Proceedings, 10th World Congress of Genetics Applied to Livestock Production

Implementation of the French Official Genomic Evaluation in Brown Swiss Dairy Cattle

A. Baur[1,2], **S. Fritz**[1,2], **J. Promp**[1,3], **O. Bulot**[4], **D. Boichard**[1], **V. Ducrocq**[1] and **P. Croiseau**[1].
[1]INRA GABI Jouy-en-Josas, [2]UNCEIA Paris, [3]Institut de l'Elevage Paris, [4]BGS France

ABSTRACT: The European Brown Swiss Federation, in collaboration with Interbull, founded in 2009 and managed Intergenomics, an international project to perform genomic evaluations of sires based on a joint analysis of all the Brown Swiss genotypes collected in the participating countries. In this paper, we describe how this project and the genotypes are used in France. After a long list of quality controls on animals and genotypes, the French routine genomic evaluation based on a Marker-Assisted BLUP (MA-BLUP) is carried out. Compared to the pedigree-based BLUP, genomic selection allows a gain in correlation between observed and predicted sire performance between 5.2 and 26.8%. The French genomic evaluation is now performed on 29 traits and has been official in the French Brown Swiss breed since June 2014.
Keywords: dairy cattle; genomic evaluation; MA-BLUP; Brown Swiss

Introduction

In 2009, the European Brown Swiss Federation, in collaboration with Interbull, funded an international project named Intergenomics (Jorjani et al, 2011), involving 7 countries: Austria, France, Germany, Italy, Slovenia, Switzerland, and USA. With this project, each country was able to develop and to perform routine genomic evaluations using genotypes collected in all participating countries. In this study, we present the work conducted in France in order to implement the official French Brown Swiss genomic evaluation.

For Brown Swiss cattle, we applied the same quality control and the same methodology as for the 3 other French dairy breeds which already benefit from an official genomic evaluation (Holstein, Normande, and Montbéliarde). The routine evaluation is based on a Marker-Assisted BLUP (Best Linear Unbiased Predictor) based on haplotypes consisting of Single Nucleotide Polymorphisms (SNP) selected by a variable selection method, namely the Elastic-Net (EN) (Croiseau et al,2011).

Materials and Methods

Data. To perform the genomic evaluation, 3 types of data are required: genotypes, pedigree and performances.

Genotypes come from the Intergenomics project and are collected in all participating countries. For this study, 5736 Brown Swiss animals genotyped with the Illumina Bovine SNP50 BeadChip® were available. Genotyped animals with a call rate lower than 0.95 were removed from the analysis. Only markers mapped on the UMD3.1 assembly covering the 29 bovine autosomes were used. SNP showing departure from Hardy-Weinberg equilibrium (p-value < 0.0001) or with more than 10% missing genotypes were removed. And after a quality control based on minor allele frequency (required to be >1% in at least one of the 4 evaluated breeds), 43,801 SNPs were retained.

Then, a compatibility check between the genotype of a bull and his sire and dam genotypes is performed. For this control, a panel of 500 highly informative SNP is used. An incompatibility is detected if more than 3% of SNP are found incompatible with the 2 parent genotypes or if more than 1% are found incompatible with only 1 parent genotype. In such a situation, the bull genotype is discarded for the evaluation.

Once the final set of genotyped animals is obtained, a search and correction for Mendelian errors is applied on all the retained SNP. For animals without genotypes, imputation of SNP without ambiguity is applied. When it is possible, phase information is also built. Finally, the Dagphase software (Druet et al, 2009; Browning and Browning, 2009) is used to phase all genotypes and impute all missing SNP.

Pedigree information comes from the French national database and is completed with the Interbull pedigree for young bulls. Pedigrees are traced back in the database on 4 generations.

