



Integration of external estimated breeding values and associated reliabilities using correlations among traits and effects

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ABSTRACT

Based on a Bayesian view of linear mixed models, several studies showed the possibilities to integrate estimated breeding values (EBV) and associated reliabilities (REL) provided by genetic evaluations performed outside a given evaluation system into this genetic evaluation. Hereafter, the term “internal” refers to this given genetic evaluation system, and the term “external” refers to all other genetic evaluations performed outside the internal evaluation system. Bayesian approaches integrate external information (i.e., external EBV and associated REL) by altering both the mean and (co)variance of the prior distributions of the additive genetic effects based on the knowledge of this external information. Extensions of the Bayesian approaches to multivariate settings are interesting because external information expressed on other scales, measurement units, or trait definitions, or associated with different heritabilities and genetic parameters than the internal traits, could be integrated into a multivariate genetic evaluation without the need to convert external information to the internal traits. Therefore, the aim of this study was to test the integration of external EBV and associated REL, expressed on a 305-d basis and genetically correlated with a trait of interest, into a multivariate genetic evaluation using a random regression test-day model for the trait of interest. The approach we used was a multivariate Bayesian approach. Results showed that the integration of external information led to a genetic evaluation for the trait of interest for, at least, animals associated with external information, as accurate as a bivariate evaluation including all available phenotypic information. In conclusion, the multivariate

Bayesian approaches have the potential to integrate external information correlated with the internal phenotypic traits, and potentially to the different random regressions, into a multivariate genetic evaluation. This allows the use of different scales, heritabilities, variance components, measurement units, or trait definitions for external and internal traits. However, one possible issue for implementing multivariate Bayesian approaches could be the availability or estimation of genetic correlations between external and internal traits.

Key words: correlated external information, integration, random regression model

INTRODUCTION

A combination of phenotypic data into joint evaluations would be theoretically optimal, but often this is not possible for different reasons (Powell and Sieber, 1992). Several studies have shown the possibilities of combining information [i.e., EBV and associated reliabilities (**REL**); hereafter called “external information”] provided by genetic evaluations performed outside a given evaluation system with genealogical and phenotypic data in a genetic evaluation at an internal level to mimic a joint genetic evaluation. One of the proposed methods is based on a Bayesian view of the linear (mixed) models. This method consists of altering both the mean and (co)variance of the prior distributions of the additive genetic effects based on the knowledge of external information [i.e., based on available external EBV and REL (e.g., Quaas and Zhang, 2006; Legarra et al., 2007; Vandenplas et al., 2014)]. The extension of the Bayesian method to multivariate settings allows the integration of external information into an internal multivariate genetic evaluation (Quaas and Zhang, 2006; Vandenplas et al., 2013). Therefore, the underlying models could be set up to represent different traits for external information and internal phenotypic data exploiting genetic correlations among them in a multivariate setting. Also, the assumed models associated with external information and internal phenotypic data

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could be different from other correlated genetic effects (e.g., regression effects).

Furthermore, the extension to multivariate Bayesian approaches leads them to share the general features and advantages of multivariate genetic evaluations. For example, multivariate evaluations allow the prediction of EBV for traits of interest for which phenotypes could be difficult, or impossible, to collect. They can also improve accuracy of EBV for the different traits under some conditions (Schaeffer, 1994; Mrode, 2005). Thereby, integration of correlated external information into a multivariate genetic evaluation could be interesting to solve different technical issues. First, accuracy of internal evaluations may be low for some traits of interest, whereas accurate external evaluations for similar traits or for correlated traits are routinely performed, potentially at an international level [e.g., multiple across-country evaluations (**MACE**) for commonly evaluated traits for dairy cattle]. For such evaluations, integration of correlated external information into a multivariate genetic evaluation could improve the accuracy for the traits of interest. Second, external information can be expressed on other scales or measurement units, or it can be associated with different heritabilities, genetic parameters, or trait definitions other than the internal traits. All these issues can lead to genetic correlations below unity.

