



J. Dairy Sci. 101:1–13
<https://doi.org/10.3168/jds.2017-13310>

© 2018, THE AUTHORS. Published by FASS Inc. and Elsevier Inc. on behalf of the American Dairy Science Association®.
 This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/3.0/>).

Differing genetic trend estimates from traditional and genomic evaluations of genotyped animals as evidence of preselection bias in US Holsteins

Y. Masuda,*¹ P. M. VanRaden,† I. Misztal,* and T. J. Lawlor‡

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

†Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD 20705-2350

‡Holstein Association USA Inc., Brattleboro, VT 05301

ABSTRACT

The objective of this study was to compare genetic trends from single-step genomic BLUP (ssGBLUP) and traditional BLUP models for milk production traits of US Holsteins. Phenotypes were 305-d milk, fat, and protein yields from 21,527,040 cows recorded between January 1990 and August 2015. The pedigree file included 29,651,623 animals and was limited to 3 generations back from recorded or genotyped animals. Genotypes for 764,029 animals were used, and analyses were by a 3-trait repeatability model as used in the US official genetic evaluation. Unknown-parent groups were incorporated into the inverse of a relationship matrix (\mathbf{H}^{-1} in ssGBLUP and \mathbf{A}^{-1} in BLUP) with the QP transformation. For ssGBLUP, 18,359 genotyped animals were randomly chosen as core animals to calculate the inverse of the genomic relationship matrix with the APY algorithm. Computations took 6.5 h and 1.4 GB of memory for BLUP, and 13 h and 115 GB of memory for ssGBLUP. For genotyped sires with at least 10 daughters, the average genetic levels for predicted transmitting ability (PTA) and genomic PTA were similar up to 2008, with a higher level for ssGBLUP later (approximately by 36 kg for milk, 2.1 kg for fat, and 1.1 kg for protein for bulls born in 2010). For genotyped cows, the average genetic levels were similar up to 2006, with a higher level for ssGBLUP (approximately by 91 kg for milk, 3.6 kg for fat, and 2.7 kg for protein for cows born in 2012). For all cows, the average levels were slightly higher for ssGBLUP, with much smaller differences than for genotyped cows. Trends for BLUP indicate bias due to genomic preselection for genotyped sires and cows. For official evaluations released in December 2016, traditional PTA had the same trend as multiple-step genomic PTA for both genotyped bulls and cows except for the youngest bulls,

who had traditional PTA slightly lower than genomic PTA. For genotyped bulls born in recent years, genetic gain for official traditional and genomic evaluations was similar in contrast to ssGBLUP and BLUP differences. Official PTA for cows were adjusted so that the Mendelian sampling variance was comparable with that for bulls, and those adjustments likely removed bias due to genomic preselection from traditional PTA, especially for genotyped cows. The ssGBLUP method seems to account partially for that bias and is computationally suitable for national evaluations.

Key words: genomic evaluation, predicted transmitting ability, single-step method, bias

INTRODUCTION

Genomic selection has been rapidly adopted by the US dairy industry since genomic PTA (**GPTA**) were officially published for young bulls in 2009. Bulls are selected based on GPTA before they have a traditional PTA (**tradPTA**) based on daughter performance records. Genomic selection has had a positive effect on recent genetic gain because of a shortened generation interval from intensive use of young bulls (García-Ruiz et al., 2016; Wiggans et al., 2017). More than 50% of all AI matings used genotyped young bulls in 2012 (Hutchison et al., 2014), and this percentage increased to 67% in 2016 (George R. Wiggans, Council on Dairy Cattle Breeding, Bowie, MD, personal communication).

One concern in current genomic selection is the underestimation of tradPTA for young bulls when genomic preselection is not accounted for in the traditional genetic evaluation (Patry and Ducrocq, 2011a,b). A biased tradPTA could lead to inaccurate GPTA because tradPTA is still needed to construct daughter yield deviations (**DYD**) for the genomic prediction (VanRaden et al., 2009). Such bias could propagate to other countries through Interbull evaluations based on tradPTA (Patry et al., 2013) if the Interbull evaluations are used as an additional source of information for national evaluations.

Received June 8, 2017.

Accepted December 10, 2017.