Performances. For each bull, Interbull estimated breeding values (EBV). For young bulls which have not yet Interbull EBV, French official EBV are used. These EBV are deregressed in order to be included in the evaluation as phenotypes. Deregressed proofs were obtained as in Garrick et al (2011), except that weights w_i were computed assuming the whole genetic variance was explained by the SNPs. This leads to $w_i = \frac{(1-h^2)r_i^2}{h^2(1-r_i^2)}$, with r_i^2 being the reliability of the estimated breeding value (EBV) of bull i due to progeny information only. The expectation of the bull EBV without progeny information is the pedigree index (PI), leading to the following deregressed proof

$$y = PI + \frac{EBV - PI}{r^2}.$$

Evaluation Method. In the French genomic evaluation for Brown Swiss, 29 traits are evaluated: 5 production traits (milk, fat and protein yields and contents), 18 type traits (udder depth, rear udder attachment height, fore udder attachment, udder support, rear udder attachment width, chest width, body depth, rump width, rear teat placement, rear leg side view, stature, rump angle, deep heel, teat placement, teat length, angularity, foot angle and overall feet and leg score), 3 fertility traits (conception rate for cows, heifer conception rate and interval calving 1st AI) and 3 functional traits (milk somatic cell SCS, clinical mastitis MAS, direct longevity DLO).

In order to implement the genomic evaluation, a list of SNP was first selected. These SNP were then combined into haplotypes and a MA-BLUP estimation of the effect of these haplotypes and of a residual polygenic component was carried out. For the SNP selection step, several approaches were tested (see Ducrocq et al., this congress). The Elastic-Net (EN) was retained for its good performances and its computational convenience. SNP retained by EN were then grouped into haplotypes of 3 to 5 SNP (Boichard et al*.,* 2012). Due to computational constraints on the number of haplotype effects to estimate, the total number of SNP selected by EN was forced to be lower than 2500 SNP. For the SNP pre-selection with EN, only genotyped bulls with a phenotype were used. Out of the 5736 genotyped animals, only about 3000 had deregressed proofs depending on the trait (including the 90 French progeny tested bulls). The training population comprised from 2327 to 2487 animals according to the trait and was composed by all bulls born at least 4 years before the youngest genotyped bull with daughter performances. The validation population was composed of the other bulls and contained between 417 and 456 animals depending on the trait.

The Marker-Assisted BLUP evaluation was applied to estimate the haplotype effects. The genetics parameters were estimated from the same datasets using an AIREML procedure. In the Marker-Assisted BLUP, an optimal residual polygenic component between 10% and 50% was retained according to the traits. Prediction equations were derived using the training population and GEBV were estimated for the validation population based on these prediction equations (Figure 1). Then, a weighted Pearson correlation between GEBV and deregressed proofs was calculated for each trait, where the weight was the Equivalent Daughter Contribution (EDC, Peers, 1996) attached to each performance. Note that the correlations were not standardized for the reliability of the deregressed proofs for each trait.

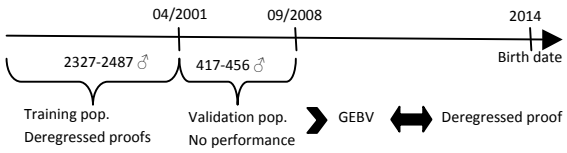

Figure 1. Schematic representation of to the validation test comparing estimated and observed deregressed proofs

Results and Discussion.

Table 2 presents the total number of SNP selected by EN and the number of haplotypes formed. The total number of SNP selected by EN varied between 195 for direct longevity and 2205 for milk yield. For most traits, it was around 2000 SNP. The number of haplotypes formed varied between 151 for direct longevity and 896 for milk yield. For direct longevity, the small number of SNP retained by EN can be explained by the low heritability of this trait and a training population with many bulls with a small reliability of the EBV. Moreover, genetic correlations between participating countries for direct longevity is lower than for the others traits, which implies that bull performances on foreign scales contribute less to prediction equations.

Table 2. Total number of SNP selected by Elastic Net and number of haplotypes formed for each trait.

