ABSTRACT: The aim of this study was to evaluate accuracy of genomic prediction for meat quality traits. The animals were slaughtered in commercial slaughterhouses from several regions of Brazil. Meat samples were evaluated for shear force (SF), lightness (LN), redness (RN) and yellowness (YN) measurement. Single-trait analyses were conducted to estimate heritability, breeding values (EBV) and reliability for all traits. Marker genotypes were obtained using the Illumina high density panel, containing 777,962 SNPs. For each trait, five-fold cross-validation was used to evaluate the genomic prediction accuracy. The heritability estimates were 0.10 ± 0.08, 0.10 ± 0.07, 0.05 ± 0.08 and 0.10 ± 0.09 for SF, RN, YN and LN, respectively. YN showed the lowest accuracy of genomic prediction (0.18) and the lowest average theoretical accuracy of genomic predictions (tACC). This was likely due to the lower heritability for YN. The genomic prediction accuracy was higher (0.23 - 0.33) for the others traits, which showed higher and similar heritability estimates. The low accuracy of prediction for all traits was likely a consequence of the low heritability and the number of animals in the training population. However, genomic selection may still be economically relevant for these meat quality traits, as they are expensive and difficult to measure.

Keywords: Bos indicus, GBLUP, Genomic selection, Meat quality traits

Introduction

The importance of meat quality traits is associated with acceptance of the product by the consumer. It is indisputable the relevance of tenderness in the purchase decision. Other relevant factor for meat quality is the meat color, which is directly related to the appearance of the product, being the first impression the consumers have about the meat. The colors have been studied based in an international standard for color measurements adopted by the Commission Internationale d’Eclairage (CIE) in 1976. L* is the luminance or lightness component, a* is associated to red color intensity and b* to yellow color (Yam and Papadakis (2004)). The a* measurement is probably more useful than b*, because it is related to metmyoglobin formation, in other words, the change in color from red to greenish brown (Page et al. (2001)). The L* measurement is also useful, because it represents the change in color from light to dark.

These traits are economically relevant for the beef industry. However, they are expensive to measure and can only be recorded post-slaughter. Usually, progeny testing is required to select for these traits, which increases costs and generation interval.

Genomic selection is an important tool to increase genetic progress, because an animal can be evaluated early in life, even at birth. Genomic selection was introduced by Meuwissen et al. (2001) and is based on genome-wide marker data to predict breeding values.

Several approaches have been proposed for estimating marker effects for genomic selection. According to Meuwissen et al. (2001), one of the approaches, BLUP, assumes that all SNP have small effect and follow the same normal distribution. GBLUP has been commonly used to estimate genomic breeding values, showing similar overall accuracy to nonlinear methods (Sargolzaei et al. (2009)).

The aim of this study was to evaluate the accuracy of genomic prediction for meat quality traits in a Nellore cattle population, using the methodology GBLUP.

Material and Methods

Phenotypic data

Nellore animals belonging to two Brazilian breeding programs with herds distributed in various regions of the country, were raised on pasture, finished in feedlots for about 90 days and slaughtered in commercial slaughterhouses with about 24 month of age. Number of observations, trait means (± SD), and the estimated heritabilities (± SE) are given in Table 1.
Meat samples were collected from 24 to 48 hours postmortem between the 12th and 13th left carcass ribs. Samples were analyzed for shear force, lightness, redness and yellowness measurements.

For this analysis samples of 2.54 cm, collected from Longissimus dorsi muscle with bone, were used. The procedure proposed by Wheeler et al. (1995) to determine shear force, using the mechanical equipment Salter Warner-Bratzler Shear Force, was applied. Eight small samples of 1/2 inch were removed from the whole sample. The value for shear force was the average of eight small samples, expressed in kilograms (kg). The meat color measures were performed using a KONICA MINOLTA - CR 400 colorimeter (Minolta Co. Ltd.) for measuring the coordinates of lightness, redness and yellowness. For convenience, in this study the acronym LN will be used for lightness, RN for redness and YN for yellowness.

Single-trait analyses were used to estimate heritabilities, breeding values (EBVs) and reliabilities for all traits. Univariate individual animal models were fit with ASREML (Gilmour et al. (2009)). The model also included fixed effects of contemporary group (farm and year of birth and management groups at weaning and yearling), age at slaughter, and time between the slaughter and the trait measurements, both modeled as covariates, including linear and quadratic effects.

Desregressed EBVs (DEBVs) (VanRaden and Wiggans (1991)) were used as pseudo-phenotypes. For each trait, a five-fold cross-validation was used to assess the accuracy of genomic predictions. The population was randomly divided into five groups, such as that each group was considered once as the validation population and the other groups as the training population.

Number of animals in training and validation groups and the estimated accuracy of the breeding values are presented in Table 2.

