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Including overseas performance information in genomic evaluations of Australian dairy cattle

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ABSTRACT

In dairy cattle, the rate of genetic gain from genomic selection depends on reliability of direct genomic values (DGV). One option to increase reliabilities could be to increase the size of the reference set used for prediction, by using genotyped bulls with daughter information in countries other than the evaluating country. The increase in reliabilities of DGV from using this information will depend on the extent of genotype by environment interaction between the evaluating country and countries contributing information, and whether this is correctly accounted for in the prediction method. As the genotype by environment interaction between Australia and Europe or North America is greater than between Europe and North America for most dairy traits, ways of including information from other countries in Australian genomic evaluations were examined. Thus, alternative approaches for including information from other countries and their effect on the reliability and bias of DGV of selection candidates were assessed. We also investigated the effect of including overseas (OS) information on reliabilities of DGV for selection candidates that had weaker relationships to the current Australian reference set. The DGV were predicted either using daughter trait deviations (DTD) for the bulls with daughters in Australia, or using this information as well as OS information by including deregressed proofs (DRP) from Interbull for bulls with only OS daughters in either single trait or bivariate models. In the bivariate models, DTD and DRP were considered as different traits. Analyses were performed for Holstein and Jersey bulls for milk yield traits, fertility, cell count, survival, and some type traits. For Holsteins, the data used included up to 3,580 bulls with DTD and up to 5,720 bulls with only DRP. For Jersey, about 900 bulls with DTD and 1,820 bulls with DRP were used. Bulls born after 2003 and genotyped cows

that were not dams of genotyped bulls were used for validation. The results showed that the combined use of DRP on bulls with OS daughters only and DTD for Australian bulls in either the single trait or bivariate model increased the coefficient of determination [(R^2) (DGV,DTD)] in the validation set, averaged across 6 main traits, by 3% in Holstein and by 5% in Jersey validation bulls relative to the use of DTD only. Gains in reliability and unbiasedness of DGV were similar for the single trait and bivariate models for production traits, whereas the bivariate model performed slightly better for somatic cell count in Holstein. The increase in R^2 (DGV,DTD) as a result of using bulls with OS daughters was relatively higher for those bulls and cows in the validation sets that were less related to the current reference set. For example, in Holstein, the average increase in R^2 for milk yield traits when DTD and DRP were used in a single trait model was 23% in the least-related cow group, but only 3% in the most-related cow group. In general, for both breeds the use of DTD from domestic sources and DRP from Interbull in a single trait or bivariate model can increase reliability of DGV for selection candidates.

Key words: genomic prediction, daughter trait deviation, deregressed proof, reliability

INTRODUCTION

The reliability of direct genomic values (DGV) is a function of the heritability of the trait, the proportion of genetic variance explained by the markers, the genetic diversity of the population, and the number of animals in the reference population where SNP effects are estimated (Daetwyler et al., 2008; Goddard, 2009). The reliability of DGV is also affected by relatedness of the candidate animals to the reference population (e.g., Habier et al., 2010), at least with 50,000 SNP. Broadening the diversity of the reference set by including more animals can improve the reliability of DGV because for each candidate, the likelihood of having related animals in the reference set increases (Clark et al., 2012; Pszczola et al., 2012).

