Implementation of DNA Markers to Produce Genomically - Enhanced EPDs in Nellore Cattle

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ABSTRACT

Background: The sequencing and publication of the cattle genome and the identification of single nucleotide polymorphism (SNP) molecular markers have provided new tools for animal genetic evaluation and genomic-enhanced selection. These new tools aim to increase the accuracy and scope of selection while decreasing generation interval. The objective of this study was to evaluate the enhancement of accuracy caused by the use of genomic information (Clarifide® - Pfizer) on genetic evaluation of Brazilian Nellore cattle.

Review: The application of genome-wide association studies (GWAS) is recognized as one of the most practical approaches to modern genetic improvement. Genomic selection is perhaps most suited to the improvement of traits with low heritability in zebu cattle. The primary interest in livestock genomics has been to estimate the effects of all the markers on the chip, conduct cross-validation to determine accuracy, and apply the resulting information in GWAS either alone [9] or in combination with bull test and pedigree-based genetic evaluation data. The cost of SNP50K genotyping however limits the commercial application of GWAS based on all the SNPs on the chip. However, reasonable predictability and accuracy can be achieved in GWAS by using an assay that contains an optimally selected predictive subset of markers, as opposed to all the SNPs on the chip. The best way to integrate genomic information into genetic improvement programs is to have it included in traditional genetic evaluations. This approach combines traditional expected progeny differences based on phenotype and pedigree with the genomic breeding values based on the markers. Including the different sources of information into a multiple trait genetic evaluation model, for within breed dairy cattle selection, is working with excellent results. However, given the wide genetic diversity of zebu breeds, the high-density panel used for genomic selection in dairy cattle (Ilumina Bovine SNP50 array) appears insufficient for across-breed genomic predictions and selection in beef cattle. Today there is only one breed-specific targeted SNP panel and genomic predictions developed using animals across the entire population of the Nellore breed (www.pfizersaudeanimal.com), which enables genomically - enhanced selection. Genomic profiles are a way to enhance our current selection tools to achieve more accurate predictions for younger animals.

Material and Methods: We analyzed the age at first calving (AFC), accumulated productivity (ACP), stayability (STAY) and heifer pregnancy at 30 months (HP30) in Nellore cattle fitting two different animal models; 1) a traditional single trait model, and 2) a two-trait model where the genomic breeding value or molecular value prediction (MVP) was included as a correlated trait. All mixed model analyses were performed using the statistical software ASREML 3.0.

Results: Genetic correlation estimates between AFC, ACP, STAY, HP30 and respective MVPs ranged from 0.29 to 0.46. Results also showed an increase of 56%, 36%, 62% and 19% in estimated accuracy of AFC, ACP, STAY and HP30 when MVP information was included in the animal model.

Conclusion: Depending upon the trait, integration of MVP information into genetic evaluation resulted in increased accuracy of 19% to 62% as compared to accuracy from traditional genetic evaluation. GE-EPD will be an effective tool to enable faster genetic improvement through more dependable selection of young animals.

Keywords: DNA Markers, Genomic Enhanced EPDs, Genetic Evaluation, Genomic Selection, Nellore Cattle, SNP.

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I. INTRODUCTION
II. MATERIAL AND METHODS
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I. INTRODUCTION

Genetic evaluation programs have significantly increased the productivity of animals and the quality as well as yield of beef products throughout the world. In Brazil, there was a significant positive genetic trend in traits of interest in beef cattle [10]. However, this genetic progress can be maximized if the best animals are identified early in life and more aggressively propagated.

After the discovery of single nucleotide polymorphism (SNP) molecular markers and the genome cattle publication, new approaches have been proposed for genetic evaluation in order to increase the accuracy of estimated breeding values and decrease the time needed for dependable evaluation of the animals (i.e. decrease generation interval and increase the genetic progress). The process of using genomic information to assist in animal selection is called genomic-enhanced selection.

The genomic-enhanced selection in dairy cattle is working with excellent results. However, given the wide genetic diversity of the zebu breeds, and considering the influence of Taurus breeds, the panel used for genomic selection in dairy cattle (Ilumina Bovine SNP50 array) appears insufficient for across-breed genomic predictions and selection in zebu cattle [10]. Despite being less informative for zebu breeds, recent efforts have proven that it is possible to use the SNP50K for effective genomic-enhanced predictions and selection. Therefore a breed specific targeted SNP panel and genomic predictions was developed by Pfizer which enables genomically-enhanced selection on Nellore cattle.

In the present study, we proposed an approach to evaluate the improvement in accuracy from integration of genomic information (Clarifide® - Pfizer) into the genetic evaluation of Brazilian Nellore cattle.

II. MATERIALS AND METHODS

Phenotypic data were collected from Nellore animals, belonging to farms participating in the Nellore Brazil Genetic Evaluation Program, coordinated by the National Association of Breeders and Researchers ("Associação Nacional de Criadores e Pesquisadores" - ANCP). Traits included in these analyses were: age at first calving (AFC), accumulated productivity (ACP), stayability (STAY), and heifer pregnancy at 30 months (HP30). Molecular value predictions (MVP) for each trait (MVP_{AFC}, MVP_{ACP}, MVP_{STAY}, MVP_{HP30}) were determined from Clarifide prediction equations (Clarifide is a registered trademark of Pfizer Animal Health) specifically developed for Nellore cattle.

AFC is a measure of the age of entry of heifers into the beef cattle production system. This is an easily measured trait that can be used as a selection criterion for earlier expressed reproductive performance. ACP is an index that evaluates female productivity, considering progeny weight at weaning and number of offspring produced. The ACP depends directly on age at first calving, the calving intervals, and on the duration of time the cow remains in the herd. ACP expresses the cow's ability to conceive and give birth regularly, to begin production early in life, and to wean heavier calves [6]. STAY is a trait that has a large impact on the costs of beef production because it is directly related to the cow's ability to produce a number of calves over a given period of time [1], and the need for resources to be used for producing replacement females. HP30 quantifies the probability of successful conception and calving by 30 months of age.