### Table 2: Descriptive statistics of data used for validation of genomic predictions

<table>
<thead>
<tr>
<th>Trait</th>
<th>Ntrain</th>
<th>accT</th>
<th>Nval</th>
<th>accV</th>
</tr>
</thead>
<tbody>
<tr>
<td>SF</td>
<td>1066</td>
<td>0.33</td>
<td>266</td>
<td>0.33</td>
</tr>
<tr>
<td>LN</td>
<td>1062</td>
<td>0.33</td>
<td>265</td>
<td>0.33</td>
</tr>
<tr>
<td>RN</td>
<td>1059</td>
<td>0.32</td>
<td>265</td>
<td>0.32</td>
</tr>
<tr>
<td>YN</td>
<td>1004</td>
<td>0.24</td>
<td>251</td>
<td>0.24</td>
</tr>
</tbody>
</table>

aTrait: SF= shear force (Kg), LN= lightness, RN= redness, YN= yellowness.
Ntrain: number of animals in the training set; Nval: number of animals in the validation set; accT: average accuracy of EBV in the training set; accV: average accuracy of EBV in the validation set.

#### Genomic Prediction

Marker genotypes were obtained using the Illumina High-Density Bovine BeadChip (Illumina Inc., San Diego, CA, USA), containing 777,962 SNPs. SNPs were deleted if minor allele frequency (MAF) < 3%, call rate <0.9. A total of 521,205 SNPs were retained for further analyses after filtering.

The software GEBV (Sargolzaei et al. (2009)), was used to calculate direct genomic values (DGV), using the GBLUP methodology.

The following model was used in genomic analysis:

\[ y = \mu + Wa + e \]

Where \( y \) is the vector of pseudo-phenotypes (DEBVs), \( \mu \) is the overall mean, \( a \) is the vector of random animal DGVs, \( e \) is the vector of random residual effects, \( I \) is a vector of 1s and \( W \) is an incidence matrix relating the animal DGVs to the observations. The DGVs were assumed normally distributed with mean zero and variance equal to \( G \sigma^2_g \), where \( G \) is the genomic relationship matrix based on the SNP markers and \( \sigma^2_g \) is the genetic variance. The random residual effects were assumed normally distributed with mean zero and variance equal to \( I \sigma^2_e \), where \( I \) is an identity matrix and \( \sigma^2_e \) is the residual variance.

The genomic prediction accuracy in the validation set was calculated as the Pearson correlation between DGV and EBV (r(DGV,EBV)). Moreover, the average individual theoretical accuracy (tACC) of DGVs, obtained using the elements of the inverse of the left hand side of the mixed model equations for GBLup, was also calculated.

### Results and Discussion

The YN measurement showed the lowest r (DGV, EBV) and tACC among all traits (Table 3). These results are most likely due to the lowest heritability estimated for this trait. For the others traits, which had similar and higher heritabilities, both r (DGV, EBV) and tACC were higher, with the best result observed for LN.

#### Table 3: Accuracy of genomic prediction for meat quality traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>r (DGV,EBV)</th>
<th>tACC</th>
</tr>
</thead>
<tbody>
<tr>
<td>SF</td>
<td>0.23</td>
<td>0.21</td>
</tr>
<tr>
<td>LN</td>
<td>0.33</td>
<td>0.19</td>
</tr>
<tr>
<td>RN</td>
<td>0.32</td>
<td>0.19</td>
</tr>
<tr>
<td>YN</td>
<td>0.18</td>
<td>0.14</td>
</tr>
</tbody>
</table>

\( ^* \text{Trait: SF= shear force (Kg), LN= lightness, RN= redness, YN= yellowness.} \)
\( r(DGV,EBV): \) Pearson correlations between direct genomic value and EBV; tACC: average of the individual theoretical accuracies of DGV.

The impact of trait heritability on the accuracy of genomic predictions has been shown in several studies (Snelling et al. (2012); Bolormaa et al. (2013)). In addition to the heritability, the number of animals in the training population also affects the accuracy resulting from genomic prediction. In this study, the training population was quite limited in size (n~1050), which added to the low heritability estimates obtained for the traits analyzed, may have yielded to the observed low genomic prediction accuracies. Balormaa et al. (2013) using GBLUP, found average accuracies of genomic EBV ranging from of 0.17 - 0.33 for
carcass and meat quality traits in *Bos Taurus*, *Bos Indicus* and composite beef cattle.

Overall, the prediction accuracies were low for all four traits in this study. However, considering the costs to measure and the difficulty to select for them, genomic selection might be a viable alternative. It potentially can accelerate genetic improvement and reduce the costs of selection. Accuracies are expected to improve with further research and an increase in the training population size.

**Conclusion**

The low heritabilities for the meat quality traits analyzed, associated with the small number of animals in the training population seemed to yield to low genomic prediction accuracies. However, it could be expected that with an increase of training population size the prediction accuracy should improve.

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**Literature Cited**