

# Predicting MACE Breeding Values on a Phantom Country Scale

*Helge Täubert, Zengting Liu and Friedrich Reinhardt*

*Vereinigte Informationssysteme Tierhaltung w.V (vit), Heideweg 1, 27283 Verden/Aller, Germany*

---

## Abstract

The estimation of international breeding values provided by INTERBULL results in MACE proofs on single trait base. These proofs can be used within each member country, but the comparison between them is not possible. A combination of several MACE proofs to a combined value helps breeders in non-Interbull member countries to select bulls from these countries disregarding national base differences.

We provide the first application of a combined MACE proof based on phantom country scale, comparing two different approaches. The country list is the PROTEJE group, which supported this project. The estimated combined proofs show an adequate trend according to single MACE proofs. Over- and underestimations, as for average proofs, cannot be seen. Double information does not bias the results. Top lists for combined proofs contain top sires of all participating countries.

---

## Introduction

International breeding value estimation provided by INTERBULL is very useful to compare bulls with different countries of origin. The used MACE-method provides proofs for each sire on each member country scale for marketing strategies within each member country. With actual 25 participating countries, the same number of different proofs is estimated for each bull. This large number makes it difficult for breeders in non-member countries, e.g. China, to compare international sires on different scales.

In the future it will not become possible for a single European country to compete against dominating global players. Only collaborations of European associations will be large and powerful enough to exist on a long term perspective. In order to put European associations on a common platform, the calculation of joint European sire proofs will be necessary to present one joint breeding value on outside European markets. This helps to support marketing strategies and enables to compete against other large breeding areas, i.e. United States of America or Canada. The development of new worldwide markets needs a powerful and compact appearance of all European countries to outside European markets, disregarding inside competition.

It has been discussed in the literature for years if a combination of INTERBULL proofs will

be helpful to calculate country-independent sire proofs. Several approaches were discussed, the most interesting and favoured approach is the 'MACE proof on a phantom country scale' (Liu, 2007; Mark, 2006; Torsell, 2007).

To combine European MACE proofs to one single European breeding value, the PROTEJE-workgroup has been founded. Goal of this project is a single European sire proof list to combine proofs on one common European scale. The method used in this project is similar to the above but used on a smaller number of countries.

## Methods

### *Average MACE proofs*

Simple approaches to combine MACE proofs are based on averaging national values. Powell and VanRaden (2002) propose a method to calculate an average proof of all single country entries of each bull, corrected for genetic standard deviation within country. This method is fast and easy to obtain, but not optimal. The most important effect is the lack of recognition of genetic correlations between countries. Daughter contributions of one bull in two different countries influence the proofs based on genetic relationships. Adding these related proofs leads to double counting of source

information and therefore to biased common values. Methods which correct for genetic standard deviation and correlation between countries have advantages. Results of an average sire proof are compared with other approaches.

### ***MACE proofs on a phantom country scale***

The computation of a combined breeding value is based on the method to calculate a breeding value for an unknown phantom country where no information is available. The most important task is in weighing single country MACE proofs, in some kind of standardisation. The approach proposed in this paper is using a standardisation of MACE-proofs of an animal according to genetic correlations and covariances:

$$\hat{a}_{im} = \mathbf{c}_m \mathbf{G}_0^{-1} \hat{\mathbf{a}}_i \quad [1]$$

where  $\hat{a}_{im}$  is the predicted proof of animal  $i$  on a phantom country scale,

$\hat{\mathbf{a}}_i$  is a vector of MACE proofs of the  $i$ -th animal from all Interbull member countries,

$\mathbf{G}_0$  is the genetic (co)variance matrix in MACE evaluation for all countries with data,

$\mathbf{c}_m$  is the vector of genetic covariances between the missing country with all countries having data in MACE evaluation.

Note that the matrix  $\mathbf{G}_0$  is not the (co)variance matrix of MACE proofs, and thus reliabilities of MACE proofs are not relevant for the prediction. The genetic covariance vector  $\mathbf{c}_m$  is:

$$\begin{aligned} \mathbf{c}_m &= \begin{bmatrix} r_{g_{m1}} \sigma_{g_m} \sigma_{g_1} & r_{g_{m2}} \sigma_{g_m} \sigma_{g_2} & \cdots & r_{g_{mn}} \sigma_{g_m} \sigma_{g_n} \end{bmatrix} \\ &= \sigma_{g_m} \begin{bmatrix} r_{g_{m1}} \sigma_{g_1} & r_{g_{m2}} \sigma_{g_2} & \cdots & r_{g_{mn}} \sigma_{g_n} \end{bmatrix} \end{aligned} \quad [2]$$

