



Single-step genomic model improved reliability and reduced the bias of genomic predictions in Danish Jersey

P. Ma,^{*1} M. S. Lund,^{*} U. S. Nielsen,[†] G. P. Aamand,[‡] and G. Su^{*}

^{*}Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, DK-8830 Tjele, Denmark

[†]SeGES, DK-8200 Aarhus, Denmark

[‡]NAV Nordic Cattle Genetic Evaluation, DK-8200 Aarhus, Denmark

ABSTRACT

A bias in the trend of genomic estimated breeding values (GEBV) was observed in the Danish Jersey population where the trend of GEBV was smaller than the deregressed proofs for individuals in the validation population. This study attempted to improve the prediction reliability and reduce the bias of predicted genetic trend in Danish Jersey. The data consisted of 1,238 Danish Jersey bulls and 611,695 cows. All bulls were genotyped with the 54K chip, and 1,744 cows were genotyped with either 7K chips (1,157 individuals) or 54K chips (587 individuals). The trait used in the analysis was protein yield. All cows with EBV were used in a single-step approach. Deregressed proofs were used as the response variable. Four alternative approaches were compared with genomic best linear unbiased prediction (GBLUP) model with bulls in the reference data (GBLUP_{Bull}): (1) GBLUP with both bulls and genotyped cows in the reference data; (2) GBLUP including a year of birth effect; (3) GEBV from a GBLUP model that accounted for the difference of EBV between dams and maternal grandsires; and (4) using a single-step approach. The results indicated all 4 alternatives could reduce the bias of predicted genetic trend and that the single-step approach performed best. However, not all these approaches improved reliability or reduced inflation of GEBV. The reliability was 0.30 and regression coefficients of deregressed proofs on GEBV were 0.69 in the scenario GBLUP_{Bull}. When genotyped cows were included in the reference population, the regression coefficients decreased to 0.59 but the reliability increased to 0.35. If a year effect was included in the model, the prediction reliability decreased to 0.29 and the regres-

sion coefficient improved to 0.75. The method in which GEBV were adjusted for the difference between dam EBV and maternal grandsire EBV led to much lower regression coefficients though the reliability increased to 0.4. The single-step approach improved both the reliability, to 0.38 and regression coefficient to 0.78. Therefore, the bias in genetic trend was reduced. The results suggest that implementing the single-step approach is an effective way to improve genomic prediction in Danish Jersey cattle.

Key words: bias of predicted genetic trend, reliability of genomic prediction, single-step method

INTRODUCTION

Genomic prediction has been widely used in dairy cattle since genome-wide dense marker chips became available. To obtain accurate prediction, a large reference population is needed (Goddard and Hayes, 2009; Hayes et al., 2009a). In dairy cattle, usually progeny-tested bulls are used to form the reference population. In some large populations, such as Holsteins, accurate prediction using genomic information has been obtained (VanRaden et al., 2009; Lund et al., 2011). For Danish Jerseys it is quite challenging to obtain a large reference population because a limited number of progeny-tested bulls are available (Thomasen et al., 2012). One way to overcome this limitation is to add genotyped cows to the reference population. However, previous studies have reported an inflation of the genomic estimated breeding values (GEBV) when cows were included into the training set (Wiggans et al., 2011; Calus et al., 2013), because the genotyped cows are usually elite and possible get preferential treatment. Another strategy is to make use of the phenotypic information from nongenotyped animals. A popular approach is to apply a single-step model which estimates genomic breeding values using the information of genotyped and nongenotyped individuals simultaneously by integrating marker- and pedigree-based relationship matrix

Received April 13, 2015.

Accepted August 14, 2015.

¹Corresponding author: peipei.ma@mbg.au.dk

into a joint relationship matrix (Miształ et al., 2009; Christensen and Lund, 2010; Aguilar et al., 2010).

