Effectiveness of Mace in Accounting for Differences in Heritabilities among Countries

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Introduction

Comparing breeding values of bulls proven in different countries is a difficult and complex task. The application of Multiple Across Country Evaluation (MACE) was introduced by Schaeffer in 1994 to compare breeding values of bulls at the international level. Following Schaeffer's suggestion research developed at the Interbull Centre in Uppsala led to the choice of deregressed proofs (DRPF) as the dependent variable in the model (Sigurdsson et al., 1995) as well as to the definition of a method to compute genetic correlations among countries (Sigurdsson et al., 1996). DRPF and the estimated parameters are then used in MACE to compute the International bull evaluation. Differences in heritability among countries are taken into account throughout all International evaluation programs.

Results of MACE international evaluation are considered official in several countries however in some countries more research is under way on topics like accuracies and conversion formulae computation, and heterogeneity of sire variance across years within countries.

Although the model and the applied procedures do take into account differences in heritability, little research has been done in determining what is the impact of changes in heritability in any specific country on the international evaluation system.

In june 1996 Italy changed the heritability to 0.30 from 0.25 and the same change was applied to genetic official evaluation in USA in August 1997. In a simulation study by Sigurdsson et al. (1996)

wrong parameters for heritability in a given country were assumed: no significant effect was found on PEV or international ranking of bulls. Little is known about the effect of heritability changes on genetic correlation which is an important parameter in determining comparison among countries (Schaeffer, 1994).

The objective of this study is to investigate the ability of international evaluation procedures in accounting for differences in heritability among countries, that is how the system behaves when one country changes the heritability in its own genetic evaluation.

Materials and methods

Lactation data for the June 1996 Italian official evaluation were used to compute three additional genetic evaluation with different heritabilities. Table 1 reports statistics on data used for the evaluation. Standard heritability for the official run was 0.30 with r = 0.50. Heritability ranged from 0.25 to 0.40 with r also changing from 0.50 to 0.60 to held permanent environmental effect to the same scale compared to phenotypic variance. Table 2 summarize the parameters used in the this four genetic evaluations.

Official data used in the Interbull official evaluation of August 1996 from The USA, The Netherlands and Canada were used for the international comparisons. Sire variances and genetic correlations were estimated using official programs of Interbull as described by Sigurdsson et al. (1996).

| Table 1. | Statistics of | on data | used for | official | genetic | evaluation | in Italy | in June | 1996. |
|----------|---------------|---------|----------|----------|---------|------------|----------|---------|-------|
|----------|---------------|---------|----------|----------|---------|------------|----------|---------|-------|

| Type of data | |
|----------------------------------|-----------|
| Lactation records | 7,463,860 |
| Cows | 2,929,829 |
| average lactation number | 2.47 |
| Animals | 3,482,960 |
| Bulls (10 daughters in 10 herds) | 5,617 |

Table 2. Parameters used in four different runs on Italian data.

| | h^2 | r | PE | TE |
|-------|-------|-----|-----|-----|
| ITA25 | .25 | .5 | .25 | .5 |
| ITA30 | .30 | .5 | .20 | .5 |
| ITA35 | .35 | .55 | .20 | .45 |
| ITA40 | .40 | .60 | .20 | .4 |

Results and discussion

Table 3 reports number of bulls in data files from four different countries used for sire variances and genetic correlations estimation.

Table 3. Data and sire variances on different countries used in the analysis.

| Country | N. of bulls | N. of ancestors | Phantom groups | Sire SD |
|------------|-------------|-----------------|----------------|---------|
| USA (0.25) | 24,696 | 1,525 | 38 | 21.4251 |
| NLD (0.35) | 4,143 | 562 | 45 | 15.7171 |
| CDN (0.33) | 5,773 | 758 | 39 | 23.0230 |
| ITA25 | 5,617 | 1,153 | 49 | 17.2244 |
| ITA30 | 5,617 | 1,153 | 49 | 17.4289 |
| ITA35 | 5,617 | 1,153 | 49 | 17.6888 |
| ITA40 | 5,617 | 1,153 | 49 | 17.8788 |

Table 4. Statistics on data used for correlation computation.

| Country pairs | N. of bulls | N. of ancestors | phantom groups |
|---------------|-------------|-----------------|----------------|
| USA-ITA | 703 | 358 | 10 |
| NLD-ITA | 225 | 181 | 9 |
| CDN-ITA | 408 | 249 | 11 |

Table 5. Genetic correlations between country pairs.

| Country | ITA25 | ITA30 | ITA35 | ITA40 |
|------------|--------|--------|--------|--------|
| USA (0.25) | 0.9424 | 0.9396 | 0.9350 | 0.9302 |
| NLD (0.35) | 0.9070 | 0.9027 | 0.8982 | 0.8930 |
| CDN (0.33) | 0.9395 | 0.9359 | 0.9312 | 0.9267 |

There is a clear trend in sire variances (Table 4) which increase as the heritability increases. Table 4 shown number of common bulls and structure of data used to estimate genetic correlation. Genetic correlation that tend to decrease as the heritability increases (Table 5). It is obvious that as the genetic correlations tend to decrease the number of bulls in the top list tend to increase on the country own scale and to decrease on other countries scales. Heritability changes tend to give more information on deregressed proofs compared to pedigree information and seem to differentiate countries more genetically as the weights move towards production data, specific of a given country. This may suggests that increase in accuracy of proofs and measurement of production may tend to increase differences among countries at the genetic level or may tend to increase the impact of G<E interaction. Also differences in repeatability parameters and in average number of lactations per daughter may have an influence in determining differences between countries that are not presently accounted for by deregression procedures.

Conclusion

Heritability changes do influence both sire variance and genetic correlation estimates among countries. The impact on international genetic evaluation is then evident. Different countries have different heritability and make use of different data structures, models and methods to estimate this parameter that clearly has an impact on international comparisons. This may suggest the need for guidelines on heritability estimation procedures among countries that may help in improve quality of international evaluation results. Further studies should investigate what is the impact on correlation estimates of differences in other parameters like repeatability or other random effect included in national evaluation that are not currently taken into account by the deregression procedure.

References

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