

Genomic Predictions of Economically Important Traits in Nelore Cattle of Brazil

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ABSTRACT: Currently, genome-wide selection methods are being successfully applied in dairy and beef breeds world-wide. Direct genomic breeding values (DGVs) in these breeds are estimated using genotypes generated either through high density SNP arrays such as Illumina BovineSNP50 BeadChip or by imputing these genotypes from low density arrays such as Illumina BovineLD BeadChip. However, research on applied genomic selection in tropical breeds such as Nelore is rather limited. The objective of this study is to estimate DGVs for several economically important traits routinely evaluated at National Association of Breeders and Researchers (Associação Nacional de Criadores e Pesquisadores - ANCP). This study also examines the increase in accuracy of genomic predictions when utilizing higher density chips such as Illumina BovineHD SNP chip (HD chip). The average accuracy for reproductive, productive, visual body conformation scores, and other traits were respectively 0.58, 0.53, 0.34, and 0.57.

Keywords:

Genomic selection

Productive and reproductive traits

Introduction

There are a number of traits recorded in Nelore national evaluation programs that contribute to the economic efficiency of beef production in Brazil. In this study, the genomic selection approach (Meuwissen et al. (2001)) was applied to enhance accuracy of selection in Nelore cattle. Reproductive traits included: age at first calving, gestation period, heifer pregnancy, scrotal circumference at 365 and 450 days and stayability. Production traits included maternal ability at 120 and 240 days, and weight at 120, 210, 365 and 450 days. Accumulated production, an index trait, takes into account cow's ability to give birth regularly (and early), and to wean heavier calves (Lobo et al. (2000)).

Visual body conformation scores have been used in Nelore cattle genetic evaluation program to predict finishing precocity and carcass maturity and quality. In this study, three such visual scores measured at weaning and yearling were studied; body conformation, muscularity, and precocity. In addition, other traits such as mature height, fat thickness, and rib eye area were also evaluated.

The Illumina BovineSNP50 BeadChip was developed for Taurus cattle; and, as a result, only half of

the markers on BovineSNP50 are segregating in Nelore cattle. The Illumina HD Beadchip was designed to include markers specifically segregating in Indicus cattle. Thus, in this study, an attempt was also made to evaluate the improvement in genomic prediction accuracy associated with use of Bovine HD Beadchip genotypes.

Materials and Methods

Data: A total of 2,241 Nelore cattle with EBVs and genotypes were available for this study: 763 of the animals were genotyped with Illumina BovineHD BeadChip (HD) and the remaining animals were genotyped with Illumina BovineSNP50 v2 BeadChip (50K). All 50K genotypes were imputed to HD using FImpute (Sargolzaei et al. (2010)).

Traits: A total of 22 EBV traits were classified into four trait groups: reproductive, productive, visual body conformation scores, and other traits. The list of specific traits in each trait group, heritability estimates, and summary statistics are presented in Table 1.

Genotypes: Markers with minor allele frequency (MAF) less than 0.05 were removed from the analysis. The number of markers utilized for genomic predictions were 25,458 and 492,887 for 50K and HD respectively.

Data splits for cross-validation and training: A subset of data consisting of higher accuracy EBVs was used to estimate genomic predictions. The accuracy cut-off thresholds for this purpose were determined based on the accuracies of weight at 120 days, body conformation at weaning and rib eye area. For each trait, the training dataset was classified into five equally sized cross-validation groups using IBS-based clustering methods (Boddhireddy et al. (2014)). Each IBS cluster consisted of animals that were more closely related to the animals within the cluster and distantly related to animals outside. This clustering strategy allows one to compute predictive correlations in distantly related group of animals through cross-validation methods. In the cross-validation approach, a prediction equation was developed using the marker effects estimated in four of the five groups and tested in the fifth group that was not used for marker effect estimation. This fifth group provided the cross-validation results from that calibration. This process was repeated five times leaving a different group out of the estimation of marker effects each time.

Computation and evaluation of DGVs: The allele substitution effect for each marker was computed using

Table 1: Heritability estimates and summary statistics for the traits used in this study. Heritability is denoted as h^2 .

Trait	h^2	Animals	Mean EPD	Mean BIF Accuracy
Reproductive traits				
Age at first calving, months	0.11	1,496	-0.53	0.26
Gestation period	0.37	1,496	0.58	0.32
Heifer pregnancy rate, %	0.24	1,496	48.97	0.18
Scrotal circumference at 365 days, cm	0.40	1,496	0.19	0.35
Scrotal circumference at 450 days, cm	0.43	1,496	0.21	0.36
Stayability, %	0.12	1,496	55.92	0.23
Productive traits				
Accumulated production, kg/yr	0.20	1,496	3.16	0.24
Maternal ability at 120 days, kg	0.11	1,496	1.22	0.29
Maternal ability at 210 days, kg	0.10	1,496	1.48	0.28
Weight at 120 days, kg	0.23	1,496	2.60	0.42
Weight at 210 days, kg	0.25	1,496	4.07	0.41
Weight at 365 days, kg	0.32	1,496	7.85	0.45
Weight at 450 days, kg	0.34	1,496	8.33	0.45
Visual scores				
Body conformation at weaning	0.53	777	56.04	0.45
Body conformation at yearling	0.51	777	60.49	0.45
Muscularity at weaning	0.53	777	52.51	0.47
Muscularity at yearling	0.44	777	55.58	0.38
Precocity at weaning	0.53	777	50.05	0.38
Precocity at yearling	0.49	777	54.60	0.38
Other traits				
Height	0.25	1,046	0.56	0.17
Fat thickness, mm	0.35	1,030	-0.02	0.35
Rib eye area, cm ²	0.35	1,053	0.20	0.35

Gensel (Fernando and Garrick (2008)), ‘BayesC’ method. The value of π denoting the proportion of markers excluded iteratively was 0.90 and 0.99 for BovineSNP50 and HD data, respectively. The description of estimation of marker effects and pooled correlation across five cross-validation groups are given in Boddhireddy et al. (2014). The DGV of each animal in the dataset was calculated by summing the products of the estimated marker substitution effects and the number of ‘A’ alleles in the genotype. Evaluation of genomic prediction accuracies was achieved by computing the correlation between DGVs and EBVs. In addition, the regression of EBVs on DGVs was calculated to evaluate prediction bias.

