



J. Dairy Sci. 100:1–12
<https://doi.org/10.3168/jds.2017-12741>
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Accuracies of breeding values for dry matter intake using nongenotyped animals and predictor traits in different lactations

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ABSTRACT

Given the interest of including dry matter intake (DMI) in the breeding goal, accurate estimated breeding values (EBV) for DMI are needed, preferably for separate lactations. Due to the limited amount of records available on DMI, 2 main approaches have been suggested to compute those EBV: (1) the inclusion of predictor traits, such as fat- and protein-corrected milk (FPCM) and live weight (LW), and (2) the addition of genomic information of animals using what is called genomic prediction. Recently, several methodologies to estimate EBV utilizing genomic information (EBV) have become available. In this study, a new method known as single-step ridge-regression BLUP (SSRR-BLUP) is suggested. The SSRR-BLUP method does not have an imposed limit on the number of genotyped animals, as the commonly used methods do. The objective of this study was to estimate genetic parameters using a relatively large data set with DMI records, as well as compare the accuracies of the EBV for DMI. These accuracies were obtained using 4 different methods: BLUP (using pedigree for all animals with phenotypes), genomic BLUP (GBLUP; only for genotyped animals), single-step GBLUP (SS-GBLUP), and SSRR-BLUP (for genotyped and nongenotyped animals). Records from different lactations, with or without predictor traits (FPCM and LW), were used in the model. Accuracies of EBV for DMI (defined as the correlation between the EBV and pre-adjusted DMI phenotypes divided by the average accuracy of those phenotypes) ranged between 0.21 and 0.38 across methods and scenarios. Accuracies of EBV for DMI using BLUP were the lowest accuracies obtained across methods. Meanwhile, accuracies of EBV for DMI were similar in SS-GBLUP and SSRR-BLUP, and lower for the GBLUP method. Hence, SSRR-BLUP could be

used when the number of genotyped animals is large, avoiding the construction of the inverse genomic relationship matrix. Adding information on DMI from different lactations in the reference population gave higher accuracies in comparison when only lactation 1 was included. Finally, no benefit was obtained by adding information on predictor traits to the reference population when DMI was already included. However, in the absence of DMI records, having records on FPCM and LW from different lactations is a good way to obtain EBV with a relatively good accuracy.

Key words: genomic prediction, feed intake, fat- and protein-corrected milk, live weight

INTRODUCTION

Feed costs represent half of the total costs of dairy production (European Union, 2011). One way to increase profitability of dairy production is to reduce feed costs by improving feed efficiency (Veerkamp, 1998; de Haas et al., 2012). Optimization of dairy cattle breeding goals for feed efficiency requires the availability of breeding values for DMI, as this is an important component of feed efficiency. To estimate accurate DMI breeding values, a large number of records is required. However, DMI is labor intensive and expensive to measure. As DMI is not a trait typically recorded in commercial herds, the amount of available data is limited. The difficulty in recording DMI has hampered direct selection for DMI previously because insufficient records were available on daughters of progeny-tested bulls. This difficulty might be overcome by jointly using predictor traits (Veerkamp and Brotherstone, 1997; Berry and Crowley, 2013; Manzanilla-Pech et al., 2016) and genomic information (Meuwissen et al., 2001). Readily available predictor traits that are easier and cheaper to record compared with DMI are fat- and protein-corrected milk (FPCM) and live weight (LW). Both traits are known to be strongly correlated with DMI (Korver, 1988; Van Arendonk, 1991; Veerkamp and Brotherstone, 1997; Veerkamp, 1998; Liinamo et al., 2012).

Received February 16, 2017.

Accepted July 16, 2017.

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Ideally, breeding values for DMI across the whole productive lifetime of cows should be predicted, but historical DMI data in the Netherlands have mainly covered just first lactations. It has been reported that DMI varies not only during lactation but also across lactations (Berry et al., 2006). For this reason, it is important to investigate the effect on the EBV of either including data (on DMI, FPCM, and LW) from only lactation 1, or using data from 3 lactations when predicting DMI in lactation 1 or in the first 3 lactations.