¹Corresponding author: yutaka@uga.edu

A simple method to reduce the bias is to blend genomic information with tradPTA (Ducrocq and Liu, 2009; Mäntysaari and Strandén, 2010; Patry and Ducrocq, 2011a). This is implemented as an extra step after genomic prediction and needs pseudo-phenotypes derived from tradPTA and GPTA. Stoop et al. (2013) implemented a multiple-trait approach to blend DYD with direct genomic values (**DGV**; Mäntysaari and Strandén, 2010) for Dutch dairy sires. They found that the method was easily applied using an animal-model framework and could partially account for preselection bias. Although the method works, the approach is ad hoc, and bias may remain because of biased pseudo-phenotypes (VanRaden, 2012).

The single-step genomic BLUP approach (**ssGBLUP**) calculates GPTA by combining all available phenotypes, pedigree, and genotypes in the same equations and can possibly account for genomic preselection (Aguilar et al., 2010; Patry and Ducrocq, 2011b). Originally ssGBLUP was considered as a method to account for preselection in dairy cattle only with a limited number of genotyped animals because of high computing cost (VanRaden, 2012). Whereas new algorithms to solve ssGBLUP-based equations were suggested (Fernando et al., 2016a,b; Taskinen et al., 2017), recent developments have removed computing limitations of ssGBLUP in dairy cattle with a large number of genotyped animals (Koivula et al., 2015; Masuda et al., 2016; Misztal, 2016; Strandén et al., 2017).

If the downward bias in the traditional evaluation is real, we should observe a higher trend in GPTA from ssGBLUP (**ssGPTA**) than in tradPTA for recent animals. The main objective of this study was to compare trends of ssGPTA and tradPTA for milk production traits in the US Holstein population. A secondary objective was to compare the recent genetic trend of official GPTA using a multi-step method with corresponding tradPTA.

MATERIALS AND METHODS

Data

The initial data set was derived from that used for the official US official genomic evaluation of Holsteins in August 2015 but with foreign data, other breeds, and crossbreds excluded. The initial data set consisted of over 80 million 305-d lactation records each for milk, fat, and yields from 34 million cows and also included 70 million pedigreed animals.

We excluded old phenotype and pedigree information to reduce computing costs and improve convergence. According to Jamrozik and Schaeffer (1991), the use of all available data in genetic evaluation is important

if the interest is in estimation of genetic trends over time. In contrast, Mehrabani-Yeganeh et al. (1999) showed that use of the last 2 discrete or 4 overlapping generations had no significant effect on selection response in traditional evaluations in simulated chicken populations. Our interest was a possible difference in estimated genetic gain after 2009 between traditional BLUP and ssGBLUP evaluations. Therefore, only lactation records from cows that calved in or after 1990 were retained, and pedigree information was limited to 3 generations back from cows with lactation records. The final phenotypic data included 21,527,040 cows with 50,970,954 records for milk and fat yields and 50,319,544 records for protein yield. The pedigree data included 29,651,623 animals. Genotypes included 60,671 SNP markers for 764,029 animals. No SNP chip included all those markers; therefore, imputation was used to fill in missing marker genotypes (Wiggans et al., 2017).

Genetic and Genomic Evaluation

Traditional Evaluation. We calculated tradPTA using the 3-trait animal model described by VanRaden et al. (2007) and VanRaden et al. (2014). Lactation records were pre-corrected for calving age, season, milking frequency, previous days open, and heterogeneous variance. The model included fixed effects for management group, parity by age, and regressions on inbreeding and general heterosis and random effects for breeding value, permanent environment, and herd-by-sire interaction. Multiple-trait equations and variance components from VanRaden et al. (2014) were used for the 3 production traits. Inbreeding coefficients were considered in the inverse of the numerator relationship matrix (\mathbf{A}^{-1}). Unknown-parent groups (215) were defined by pedigree path, national origin, and birth year.

Mixed-model equations were solved with the BLUP90IOD2 program that implemented the preconditioned conjugate gradient (**PCG**) method with parallel processing using OpenMP (Tsuruta et al., 2001; OpenMP Architecture Review Board, 2015). Iteration finished when the squared ratio of the Euclidean norm of residual and right-hand-side vectors:

$$\frac{\|\mathbf{b} - \mathbf{Cx}\|^2}{\|\mathbf{b}\|^2} = \frac{(\mathbf{b} - \mathbf{Cx})'(\mathbf{b} - \mathbf{Cx})}{\mathbf{b}'\mathbf{b}},$$

where \mathbf{C} is the left-hand-side matrix, \mathbf{b} is the right-hand-side vector, and \mathbf{x} is the solution in the current iteration, which was less than 10^{-15} . The same software and convergence criterion were also used in ssGBLUP.

Download English Version:

<https://daneshyari.com/en/article/8501138>

Download Persian Version:

<https://daneshyari.com/article/8501138>

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