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For national dairy cattle genomic evaluations, one way to diversify and increase the size of the reference set would be to use genotype of animals with performance records in other countries, for example bulls with daughters in other countries. Currently several countries exchange genotype data to increase their reference set for genomic evaluation and use deregressed multiple trait across-country evaluation (**MACE**) proofs as a response variable. Including information from other countries for genomic predictions has resulted in small to substantial increases in reliability of genomic evaluations (Brøndum et al., 2011; Lund et al., 2011; VanRaden et al., 2012). Including overseas (**OS**) information for genomic prediction is more likely to improve reliability when genetic correlations among countries are reasonably high, that is limited genotype by environment interaction (**G×E**) exists between the countries. For example, the genetic correlation between the Eurogenomics consortium countries is high (~0.9 for most traits; Interbull, 2013), this means there is weak **G×E** and treating performance in the Eurogenomics consortium countries as a single trait works well (Lund et al., 2011). Studies in Europe (Lund et al., 2011) and the United States (VanRaden et al., 2012) have shown that the increase in reliability of bull proofs from using data from other countries was greater for traits with higher genetic correlations among countries (e.g., protein) than for traits that have lower correlations between countries (e.g., fertility or survival). Furthermore, VanRaden et al. (2012) suggested that countries with more diverse populations and where trait definitions are more variable would be expected to benefit more from implementing multitrait genomic evaluation models (with performance in different countries treated as different traits) rather than single-trait models. The genetic correlation of the same trait measured in Australia with most of the northern hemisphere countries is typically about 0.8 or less (Interbull, 2013) for Jersey and Holstein. This is likely to be because the majority of Australian (**AUS**) herds practice pasture-based seasonal calving, whereas most herds in northern hemisphere largely rely on TMR. Thus, simply including OS information in the reference set for AUS genomic evaluations in a single-trait model could potentially create biases or reduce the value of including the information. Australia is an interesting test case to investigate the best approach to include OS daughter information in the reference population, as the **G×E** between Australia and other countries is considerable.

The main aim of our study was to evaluate alternative approaches (including multitrait) for using OS information in AUS genomic evaluations. The main criteria for evaluation were how well DGV from these alternative approaches predict a bull's AUS daughter

performance. This is done by predicting DGV either (1) using domestic daughter trait deviations (**DTD**) as response variables, using OS information by including deregressed proofs (**DRP**) from MACE for bulls with only OS daughters as well as domestic DTD as the response variable in a single trait model; or, (2) using a multitrait approach where DTD for bulls with AUS daughters and **DRP** for bulls with only OS daughters were considered as different traits. The second objective was to test if improvement in reliability of DGV as a result of using OS information was relatively larger if the candidate animals were less related to the current reference set. In addition to bulls, cows were used to test this hypothesis, as the degree of relatedness of the genotyped cows available to us was more diverse than that of bulls. Separate analyses were conducted using Holstein and Jersey data.

MATERIALS AND METHODS

Genotype Data

Bulls in the AUS reference set were genotyped for the 50,000 panel (Matukumalli et al., 2009); quality filters were imposed as described in Hayes et al. (2009) and Nieuwhof et al. (2010). Genotypes were also available for about 8,478 Holstein and 3,917 Jersey cows that were used in the reference set for AUS genomic evaluations, but here we used a subset of them as validation animals. For both Holsteins and Jerseys, 43,990 SNP were retained for genomic prediction.

Raw genotype data files were obtained for 5,720 bulls from the Cooperative Cattle Improvement Organization [**CRV**; Arnhem, the Netherlands (**NLD**)] and 3,072 bulls from Livestock Improvement Corporation [**LIC**; Hamilton, New Zealand (**NZL**)]. Of the 5,720 bull genotypes received from CRV, 4,228 Holstein and 561 Jersey were not genotyped in AUS and were included in this study. Of the 3,072 bull genotypes received from LIC, 1,472 Holstein and 1,182 Jersey bulls were not genotyped in AUS and none had AUS daughters for inclusion in the Australian Dairy Herd Improvement Scheme (**ADHIS**) routine genetic evaluation. The genotype data of these bulls, which were evaluated using the commercial Illumina BovineSNP50 chip (Illumina, San Diego, CA), were edited for imputation up to the same number of SNP (43,990) as the AUS data. When imputing these Holstein and Jersey bulls, the genotype data of AUS Holstein and Jersey bulls, respectively, were used as a reference set, and Beagle (Browning and Browning, 2009) was used for imputation.

The genotype data provided by CRV were carried out using 1 of the 2 versions of a custom 50,000 SNP chip. The CRV custom 50,000 SNP panel and the commercial

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