

Comparison of National Genomic Predictions of EuroGenomics Exchanged Young Bulls

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Abstract

Since the formation of EuroGenomics Consortium in 2009, member countries exchange routinely genotypes of reference bulls for Holstein breed. By April 2013, a total of 25,903 Holstein bulls were included in EuroGenomics common bull reference population. It was of interest to investigate consistency of national genomic predictions based on the same reference population. The objective of this study was to compare national genomic predictions of the EuroGenomics member countries using common young bulls. Genotypes of all male candidates, culled or selected, born in 2010 (N=12,336) were exchanged between Germany (DEU), Nordic countries (DFS), France (FRA), and The Netherlands (NLD). National genomic breeding values and their associated reliabilities were provided by the four countries for four selected traits: protein yield, udder depth, somatic cell scores, and cow's ability to conceive. For protein yield, GEBV correlations between any two country scales reached 0.90. Similar levels of GEBV correlations were found also for udder depth and somatic cell scores. The fertility trait with lowest heritability had somewhat lower GEBV correlations between country scales. It can be clearly seen that foreign bulls had equal variance in GEBV as domestic ones. Around two thirds of top 500/1000 bulls were common for protein between DEU, DFS or NLD scales. The highly correlated national GEBV of the exchanged young bulls can be attributed to the high genetic correlations between the countries and the sharing of the common bull reference population and using the same pedigree and similar phenotypes for national genomic predictions in the EuroGenomics countries. Foreign bulls were no longer disadvantaged in ranking, compared to domestic bulls. The highly consistent national GEBV of the EuroGenomics countries confirmed a high quality of the EuroGenomics genomic predictions and increased the trust of breeders in the EuroGenomics genomic evaluations.

Key words: genomic prediction, reference population, genotype exchange

Introduction

EuroGenomics Consortium (EG) was formed in 2009 by combining genetic resources together from four European countries, Germany (DEU), France (FRA), Nordic countries (DFS) and The Netherlands (NLD), in order to improve reliability of genomic predictions. Later, Spain and Poland also joined the Consortium. By April 2013, more than 25,000 Holstein bulls were included in EG common bull reference population. With the large number of shared reference bulls, national genomic predictions of the EG countries are expected to be highly consistent. In order to verify consistency of genomic predictions between EG member countries, genotypes of all young bulls born in 2010 were exchanged, followed by national genomic

evaluations in all the member countries. The objective of this study was to compare national genomic predictions of the exchanged young bulls.

Materials and Methods

EuroGenomics bull reference population

Figure 1 shows composition of the EG common bull reference population for Holstein breed. A total of 25,903 Holstein bulls, representing 33 million cows, were included in reference population of EuroGenomics genomic predictions of milk yield in April 2013. The number of genotyped Holstein bulls with conventional EBV increased from approximately 700 in birth years 1991 to 1997

to c.a. 2200 in recent birth years from 2003 onwards. DEU and FRA, with a respective share of 33% and 21% overall years, contributed more younger reference bulls; whereas DFS and NLD with a share of 19% each had more older reference bulls. On a yearly basis, DEU share of reference bulls increased from c.a. 10% in birth years 1991 - 1997 to approximately 45% in youngest years 2003 - 2007.

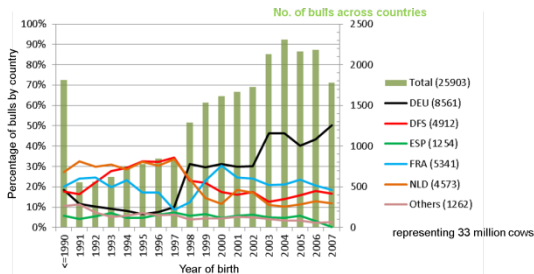


Figure 1. EuroGenomics common bull reference population for Holstein breed.