Table 2: Genomic prediction accuracies in 50K and HD datasets. Accuracy is measured as correlation between EBVs and DGVs. Cor_50K and Cor_HD denotes accuracies and Reg_50K and Reg_HD denotes bias associated with prediction accuracies respectively for 50K and HD datasets.

Trait	Cor_50K	Reg_50K	Cor_HD	Reg_HD
Age at first calving, months	0.64	0.89	0.64	0.90
Gestation period	0.46	0.71	0.50	0.79
Heifer pregnancy rate, %	0.64	0.87	0.64	0.89
Scrotal circumference at 365 days, cm	0.57	0.89	0.59	0.95
Scrotal circumference at 450 days, cm	0.56	0.86	0.59	0.93
Stayability, %	0.58	0.70	0.59	0.77
Reproductive Average	0.58	0.82	0.59	0.87
Accumulated production, kg/yr	0.51	0.70	0.54	0.79
Maternal ability at 120 days, kg	0.48	0.73	0.50	0.81
Maternal ability at 210 days, kg	0.48	0.74	0.51	0.82
Weight at 120 days, kg	0.63	0.94	0.63	0.94
Weight at 210 days, kg	0.61	0.84	0.64	0.89
Weight at 365 days, kg	0.56	0.79	0.52	0.69
Weight at 450 days, kg	0.44	0.53	0.46	0.60
Productive Average	0.53	0.75	0.54	0.79
Body conformation at weaning	0.31	0.40	0.36	0.44
Body conformation at yearling	0.29	0.35	0.30	0.36
Muscularity at weaning	0.30	0.38	0.28	0.34
Muscularity at yearling	0.40	0.52	0.32	0.34
Precocity at weaning	0.37	0.47	0.34	0.42
Precocity at yearling	0.37	0.47	0.38	0.48
Visual Scores Average	0.34	0.43	0.33	0.40
Height	0.72	0.98	0.71	0.97
Fat thickness, mm	0.41	0.68	0.42	0.72
Rib eye area, cm ²	0.58	0.87	0.59	0.89
Other Traits Average	0.57	0.84	0.57	0.86

Results and Discussion

The accuracy of genomic predictions in cross-validation datasets with 50K and HD data is presented in Table 2. The five-fold cross validation correlations for reproductive traits ranged from 0.46 to 0.64 with a mean of 0.58 with 50K dataset and from 0.50 to 0.64 with a mean of

0.59 with HD dataset; for production traits, the correlations ranged from 0.44 to 0.63 with a mean of 0.53 with 50K dataset and from 0.46 to 0.64 with a mean of 0.54 with HD dataset; for visual body conformation scores, the correlations ranged from 0.29 to 0.40 with a mean of 0.34 with 50K dataset and from 0.28 to 0.38 with a mean of 0.33 with HD dataset, and the correlations for rest of the traits ranged from 0.41 to 0.72 with a mean 0.57 with 50K dataset and from 0.42 to 0.71 with a mean 0.57 with HD dataset. The regression coefficients on average were 0.82, 0.75, 0.47, and 0.84 with 50K dataset and were 0.87, 0.79, 0.40, and 0.86 with HD dataset respectively for reproductive, productive, visual body conformation scores, and other traits. The regression coefficients are lower than one, indicating that estimates were biased upwards.

For reproductive and productive traits, the accuracies were slightly lower than those observed for the same traits in recent studies in Angus cattle (Boddhireddy et al., (2014), and Saatchi et al. (2013)), likely due to fewer available records in this study. Genomic predictions of visual body conformation scores were estimated for the first time in cattle and no comparable studies are available. The accuracies for visual scores were generally lower than other trait categories despite high BIF accuracy. The accuracies of height, fat thickness, and rib-eye area traits were slightly lower than those observed in Angus study mentioned above. Increasing the marker density from 50K to HD resulted in only a slight improvement in accuracy (about 2 to 3%) for production and reproduction traits. However, across all traits evaluated in this study, there were no significant differences between prediction accuracies between 50K and HD, which is in agreement with the results in dairy cattle (VanRaden et al. (2013)).

For a given trait, only animals with high BIF accuracy were used for the estimation of SNP effects, even though greater numbers of genotyped animals with EBVs were available. For instance in the category of productive and reproductive traits, out of 2,250 available records, only 1,496 animals were used for the analysis. Further the EBVs were weighted by their respective accuracies in Bayes C method to ensure robust SNP effect estimates. While the accuracies obtained here suggests potential application of genomic selection for all the traits evaluated in this study, the predictions are most beneficial for low heritability and difficult to measure traits such as age at first calving, stayability, accumulated production, and maternal ability.

Conclusion

In this study, we report for the first time the results from a comprehensive analysis of genomic selection across several economic traits in Nelore cattle using high density SNP genotypes such as 50K chip and HD chip. Increasing the marker density from 50K to HD did not improve prediction accuracy. The genomic breeding values can be successfully integrated into genetic evaluation programs to compute genomically enhanced breeding values (GEBVs) to further increase the accuracies of breeding values to enable better selection decisions.

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