A single-step, multiple-trait genomic evaluation model increase the accuracy for suckling performance in beef cows

A. Michenet[1,2], D Boichon[3], R Saintilan[2,4], F Phocas[5] and E Venot[5]

[1]Interbull, Uppsala, Sweden
Corresponding Author : alexis.michenet@slu.se
[2]ALLICE, 149 rue de Bercy, 75012 Paris, France
[3]AURIVA, Les Nauzes, 81580 Soual, France
[4]GenEval, 78350 Jouy en Josas, France
[5]GABI, INRA, AgroParisTech, Université Paris-Saclay, 78350 Jouy en Josas, France

Abstract

Suckling performance of beef cows is of major importance for the income of livestock farmers. This trait is estimated with commercial farm data recording by the maternal genetic effect on weaning weight which is lowly heritable (0.09). In the Blonde d'Aquitaine breed, the breeding program includes a progeny testing station where eight sires are tested each year. Milk yield is recorded by the weigh-suckle-weigh technique on daughters and constitute a heritable (0.40) early selection criterion for bulls intended for artificial insemination. A dataset with 2403 milk yield records collected in station and 137,943 weaning weights from field records was used to genetic parameters in relation with suckling performance. A strong genetic correlation (0.75) was obtained and allowed performing a multiple-trait evaluation model. BLUP animal model and single-step genomic BLUP models were tested and theoretical average accuracies on a population of 813 candidates for selection were compared.

The reference population was made of 1 039 animals phenotyped and genotyped or imputed in 50K SNP density. Best correlations (0.20 to 0.30) were obtained with candidates that were moderately or strongly related to the station reference population. For other cases, accuracies were below 0.15.

The combination of farm and station performance is a good way to increase accuracy of candidate for selection, in particular for animal related to the reference population. The single-step GBLUP including performance from many non-genotyped animals leads to a more efficient use of maternal EBV in beef cattle breeding programs. In the near future, this method associated with an increase of genotyped animals will help to improve breeding choice accuracy and genetic progress.

Introduction

Considering maternal traits in beef cattle selection programs is of major importance because these traits directly impacts the income of the breeders (Roughsedge *et al.*, 2008). It concerns in particular the suckling performance of the cow-calf pair which influences the calf growth and weaning weight (Phocas *et al.*, 1998). The performance record is difficult to establish at farm level and there is a lack of efficient selection tools to improve such traits.

In Blonde d'Aquitaine breed, the French artificial insemination bulls selection program relies on progeny testing in station to evaluate the primiparous daughters' performance, since the mid-eighties. The weigh-suckle-weigh technique applied to the daughters' calves of 8 AI candidates for selection are evaluated for milk yield (MY) each year. Recording phenotypes on testing station following a strict protocol (homogeneous farming conditions, limited number of technicians that record the phenotypes) leads to high heritability estimates (0.35), (Michenet *et al.*, 2016). Moreover, the French official farm indexation allowed evaluating hundreds of natural service bulls for their maternal genetic effects on weaning weight (WW), since the mid-nineties. The heritability of this trait is lower (0.10) because it is a more complex trait accounting for milk quality, maternal and calf behaviours, and impacted a lot by the environmental conditions.

Based on a reference population of 2327 genotyped animals in Blonde d'Aquitaine breed (Venot *et al.*, 2016), the new statistical methodologies provides now solutions to develop efficient genomic selection for these complex traits.

This study was focused on two objectives: the first was to estimate the genetic correlation between maternal weaning weight recorded on farm and milk yield recorded in station, and then the second objective was to assess the interest of a single-step and multiple-trait genomic model for suckling performance to estimate the breeding values for maternal traits the most accurately possible.

Materials and methods

Phenotypes

The weigh-suckle-weigh technique was used to assess the milk yield in progeny testing station (Pabiou, 2005). A total of 2403 females were recorded from 1996 to 2014. Measurements were performed in the morning and evening on the 60th and 120th days after calving. MY was estimated from the weighted average of the 60-day measurement and 120-day measurement, with respective weightings of one-third and two-thirds. The average MY was 5.66 kg, with a standard deviation of 1.46 kg.