Trait	SNP	Haplotypes
Milk yield	2205	896
Fat	2056	835
Protein	2074	839
Somatic Cells Score	2158	883
Clinical Mastitis	1895	761
Cow Conception Rate	1314	594
Interval Calving 1st AI	2112	835
Direct longevity	195	151
Stature	2140	868
Udder Depth	2087	857
Feet and legs	797	444
Average	1848	763

Table 3 presents for 11 traits the weighted correlation between deregressed proofs and GEBV obtained from our genomic evaluation. It also presents the corresponding correlations obtained with pedigree-based BLUP. We first observe that genomic selection improved correlations whatever the trait. Genomic selection allowed a gain in correlation between 5.2 and 26.8%. For example, if we compare these correlations with those of Montbéliarde, another French breed with a much larger national population (see Ducrocq, in this congress), genomic selection in French Brown Swiss had nearly the same efficiency. This is not surprising because the training and validation populations had comparable size. Such a result

was achieved for a breed with only 90 French bulls in the reference, thanks to the international collaboration. Another appealing feature is that MA-BLUP is really fast even for a very large population.

Table 3. Weighted correlation between GEBV and deregressed proofs for French Brown Swiss.

Trait	Pedigree BLUP	MA-BLUP
Milk yield	0,333	0,550
Fat	0,410	0,627
Protein	0,433	0,603
Somatic Cells Score	0,493	0,622
Clinical Mastitis	0,306	0,437
Cow Conception Rate	0,290	0,345
Interval Calving 1st AI	0,384	0,591
Direct longevity	0,368	0,420
Stature	0,259	0,527
Udder Depth	0,447	0,584
Feet and Legs	0,432	0,587
Average	0.401	0.547

The implementation of the genomic evaluation in French Brown Swiss allows BGS (the French Brown Swiss Association) a better choice of bulls because of a higher (G)EBV reliability and a larger number of genomically evaluated bulls. In the future, genotypes will continue to be exchanged within the Intergenomics consortium. A large population of bulls will be evaluated and available for the French selection scheme.

Moreover, this large reference population made possible the use of low density genotypes, as for the 3 other French breeds with a genomic evaluation. This cheaper chip allows to increase the number of genotyped animals (especially females) and to broaden the population screened.

For being in the reference population, a bull must have a genotype and a performance. The difficulty with such international reference populations is the implementation of a genomic evaluation for new traits: if a country wants to include selection for a new trait, an international agreement must be obtained and Interbull must implement it at first into an international polygenic evaluation.

Conclusion

This study described how the French genomic evaluation has been implementing for the French Brown Swiss cattle breed. The chosen methodology is a Marker-Assisted BLUP applied to estimate haplotype effects formed by a maximum of 2500 maximum SNP selected by Elastic Net.

Genomic selection allowed a substantial gain in correlation between estimated GEBV and deregressed proofs. With only 90 French bulls in the training population, genomic evaluation performed well thanks to the collaboration within the Intergenomics international project.

France has now implemented genomic evaluation for the French Brown Swiss breed, a minor breed in the country. Three times per year, 29 traits have been routinely evaluated and officially published since June 2014.

Acknowledgements

This work was performed within the Mixed Technology Unit “Génétique, Génomique et Gestion de populations bovines” (UMT3G), located at INRA Jouy-en-Josas.

Literature Cited

Boichard, D., Guillaume, F., Baur, A., et al. (2012). Anim. Prod. Sci. 52: 115-120.

Browning, B.L. and Browning, S.R. (2009) Am J Hum Genet 84, 210-223.

Croiseau, P., Legarra, A., Guillaume, F., et al (2011) Genet. Res. 93, 409-417.

Druet, T. and Georges, M. (2009). Genetics. 184, 189-198.

Garrick, D.J., Taylor, J.F., and Fernando, R.L. (2009) Genet Sel Evol 41:55

Jorjani, H., Jakobsen, J., Nilforooshan, M.A., et al (2011) Interbull bull. 43

Peers, I. (1996). Ed. The Falmer Press. Washington, DC.