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Comparison of genomic predictions for lowly heritable traits using multi-step and single-step genomic best linear unbiased predictor in Holstein cattle

A. R. Guarini,* D. A. L. Lourenco,† L. F. Brito,* M. Sargolzaei,*‡ C. F. Baes,* F. Miglior,*§ I. Misztal,† and F. S. Schenkel*¹

*Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, Ontario, Canada, N1G-2W1

†Department of Animal and Dairy Science, University of Georgia, Athens, 30602

‡The Semex Alliance, Guelph, Ontario, Canada, N1H-6J2

§Canadian Dairy Network, Guelph, Ontario, Canada, N1K-1E5

ABSTRACT

The success and sustainability of a breeding program incorporating genomic information is largely dependent on the accuracy of predictions. For low heritability traits, large training populations are required to achieve high accuracies of genomic estimated breeding values (GEBV). By including genotyped and nongenotyped animals simultaneously in the evaluation, the single-step genomic BLUP (ssGBLUP) approach has the potential to deliver more accurate and less biased genomic evaluations. The aim of this study was to compare the accuracy and bias of genomic predictions for various traits in Canadian Holstein cattle using ssGBLUP and multi-step genomic BLUP (msGBLUP) under different strategies, such as (1) adding genomic information of cows in the analysis, (2) testing different adjustments of the genomic relationship matrix, and (3) using a blending approach to obtain GEBV from msGBLUP. The following genomic predictions were evaluated regarding accuracy and bias: (1) GEBV estimated by ssGBLUP; (2) direct genomic value estimated by msGBLUP with polygenic effects of 5 and 20%; and (3) GEBV calculated by a blending approach of direct genomic value with estimated breeding values using polygenic effects of 5 and 20%. The effect of adding genomic information of cows in the evaluation was also assessed for each approach. When genomic information was included in the analyses, the average improvement in observed reliability of predictions was observed to be 7 and 13 percentage points for reproductive and workability traits, respectively, compared with traditional BLUP. Absolute deviation from 1 of the regression coefficient of the linear regression of de-regressed estimated breeding values on genomic predictions went from 0.19 when using

traditional BLUP to 0.22 when using the msGBLUP method, and to 0.14 when using the ssGBLUP method. The use of polygenic weight of 20% in the msGBLUP slightly improved the reliability of predictions, while reducing the bias. A similar trend was observed when a blending approach was used. Adding genomic information of cows increased reliabilities, while decreasing bias of genomic predictions when using the ssGBLUP method. Differences between using a training population with cows and bulls or with only bulls for the msGBLUP method were small, likely due to the small number of cows included in the analysis. Predictions for lowly heritable traits benefit greatly from genomic information, especially when all phenotypes, pedigrees, and genotypes are used in a single-step approach.

Key words: genomic evaluation, dairy cattle, reference population, reliability, single-step model

INTRODUCTION

In Canada, genomic evaluation for a series of traits has been successfully implemented in Holstein cattle since 2009 through a multi-step genomic BLUP method (**msGBLUP**; Van Doormaal et al., 2009). This procedure consists of (1) running a traditional genetic evaluation based solely on pedigree and phenotypic information, (2) calculation of pseudo-phenotypes such as de-regressed estimated breeding values (**DEBV**) using results obtained from the previous step, (3) estimation of SNP effects to obtain direct genomic values (**DGV**) for genotyped animals, and (4) blending of genomic predictions with EBV or parent averages (**PA**). Loss of information during the de-regression step can introduce bias and errors into the evaluation (Legarra et al., 2014), thus reducing the contribution of genomic information. Moreover, in msGBLUP, only information on genotyped animals is directly used. Given that only a small portion of the animals are genotyped, bias can also be introduced by the fact that not all information used for selection decisions is accounted for.

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¹Corresponding author: schenkel@uoguelph.ca

To overcome potential problems, Misztal et al. (2009), Aguilar et al. (2010), and Christensen and Lund (2010) developed single-step genomic BLUP (**ssGBLUP**), a methodology that combines genotypic, pedigree, and phenotypic information into a single evaluation. It consists of augmenting the pedigree relationship matrix with contributions from genomic relationships into a matrix of realized (observed or imputed) relationships, the inverse of which is used in the BLUP mixed model equations. In this way, genotyped and nongenotyped animals can be included simultaneously in the evaluation. As several steps are avoided, ssGBLUP is, in many instances, simpler to use and has the potential to deliver more accurate and less biased genomic evaluations. The main advantage of ssGBLUP, especially for dairy cattle, is its ability to account for genomic pre-selection (Legarra et al., 2014). Accuracy of ssGBLUP is usually as high as, if not greater than, other methods of genetic merit evaluation (Christensen et al., 2012; Baloché et al., 2014; Lourenco et al., 2014a).