These data overlapped farm data since some primiparous daughters recorded in station for MY were recorded on farm for their own weaning weight (WW) and WW of their descendants. The field data considered in this study was collected from the 484 largest herds (contemporary group sizes above 10) out of the 1122 herds of birth for the 2403 females recorded in station. A total of 137,943 WW records were retained for the analysis. The average WW (standardized at 210 days) was 285.4 kg, with a standard deviation of 45.1 kg.

Genotypes

The station reference population was made up of 1155 females recorded for MY from 2005 to 2014. They were genotyped either with the Bovine SNP50 BeadChip® medium-density chip with 54,000 single nucleotide polymorphisms (SNP) (223 females) or the EuroG10K BeadChip® low-density chip with 10,000 SNP (933 females). Among the farm reference population, 1039 animals with weaning weight data collected in the 484 herds of the current study were genotyped as followed: 62 AI sires with the Bovine HD BeadChip®, 650 bulls with the Bovine SNP50 BeadChip® and 327 animals with the EuroG10K BeadChip®. In addition, a population of 813 young candidates for selection were genotyped with the Bovine SNP50 BeadChip®. After quality controls that included a call rate higher than 90% and a Hardy-Weinberg equilibrium test (P-value > 10-4), 43,801 SNP from the medium-density chip were retained, and 7,660

SNP for the low-density chip. A total of 2690 medium-density genotypes were used for the imputation of the female genotypes from low to medium density with BEAGLE 3.3.0 software (Browning and Browning, 2007). Allelic imputation error rates were estimated at 1.3% (Saintilan *et al.*, 2014).

The population of the 813 young bulls candidates for selection only have their own WW recorded on-farm. The birth years of the candidates and the degree of their relationship with the station reference population is described in Figure 1. A kinship analysis was performed to split the candidate population into three categories: 463 male progeny of sires tested on the station which are strongly related to the reference population, 189 candidates having one grandsire tested on the station which are moderately related to the reference population, and the remaining 161 which have a low relationship to the reference population.

Models

As a reference for accuracies of MY and WW, a pedigree BLUP-animal models was performed with univariate analysis. The model for MY only considered the animal breeding values as a random effect. The model for WW performance (y) involved the calf's direct genetic effect, the maternal genetic effect and the permanent environment effect of its dam as follows: $y = X\beta + Z_1u + Z_2m + Z_3p + e$ where **y**, ², **u**, **m**, **p** and ***e*** are the vectors of performance, fixed effect, direct genetic effect, maternal genetic effect, permanent environmental random effect and the residuals of the model. **X**, $\mathbf{Z}_1$, $\mathbf{Z}_2$ and $\mathbf{Z}_3$ are the incidence matrices for ², **u**, **m** and **p** respectively. Hereafter, the direct genetic effect on WW is named WWd and the maternal genetic effect WWm.

