimated sire variances and the true genetic correlation were used in the Mace analysis. The approximation method described by Harris and Johnson (1998^a) was used to calculate international reliabilities.

Genetic groups in the de-regression, sire variance estimation and Mace analysis were defined according to population of origin, generation and selection path.

For each of the 15 replicates four international genetic evaluations were done. In

population 1, $n_{e,cn}$ was always used as the weighting factor, whereas for population 2 the four alternative weighting factors were used.

Results and Discussion

Table 1. Ratio n_e/n_d in population 2

Weighting factor	Mean	SD
$n_{e,cn}$	1.86	.00
$n_{e,bias}$	0.99	.00
$n_{e,var}$	1.94	.01
$n_{e,low\ h2}$	1.56	.00

Lower domestic reliabilities ($n_{e,bias}$ and $n_{e, low\ h2}$) resulted in lower ratios of n_e/n_d , as expected (Table 1). The higher ratio $n_{e,var}/n_d$ was due to the non-linear relationship between number of daughters and reliability. A unit increase in reliability requires a greater number of effective records than a unit decrease, in reliability, so the effect of equal distributions of increases and decreases in reliability was a net increase in the average $n_{e,var}$. The ratio $n_{e,cn}/n_d$ was slightly lower than DE_{milk} , as expected, due to the use of information for the estimation of contemporary group effects (Meyer, 1987).

Table 2. Relative bias^a in estimated genetic variance in population 2

Weighting factor	Mean	SD
$n_{e,cn}$	-0.06	1.29
$n_{e,bias}$	8.75	1.32
$n_{e,var}$	0.13	1.30
$n_{e,low\ h2}$	2.12	1.30

^a Relative bias computed as deviation between estimated and true genetic variance, as percentage of the true genetic variance. Mean and SD of 15 replicates

N_e 's from unbiased national reliabilities yielded empirically unbiased sire variance estimates (Table 2). Bias for $n_{e,bias}$ agreed well with the result obtained by Fikse and Banos (1999) for the same simulation alternative and n_d as the weighting factor. In both cases where n_e 's from downwards biased national reliabilities were used precision of the breeding values was underestimated, and the portion of the REML equation to account for that was overestimated.

Table 3. Prediction error variance of international breeding values on foreign scale for bulls with evaluation in only one population (mean and SD of 15 replicates)

Weighting factor	local scale		foreign scale	
$n_{e,cn}$	7.75	0.35	23.78	1.03
$n_{e,bias}$	7.75	0.34	24.83	1.27
$n_{e,var}$	7.75	0.35	23.78	1.06
$n_{e,low\ h2}$	7.75	0.35	23.84	0.88

For bulls with information in only one country, PEV on the local scale was unaffected by the choice of weighting factor. More generally, the international proofs were unaffected and, as expected, matched the original national proofs. The increased PEV on

the foreign scale for $n_{e,bias}$ (Table 3) was significant ($P < .05$), but the effect was not of practical importance. PEV for bulls with a proof in both populations differed significantly ($P < .05$) for both $n_{e,bias}$ and $n_{e,var}$, but the difference in each case was less than .25.

Table 4. Number of local bulls in top 10/100 on local scale^a

Weighting factor	population 1		population 2	
	top 10	top 100	top 10	top 100
$n_{e,cn}$	6.7	61	7.6	64
$n_{e,bias}$	7.3	65	7.1	60
$n_{e,var}$	6.7	61	7.6	63
$n_{e,low h2}$	6.8	62	7.5	63

^a Top bull lists considered both proven and young bulls

Both populations were simulated with equal genetic level, but due to chance population 1 was slightly inferior. The number of local bulls in the top bull list was therefor higher for population 2 (Table 4). The largest changes in top rankings were for $n_{e,bias}$. The ratio of sire variances changed unfavorably for population 2, resulting in relatively more top bulls from population 1 on both scales. This observation was supported by a higher foreign-scale mean for the best 10 young bulls originating from population 1, and a lower foreign-scale mean for the best 10 young bulls from population 2.

Conversion equations, estimated from young bulls in the last generation, were slightly affected, but converted breeding values for top bulls were nearly the same for all alternatives.

For young bulls with a proof in one population, the parent-average contribution to their foreign-scale predicted breeding value reduces the effect of error from prediction of

their foreign-scale Mendelian sampling term. Many parents would have proofs in both populations in the present study, because of the extensive semen exchange that was simulated. Effects of the alternative weighting factors on converted proofs may be larger when there is less semen exchange between populations, because a greater percentage of parents averages would have to be predicted in MACE based on the estimated sire variances for each country.

Table 5. International reliabilities on local and foreign scale^a for bulls with information in only one population, and difference between national and international reliabilities on local scale

Weighting factor	local scale	nat'l - int'l reliability	foreign scale
$n_{e,cn}$	92.9	.0	77.2
$n_{e,bias}$	90.5	-.4	75.4
$n_{e,var}$	92.8	.0	77.2
$n_{e,low h2}$	92.2	-.1	76.7

^a Mean over 15 replicates; SD < .05

It is clear that the alignment procedure gives international reliabilities that are close to the domestic reliabilities (Table 5). Apart from biased n_e 's, the computed reliabilities agreed well with the empirical prediction error variances, which was not the case for the currently used weighting factor: n_d .

In conclusion, the procedure to re-engineer effective number of records from domestic reliabilities works well when domestic reliabilities are unbiased. Downwards biased reliabilities yields an overestimated sire variance, and disadvantages bulls from the population with biased reliabilities. The effect is of minor importance for internationally proven bulls, and is relatively small for superior young bulls if there is substantial semen exchange between populations.

References

- Fikse, W.F. & Banos, G. 1997. Alternative weighing factors for daughter information in international genetic evaluations: progress report. *Interbull bulletin*, 16, 3-7.
- Fikse, W.F. & Banos, G. 1999. Weighting factors of daughter information in international genetic evaluation for milk production traits: effect on (co) variance components. *J. Dairy Sci.* 82 (suppl. 1)72. (Abstr.)
- Harris, B. & Johnson, D. 1998^a. Information source reliability method applied to MACE. *Interbull Bulletin* 17, 31-36.
- Harris, B. & Johnson, D. 1998^b. Approximate reliability of genetic evaluations under an animal model. *J. Dairy Sci.* 81, 2723 - 2728.
- Meyer, K. 1987. Approximate accuracy of genetic evaluation under an animal model. *Livest. Prod. Sci.* 21, 87-100.
- Rozzi, P. & Schaeffer, L.R. 1996. New deregression procedure used on type traits. Paper presented at INTERBULL workshop Nov. 25-26, Verden, Germany.
- Schaeffer, L.R. 1994. Multiple-country comparison of dairy sires. *J. Dairy Sci.* 77, 2671-2678.
- Sigurdsson, A. & Banos, G. 1995. Dependent variables in international sire evaluations. *Acta Agric. Scand. Sect. A, Anim. Sci.* 45, 209-217.
- Sigurdsson, A., Banos, G. & Philipsson, J. 1996. Estimation of genetic (co)variance components for international evaluation of dairy bulls. *Acta Agric. Scand. Sect. A, Animal Sci.* 46, 129-136.
- Sullivan, P.G., Harris, B. & Fikse, W.F. 1998. Aligning domestic and MACE reliabilities for conformation. Paper presented at INTERBULL workshop Oct. 12-13, Cremona, Italy.
- VanRaden, P.M. & Wiggans, G.R. 1991. Derivation, calculation, and use of national animal model information. *J. Dairy Sci.* 74, 2737-2746.