Accuracy of genomic predictions is critical for the expected genetic gains resulting from genomic selection and is dependent on many factors, such as heritability of the trait, the statistical method used to estimate SNP effects in the training population, and most importantly, the size of the training population (Goddard, 2009; Hayes et al., 2009; Hozé et al., 2014). For the latter, the number of genotyped progeny-tested bulls could be a limitation, especially for lowly heritable traits or those traits that are difficult or expensive to measure. One way of overcoming this problem is by incorporating genomic information of cows into the evaluation (Calus et al., 2013; Tsuruta et al., 2013; Uemoto et al., 2017). However, it is important that cow and bull traditional evaluations are comparable to avoid a decrease in reliability of genomic predictions, especially due to preferential treatment. Wiggans et al. (2011) reported a decrease in reliability of genomic predictions with the inclusion of cows in the training population. The authors hypothesized that many cows were subject to preferential treatment for having higher genetic merit. A pre-adjustment was then developed to reduce the mean and variance of cows' EBV so they would be comparable to those of bulls (Wiggans et al., 2012). Tsuruta et al. (2013) suggested that by using ssGBLUP, the inclusion of cows in the training population would be possible without any pre-adjustments.

In Canada, genomic evaluations are currently based solely on bulls' genomic information and there is still a lack of studies investigating the feasibility of ssGBLUP in Canadian dairy cattle. The incorporation of genomic information into breeding programs using alternative approaches to improve genomic predictions for lowly heritable traits is needed. In addition, the importance

of workability and reproduction traits have increased over time in the dairy cattle industry. Advantages of incorporating genomics into a breeding program are the greatest for lowly heritable traits, especially due to the higher relative increase in reliabilities of predictions achieved for these traits by using genomic information (García-Ruiz et al., 2016; Wiggans et al., 2017). Therefore, the objective of this study was to compare the accuracy and bias (spread) of genomic predictions for various workability and reproductive traits in Canadian Holstein cattle using multi-step and single-step GBLUP methods under different strategies, such as adding genomic information of cows in the analysis, testing different adjustments of the genomic relationship matrix, and using a blending approach to obtain GEBV from the multi-step method.

MATERIALS AND METHODS

Data

Genotypic data consisted of 10,590 bulls born between 1960 and 2012 genotyped with the Illumina Bovine SNP50 BeadChip (**50K**, Illumina Inc., San Diego, CA) or a higher density panel. The SNP present in the higher density panel that overlapped with the 50K panel were imputed to the 50K panel using the FImpute software (Sargolzaei et al., 2014). In addition, 6,842 cows born between 1997 and 2015 genotyped either with the 50K SNP panel or a low-density panel (6K) were imputed to the 50K panel by also using the FImpute software. Thus, all animals had information on the same SNP set. Genotypes were coded as 0, 1, or 2 for calculation of the genomic relationship matrix (**G**). Genotype quality control excluded monomorphic SNP, SNP and individuals with call rate lower than 90%, SNP that were out of Hardy-Weinberg equilibrium with very low probability ($P < 10^{-6}$) or with minor allele frequency less than 0.05, and individuals with parent-progeny Mendelian conflicts. After quality control, the number of genotyped animals retained was 17,430 and the final genotype data set included 40,635 informative SNP. The PREGSF90 software was used for SNP and sample quality control (Misztal et al., 2002).

Data on Holstein reproductive and workability traits were extracted from the April 2017 genetic evaluation carried out by the Canadian Dairy Network (Guelph, Ontario, Canada, www.cdn.ca). The traits selected for this study were milking speed (**MS**), milking temperament (**MT**), age at first insemination (**AFS**), days from calving to first insemination (**CTFS**), number of services (**NS**), 56-d nonreturn rate (**NRR**), days from first service to conception (**FSTC**), calving ease (**CE**), stillbirth (**SB**), gestation length (**GL**), and calf size

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