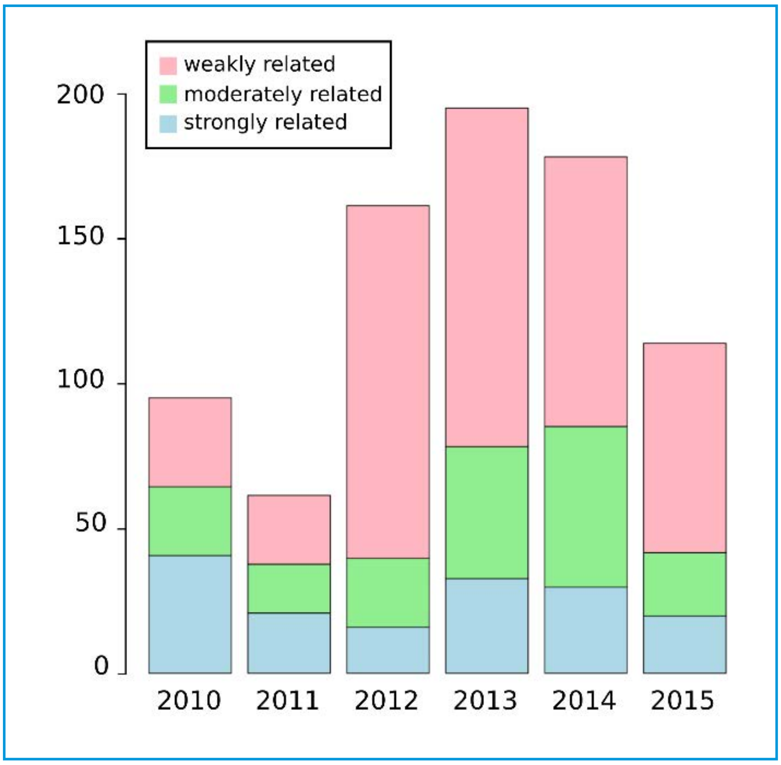

Figure 1. Distribution of the population of candidates for selection according to their birth year and their degree of relationship with the station reference population.

The fixed effects were the contemporary group, whether the calving was assisted (hard pull or caesarian) or not, and the age of the heifer at calving as a covariable for MY. The calf contemporary group (combination of birth year, herd and calf sex), the calf birth season and its dam parity were considered for WW.

The two traits were combined in a multiple-trait pedigree BLUP with maternal effects. A single-step genomic BLUP (ssGBLUP) was used to combine pedigree information for all phenotyped animals and genomic information for the subset of animals with genotypes (Aguilar *et al.* 2010).

A population of 813 young bulls candidate to selection was used to estimate the potential advantage of combining two kinds of phenotypic information for increasing EBV accuracies for suckling performance. Results from the univariate pedigree BLUP were compared to the multiple-trait model pedigree BLUP and ssGBLUP. The BLUPF90 software package (Misztal *et al.*, 2002) was used to estimate genetic parameters by AIREML and to solve pedigree BLUP and ssGBLUP.

Results and discussion

Genetic parameters

With more data and considering an animal model, the heritability estimate of MY was higher (0.41) than the earlier estimate (0.30) from data collected in the same station (Phocas and Sapa, 2004). The study of MacNeil and Mott (2006) also provided a lower heritability of 0.25 for MY recorded in station for 403 Hereford cows. For WWd and Wwm, the heritabilities are in accordance with the estimates obtained in the same breed (Phocas and Laloë, 2004) and also in Hereford (Torres-Vázquez and Spangler, 2016).

A negative genetic correlation (-0.39) was estimated between direct and maternal effects on WW. However, the genetic correlation between WWd and MY was estimated to be null. A strong (0.75) genetic correlation was computed between MY and Wwm, in agreement with the MacNeil and Mott (2006) study. Even if MY is a good estimator of suckling performance, it does not take into account the quality of the milk that could impact WWm. Meyer *et al.* (1994) also showed that MY was the main factor affecting WWm and was not correlated with WWd. Negative genetic correlations between direct and maternal effects on WW are frequently seen in literature (Vargas *et al.*, 2014). These negative estimates are more likely to be statistical artefact rather than a biological antagonism due to the difficulty of estimating covariances without bias in maternal effect models (Robinson *et al.*, 1996, Dodenhoff *et al.*, 1999, Clément *et al.*, 2001).

The study of Michenet *et al.* (2016) highlighted several common quantitative trait loci detected for MY and WWm. These results are in accordance with the strong genetic correlation estimated between the two traits.

Table 1. Heritabilities and genetic correlations of milk yield (MY), direct (WWd) and maternal (WWm) genetic effects on weaning weight.

	MY	WWd	WWm
MY	**0.41** (0.07)[1]	0.01 (0.12)	0.75 (0.10)
WWd		**0.30** (0.02)	-0.39 (0.04)
WWm			**0.09** (0.01)

[1] Heritabilities in bold on the diagonal, genetic correlations above the diagonal (standard errors in brackets)

Accuracy of multiple-trait EBV

A multiple-trait model combining correlated traits is supposed to increase accurracy. On the figure 2, the mean accuracy of the EBV of candidates for selection were plotted for MY and WWm comparing multi-trait model and single trait models.

