Genetic parameters estimates for growth, reproduction and carcass traits in Nellore cattle

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Summary

The aim of this study was to estimate heritabilities and genetic correlations between adjusted weight at 210 (W210) and 450 (W450) days of age, adjusted scrotal circumference at 365 (SC365) and 450 (SC450) days of age, age at fist calving (AFC), probability of precocious calving (PPC), stayability (STAY), rib eye area (REA), subcutaneous fat thickness (SFT), and rump fat (RF) for Nellore animals using ssGBLUP. Genetic parameter estimates were performed using linear and threshold animal models for single traits and linear models for two-trait analysis. For PPC and STAY, a linear-threshold or threshold animal model was used. The heritabilities for single-trait analysis were 0.21, 0.43, 0.47, 0.52, 0.11, 0.12, 0.37, 0.33, 0.17 and 0.33 for W210, W450, SC450, AFC, PPC, STAY, REA, SFT and RF, respectively. Overall, the genetic correlations between the traits ranged from -0.64 to 0.95. Most of the residual correlation estimates showed moderate to low magnitude, indicating that the extent of the environmental effects for two-trait selection were small or close to null. Greater gains by direct selection would be obtained for W450, SC365, SC450, STAY, REA and RF since they displayed the highest heritabilities estimates. In addition, selecting animals for weight (W210 and W450) would result in greater gains for SC365, SC450 and REA by indirect selection. The same pattern can be achieved when selecting for SC, resulting in gains for female reproductive traits (AFC, PPC, and STAY). Further, selection for STAY can increase the AFC and PPC genetic gains, as selection for SF can increase RTF.

Keywords: Bos indicus, genetic gain, heritability, indirect selection

Introduction

Several traits have been simultaneously selected in the beef cattle industry and selection has been performed by identifying and selecting superior animals for traits that are a determining factor for the beef cattle industry profit. In this regard, reproductive traits have a prominent importance upon breeding programs, followed by growth and carcass quality traits (Laske et. al. 2012; Eler et. al. 2014). Within the reproductive traits, i.e. fertility and sexual precocity, genetic gains can be achieved by direct and indirect selection. Therefore, the aim of
this study was to estimate (co)variance components with single step genomic BLUP (ssGBLUP) method for growth, reproductive and carcass traits used in the bioeconomic total genetic merit index (MGTe) of a Brazilian breeding program.

Material and methods

The dataset was provided by the National Association of Farmers and Researchers (ANCP, Ribeirão Preto-SP, Brazil). Information from 18 Nellore herds which participate in the Nellore Brazil breeding program was used. The relationship matrix was composed of 23 generations and 129,369 animals, in which 5,257 bulls and 50,742 cows had phenotypic records. A total of 4,294 animals were genotyped with the low-density panel (Clarifide Nelore 2.0 – 22k) and then imputed to a panel containing 735,044 markers using the FImpute software (Sargolzaei et al., 2014). Markers with MAF lower than 0.05, call rate lower than 90%, with redundant position, and those located in non-autosome chromosomes were excluded. After quality control, there were 461,554 markers and 4,256 animal samples left for analyses.

The traits used were classified as: 1) growth: adjusted weight for 210 (W210) and 450 (W450) days; 2) reproductive: scrotal circumference adjusted for 365 (SC365) and 450 (SC450) days, age at first calving (AFC) in days, probability of precocious calving (PPC) and stayability (STAY), and 3) carcass: rib eye area (REA-cm²), subcutaneous fat thickness (SFT-mm) and rump fat (RF-mm). Carcass traits were obtained by ultrasonography using ALOKA 500 V device, with a 3.5 MHz linear probe. For PPC, animals were categorized as success (2) if their first calving happened when they were up to 30 months old or failure (1) otherwise. For STAY, animals were categorized as success (2) if dams had at least three calving up to 76 months old or failure (1) otherwise. The contemporary groups (CG) for W210, W450, SC365, SC450, REA, SFT and RFT were composed by farm, year and season of birth, sex, and management group. For AFC, PPC and STAY the CG were composed by farm, year, and season of birth. The CG with less than five animals were excluded. The (co)variances and genetic parameters for W210, W450, SC365, SC450, AFC, REA, SFT and RF were estimated considering an animal model and ssGBLUP. The ssGBLUP model is a modification of BLUP with the numerator relationship matrix $A^{-1}$ replaced by $H^{-1}$ (Aguilar et al., 2010). The model used for PPC and STAY was proposed by Mrode and Thomson (2005).

