Accuracy of Genomic Selection for Growth Traits in Nellore Cattle


1The study was funded by National Counsel of Technological and Scientific Development (CNPq), Brasilia, DF, Brazil, 2Universidade Estadual de Sào Paulo, Jaboticabal, SP, Brazil, 3Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil 4Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada.

ABSTRACT: The objective of this study was to evaluate the accuracy of prediction of genomic breeding values using GBLUP method for genomic selection of weight gain from birth to weaning (GBW) and from weaning to yearling (GWY) in Nellore cattle. The genotyping of 2,660 Nellore animals was performed using the Illumina BovineHD BeadChip (777,962 SNPs). The accuracy of genomic prediction was assessed by 5-fold cross-validation. De-regressed estimated breeding values (DEBVs) were calculated using VanRadens’s method and then used as pseudo-phenotypes in the genomic analyses. The accuracy of genomic prediction was evaluated by the correlation (CORR) between EBVs and predicted direct genomic values (DGVs) for animals in the validation group. The regression coefficient of the regression of EBVs on the DGVs (b) was calculated to evaluate the degree of inflation/deflation of genomic predictions. Low accuracies of genomic predictions (CORR = 0.21) for both traits, with highly inflated DGVs (b = 0.25 and 0.38 for GBW and GWY, respectively) were found. The results suggest the need for further studies using alternate prediction methods in genomic analysis and possibly the need for a larger training population for obtaining more accurate genomic predictions.

Keywords: beef cattle genomic breeding value Nellore weight gain

Introduction

In recent years, after the sequencing of the human genome and several species of domestic animals, a significant amount of work on the application of genomic data to animal breeding has been published around the world. Despite major advances in molecular biology that permit to genotype thousands of animals, the methodologies that enable application of genomic data in breeding programs are still being developed. According to Schaeffer (2006) the advantages of genomic selection are too large to be ignored, because the genetic gains can be two times higher when compared to the traditional progeny testing and the value of logistics costs can be reduced by up to 92% compared to costs of traditional progeny test schemes. Genotyping costs are likely to decrease over time, which makes the implementation of genomic selection more accessible. Schrooten et al. (2005) reported increased genetic progress from 19 to 31% compared to progeny testing, when the molecular markers explained 50% of the genetic variance. For Zhang et al. (2011) the genomic selection is a reformulation of animal breeding system, and can replace the traditional genetic evaluation in a short period of time.

The objective of this study was to evaluate the accuracy of prediction of genomic values obtained by GBLUP method for genomic selection of weight gain from birth to weaning (GBW) and from weaning to yearling (GWY) in Nellore cattle.

Materials and Methods

Data and Statistical analysis. Data from 2,660 Nellore animals (1,658 females and 1,002 males) belonging to farms from the Midwestern, Northeastern and Southeastern regions of Brazil were used. Estimated breeding values (EBVs) and corresponding accuracies for weight gain from birth to weaning (GBW) and weight gain from weaning to yearling (GWY) were estimated using the ASREML software (http://www.vsni.co.uk/software/asreml I; VSN International Inc., Hemel Hempstead, UK). The EBVs were then deregressed (VanRaden and Wiggans (1991)) for further genomic analyses.

The animals were genotyped using the Illumina BovineHD SNP panel (Illumina Inc., San Diego, CA, USA), which contains 777,962 SNPs. The following exclusion criteria for SNPs were applied: Not autosomal SNPs, SNPs located at the same position, minor allele frequency (MAF) < 3%, SNP genotyping call rate < 98%. Samples with call rate < 95% were also excluded from the analysis. After quality control, 2,649 animals and 512,744 SNPs for GBW and 1,234 animals and 513,134 SNPs for GWY were used in the genomic analyses. Accuracy of genomic predictions was assessed by 5-fold cross-validation. Data were randomly divided into 5 groups with approximately 531 and 246 animals for GBW and GWY, respectively. Four groups were used for training and 1 group for validation and after the cross-validation process each group was considered once as a validation group. The genomic analyses were performed using the GEBV program (Sargolzaei et al. (2009)), using the GBLUP method, applying the following model:
Accuracy of genomic prediction was measured as either the correlation (CORR) between the EBVs and DGVs of the animals in the validation group, or the theoretical accuracy of DGVs (Accd), obtained from the elements of the inverse of the left hand side of the mixed model equation for the GBLUP method. The regression coefficient of the regression of the EBVs on the DGV (b) was calculated to evaluate the degree of inflation/deflation of genomic predictions.