In case that the number of countries having data is one, then formula 1 is simplified to:

$$\hat{a}_{im} = r_{g_{m1}} \frac{\sigma_{g_m}}{\sigma_{g_1}} \hat{a}_i \quad [3]$$

The term  $\mathbf{c}_m \mathbf{G}_0^{-1}$  standardises MACE proofs of an animal and weights them according to genetic correlations and genetic (co)variances. Note that the standardisation of MACE proofs is not conducted on a single country basis, because of the use of matrix  $\mathbf{G}_0^{-1}$ . Genetic correlations among countries having data as well as the genetic correlations between the missing country and the others are used as weighting factors to combine MACE proofs from all the observed country scales.

Compared to the average proof approach, the proposed method is a generalization of it. The average proof is a special case of the phantom country approach, when no correlation between countries exists and correlations between single and phantom countries are one. Taking genetic correlations between countries into account automatically leads to the phantom country approach.

Reliabilities of the phantom country proofs are available using the approximation formula:

$$rel(\hat{a}_{im}) = \frac{\text{var}(\hat{a}_{im})}{\text{var}(a_{im})} \text{ which is the relationship}$$

of the (co)variance of estimated and true breeding values of bull  $i$  in phantom country  $m$ . The variance of true breeding values can be derived from

$$\text{var}(a_{im}) = \mathbf{c}_m \mathbf{G}_0^{-1} \mathbf{c}_m' \quad [4]$$

the variance of estimated breeding values from

$$\text{var}(\hat{a}_{im}) = \mathbf{c}_m \mathbf{G}_0^{-1} \text{var}(\hat{\mathbf{a}}_i) \mathbf{G}_0^{-1} \mathbf{c}_m' \quad [5]$$

The variance of estimated breeding values within countries can only be derived approximately, because only diagonal elements of the corresponding matrix are available. The covariance will be estimated using  $R_{i1}^2 R_{i2}^2 \sigma_{i2}$ , with  $R_{i1}^2$  as the reliability of the estimated single country proof of bull  $i$  in country 1. In case reliabilities are one, true and estimated breeding values are equal and the reliability of the phantom country proof will be one.

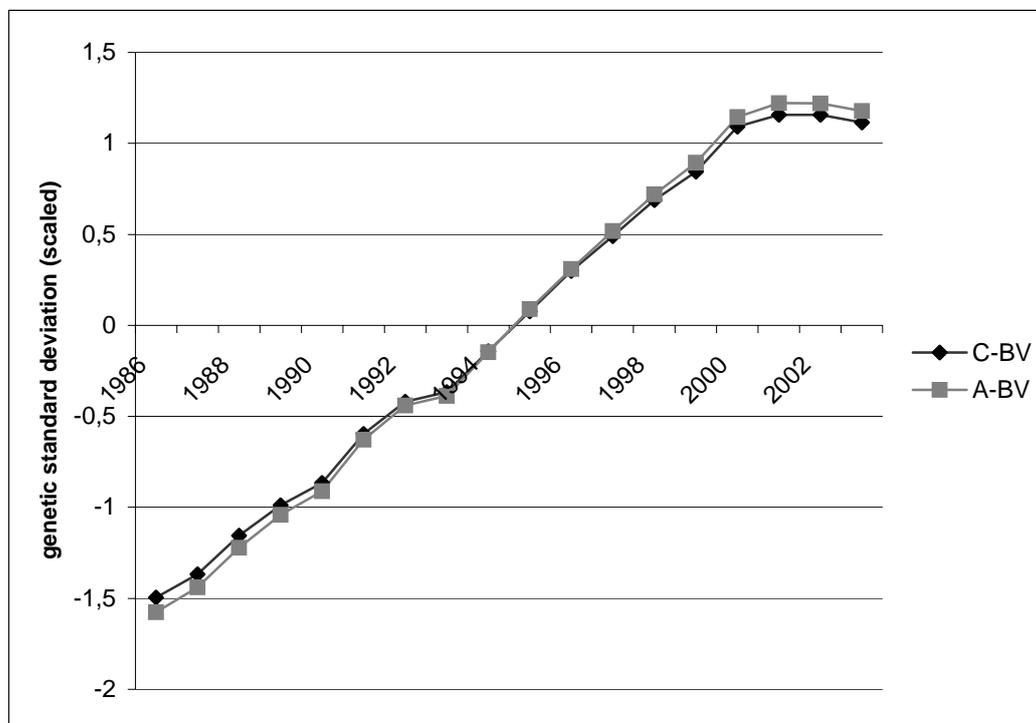
## Application of the method on MACE proofs of PROTEJE-countries

### Results and discussion

To show the properties and advantages of a combined MACE proof, single country MACE sire proofs of all 6 participating PROTEJE countries were combined. Results are shown for protein yield only, due to complexity of multi-trait indexes.

