

Use of MACE Results as Input for Genomic Models

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Abstract

With genotype exchanges between countries genomic evaluations have to be based on phenotypic information from international conventional MACE evaluation. As dependent variable of genomic model, bulls' deregressed MACE EBV are usually used in SNP effect or DGV estimation. Corresponding to the deregressed proofs, EDC or daughter reliability contributed by all domestic and foreign daughters need to be calculated as well. For routine prediction of GEBV of young candidate animals, parental average or male pedigree index and their associated reliabilities need to be calculated using the most recent conventional MACE evaluation. At the Interbull Technical Workshop on Genomics held in Guelph, Canada, March 2011, a group of animal geneticists discussed on the use of MACE results as input for genomic models. The group focused on four main questions, which were then discussed in a following plenary discussion. Different statistical methods have been applied by countries to obtain the deregressed MACE proofs and their reliabilities or EDC. All member countries and Interbull centre were encouraged to exchange their experience, statistical procedures, and computer software to make the best use of conventional MACE evaluation results for own genomic prediction.

1. Introduction

As foreign genotypes become available via genotype exchange between countries, conventional MACE EBV must be used to make foreign genotyped bulls qualified for own national genomic reference population. In addition, conventional parental average (PA) or male pedigree index (mPI) are required, based on MACE EBV information, for predicting GEBV of young animals in routine genomic evaluation. These two applications highlight the importance of conventional MACE evaluation for genomic evaluation and selection using genotypes of foreign bulls. Prior to the Interbull Technical Workshop on "Establishing the Framework for International Genomic Evaluations" held in Guelph, Canada, a questionnaire had been sent out to the designated animal geneticists worldwide. The purpose of this paper was to summarise both the group and plenary discussions on the topic of using MACE results as input for genomic models and to make proposals for further developments.

2. A questionnaire

A total of 13 designated participants, chosen by Interbull centre, discussed the following questions that had been prepared and sent out by the author prior to the Workshop:

1. How do you derive the phenotypic information for genomic model using MACE evaluation?
 - a. Using DYD of bulls or yield deviations of cows derived from national conventional evaluation
 - b. Using MACE EBV as dependent variable
 - c. Deriving deregressed proofs (DRP) on an animal by animal basis
 - d. Deriving DRP by processing all animals in pedigree:
 - i. Using sire-dam pedigree
 - ii. Using sire-maternal grandsire pedigree
 - iii. Deregression based on a single country model
 - iv. Deregression based on a multi-country model as the MACE model.

2. How do you derive EDC of all bulls in MACE evaluation, including those having no daughters in your country?
 - a. Deregressing reliability values of MACE EBV using pedigree file
 - b. Using national EDC from all countries and genetic correlations between countries on a bull by bull basis.
3. What phenotypic information do you need to obtain from conventional MACE evaluation for your SNP effect or DGV estimations of reference bulls?
 - a. Deregressed MACE EBV
 - b. EDC of all bulls, also including foreign bulls without daughters in own country, or
 - c. More accurate reliability values of MACE EBV (e.g. with more digits).
4. What information do you need from conventional MACE evaluation for your prediction of GEBV of young animals?
 - a. PA or mPI
 - b. Reliability of PA or mPI
 - c. EBV information of unofficial bulls which are present in e.g. 010 file but missing in 030 file.

Because DRP of bulls from MACE evaluations are used as the dependent variable for genomic evaluation in most countries as a result of genotype exchange, it is important to address a relevant issue related to DRP: calculating EDC for all bulls in MACE evaluation that are needed to deregress MACE EBV. There have been at least two statistical methods available which can be used to derive EDC of all bulls in MACE evaluation: deregression of reliability (Harris and Johnson, 2010) and calculating MACE EDC using national EDC and genetic correlations between countries. The second approach is described below in details.

3. A statistical procedure for estimating EDC of all bulls from MACE evaluation

For a bull i we wish to calculate his EDC in own country k using his daughter information from all countries in a MACE evaluation for a given trait. A diagonal matrix, Ψ_i , can be set up using his national EDC from all the countries:

$$\Psi_i = \text{diag} \left\{ \varphi_{i1} \sigma_{e_1}^{-2} \quad \varphi_{i2} \sigma_{e_2}^{-2} \quad \cdots \quad \varphi_{im} \sigma_{e_m}^{-2} \right\} [1]$$

where φ_{ij} denotes national EDC of the i -th bull in country j ($j=1, \dots, m$), m is the number of countries in MACE evaluation, and $\sigma_{e_j}^2$ is residual variance of country j . If the bull i has no daughters in country j , then his national EDC of country j is $\varphi_{ij} = 0$. Let \mathbf{G}_0 represent genetic (co)variance matrix of all the m countries, which can be obtained by using sire standard deviations and country genetic correlations from Interbull evaluation. Matrix