EuroGenomics national genomic models

Lund *et al.* (2011) demonstrated an increase of 11% reliability of genomic prediction by upgrading national to EG reference population. The four EG countries applied different statistical models to genomic predictions. For DEU Holstein breed, a BLUP SNP model (Liu *et al.*, 2011) was used that included a residual polygenic effect. A genomic BLUP model (GBLUP) was applied in genomic evaluation of DFS Holsteins (Lund *et al.*, 2011). In comparison to the two BLUP models assuming equal SNP marker variance, NLD used, along with a polygenic effect, a Bayes stochastic search variable selection (Calus *et al.*, 2008) that assumed most SNPs had small effects and a few had moderate or large effects. In contrast to the three genomic models essentially fitting all SNP markers, French genomic prediction was based on a BLUP QTL model (Ducrocq *et al.*, 2009) that considered about 400 QTLs jointly with a polygenic effect explaining c.a. 40% genetic variance.

For calculating combined genomic values (GEBV) of candidates, direct genomic values (DGV) were combined with male pedigree index in DEU, DFS and NLD in a posterior step, whereas the French QTL model jointly estimated and combined QTL and polygenic effects in a single step. An important fact about the EG genomic predictions was that no cows were included in the reference population due to a concern of overestimated EBV of elite cows. In addition, calculation of pedigree index did not use directly dam EBV. Both procedures prevented overestimated bull dams from distorting genomic predictions.

Phenotypes used for genomic predictions were deregressed national or MACE proofs (DRP). DFS and NLD used national DRP, when a bull had a sufficient number of national daughters. In case of DEU Holstein, MACE DRP were used whenever available and national DRP were chosen only for traits not evaluated by Interbull or for bulls without MACE evaluation. FRA used national daughter yield deviations when bulls had a sufficient number of daughters in France.

Genotype and phenotype data

In order to properly compare the national genomic predictions, genotypes of all male animals born in 2010, culled or selected, were exchanged among the four EG countries in March 2013. Pedigree of these exchanged bulls was made available as well. For all the bulls, four national GEBV and associated reliabilities were provided. Table 1 describes the genotype and GEBV data sets. Of a total of 12,336 genotypes, DEU submitted 43%, followed by FRA 34%, NLD 14% and DFS 9%. There were multiple genotype records for c.a. 300 bulls. Depending on genotype editing procedures applied in each country, e.g. minimum call rate on animal level, the number of genotyped bulls with national GEBV available varied a little between country scales.

Overall, a vast majority of the exchanged bulls received GEBV from all four countries. It is important to note that only a relatively low fraction of sires of the exchanged bulls came from the other EG countries.

Table 1. Genotype data and national GEBV of the exchanged young bulls.

Country providing genotypes					
Genotypes / %	DEU	DFS	FRA	NLD	Total
	5269	1164	4169	1734	12336
	43%	9%	34%	14%	
Country providing national GEBV					Total
DEU	4888	1031	4102	1686	11707
DFS	4809	988	4096	1661	11554
FRA	4052	1048	4163	1344	10607
NLD	4868	1159	4010	1747	11784

National genomic predictions were conducted based on phenotypic data from December 2012 conventional evaluation. Four traits included in Interbull MACE evaluation were selected, protein yield (pro) representing milk production, udder depth (ude) representing conformation, somatic cell scores (scs) representing udder health, and cow's ability to conceive (cc2) representing female fertility. For the fertility trait cc2, trait definition in FRA was cow conception rate, while DEU, DFS and NLD had interval from first to last insemination. The four selected traits covered traits with low (cc2) to medium (scs) to high (pro) heritability, so that we could investigate consistency of genomic predictions for traits with all levels of heritability.

Results and Discussion

Correlations of national GEBV

Pearson correlations of GEBV between country scales were calculated using the common exchanged bulls. Table 2 shows country correlations for protein. Interbull genetic correlations for conventional evaluations did not differ much between any pairs of countries, 0.88 to 0.90, though a larger

variation existed in heritability values, from 0.30 for FRA protein conventional evaluation with a lactation model to 0.48 and 0.50 for DEU and NLD with a test-day model. GEBV correlations between any two of DEU, DFS and NLD were around 0.90. As a result of the contrasted QTL model, FRA had lower GEBV correlations with the other countries, ranging from 0.79 with DEU or DFS to 0.85 with NLD. Despite relatively low reliability, GEBV correlations reached almost to the level of genetic correlations between the countries.

