



J. Dairy Sci. 100:1–12
<https://doi.org/10.3168/jds.2016-11811>
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Accuracy of genomic predictions in Gyr (*Bos indicus*) dairy cattle

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ABSTRACT

Genomic selection may accelerate genetic progress in breeding programs of indicine breeds when compared with traditional selection methods. We present results of genomic predictions in Gyr (*Bos indicus*) dairy cattle of Brazil for milk yield (MY), fat yield (FY), protein yield (PY), and age at first calving using information from bulls and cows. Four different single nucleotide polymorphism (SNP) chips were studied. Additionally, the effect of the use of imputed data on genomic prediction accuracy was studied. A total of 474 bulls and 1,688 cows were genotyped with the Illumina BovineHD (HD; San Diego, CA) and BovineSNP50 (50K) chip, respectively. Genotypes of cows were imputed to HD using FImpute v2.2. After quality check of data, 496,606 markers remained. The HD markers present on the GeneSeek SGGP-20Ki (15,727; Lincoln, NE), 50K (22,152), and GeneSeek GGP-75Ki (65,018) were subset and used to assess the effect of lower SNP density on accuracy of prediction. Deregressed breeding values were used as pseudophenotypes for model training. Data were split into reference and validation to mimic a forward prediction scheme. The reference population consisted of animals whose birth year was ≤ 2004 and consisted of either only bulls (TR1) or a combination of bulls and dams (TR2), whereas the validation set consisted of younger bulls (born after 2004). Genomic BLUP was used to estimate genomic breeding values (GEBV) and reliability of GEBV (R^2_{PEV}) was based on the prediction error variance approach. Reliability of GEBV ranged from ~ 0.46 (FY and PY) to 0.56 (MY) with TR1 and from 0.51 (PY) to 0.65 (MY) with TR2. When averaged across all traits, R^2_{PEV} were substan-

tially higher (R^2_{PEV} of TR1 = 0.50 and TR2 = 0.57) compared with reliabilities of parent averages (0.35) computed from pedigree data and based on diagonals of the coefficient matrix (prediction error variance approach). Reliability was similar for all the 4 marker panels using either TR1 or TR2, except that imputed HD cow data set led to an inflation of reliability. Reliability of GEBV could be increased by enlarging the limited bull reference population with cow information. A reduced panel of $\sim 15K$ markers resulted in reliabilities similar to using HD markers. Reliability of GEBV could be increased by enlarging the limited bull reference population with cow information.

Key words: indicine, genomic selection, small population, genotyping females

INTRODUCTION

The past decade has seen increasing adoption of genomic evaluations (termed as genomic selection; **GS**) in taurine dairy cattle populations around the world. The benefit of using whole-genome dense marker panel information for estimating genomic breeding values (**GEBV**) has been seen for several plant and animal populations. In dairy cattle populations, genomic evaluation has caused an increase in genetic gain (Hutchison et al., 2014) and accuracy of selection (VanRaden et al., 2009; Su et al., 2010) and a drastic decrease in generation interval (Schaeffer, 2006; Hutchison et al., 2014) compared with traditional selection methods. Genomic breeding values are estimated for genotyped individuals using estimate of marker effects (Meuwissen et al., 2001; Habier et al., 2011; Erbe et al., 2012). Alternatively, genomic relationships obtained from dense genome-wide SNP markers or a combination of marker genotypes and pedigree information are also widely used (VanRaden, 2008; Legarra et al., 2009).

In most dairy cattle populations, the reference population for genomic selection are mainly made up

Received August 1, 2016.

Accepted January 3, 2017.

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Table 1. Total number of animals with phenotypes and genotypes for milk (MY), protein (PY), and fat (FY) yield and age at first calving (AFC)

| Trait | Total number of animals | Number of bulls | Number of cows |
|-------|-------------------------|-----------------|----------------|
| MY | 2,023 | 433 | 1,590 |
| FY | 1,871 | 400 | 1,471 |
| PY | 1,556 | 379 | 1,177 |
| AFC | 2,004 | 422 | 1,582 |