For linear traits, the REMLF90 and AIREMLF90 software (Misztal et al., 2015) were used. For categorical traits, the variance components and genetic parameters were estimated in single-trait Bayesian analyzes using TRHGIBBSF90 software and a threshold model. Gibbs chains of 1,000,000 iterations were generated, with an initial burn-in of 100.000 and a sampling interval of 100. High-density regions were constructed for all variance components and genetic parameters estimated at 90% level of credibility. The convergence was tested using the Bayesian Output Analysis (BOA) implemented in R (2010) program.

Results and Discussion

Heritabilities ranged from low to moderate magnitude, with values varying from 0.11 to 0.52 (Table 1). Weight-related traits (W210 and W450) displayed favourable genetic correlations with SC and REA and unfavourable with AFC, PPC and STAY. These results indicates that selection for weight at young age would not affect the female sexual precocity and the cow’s longevity and it would also improve fat carcass traits, thus, establishing a synergism between breeders and fattening systems. The genetic correlations between SC-AFC and SC-PPC point out that selection for SC remains useful to improve precocity in females and it is also
included in the indexes as an indicator trait for age to puberty and fertility (Van Melis et al., 2010). AFC showed a negative genetic correlation with STAY, REA, SFT and RF, however, this negative correlation is not considered unfavourable, especially for STAY and REA which had moderate to high magnitude. Eler et al (2014) described similar genetic correlation between AFC-STAY (-0.64). Among the carcass traits, the highest genetic correlation was observed between SFT-RF. Most of the residual correlations estimates displayed moderate to low magnitude, indicating that the extent of the environmental effects for two-traits were small or close to null.

Table 1. Estimates of heritabilities (diagonal), genetic correlations (above the diagonal) and residuals correlations (below the diagonal) for the traits analysed.

