MARKER ASSISTED SELECTION FOR MEAT QUALITY TRAITS

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Abstract – This paper evaluated the impact of the inclusion of molecular breeding values provided by a commercial panel of very low density of genetic markers (Nellore Profile IGENITY® V3) on a beef cattle breeding program under marker assisted selection. Data of 1,849 genotyped animals, corresponding to 9,802 animals on the relationship matrix, were used. From those, 602 animals presented measurements for Warner-Bratzler shear force after 7, 14 and 21 days of ageing (WBSF7, WBSF14 and WBSF21, kg) and total lipid content at *Longissimus* muscle (LIPID). The impact of using molecular breeding values as a third source of information on selection for meat quality traits was evaluated comparing the accuracy of estimates of breeding values obtained on single and two-trait analyses within categories of animals. The effect of including molecular breeding values on classical genetic evaluation varied with subgroups of animals as well as different traits, but was greater for young animals (STEER and HEIFER). It is hence concluded that this low-density SNP marker panel was useful in marker-assisted selection programs for meat quality traits on the Nellore population analyzed.

Key Words – Accuracy, Enhanced EPD, Molecular breeding value

- INTRODUCTION

The selection for carcass and meat quality traits in beef cattle breeding programs were limited by the costs and difficulties to get a large number of measurements. However, the advances on molecular biology enabled the identification of polymorphisms on animals' genome related to the expression of those traits. This knowledge offers great potential to enhance selection for economically relevant traits for which expected progeny differences (EPDs) don't exist or are of low accuracy.

In Brazil, two companies validated the influence of some polymorphisms described on *Bos taurus* cattle on Nellore, the most prevalent *Bos indicus* breed in Brazilian herd, and constructed very low density SNP panels. These panels have been commercialized as an additional tool to the selection of this breed for growth, reproduction and carcass and meat quality traits.

Based on those panels, companies provide the molecular breeding values of genotyped animals, which can be used as a third source of information, jointly with pedigree and phenotype, on marker assisted selection.

The molecular breeding values represent the sum of allelic substitution effect weighted by the number of favorable alleles for all markers that influence trait expression. On this way, it can be assumed that the molecular breeding value has a high genetic correlation with the phenotype, and it can be used to refine the accuracy of animals' genetic merit predictions.

The aim of the present study was to evaluate the usefulness of Nellore Profile IGENITY® V3, a

very low density SNP markers panel, on a Nellore beef cattle breeding program, considering the molecular breeding values as a third source of information and measuring the impact on the accuracy of the predictions of additive genetic values.

- MATERIALS AND METHODS

- *Population*

Data of 1,849 Nellore animals, corresponding to 9,802 animals on the relationship matrix was used. From that dataset, a sample of 602 animals, that are progenies of bulls selected for production and reproduction traits, were raised under pasture conditions until 18 months of age and, after, fed in feedlots until slaughter between 21 and 27 months of age. The slaughter occurred in six different dates, always in the mornings, and after, approximately, 16 hours of fastening. All animals were perfectly identified for sample collection and measurements.

- *Phenotypic traits*

Animals were evaluated for meat quality traits. Meat tenderness was measured as Warner-Bratzler shear force after 7, 14 and 21 days of ageing (WBSF7, WBSF14 and WBSF21, kg). To measure Warner-Bratzler shear force, steaks were cooked and sheared as described by [1]. From each steak were taken 8 sub-samples of ½" of diameter and the average of these were considered as beef tenderness. Determination of total lipid content at *Longissimus* muscle (LIPID) was based on methodology described by [2]. Descriptive statistics of observed phenotype for evaluated traits are described in Table 1.

Table 1 Descriptive statistics for observed phenotypes

Trait	N	AVG	SD	MIN	MAX
WBSF7, kg	599	5.91	1.46	1.82	9.99
WBSF14, kg	602	4.92	1.27	1.38	9.34
WBSF21, kg	599	4.38	1.12	1.61	8.53
LIPID, g/100 g	527	2.18	0.65	0.96	4.60

N = number of observations; AVG = average; SD = standard deviation; MIN = minimum; MAX = maximum.

- *Genotyping process*

DNA was extracted from blood samples collected using EDTA vacuum tubes and impregnated on FTA cards by NaCl extraction and precipitation method described for [3].