of progeny-tested bulls with reliable pseudophenotypes [mostly, deregressed breeding values (**dEBV**) or daughter yield deviations]. However, in populations with a limited number of progeny-tested bulls, several other alternatives have been suggested. Some of the adopted approaches include sharing genotypes within and across countries by several breeding organizations such as Interbull (<http://www.interbull.org/ib/interbullcentremain>; Wiggans et al., 2015), combining information across breeds (Hayes et al., 2009; Hozé et al., 2014), and adding genotyped cows to the reference populations (Wiggans et al., 2011; Ding et al., 2013; Thomasen et al., 2014; Lourenco et al., 2014). Addition of cows to reference populations is an attractive alternative, as cow information is more readily available; however, GEBV have been reported to be biased when elite cows are added to reference population in genomic evaluations (Dassonneville et al., 2012).

Genomic selection has been well studied in both large and small populations of *Bos taurus* dairy cattle breeds (VanRaden et al., 2009; Luan et al., 2009; Mulder et al., 2010; Brøndum et al., 2011). However, a dearth of knowledge exists on the potential of GS in *Bos indicus* dairy cattle populations. Recent studies in an indicine beef cattle population (Nelore) suggested that GS is a feasible alternative to traditional selection approaches (Neves et al., 2014). The present study was undertaken on Gyr (*Bos indicus*), which is an important dairy cattle breed of Brazil. The Brazilian Gyr cattle have gained prominence as an efficient milk production breed in the tropics, producing relatively high amount of milk (~3,000 kg of milk per 305 DIM) and having good adaptability to tropical conditions, such as resistance to ticks, worms, and mastitis (Santana et al., 2014). In Brazil, about 80% of dairy herds are composed of Gyr and their crosses with Holstein. The Gyr breed is known to have about 400,000 registered animals in its national herdbook; however, progeny testing of bulls began only about 3 decades ago and the number of bulls that have been involved in the program is about 450 (Santana et al., 2014). Furthermore, DNA samples from some progeny-tested bulls and most of the non-progeny-tested bulls from the Brazilian population were

not stored. Thus, in Gyr, a large reference population for preliminary GS study required the addition of cow data to the limited bull data set. The overall aim of the current study was to test the feasibility of genomic selection in Brazilian Gyr on milk production traits and age at first calving.

MATERIALS AND METHODS

Phenotype Data

Pseudophenotypes used as response variables in genomic models were dEBV for milk yield (**MY**), fat yield (**FY**), protein yield (**PY**), and age at first calving (**AFC**), computed for both bulls and cows of Brazilian Gyr dairy cattle. Deregression of EBV followed the procedure of Garrick et al. (2009). The EBV were obtained from the 2014 routine genetic evaluation with 28,133 individuals of Embrapa Gado de Leite, Juiz de Fora, Brazil. For genomic prediction analysis, individuals (bulls and cows) with EBV reliability <0.25 were discarded. Heritability estimates were 0.28 for MY, 0.22 for both FY and PY, and 0.18 for AFC. Table 1 shows the number of animals used for genomic prediction after quality check of both phenotype and genotype data set. The distribution of sires and dams across birth years is presented in Figure 1.

Genotype Data

Four hundred seventy-four bulls and 1,688 cows were genotyped with the Illumina BovineHD (**HD**; Illumina, San Diego, CA) and Illumina BovineSNP50 (**50K**) BeadChip, respectively. Quality check (**QC**) was performed using PLINK v1.07 (Purcell et al., 2007). Samples with a call rate <90% were removed from the analysis. Nonautosomal and unmapped SNP were discarded. Markers deviating from Hardy-Weinberg equilibrium (Fishers exact test; P -value <10⁻⁶) and those with call rate <90% were also removed. In addition to the above QC, markers with minor allele frequency <2% were deleted for Illumina HD. Mendelian inconsistencies were checked and pedigree relationships as well as discordant markers were set to unknown and missing. After QC, 471 bulls with 496,606 SNP and 1,644 cows with 47,668 SNP remained. Out of the 47,668 markers, 22,152 were present on the quality checked Illumina HD.

To be able to undertake genomic prediction with the HD markers using data from bulls and cows, the latter were imputed from Illumina 50K to HD with FImpute version 2.2 (Sargolzaei et al., 2014). Genotyped bulls were used to generate the haplotype library needed for the imputation of cows genotypes to Illumina HD. Ad-

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