<table>
<thead>
<tr>
<th>Trait</th>
<th>W210</th>
<th>W450</th>
<th>SC365</th>
<th>SC450</th>
<th>AFC</th>
<th>PPC</th>
<th>STAY</th>
<th>REA</th>
<th>SFT</th>
<th>RF</th>
</tr>
</thead>
<tbody>
<tr>
<td>W210</td>
<td>0.22±0.01</td>
<td>0.95±0.01</td>
<td>0.66±0.02</td>
<td>0.49±0.03</td>
<td>0.09±0.06</td>
<td>-0.03 (0.10±0.22)</td>
<td>0.01 (0.21±0.23)</td>
<td>0.48±0.04</td>
<td>0.20±0.01</td>
<td>-0.07±0.07</td>
</tr>
<tr>
<td>W450</td>
<td>0.63±0.01</td>
<td>0.44±0.01</td>
<td>0.39±0.02</td>
<td>0.30±0.02</td>
<td>-0.02±0.03</td>
<td>0.20 (0.04±0.44)</td>
<td>0.18 (0.01±0.35)</td>
<td>0.47±0.03</td>
<td>0.11±0.05</td>
<td>0.06±0.04</td>
</tr>
<tr>
<td>SC365</td>
<td>0.33±0.01</td>
<td>0.42±0.01</td>
<td>0.48±0.02</td>
<td>0.95±0.01</td>
<td>-0.28±0.06</td>
<td>0.39 (0.19±0.59)</td>
<td>0.38 (0.22±0.55)</td>
<td>0.19±0.05</td>
<td>0.13±0.06</td>
<td>0.10±0.05</td>
</tr>
<tr>
<td>SC450</td>
<td>0.34±0.01</td>
<td>0.49±0.02</td>
<td>0.77±0.01</td>
<td>0.52±0.02</td>
<td>-0.29±0.06</td>
<td>0.52 (0.31±0.74)</td>
<td>0.35 (0.20±0.50)</td>
<td>0.17±0.05</td>
<td>0.17±0.06</td>
<td>0.17±0.05</td>
</tr>
<tr>
<td>AFC</td>
<td>-0.09±0.01</td>
<td>0.12±0.01</td>
<td>—</td>
<td>—</td>
<td>0.11±0.01</td>
<td>—</td>
<td>—</td>
<td>-0.64 (0.83±0.44)</td>
<td>-0.02±0.08</td>
<td>-0.29±0.10</td>
</tr>
<tr>
<td>PPC</td>
<td>0.25 (0.12±0.37)</td>
<td>0.15 (0.03±0.26)</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>0.12 (0.07±0.16)</td>
<td>0.64 (0.45±0.97)</td>
<td>0.11 (0.33±0.52)</td>
<td>0.35 (0.10±0.59)</td>
</tr>
<tr>
<td>STAY</td>
<td>0.10 (0.05±0.15)</td>
<td>0.10 (0.06±0.15)</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>0.15 (0.19±0.12)</td>
<td>0.14 (0.03±0.24)</td>
<td>0.37 (0.26±0.48)</td>
<td>0.31 (0.04±0.64)</td>
<td>0.24 (0.06±0.49)</td>
</tr>
<tr>
<td>REA</td>
<td>0.35±0.01</td>
<td>0.42±0.01</td>
<td>0.14±0.03</td>
<td>0.18±0.03</td>
<td>-0.06±0.02</td>
<td>0.07 (0.18±0.29)</td>
<td>0.05 (0.04±0.15)</td>
<td>0.34±0.02</td>
<td>0.06±0.06</td>
<td>0.09±0.05</td>
</tr>
<tr>
<td>SFT</td>
<td>0.18±0.01</td>
<td>0.20±0.02</td>
<td>0.03±0.03</td>
<td>0.03±0.03</td>
<td>-0.03±0.02</td>
<td>0.10 (0.00±0.21)</td>
<td>0.04 (0.01±0.11)</td>
<td>0.19±0.02</td>
<td>0.17±0.01</td>
<td>0.73±0.03</td>
</tr>
<tr>
<td>RF</td>
<td>0.09±0.24</td>
<td>0.21±0.02</td>
<td>0.01±0.03</td>
<td>0.01±0.03</td>
<td>-0.07±0.02</td>
<td>0.26 (0.12±0.38)</td>
<td>0.05 (0.06±0.10)</td>
<td>0.18±0.02</td>
<td>0.54±0.01</td>
<td>0.33±0.02</td>
</tr>
</tbody>
</table>

1W210: weight to 210 days; W450: weight to 450 days; SC365: scrotal circumference to 365 days; SC450: scrotal circumference to 450 days; AFC: age at first calving; STAY: stayability; 3P: probability of precocious calving; REA: rib eye area; SFT: subcutaneous fat thickness; RF: rump fat.

Selection indexes keep growing in the beef industry since their use facilitates the breeder’s decision-making, allows for the selection of multiple traits simultaneously, and can account for several production levels (Parish et al., 2011). The bioeconomic total genetic merit index (MGTe) developed by the National Association of Farmers and Researchers is a useful tool to rank candidates to selection. The most important traits included in the MGTe are W450 and STAY (24% and 22%, respectively). Besides, STAY has a low heritability and it measurement is performed only in later in life, delaying young females evaluation. In this
regard, it could be of interest to increase the relative importance of precocity traits in the indexes, and thus, improving STAY as a correlated trait.

**Conclusion**

Estimates ofheritabilities showed that traits have enough genetic variability to respond to selection. Higher gains by direct selection would be obtained for W450, SC365, SC450, STAY, REA, and RF. Most of the traits included in the index showed moderate to highheritabilities, hence, the application of the MGTe to select candidates to selection would bring significant gains on the profitability of the beef cattle production systems. In addition, selecting animals for weight (W210 and W450) would result in greater gains for SC365, SC450 and REA by indirect selection. The same pattern can be achieved when selecting for SC, resulting in gains for female reproductive traits (AFC, PPC, and STAY). Further, selection for STAY can increase the AFC and PPC genetic gains, as selection for SF can increase RTF.

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