Nordic routine genomic genetic evaluation has observed a bias of predicted genetic trends in Danish Jerseys. Bias of predicted genetic trends was defined as the annual deviation of GEBV from the deregressed proofs (**DRP**) of the animals in the test population. Bias of predicted genetic trends may lead to an unfair comparison of animals across birth years. The bias could be caused by a discrepancy between assumptions of the genomic prediction models and the selection histories of the practical populations (Vitezica et al., 2011). The genomic prediction models assume there is no selection in the population, which is used for implementing genomic prediction (Hayes et al., 2009b). However, in practice, the genotyped populations usually consist of selected animals such as progeny-tested bulls and elite cows. The single-step approach accounts for the selection by including all records in the model. Therefore, this approach is expected to minimize the bias. Another possible solution to reduce the bias is to add a year of birth effect in the model, which may lead to a robust estimation of genetic trend (Ducrocq, 2010). Therefore, the genetic progress on the maternal side could be taken into account by the year trend. Similarly, adjusting GEBV for the difference between EBV of dam and maternal grandsire (**MGS**) may reduce bias of predicted genetic trend.

The objectives of our study were to investigate the prediction reliability and bias of predicted genetic trend in Danish Jersey. A second objective was to increase prediction reliability and reduce bias of predicted genetic trend using various strategies such as adding genotyped cows to the reference population, including year effect into the prediction model, accounting for the difference of EBV between dam and MGS, and applying a single-step approach.

MATERIALS AND METHODS

Data

Danish Jersey data were used in our study. There were 2,982 genotyped individuals comprising 1,238 bulls born between 1981 and 2009 and 1,744 cows born between 2000 and 2011, with most of them (1,733) born after 2004. Most cows (1,157) were randomly selected from a few herds, whereas the others (587) were selected as potential bull dams by individual farms according to their own breeding schemes. The **DRP** of protein used in different scenarios were calculated from EBV of genetic evaluation in November 2013. When using the single-step approach, all cows with EBV for protein were used in the analysis. After tracing the pedigree

to as many generations as possible for the cows with EBV and bulls with genotypes, the pedigree used for single-step prediction included 819,988 individuals. The **DRP** for all cows were calculated using Mix99 (Lidauer and Strandén, 1999; Strandén and Mäntysaari, 2010); it required that the cows had an effective record contribution (**ERC**) larger than 0.1. This reduced the number of cows with **DRP** to be 611,695. Cows which are daughters of the test bulls (described later) were excluded. After filtering, the number of cows with **DRP** used in the single-step approach was 577,405.

The bulls were genotyped with Illumina BovineSNP50 BeadChip (**54K**; Illumina, San Diego, CA), which includes 54,001 SNP. Bull dams (587) were genotyped with 54K chips. Randomly selected cows (1,157) were genotyped with Illumina BovineLD BeadChip (**LD**) which includes 6,909 SNP. The LD data were imputed to 54K with Beagle (Browning and Browning, 2009) using the 54K genotyped animals as imputation reference population. The markers used for prediction were from 29 autosomes. The genotypes for genomic prediction were edited by deleting the markers with minor allele frequency less than 0.01 and the markers in complete linkage disequilibrium ($r^2 = 1$) with the previous marker. After editing, 38,967 markers were used for genomic prediction.

Methods

To validate the prediction accuracy and unbiasedness, the Jersey bulls were divided into reference and test sets using a cut-off date of birth of January 1, 2005. The bulls born after this date were used as validation animals (208 bulls). Thus, in the scenario using only bull reference data, 1,030 bulls were used as reference population.

Besides the genomic BLUP model (**GBLUP**) with bulls in the reference data (**GBLUP_{Bull}**), 5 alternative approaches were used in our study. The first was including pedigree relationships to weight the genomic relationship (**GBLUPW_{Bull}**). Approach 2 was the **GBLUP** model with both bulls and genotyped cows in reference set (**GBLUP_{Cow}**), in which, 25 cows were dams of test bulls. Approach 3 included a year of birth effect in the **GBLUP** model (**GBLUP_{Year}**) to account for the part of genetic trend that is not accounted for by SNP markers. Approach 4 was to adjust GEBV using the difference of EBV between dams and maternal grandsires (**GBLUP_{Dam_mgs}**). Approach 5 was a single-step method to integrate the information of genotyped and nongenotyped animals for genomic prediction. Two scenarios of this approach were investigated, which were the predictions either using cow genotypes (**SS_{PG}**) or without using cow genotypes (**SS_P**). The numbers of

Download English Version:

<https://daneshyari.com/en/article/10973437>

Download Persian Version:

<https://daneshyari.com/article/10973437>

[Daneshyari.com](https://daneshyari.com)