Our study used the Bayesian approach in the context of dairy cattle production evaluations. In this context, exchanged EBV and REL (e.g., from Interbull, Uppsala, Sweden) are mostly expressed as an average yield on 305 d for 3 lactations, whereas the underlying genetic evaluations are often based on a (random regression) test-day model (e.g., Auvray and Gengler, 2002). Also, trait definitions and measurement methods for some dairy cattle production traits are not completely harmonized across countries. A good example is the use of different protein traits; most countries use CP, whereas others (e.g., France, United States) use true protein (VanRaden and Powell, 2015). Integration of this type of external information back into underlying genetic evaluations can be considered as a specific case where a multivariate Bayesian approach could be optimal to evaluate genetic merits of animals without the need to convert or deregress external information to be integrated. Therefore, even if the theoretical developments were previously reported, the aim of our study was to test the integration of external information (i.e., EBV and associated REL expressed on a 305-d basis) into a random regression test-day model using correlations among traits and among random regression effects in the context of dairy cattle.

MATERIALS AND METHODS

Data

Data, hereafter called “full data set,” were provided by the Interreg IVa France-Wallonie-Vlaanderen (Brussels, Belgium) project BlueSel. It consisted of test-day records between 5 and 365 DIM for first-parity, dual-purpose Belgian Blue cows for 2 traits: (1) for protein yield expressed as CP (kg) and measured in the Walloon Region of Belgium [hereafter called the Belgian trait (**B**)], and (2) for protein yield expressed as true protein (kg) and measured in France [hereafter called the French trait (**F**)]. Trait F was assumed to be the trait of interest for our study. In addition, only records of cows which were at least 21 mo old at first calving were selected. After edits, the full data set included 106,606 records for trait B from 14,590 Walloon cows and 38,455 records for trait F from 5,080 French cows. The pedigree (hereafter called “full pedigree”) was also provided by the BlueSel project and consisted of the Belgian and French data combined into a file including 35,978 animals (cows with records and ancestors). The pedigree was traced back to 10 generations starting from the cows with records. A total of 848 bulls sired at least one cow with records in one or in both populations. Among these 848 sires, 104 bulls had progeny in both Belgian and French populations, showing a good genetic link between these 2 populations.

Bivariate Genetic Evaluations

To be completely independent from differences existing between evaluation methods in routine evaluations in Belgium and France, a harmonized evaluation model was used. The base genetic evaluation model was a bivariate random regression test-day model for traits B and F. This bivariate model was based on the model used for the Walloon genetic evaluation of production traits (Auvray and Gengler, 2002; Croquet et al., 2006) and was written as

$$\begin{bmatrix} \mathbf{y}_B \\ \mathbf{y}_F \end{bmatrix} = \begin{bmatrix} \mathbf{X}_B & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_F \end{bmatrix} \begin{bmatrix} \boldsymbol{\beta}_B \\ \boldsymbol{\beta}_F \end{bmatrix} + \begin{bmatrix} \mathbf{Q}_B & \mathbf{0} \\ \mathbf{0} & \mathbf{Q}_F \end{bmatrix} \\ \left(\begin{bmatrix} \mathbf{Z}_{hB} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{hF} \end{bmatrix} \begin{bmatrix} \mathbf{h}_B \\ \mathbf{h}_F \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{aB} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{aF} \end{bmatrix} \begin{bmatrix} \mathbf{a}_B \\ \mathbf{a}_F \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{pB} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{pF} \end{bmatrix} \begin{bmatrix} \mathbf{p}_B \\ \mathbf{p}_F \end{bmatrix} \right) + \begin{bmatrix} \mathbf{e}_B \\ \mathbf{e}_F \end{bmatrix}, \quad [1]$$

where \mathbf{y}_i ($i = B, F$) is the vector of observations for the traits B and F, respectively; $\boldsymbol{\beta}_i$ ($i = B, F$) is the vector of fixed effects for each trait, B or F [i.e., herd

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