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# Influence of Foreign Genotypes on Genomic Breeding Values of National Candidates in Brown Swiss

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**ABSTRACT:** By using principal component analyses and calculating Fst statistics we found indications for a moderate subdivision of the current Brown Swiss population. Motivated by these results we started an investigation where we extended a strictly national calibration set used in genomic prediction with foreign genotypes in a stepwise manner to assess the dimension and relevance of resulting changes in predictions for national candidates. National candidates were further divided into a set of national descent and a set of partly mixed ancestry and differences between both groups were investigated. Results of this pilot study indicate that changes in genomic breeding values by augmenting the calibration group might be substantial. There are differences observable between the two groups of candidates. The mechanisms causing these effects are still not fully understood although joining international calibration sets is a common practice in genomic selection.
**Keywords:** dairy cattle; genomic breeding values; population subdivision

## Introduction

For the Brown Swiss breed the availability of international breeding values was decisive for a closer cooperation between the national breeding programs of Germany and Austria and other European and American breeding programs in the frame of the project 'Intergenomics' hosted and organized by Interbull. Within 'Intergenomics', participating countries are free to use commonly exchanged genotypes in their national genomic evaluations. It is generally assumed that increasing the calibration set improves the prediction of genomically enhanced breeding values (GEBV) of national candidates.

The aim of this preliminary study was to clarify the consequences of the inclusion of international genotypes for the German-Austrian genomic evaluation system. The present work is divided into two main parts: i) analyzing the subdivision of the current Brown Swiss population, and ii) assessment of the dimension of changes in genomic predictions derived from various calibration sets.

These analyses are part of a larger research project. The aim of this project is a better understanding of the consequences of exchanging international genotypes in genomic evaluation.

## Material and Methods

**Animals.** The analyses were done for a total number of 2,231 German-Austrian (DEA) selection candidates born in 2012 and 2013. Candidates were divided into two groups, according to the origin of their sire and/or maternal grandsire (MGS). The first group (called '*pure*') consists of 1,466 candidates whose sire and MGS were born in Germany or Austria. The second group (called '*cross*') consists of 765 candidates, where either sire or MGS or both are imported bulls.

The total number of 4,310 animals of the calibration was divided in four different groups as explained in Table 1.

**Table 1: Explanation of the differences shown in the graphs. DEA: German and Austrian, EU: Swiss and Italian, US: American and OB: Original Braunvieh breed**

| Calib Sets | Differences | | | N calib |
|---|---|---|---|---|
| **DEA** | +EU | +EU +US | +EU +US+OB | 2,049 |
| **DEA+EU** | | +US | / | 3,729 |
| **DEA+EU+US** | | | +OB | 4,171 |
| **DEA+EU+US+OB** | | | | 4,310 |

**Methods.** Population subdivision was analyzed using principal component analysis (PCA) as explained by Patterson et al. (2006) and Fst statistics (Weir and Cockerham (1984)). Based on these Fst statistics we created so-called 'neighbor joining trees'.

Genomic predictions were conducted using four different calibration sets for the two candidate sets (*pure* and *cross*). The whole process of preparation of genomic data and genomic prediction with GBLUP as currently employed in the national genomic evaluation in the DEA system was repeated for each calibration set. For details on the methodology involved see Edel et al. (2011) or Ertl et al. (2014). Results are presented for direct genomic values (DGV) and GEBV. Reliabilities presented throughout this paper are model-based reliabilities derived by direct inversion of the genomic system.

Breeding values were estimated for protein yield (PY) and stature (STA). Deregressed MACE breeding values were used as phenotypes.

In order to assess the influences of foreign genotypes on national breeding values, differences were calculated as shown in Table 1.

## Results and Discussion

**Population subdivision.** PCA and Fst statistics show that there is some degree of genetic separation detectable within the Brown Swiss population. Subpopulations within the joint set of calibration animals additionally show a varying distance to the current full candidate set (Figure 1). The populations of Germany, Italy (IT), Switzerland (CH) and the United States (US) might be defined as belonging to a main population of the Brown Swiss breed. The Original Braunvieh breed (OB) on the other hand is considerably distant from the main population (Figure 2). The EU group (IT and CH) are genetically closer to the US population. In the German-Austrian breeding program the use of American sires decreased in the past few years and candidates are genetically more distant from the US population than the DEA calibration.