The best way to implement the genomic information into breeding programs is to simply integrate the genomic predictions into traditional genetic evaluation. Using this approach, traditional expected progeny differences based on phenotypic and pedigree information is combined with genomic predictions based on markers. Another approach is to include the two sources of information into a multiple trait genetic evaluation model [10].

We analyzed reproductive traits in Nellore cattle with two different animal models. The traditional single trait model and a two-trait model where the MVP was fit as a correlated trait were analyzed. The linear mixed model used to estimate MVP genetic variances and covariances, breeding values and respective accuracy is described in [8]. All mixed models analyses were performed using the

statistical software ASREML 3.0 [3] fitting an animal model similar to those used in the Nellore Brazil Genetic Evaluation to all traits analyzed. MVP models included just the overall mean. We analyzed 813 animals with MVP for all traits evaluated. The data available for each trait are described on Table 1.

Estimated accuracies of EPD from analyses with and without MVP information were compared to calculate the increase in accuracy caused by the inclusion of MVP in the genetic evaluation of animals for these traits.

III. RESULTS

Mean values, standard deviations, minimums and maximums for AFC, ACP, STAY, HP30 and respective MVPs are provided in Table 2.

The estimated heritabilities for AFC, ACP, STAY and HP30 were 0.11, 0.20, 0.12 and 0.24, respectively and for MVP_{AFC}, MVP_{ACP}, MVP_{STAY} and MVP_{HP30} the heritabilities ranged from 0.95 to 0.98. Genetic correlation estimates between AFC, ACP, STAY, HP30 and respective MVPs ranged from 0.29 to 0.46.

The difference between the average GE-EPD and the average of traditional EPD ranged from 1 to 11%. This variation occurs because the MVP is new information that can move up or down the traditional EPD. However, the GE-EPD estimates are in average more accurate than traditional EPD (Table 3).

Table 3. shows the accuracy increase for all traits when the MVP information was included in the genetic evaluation.

Table 1. Description of data used to estimate the variance components and genomic-enhanced expected progeny difference for age at first calving (AFC), accumulated productivity (ACP), stayability (STAY) and heifer pregnancy at 30 months (HP30).

Trait	N	Phenotype	MVP
AFC	18462	18457	813
ACO	10325	9837	813
STAY	17218	16694	813
HP3O	4014	3760	813

Table 2. Means, standard deviations (SD), and minimum (Min) and maximum (Max) values for age at first calving (AFC), accumulated productivity (ACP), stayability (STAY) and heifer pregnancy at 30 months (HP30) and respective molecular value predictions (MVP).

Trait	N	Min	Max	Mean+SD
$AFC_{(months)}$	18457	21.00	49.00	35.80±5.59
$MVP_{AFC(months)}$	813	-2.21	1.28	-0.33±0.55
$ACP_{(kilograms)}$	9837	55.00	264.00	150.99±29.87
$MVP_{ACP(kilograms)}$	813	-5.48	12.01	1.51±3.03
$STAY_{(probability)}$	16694	0.00	1.00	0.43±0.50
$MVP_{STAY(probability)}$	813	46.96	63.74	53.40±3.00
$HP30_{(probability)}$	3760	0.00	1.00	0.26±0.44
$MVP_{HP30(probability)}$	813	43.81	58.68	49.42±2.59

Table 3. Mean accuracy of expected progeny difference estimated in the analysis without using Clarifide predictions (without MVP) and considering the molecular value predictions (with MVP) in the model for age at first calving (AFC), accumulated productivity (ACP), stayability (STAY) and heifer pregnancy at 30 months (HP30).

Trait	Accuracy Mean[a]		Increase	
	Without MVP	With MVP	Difference	(%)[b]
AFC	0.16	0.25	0.09	56
ACP	0.14	0.19	0.05	36
STAY	0.13	0.21	0.08	62
HP30	0.16	0.19	0.03	19

[a]Beef Improvement Federation (BIF) accuracy; [b]Increase observed by inclusion of predicted molecular value (MVP) in animal genetic evaluation.

IV. DISCUSSION

The observed means are similar to those reported for the Nellore breed [7], showing that the data file analyzed is representative of the breed in Brazil.

Estimated heritabilities are consistent with those previously reported to Nellore cattle [5,14], except for HP30 where [2,12] reported large heritabilities. However, the data used was smaller than those considered by [2,12]. In despite of the large MVP heritabilities estimates, it was expected since MVPs are the sum of SNP additive genetic effects present on Clarifide® panel and it should have a smaller environment variance component.

Considering that heritabilities account for correlation between estimated breeding values and phenotypes and that the MVP genetic correlation with the phenotype (from 0.29 to 0.46) are higher than the estimated heritabilities (from 0.11 to 0.24), we can summarize that GE-EPD are more correlated with phenotype than traditional EPD. It will result in greater response to selection consequently more genetic gain per generation when used GE-EPD as a selection criterion.

The increase in accuracy observed in this research (Table 3) are similar with those reported by [8] in carcass marbling trait of Angus cattle that found an accuracy increase ranging from 36 to 85%. It should be recognized from this results that the use of Clarifide® information can provide more accurate EPDs for these traits.

V. CONCLUSIONS

Depending upon the trait, integration of MVP information into genetic evaluation resulted in increased accuracy of 19% to 62% as compared to accuracy from traditional genetic evaluation. GE-EPD will be an effective tool to enable faster genetic improvement through more dependable selection of young animals.

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