**Results and Discussion**

The heritability estimates (± SE) for GBW and GWY were 0.41 ± 0.006 and 0.20 ± 0.006, respectively. Table 1 and Table 2 show a summary of the genomic prediction for GBW and GWY, respectively. The values are presented for each of the cross-validation analyses and for the average values over all 5 cross-validations. The average accuracy of the GBW EBVs for both training and validation groups was 0.72. For GWY the average accuracy of EBVs was lower (0.56), but again similar for both training and validation groups.

**Table 1. Summary statistics of genomic prediction for weight gain from birth to weaning (GBW).**

<table>
<thead>
<tr>
<th>C-Val</th>
<th>Ntr</th>
<th>Acctr</th>
<th>Nval</th>
<th>Accval</th>
<th>CORR</th>
<th>Accd</th>
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<td>529</td>
<td>0.72</td>
<td>0.20</td>
<td>0.48</td>
<td>0.36</td>
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<td>0.72</td>
<td>530</td>
<td>0.72</td>
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<tr>
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<td>0.25</td>
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<tr>
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<tr>
<td>Mean</td>
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<td>530</td>
<td>0.72</td>
<td>0.23</td>
<td>0.48</td>
<td>0.38</td>
</tr>
</tbody>
</table>

C-Val: Cross-validation 1, 2, 3, 4 and 5; Ntr: number of animals in the training population; Acctr: accuracy of EBVs in the training population; Nval: number of animals in the validation population; Accval: accuracy of EBVs in the validation population; CORR: Pearson correlation between EBVs and the predicted direct genomic values (DGVs); Accd: direct theoretical accuracy of genomic values (DGVs) obtained from the elements of the inverse of the left hand side of the GBLUP mixed model equations; b: coefficient of regression of EBVs on DGVs.

The estimated average correlation between EBVs and DGVs (CORR) was 0.21 for both traits, while the theoretical direct accuracy of DGVs (Accd) was 0.48 and 0.28 for GBW and GWY, respectively.

An average value much smaller than 1 was found for the coefficient of regression of EBVs on DGVs, indicating an inflation on DGVs values, so that DGVs would predict larger differences among individuals compared to EBVs.

Saatchi et al. (2011), using a larger number of animals and BayesC method investigated the Accd (defined as the correlation between true genetic values and DGV) for 16 economically important traits in Angus breed, obtained by Kmeans and random clustering methods. These authors found Accd values ranging from 0.22 to 0.85 for all traits, where the value found for growth traits (weaning weight and yearling weight) were 0.33 and 0.36, respectively. Garrick (2011) found higher accuracies, ranging from 0.52 to 0.56 for growth traits in beef cattle. On the other hand, Pryce et al. (2011), working with growing heifers and using a 600k panel, reported accuracies of genomic breeding values ranging from 0.25 to 0.40 for 250-d body weight when using GBLUP method.

**Conclusion**

Results suggest that genomic selection might be implemented in the future for Nellore growth traits, but more studies will be necessary to increase accuracy of genomic prediction by using a larger training population size and/or alternative prediction methods. More research is, therefore, warranted.

**Literature Cited**


Acknowledgements

The authors would like to thank GenSys and the breeding programs of beef cattle (DeltaGen, Qualitas and PAINT) that have provided the data.
The National Counsel of Technological and Scientific Development (CNPq) for granting the fellowships.
The Centre for Genetic Improvement of Livestock (CGIL) for the contribution in the analyses.