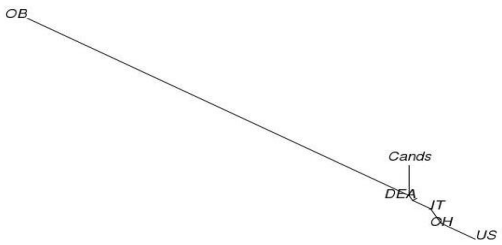


**Figure 1: Neighbor joining tree created with Fst statistics of calibration group 4, EU was divided into Switzerland and Italy and the DEA population was divided into calibration and candidates.**

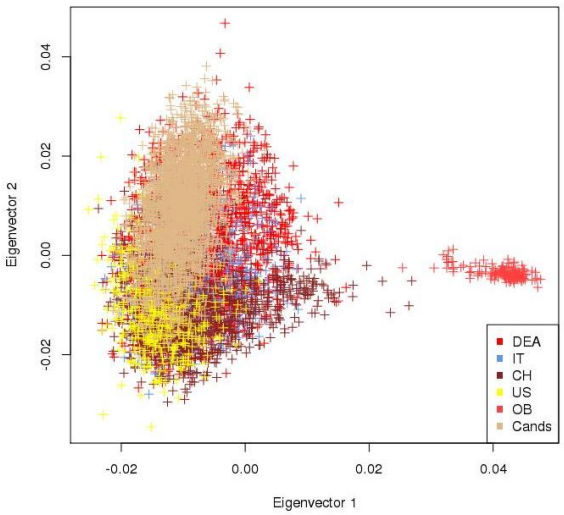


**Figure 2: First and the second eigenvector of the IBS matrix calculated for full set of calibration animals. Color separations are by country, the DEA population was divided into calibration and candidates.**

**Genomic prediction.** *DGV:* The inclusion of foreign bulls in the calibration set had a higher impact on *cross* than on *pure* candidates, with standard-deviations of differences between DGV-estimates being on average 13.7% higher for the *cross* than for *pure*. In PY the largest impact came from adding bulls from other EU-countries, whereas adding US or OB genotypes to the calibration only gave marginal effects. For STA EU-sires alone had only a small effect, which increased when US-sires were added. A directional shift of the median was observed for both traits in *cross.* Supposedly as a consequence of adding positive mendelian-sampling deviations of previously unknown sires or MGS for the *cross* group (Figure 3). Correlations between the DGV estimated with the various calibration sets were the smallest between DEA and DEA+EU+US+OB for both groups and traits (0.86/0.87).

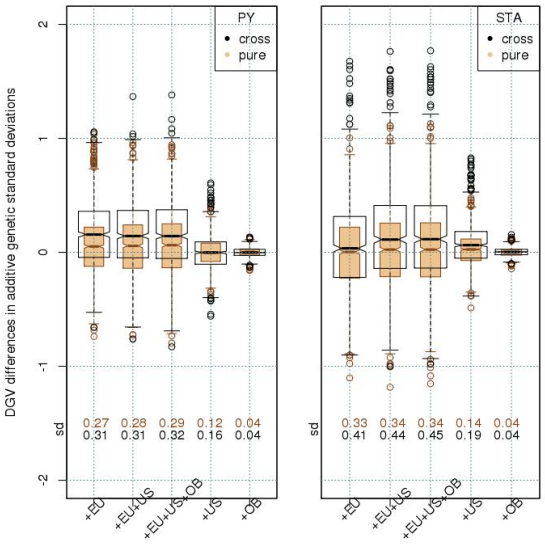


**Figure 3: Distribution of differences for candidate-datasets *pure* and *cross* when DGVs are estimated with increasingly complete subsets of all calibration animals (sd = standard deviation of differences, base variant = only national animals in calibration)**

*GEBV:* Differences between *pure* and *cross* were smaller than the differences observed in DGV. The shift in the median of the differences that was observed in the DGV can no longer be observed. Blending of mendelian-sampling information of ungenotyped ancestors seems at least partly prevent biasing effects on genomic breeding values when a relevant amount of ancestors is not genotyped (Figure 4).

*$r^2$ DGV:* The changes of the model based reliabilities for *cross* are much stronger than for *pure*. The effect of adding EU-genotypes was larger than when US-genotypes were added. Surprisingly, overall reliabilities decreased considerably, when 139 OB-genotypes were added to the calibration set (Figure 5).