Best linear unbiased prediction is a widely used method in genetic improvement of livestock that uses pedigree relationships to estimate the EBV of an animal. In our study, we used this method as the base traditional method to compare the other BLUP methods [genomic BLUP (**GBLUP**), single-step GBLUP (**SS-GBLUP**), and single-step ridge-regression BLUP (**SSRR-BLUP**)].

Genomic BLUP uses genomic relationships to estimate the genetic merit of an individual (VanRaden, 2008). The genomic relationship matrix (**GRM**) constructs the relationship between individuals based on genomic information, instead of pedigree information. The main limiting factor of this method is that only phenotypic information of genotyped animals is used, thereby ignoring important phenotypic information from nongenotyped relatives.

Single-step GBLUP (Aguilar et al., 2010; Christensen and Lund, 2010) allows for adding phenotypic information of nongenotyped animals into the GBLUP model. This method combines, in a single step, the GRM (**G**) with the pedigree relationship matrix (**A**) into a new relationship matrix (**H**), whose inverse is used to solve the mixed model equations to obtain the EBV. The SS-GBLUP is a well-known method due to its simplicity, which has been adopted in several countries for routine evaluations. However, this method has the limiting factor (in common with ordinary GBLUP) that the computation time required to invert the G-matrix more than quadratically increases with the number of genotyped animals.

In this work, a novel method will be evaluated being implemented in the software package MiXBUP, which combines information about genotyped and nongenotyped animals with phenotypes using SNP estimates, instead of GRM, using BLUP methodology, namely, SSRR-BLUP. This methodology is based on the theory behind a previously presented Bayesian regression method (Fernando et al., 2014). The Bayesian regression method uses imputed SNP genotypes for animals that are not genotyped, together with a residual genetic effect of the deviations between true and imputed genotypes (Fernando et al., 2014). In theory, the accuracy of prediction of SSRR-BLUP is expected to be identical

to SS-GBLUP, but its advantage is that it does not require the computation of **G** or its inverse.

In 2016, a breeding value for DMI was introduced in the Netherlands. As a consequence, more historical DMI data have been collected and combined for genetic analysis. Therefore, the objective of this study was to estimate genetic parameters using this uniquely large data set with DMI records, as well as compare accuracies in the prediction of the EBV of DMI, obtained by applying 4 different methods (i.e., BLUP, GBLUP, SS-GBLUP, and SSRR-BLUP) using records from different lactations, with or without predictor traits (FPCM and LW), in the model.

MATERIALS AND METHODS

Phenotypes

Data Collection. A total of 459,096 daily records on DMI were available from 3,954 Dutch dairy cows in 6,820 lactations. These records came from cows that participated in nutritional experiments, which were conducted from 1987 to 2015 on several farms in the Netherlands (e.g., Aver Heino, Heino; Bosma Zathe, Ureterp; Cranendonck, Soerendonk; 't Gen, Lelystad; Minderhoudhoeve, Swifterbant; Waiboerhoeve Dairy Unit 2, 3, Lelystad; Zegveld farm, Zegveld; Hoorn, Lelystad; and New Wairboerhoeve, Lelystad). A full description of the methodology of most of the experiments and diets has been summarized previously (Veerkamp et al., 2000; Beerda et al., 2007; Zom et al., 2012). Diets primarily included grass silage, fresh grass, dehydrated grass, corn, corn silage, cereal, concentrates, or beet pulp. All cows were kept indoors in conventional cubicle housings, offered complete mixed rations ad libitum and milked twice a day, except for 50% of the cows at Bosma Zathe ($n = 50$), which were milked 3 times per day.

Recorded Traits. Recording frequencies of DMI varied by experiment: it was recorded 1, 2, 3, or 5 times per week (Veerkamp et al., 2000; Beerda et al., 2007; Zom et al., 2012). An overview of the experiments, treatments and diets is summarized in Manzanilla-Pech et al. (2014). Weighing platforms were used to automatically monitor LW 3 times a week or daily, depending on the experiment. Fat- and protein-corrected milk was calculated, using milk yield and fat and protein content. Milk yield was recorded daily, but averaged per week because fat and protein contents in milk were measured weekly. The following formula was used to calculate FPCM (FAO, 2010):

$$\text{FPCM (kg)} = \text{raw milk (kg)} \times [0.337 + 0.116 \times \text{fat content (\%)} + 0.06 \times \text{protein content (\%)}].$$

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