

Effects of use of external information in Single-Step evaluations for linear type traits in Brown Swiss

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Abstract

The German-Austrian official genomic evaluation for conformation traits in Brown Swiss has used information from foreign bulls since its introduction in 2011. Access to genotypes of foreign bulls has been possible through the participation in the InterGenomics consortium. Initially, genotypes and de-regressed MACE breeding values of foreign bulls were integrated in a calibration set of a two-step genomic evaluation system. In April 2021, the first official genomic breeding values for conformation traits from a single-step system including foreign information were published. The objective of this work is to present an overview of the effects of the inclusion of foreign information in the new single-step system. Data from the December 2020 run of the German-Austrian official genomic evaluation for 29 conformation traits in Brown Swiss were used. Benefits from the inclusion of external MACE information were assessed in a minus 4 years validation framework and quantified in terms of validation reliability. For that, data was truncated to the status of December 2016 and evaluations were conducted with and without external MACE breeding values. The truncated dataset included 23 992 genotyped animals, from which 5 757 originated from the exchange with InterGenomics partners. External MACE breeding values were corrected to remove information on domestic daughters and then de-regressed. Final observations used in the analyses comprised yield deviations of domestic cows and de-regressed corrected MACE breeding values as pseudo-phenotype of bulls with additional foreign information. The number of foreign bulls contributing a phenotype to the evaluations ranged from 2 968 to 6 607, with an average of 5 270. Validation reliabilities with the inclusion of external MACE breeding values increased by on average 6 reliability percentage points. The gains ranged from 2 to 13 depending on the trait. In udder score, for example, the reliability increased from 0.40 to 0.45. In conclusion, integration of foreign information in the new single-step system resulted in notable increase in validation reliabilities.

Key words: genomic breeding value, cow genotypes, MACE, reliability, validation

Introduction

Genomic evaluations for Brown Swiss in Germany and Austria were introduced in 2011. The initial strategy was to genotype male animals and run a two-step genomic system. The calibration set comprised daughter proven domestic bulls and foreign bulls, whose genotypes were available through participation in the InterGenomics Consortium. The external information from foreign daughters of genotyped bulls were included in the

calibration step through the use of de-regressed MACE breeding values.

Since the introduction of genomic evaluations, all male selection candidates have been genotyped, so that the information potential on the male side is exhausted. On the female side, there was and there still is a large potential for information gain though. Therefore, projects for genotyping cows were started, which also due to decreasing genotyping costs enabled a broad female genotyping strategy.

As of December 2020, the German-Austrian Brown Swiss genotype pool comprised 68 236 genotypes in total, from which 6 055 were of calibration bulls (e.g. for udder score) and 38 972 were from females, of which 13 239 had a phenotype for linear type traits. This additional information from genotyped cows with phenotypes needed to be integrated in the evaluation system somehow. The method chosen was to include them in a single-step model, which should combine all information in the best possible way.

In April 2021 official genomic evaluations were switched from a two-step model with a bull calibration set to a single-step model including all genotypes of male and female animals. The external information from MACE was also included in the new single-step system. The objective of this study is to present an overview of the method used for integration of external MACE information and to illustrate the effects of including this external information in terms of validation reliabilities.

Materials and Methods

To perform a minus 4 years validation study, data from the official German-Austrian Brown Swiss genomic evaluation were truncated to the status of December 2016. At that time there were 23 992 genotypes in total, from which 5 272 were daughter proven bulls (e.g. in the calibration set for udder score) and 4 717 were from females, of which 962 had a phenotype for linear type traits. Furthermore, 5 757 genotypes originated from the genotype exchange within InterGenomics and 1 747 originated from earlier bilateral exchanges with the USA, Italy and Switzerland. Single-Step evaluations for 29 linear type traits were performed including or not the external information from MACE. The number of bulls with MACE EBVs ranged from 2 968 to 6 607 depending on the trait. Some of these bulls are domestic bulls that also have daughters abroad, and some are foreign bulls that also have

daughters in the domestic system. Any MACE external information from a bull was integrated, irrespective of whether the bull was genotyped or not. Validation reliabilities were estimated as the squared correlations between single-step EBVs from December 2016 and de-regressed proofs from December 2020 of the validation bulls, i.e., bulls that had no daughter information in December 2016 and at least 20 EDCs in December 2020. All Single-Step evaluations were performed using the software package MiX99 Release XI/2019 version 19.1129 (MiX99 Development Team, 2019) for solving the mixed model equations.

Adjustment to avoid double counting

Because MACE breeding values also include information from domestic daughters, an adjustment must be made to avoid double counting of this domestic information. Such adjustment was conducted following the formulas described in Guarini et al. (2019):

$$EBV^* = \frac{[(DE_M + k) \times EBV_M] - [(DE_D + k) \times EBV_D]}{(DE_M - DE_D) + k},$$

$$Rel_{EBV^*} = \frac{DE_M - DE_D}{(DE_M - DE_D) + k},$$

where EBV_M and EBV_D are the MACE EBV obtained from Interbull and the domestic EBV from a conventional run (i.e., without genomic information); DE_M and DE_D are daughter equivalents calculated from the reliabilities of the EBV_M and EBV_D ; and k is a variance ratio computed as $(4-2h^2)/h^2$.