*$r^2$ GEBV:* The differences of the reliability for *cross* are still larger than for *pure*, although not

as large as for the DGV. Otherwise results were similar as for the DGV (Figure 6).

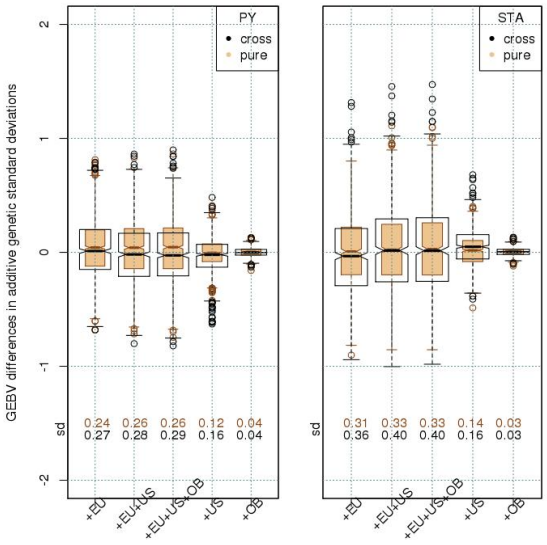


**Figure 4: Distribution of differences for candidate-datasets *pure* and *cross* when GEBVs are estimated with increasingly complete subsets of all calibration animals (sd = standard deviation of differences, base variant = only national animals in calibration)**

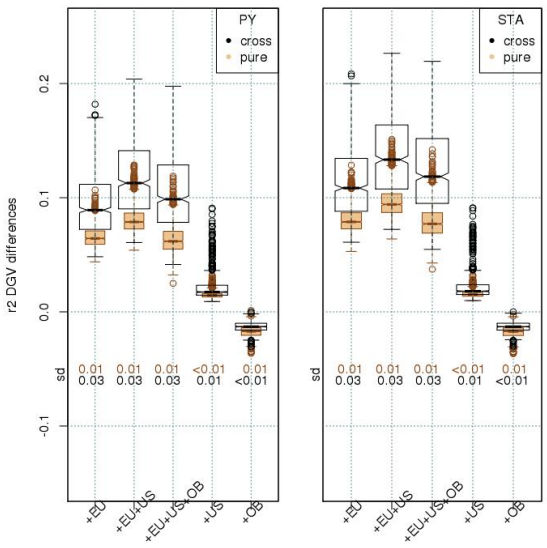


**Figure 5: Distribution of differences for candidate-datasets *pure* and *cross* when r2 of the DGVs are estimated with increasingly complete subsets of all calibration animals (sd = standard deviation of differences, base variant = only national animals in calibration)**

## Conclusion

- Inclusion of foreign genotypes in the calibration affects the breeding values of DEA candidates considerably.
- Results indicate that there might be effects beyond a simple numerical enlargement of the calibration as a consequence of population subdivision.
- Importance of foreign genotypes for DEA candidates can be ranked as follows:

  EU > US >>> OB
- An increase of the calibration set does not necessarily lead to an increase in model based reliabilities as observed in the OB case.

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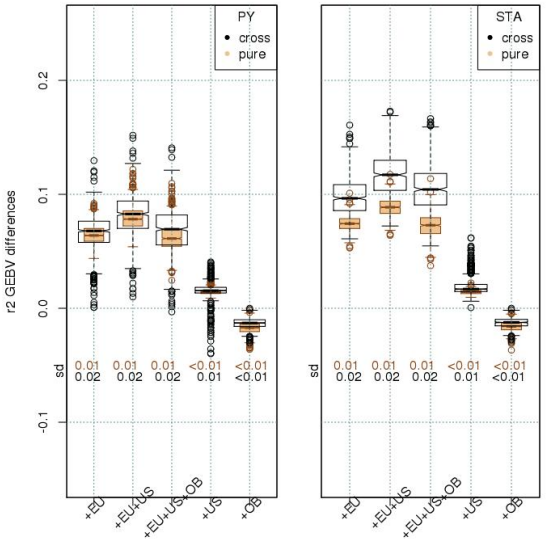


**Figure 6: Distribution of differences for candidate-datasets *pure* and *cross* when r2 of the GEBVs are estimated with increasingly complete subsets of all calibration animals (sa = additive genetic standard deviation, sd = standard deviation of differences, base variant = only national animals in calibration)**