Genotyping process was carried out on laboratories located in USA and licensed by Neogen/Igenity®. All animals were genotyped on Nellore Profile IGENITY® V3 SNP panel and the estimates of molecular breeding value for Warner-Bratzler shear force (MBV_{WBSF}) and backfat thickness (MBV_{BFT}) were provided by Neogen®.

- *Statistical analysis*

Single and two-trait analyses under animal model were performed using MTDFREML software [4]. Two single trait analyses were realized to estimate variance components and genetic parameters for observed phenotypes and molecular breeding values. First, a classical genetic evaluation was realized assuming observed phenotypes as dependent variable and including the fixed effects of batch and sex, age of animal at slaughter, meat temperature at Warner-Bratzler

shear force measurement and pH after 24 hours of slaughter as covariates and the random effects of direct additive genetic and residual effects. Next, molecular breeding values were used as dependent variable, assuming only direct additive genetic and residual effects as random effects.

Finally, a two-trait analysis was performed, considering as one trait the observed phenotypes and, as correlated attribute, the MBV_{WBSF} for WBSF7, 14 and 21 and the MBV_{BFT} for LIPID. The same effects described for single trait analyses were fitted here and the variance components were kept fixed. Descriptive statistics of molecular breeding values used on two-trait analysis are described in Table 2.

Table 2 Descriptive statistics for molecular breeding values

Trait	N	AVG	SD	MIN	MAX
MBV_{WBSF}, kg	1,849	0.02	0.36	-1.82	1,22
MBV_{BFT}, mm	1,823	0.005	0.06	-1.17	0,22

N = number of observations; AVG = average; SD = standard deviation; MIN = minimum; MAX = maximum.

The impact of using molecular breeding values as a third source of information on selection for meat quality traits was evaluated comparing the accuracy of estimates of breeding values obtained on single and two-trait analyses. This was applied within categories of animals defined by its importance within the herd, given the potential to transmit their alleles to future generations. The categories considered were HERD (all animals in pedigree matrix), SIRE (males that have at least one progeny in dataset), DAM (females that have at least one progeny in dataset), STEERS (males without progeny in dataset), HEIFER (females without progeny in dataset) and SIBTEST (steers that present measures of meat quality traits).

- RESULTS AND DISCUSSION

The estimates of heritability and their standard errors for WBSF7, WBSF14, WBSF21 and LIPID were 0.17 (0.12), 0.19 (0.00), 0.12 (0.00) and 0.30 (0.00), respectively, and for MBV_{WBSF} and MBV_{BFT} were 0.70 (0.07) and 0.74 (0.06), in this order. The genetic correlations estimates were 0.85 (WBSF7 x MBV_{WBSF}), 0.75 (WBSF14 x MBV_{WBSF}), 0.77 (WBSF21 x MBV_{WBSF}) and 0.27 (LIPID x MBV_{BFT}). Those values indicates that molecular breeding values were higher correlated with the phenotype than the additive genetic values, once genetic correlations between observed phenotypes and molecular breeding values were upper than estimates of heritability, which represents the correlation between phenotype and classical additive genetic values.
The mean accuracy of accuracy of the predictions of additive genetic values for WBSF7, WBSF14, WBSF21 and LIPIDS estimated in single and two-trait analyses were presented on Table 3.

Table 3 Mean accuracy of expected of the predictions of additive genetic values estimated in single and two-trait analyses

Trait	Single trait	Two-trait
WBSF7, kg	19,70	36,35
WBSF14, kg	20,49	32,91
WBSF21, kg	17,56	33,39
LIPID, g/100 g	22,76	21,46

The mean increments on the accuracy of estimates of breeding values for WBSF7, WBSF14, WBSF21 and LIPIDS observed for each category of animals were presented on Figures 1.

Figure 1. Graph of mean increments on accuracy of estimates of breeding values

Increments on accuracy were observed for all analyzed traits and animals' categories. Because of that it's expected that the genetic gain must be greater when molecular breeding values information is incorporated on genetic evaluation to estimate expected progeny differences (EPDs) for meat quality traits that, usually, are low accuracy traits.

- CONCLUSION

Those outcomes demonstrated the potential of marker assisted selection for meat quality traits on a Nellore beef cattle breeding program, using a very low density SNP markers commercial panel.

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