Figure 1 shows average sire proofs by birth year (genetic trend) for average (A-BV) and combined breeding value of countries participating in PROTEJE (C-BV). The development of genetic trends of average and combined proofs show clear differences. In the middle part, where breeding values are on an average scale, both procedures result in nearly equal proofs. For old and young bulls, having high negative or positive proofs, the average proof is over- and underestimated. This effect can be derived from the effect of double counting information, positive results are exaggerated as well as negative.

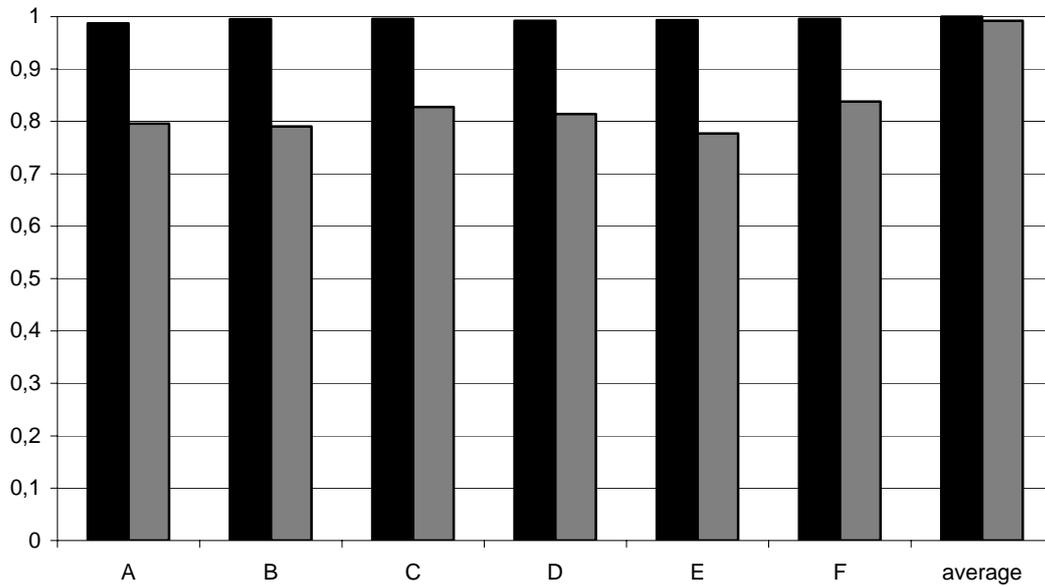
**Figure 1.** Genetic trend of average (A-BV) and combined breeding value (C-BV).



Compared to single mace proof genetic trends the combined breeding value reflects the average development of all single country proofs (results not shown). Based on increasing international exchange of bulls the development of single country proofs are more or less similar but on different scales. This is reflected by more or less parallel development of the trends. A combined value breeding value (C-BV) should reflect the same development over years. The calculated values are positioned in the centre of all curves and shows the same amount of genetic progress as all single countries.

The correlation of ranks between single country and combined proofs are shown in Figure 2. Two scenarios are presented, one value for proofs of all bulls, one for the top 1000 bulls. Correlations of rank are very high ( $> .95$ ) taking all bulls into account, for top 1000 bulls the values are lower (.77 - .83) but still on a very high level. The high rank correlation even for a sub sample of bulls is a clear sign for only small changes of rankings between single country and PROTEJE scale. Bulls with a top ranking on all single country lists are also top-ranked on a combined list.