Integration of external observations

Final observations included in the analyses were yield deviations of domestic cows and de-regressed adjusted MACE EBVs of MACE bulls (EBV^*/Rel_{EBV^*}), which were weighted by the corresponding effective number of own performances (EOP, Edel et al., 2009).

Some of the 29 linear type traits are evaluated in univariate models and some in

multivariate models. Most multivariate models include the target trait, so the pseudo-phenotypes of MACE bulls were integrated as observations for the target trait. The only exception to that is the overall conformation score (OCS), in which the multi-trait model includes the traits overall rump, udder score, feet & legs and frame. The final breeding value for OCS is then computed as an index combining the multi-trait breeding values for the four traits. Integration of external observations for OCS were the pseudo-phenotypes of MACE bulls for the four component traits. This is somewhat different than what had been done with the previous two-step model, in which the de-regressed EBVs of MACE bulls for OCS were included in the calibration step. When integrating external MACE information in the model, uniformization of trait definition across countries plays an important role. Therefore, the inclusion of pseudo-phenotypes for the four component traits in the new system allows for a better integration and the resulting single-step EBVs are based on the domestic definition of OCS.

Results & Discussion

Integration of external information from MACE resulted in a considerable amount of additional information in the system. For instance, the number of MACE bulls contributing a pseudo-phenotype for udder score was 5 686, from which 5 163 were genotyped. The number of exclusively foreign genotyped bulls ($DE_D=0$) was 2 879, from which 2 454 had $DE_M>20$. This number is almost a half of the total number of genotyped bulls with more than 20 daughters available at that time.

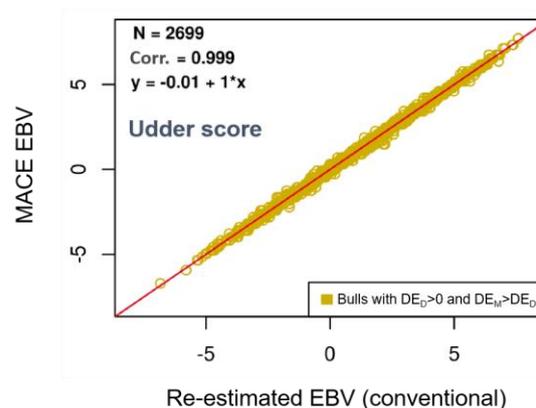


Figure 1. Original MACE EBVs against re-estimated EBVs from a conventional model with integrated external MACE information adjusted to avoid double counting (trait is udder score).

To check how well the adjustment for double counting worked, we performed evaluations with conventional models including external information and compared the EBVs of MACE bulls from these models with the original MACE EBVs. Results from these comparisons are illustrated in Figure 1 using udder score as an example. The EBVs re-estimated with the conventional model with MACE integration were pretty much the same as the original MACE EBVs. Similar results were obtained for the other traits, showing that the method used to avoid double counting worked well.

Distributions of validation reliabilities for the 29 traits with and without integration of external MACE information are presented in Figure 2 in form of boxplots. On average, the inclusion of external MACE information resulted in an increase of 6 reliability percentage points. The gains ranged from 2 to 13 depending on the trait. Differences among traits can be explained by the different amounts of external information available for each trait, different heritabilities and different base levels of validation reliability.

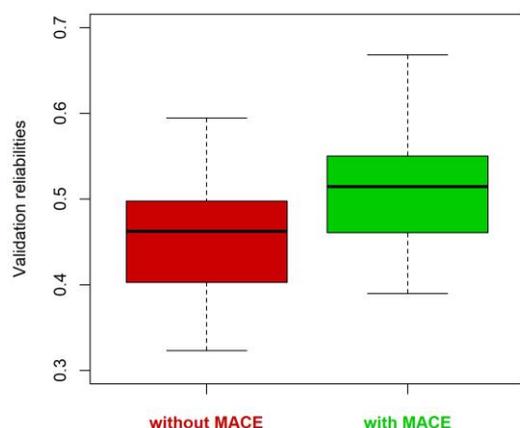


Figure 2. Distributions of validation reliabilities for the 29 linear type traits, with and without integrated external MACE information.

Validation reliabilities for the five main linear type traits with and without integration of external MACE information are presented in Table 1.

Table 1. Validation reliabilities for the 5 main linear type traits, with and without integration of external MACE information

Trait	without MACE	with MACE
Frame	0.538	0.579
Overall Rump	0.369	0.447
Feet & Legs	0.385	0.444
Udder score	0.402	0.450
OCS	0.463	0.485

Conclusions

Integration of foreign information in the new single-step system resulted in notable increase in validation reliabilities. The method used for integration seemed to work well and allowed for a better combination of information in the overall conformation score.

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