Table 2. GEBV correlations between countries for protein below diagonal (heritability on and Interbull genetic correlations above diagonal).

	DEU	DFS	FRA	NLD	Mean
DEU	0.48	0.90	0.85	0.89	0.88
DFS	0.90	0.42	0.90	0.89	0.90
FRA	0.79	0.79	0.30	0.87	0.88
NLD	0.90	0.91	0.85	0.50	0.89
Mean	0.87	0.87	0.81	0.89	

For udder depth with nearly unity country genetic correlations, GEBV from DEU, DFS or NLD were also highly correlated with correlations of 0.91 to 0.93 (Table 3). Somewhat lower GEBV correlations were found for FRA due to the model difference.

Table 3. GEBV correlations between countries for udder depth below diagonal (heritability on and genetic correlations above diagonal).

	DEU	DFS	FRA	NLD	Mean
DEU	0.27	0.98	0.97	0.98	0.98
DFS	0.93	0.37	0.98	0.98	0.98
FRA	0.78	0.78	0.36	0.98	0.98
NLD	0.91	0.92	0.82	0.40	0.98
Mean	0.87	0.88	0.79	0.88	

Similar to udder depth, somatic cell scores (Table 4) had also very high country genetic correlations between the EG countries, between 0.94 and 0.97. GEBV from DEU, DFS and NLD were found highly correlated as well with correlation around 0.90, they had slightly lower correlations with FRA GEBV.

Table 4. GEBV correlations between countries for scs below diagonal (heritability on and MACE genetic correlations above diagonal).

	DEU	DFS	FRA	NLD	Mean
DEU	0.23	0.95	0.94	0.95	0.95
DFS	0.91	0.23	0.97	0.95	0.96
FRA	0.79	0.79	0.15	0.94	0.95
NLD	0.89	0.90	0.84	0.37	0.95
Mean	0.86	0.87	0.81	0.88	

The fertility trait, cow’s ability to conceive, represented a functional trait in this study with a low heritability, ranging from 0.01 for DEU to 0.08 for NLD cc2 trait. Country genetic correlations were more variable and somewhat lower than the other traits, but GEBV correlations reached also to a reasonably high level, e.g. 0.85 of DEU with DFS or NLD (Table 5).

Table 5. GEBV correlations between countries for cc2 below diagonal (heritability on and country genetic correlations above diagonal).

	DEU	DFS	FRA	NLD	Mean
DEU	0.01	0.91	0.84	0.91	0.89
DFS	0.85	0.02	0.71	0.91	0.84
FRA	0.73	0.67	0.02	0.79	0.78
NLD	0.85	0.74	0.65	0.08	0.87
Mean	0.81	0.75	0.68	0.75	

Across the traits, NLD exhibited higher GEBV correlations with FRA, except cc2, than DEU or DFS, which may be attributed to that the NLD Bayes genomic model treated SNP effects in a more similar way as the FRA QTL model than the DEU or DFS BLUP models.

Reliability values of national GEBV

Table 6 shows GEBV reliabilities for protein by all the countries. It can be seen that the four countries differed in GEBV reliabilities, which was mostly caused by different reliability approximation methods applied, because all four countries had nearly equal level of correlation of GEBV with daughter DRP in a validation study (Lund *et al.*, 2011). There does not seem to have lower reliabilities for

foreign bulls (off-diagonals) than own bulls (on the diagonal), indicating that the foreign and domestic bulls had similar completeness of pedigree and the same reference bulls were used in the four countries. The GEBV reliability approximation methods need to be harmonised or standardised.

Table 6. National reliabilities of GEBV by owner countries on all country scales.