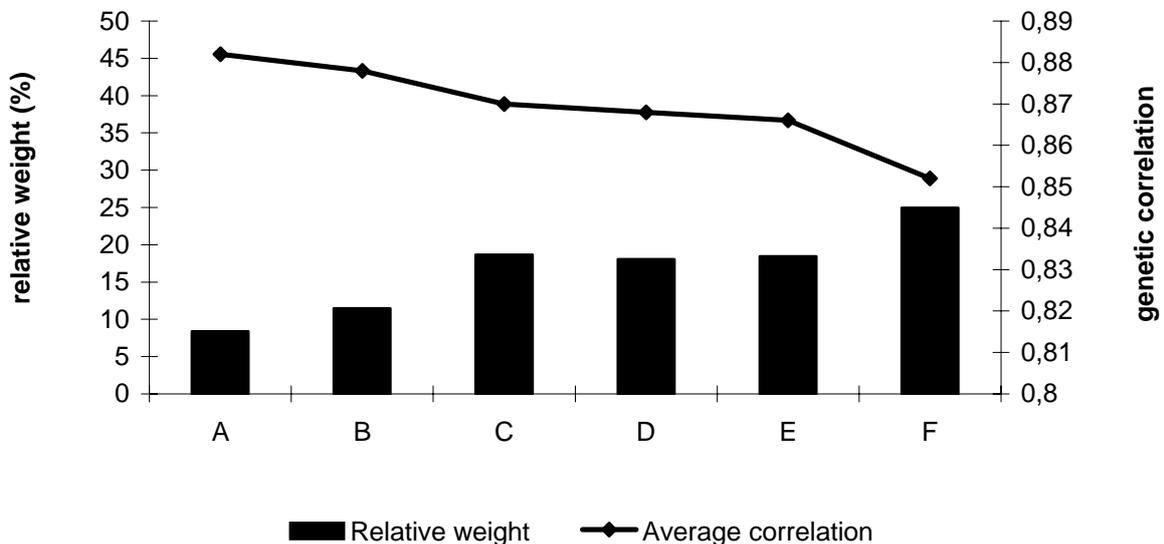
**Figure 2.** Correlation of ranks between single country and average MACE and combined PROTEJE proofs.



The correction for double counting information using the phantom scale approach can also be shown presenting the relative weight for each single country proof within the combined proof. The relative country weights for each single country proof are shown in figure 3. They are combined with presenting the average genetic correlation of each country to all the others in this index. The weight of each country does not reflect any importance of this country. They are all treated equally.

The differences in weighting proofs are caused by different genetic correlations between the countries. Countries A and B have the lowest weight in the combined proof, based not on any importance of these countries but on the high genetic correlations of these countries to all others. A proof of A is based on more common information than a proof of F. This shared information causes a loss in relative weight.

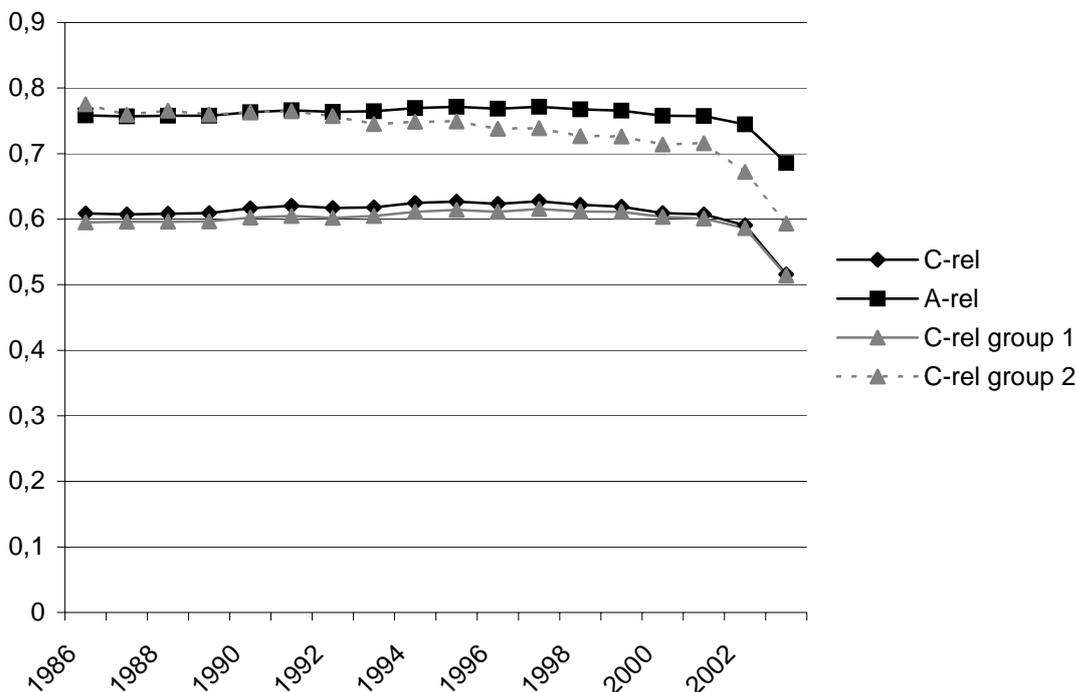
**Figure 3.** Relative weights and average genetic correlations of single country proofs.