$$\mathbf{C}_i = (\Psi_i + \mathbf{G}_0^{-1})^{-1} [2]$$

can be used to calculate daughter reliability of this bull in country k , R_{ik}^2 , based on daughter information from all the countries:

$$R_{ik}^2 = \mathbf{v}_k' (\mathbf{G}_0 - \mathbf{C}_i) \mathbf{v}_k / \mathbf{v}_k' \mathbf{G}_0 \mathbf{v}_k. [3]$$

where vector \mathbf{v}_k is a vector of 0s with 1 in position k . This daughter reliability is then converted to EDC with:

$$\varphi_{ik}^M = \lambda_{ik} \frac{R_{ik}^2}{1 - R_{ik}^2} [4]$$

$$\text{where } \lambda_k = \frac{4 - h_k^2}{h_k^2} [5]$$

and h_k^2 is the heritability of own country k . The MACE EDC φ_{ik}^M of the bull i in own country k scale is always greater than or at least equal to his national EDC φ_{ik} , because his foreign daughters contribute information to his MACE EBV.

Using the MACE EDC φ_{ik}^M of all bulls in MACE evaluation file and Interbull pedigree file, MACE EBV can be deregressed by treating the MACE EBV on the country k scale as a single trait. A similar deregression could also be performed for the case that the MACE EDC φ_{ik}^M are obtained by deregressing reliabilities of MACE EBV (Harris and Johnson, 2010).

4. Results of group and panel discussions

A total of 13 people representing 11 countries participated in the group discussion on the use of MACE results as input for genomic models. They debated about the four questions from the questionnaire.

None of the represented countries used MACE EBV as dependent variable in genomic models. As a lack of cow EBV from Interbull evaluation, yield deviations of cows could be considered as phenotype in national genomic evaluation. Two countries derived DRP on an animal by animal basis without processing the whole pedigree, whereas four other countries utilised the complete pedigree file to obtain DRP for bulls with daughters. One of the four countries considered sire-maternal grandsire pedigree, in contrast to the full animal pedigree used by the other three countries. All of the countries treated MACE EBV on own country scale as if they were obtained from a single country MACE model when deriving DRP, although applying a multiple-country MACE model to all MACE EBV in all country scales jointly would result in more accurate DRP.

For calculating EDC of bulls, in particular foreign bulls without daughters in own country, there seems to a need for further development and proper implementation. At least two methods have been available: Harris and Johnson's deregression of reliability and the one presented here in this paper. The EDC corresponding to MACE EBV, φ_{ik}^M , are required for SNP effect or DGV estimation and for combining conventional PA/mPI with DGV.

All the participants agreed on the need for deregressed MACE EBV for national genomic evaluation. Either EDC or reliability contributed by daughters from all countries were needed for all the bulls included in MACE conventional evaluation. In case of using MACE reliability values (Harris and Johnson 2010), more digits (at least four digits) were considered to be necessary than the current two digits.

Predicting GEBV of young candidate animals is usually done more frequently than SNP effect or DGV estimation for genomic reference population. Besides the calculation of DGV of the young candidates, conventional PA or mPI need to be obtained from the most recent MACE evaluation on a regular basis, e.g. once per month. Reliability values of PA or mPI must be calculated for the combination with DGV of the young candidates. Most of the participants were opposed to the idea of making MACE EBV of unofficial bulls available that may have become sires of the young candidates. However, an additional file containing the unofficial MACE EBV might be provided by Interbull to countries on request.

In the following panel discussion some technical details were raised and discussed on the calculation of EDC for foreign bulls and the pedigree used in deregressing MACE EBV.

5. Recommendations

A variety of statistical methods have been applied by Interbull member countries to make use of MACE evaluation for national genomic prediction. There seems to be a need to identify or develop the optimal statistical methods for deregressing MACE EBV and calculating MACE EDC or daughter reliability for all bulls, in particular for foreign bulls. PA/mPI and their associated reliabilities may be required from the most recent MACE evaluation, e.g. for more frequent GEBV prediction for young candidate animals. Interbull centre and member countries were encouraged to exchange experience, statistical methods or computer software to make the best use of conventional MACE results as input for genomic evaluation.

6. References

Harris, B.L. & Johnson, D. J. 2010. Genomic predictions for New Zealand dairy bulls and integration with national genetic evaluation. *J. Dairy Sci.* 93, 1243-1252.