Country scale	Country providing genotypes			
	DEU	DFS	FRA	NLD
DEU	73.1	72.4	72.7	72.9
DFS	56.3	57.4	56.1	56.0
FRA	68.0	66.6	68.9	67.8
NLD	65.5	65.2	65.3	66.0

GEBV variance of foreign bulls

In conventional MACE evaluation foreign bulls showed lower EBV variance than own domestic bulls as a result of country genetic correlation less than unity. However, this phenomenon may no longer exist as a result of sharing the same genomic reference population and exchange of genotypes. Figures 2 and 3 show ratios of GEBV standard deviations of foreign to own bulls for all the traits on four country scales. It is very evident that foreign bulls had almost equal GEBV variation as own domestic bulls in all the national genomic predictions. It can be concluded that foreign bulls were no more disadvantaged in GEBV ranking when countries share the same reference population and exchange genotypes.

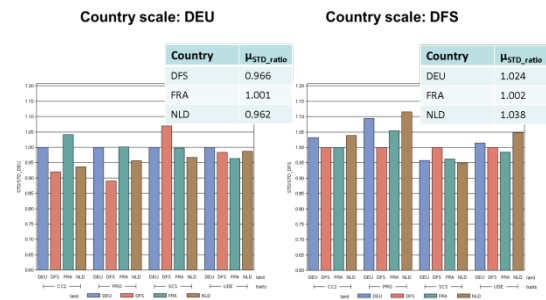


Figure 2. Ratio of GEBV standard deviations of foreign to domestic bulls on country scales DEU and DFS.

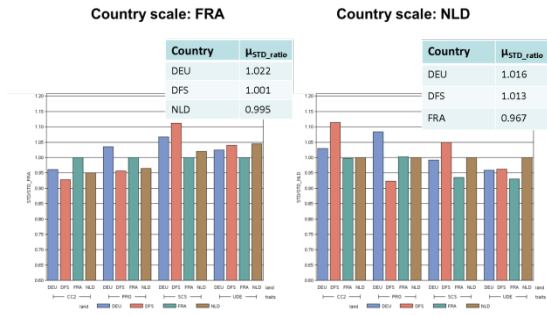


Figure 3. Ratio of GEBV standard deviations of foreign to domestic bulls on country scales FRA and NLD.

Genomic top rankings across countries

In addition to the GEBV correlations between countries, breeders may be also interested in similarity of top rankings between the country scales. Table 7 shows number of common bulls in top 500 or 1000 lists between the country scales. Around two-thirds of the top bulls were common between DEU, DFS or NLD, whereas c.a. 50% top bulls on FRA scale were also present in the other top lists.

Table 7. Number of common bulls in top 500 (below)/1000 (above diagonal) lists for protein.

Country scale	DEU	DFS	FRA	NLD
DEU		670	517	669
DFS	323		484	682
FRA	240	224		547
NLD	310	328	239	

Conclusions

National genomic predictions of the EuroGenomics countries were highly correlated despite the differences in genomic prediction models. A common reference population, same pedigree, similar phenotypes, and exclusion of bull dams from reference population and calculation of pedigree index helped make the national predictions more consistent. In contrast to conventional MACE, foreign bulls were no longer disadvantaged in ranking as they had almost equal GEBV variance as domestic bulls. Genotype exchange removed the

unfavourable regression effect for foreign bulls and avoided negative impacts of different trait definitions and low genetic correlations between countries. The highly consistent genomic predictions between the EG countries unquestionably confirmed a high quality of EG genomic prediction models and clearly increased the trust of breeders in EG genomic predictions.

Acknowledgements

EuroGenomics Consortium is kindly thanked for initialising this study. EG Steering Committee members, R. Reents, A. de Vries, S. Borchensen, X. David, E. Feddersen, and C. Patry, supported the project. Colleagues from member countries provided important technical support: H. Alkhoder, E. Pasman, T. Senftleben and F. Reinhardt from vit, Germany; B. Guldbrandtsen, U.S. Nielsen, J. Pedersen from NAV, DFS; A. Baur and V. Ducrocq from France.

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