The accuracy of EBV for MY in the single-trait BLUP varied greatly depending on the degree of relationship of the candidates to the reference population, from 0.02 for weak relationships to 0.18 for strong relationships with the reference population. The average gain in EBV accuracy for MY in a multiple-trait BLUP was +0.05 across the three categories of candidates. The accuracy of the BLUP-EBV for WWm (0.16) was on average higher than for BLUP-MY (0.09). This difference is due to th fact that WW records were available for at least one parent of the candidates whatever its category. In consequence, the increase in the accuracy of the BLUP-EBV for WWm when considering a multiple-trait model was low. The candidates strongly related to the reference population had the highest gain (+0.03).

According to the reference population size, the heritability of the trait, and the effective population size, genomic information is theoretically expected to increase the accuracy of EBV in comparison to the pedigree BLUP (Goddard and Hayes, 2009). The gain in accuracy was of the same order when integrating genomic infornation into the single-trait ssGBLUP across the three categories of candidates (+0.07 for MY, +0.02 for Wwm). These gains were comparable to those obtained in Angus breed (Lourenco *et al.*, 2015) with a reference population that includes 1628 bulls.

The multiple-trait ssGBLUP model gace the best results in term of accuracy. The gain in EBV accuracy compared to the multiple-trait BLUP was on average +0.07 for MY and +0.05 for WWm across the categories of candidates. Moreover, the average accuracy gain was +0.05 for MY compared to the single-trait ssGBLUP EBV. Concerning WWm, the gain was +0.06 for candidates which were strongly related to the station reference population while it was only +0.03 for the two other categories of candidates.

Conclusion

Increase in accuracy of EBV for suckling performance is possible pooling correlated traits with differents heeritabilities (a low heritable trait (WWm) and a higher heritable trait (MY)) from different origins (recorded on farm and on progeny testing station).

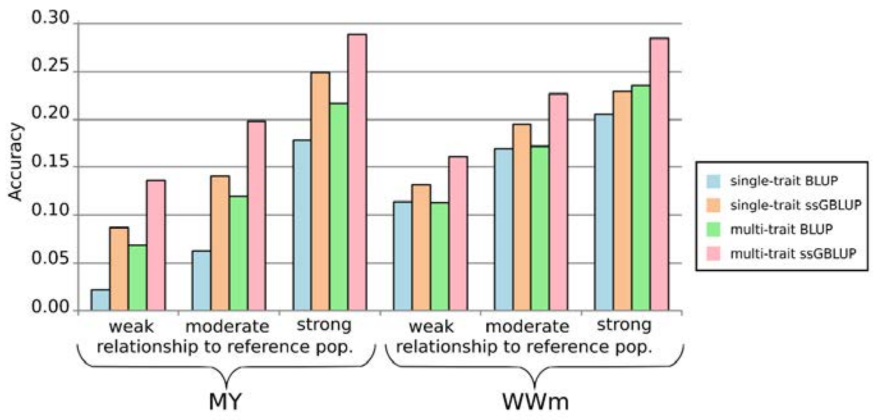

Figure 2. Mean accuracy of EBV for MY and WWm for the candidates according to their degree of relationship to the station reference population and the genetic evaluation model: single-trait pedigree BLUP or ssGBLUP and multi-trait pedigree BLUP or ssGBLUP models.

These results are confirmed by other studies with pedigree-BLUP models (Jia *et al.*, 2012 and Ismael *et al.*, 2017) for other performance traits.

The single-step and multi-trait genomic BLUP model is the one leading to the highest EBV accuracies for maternal traits. However, for animals that are only weakly related to the station reference population, accuracy of maternal EBV remained very low (below 0.15). The multi-trait ssGBLUP provided EBV accuracies for MY and WWm in average between 0.20 and 0.30 for the populations of candidates for selection which are moderately or strongly related to the station reference population. These categories of young bulls represent half of the candidate population in the breeding programmes now. These results paved the way for an efficient use of the maternal EBV in beef cattle breeding programmes using multi-trait ssGBLUP.

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