The calculated reliabilities for average and combined proofs are shown in figure 4. The reliabilities for combined proofs are split in two different groups, one group of bulls with daughters in one country only, the second group of bulls with daughters in more than one country. It is shown, that the average reliability is higher than for combined proofs, especially for younger bulls. The two split groups show the reason for this. Bulls having daughters in one country only get lower reliabilities for combined proofs than bull with daughters in several countries. Calculating a combined proof over different countries the amount of single country information has to be accounted for. The phantom country approach takes different sources of information into account, reflected by the reliability of the total proof which is of course lower, when information within one country only was available.

Information of different countries in combination result in a higher reliability of the overall proof. The approach of an average proof does not take this information into account, resulting in high reliabilities of the average proof, although not all of these proofs are based on the same amount of information. It has to be mentioned, that the reliabilities of the combined proofs are based on the relationship of true and estimated breeding values. To calculate the variance of true breeding values all needed parameters are known, for estimated breeding values only variances (diagonal elements) are available and the off-diagonal elements have to be reconstructed (as described in a section above). This results in an underestimation of reliabilities for the combined proofs, which is small but conservative.

**Figure 4.** Reliabilities of average (A-Rel) and combined (C-Rel) proofs compared for different birth years. Reliabilities of combined proofs are shown in split groups, group 1 for bulls with daughters in one country only, group 2 for bulls having daughters on more than one country.



The representative reflection of all countries by C-BVs are shown in table 1. In this table the number of co-selected bulls between all PROTEJE countries and the C-BV top list is shown for the 1000 highest ranked bulls. The number of bulls shared on each country top 1000 list is within all single countries less than

800. The number of common bulls shared between each participating country and the common list (C-BV) is always higher than 800. This result shows clearly the good fit of the common breeding value and the single country lists which show higher differences between single countries than the combined list.

**Table 1.** Number of co-selected bulls on top 1000 lists of countries A-F and combined proofs (C-BV)

	C-BV	A	B	C	D	E	F
C-BV	1000	828	854	825	805	855	790
A		1000	769	700	736	755	755
B			1000	759	776	794	690
C				1000	753	765	693
D					1000	705	632
E						1000	756

## Conclusions

The proposed method of combining MACE sire proofs on a phantom country scale has been tested on the list of participating PROTEJE countries. The results were compared to single country proofs and an average of MACE proofs. We were able to show the properties of the phantom country approach, which on the one hand reflects all single country developments as genetic trends and number of bulls in top lists, on the other hand corrects for double counting information, which is the biggest disadvantage of an average MACE proof. It could be shown that the average MACE proof is a special case of the phantom country approach, when the genetic correlation between countries is zero. The phantom country MACE proof is useful for marketing bulls in non-INTERBULL countries, bringing all PROTEJE countries on the same scale using an index-type approach. The use of MACE proofs makes the approach independent of relationships and the PROTEJE proof can be calculated on a single bull basis. The list can easily be extended to a higher number of participating countries, as long as INTERBULL proofs are available for each country and trait. Although results presented here are valid for protein yield only, all other trait proofs provided by INTERBULL can be combined. A combined PROTEJE proof for fertility traits has already been successfully tested (data not shown), although trait definitions are not consistent within the PROTEJE group.

Further investigations need to be done in order to combine single trait PROTEJE results to overall indices, e.g. PROTEJE-production index, fertility index etc. Overall indices will represent the best tool for marketing European bulls in non-INTERBULL countries.

## Acknowledgements

We thank the European Holstein and Red Holstein Confederation (EHRC) and the PROTEJE group for their support.

## References

- Mark, T., Fikse, F., Sullivan, P.G. & VanRaden, P.M. 2007. Prediction of Genetic Correlations and International Breeding Values for Missing Traits. *J. Dairy Sci.* 90, 4805-4813.
- Powell, R.L. & VanRaden, P.M. 2002. International Dairy Bull Evaluations Express on National, Subglobal and Global Scales. *J. Dairy Sci.* 85, 1863-1868.
- Torsell, A., Jorjani, H. & Fikse, W.F. 2008. Prospects of Performing Multiple-Country Comparison of Dairy Sires for Countries not Participating in Interbull International Genetic Evaluations. *Interbull Bulletin* 37, 111-114.
- Liu, Z. 2007. MACE Proofs on Phantom Country Scale, do we double count information? *Personal communication*.