Genetic relationship amongst reproductive traits in Nellore cattle

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ABSTRACT: This study aimed at estimating genetic parameters for reproductive traits (RT); and also the genetic relationship amongst scrotal circumference (SC), number of calvings at 53 months (NC53), heifers rebreeding (HR) and stayability. The (co)variances and genetic parameters were estimated using Bayesian inference. NC53, HR and stayability were analyzed assuming a threshold model while SC a linear model. The heritability estimated for NC53 was 0.22 and it was correlated with stayability (0.99), meaning selection for NC53 would improve productive longevity of cows. Correlations estimated between HR and stayability and between HR and NC53 allow an improvement on HR rates if selection were applied to traits related to longevity. Genetic correlations amongst SC and female RT were positive but with small magnitude, suggesting the need to use RT directly measured in females in order to obtain improvements in sexual precocity and longevity.

Keywords: Bayesian inference, reproductive efficiency, threshold model

Introduction

Reproductive traits in beef cattle, directly measured in females, have been little explored by researchers and animal breeding programs, which leads to a slower development of analysis methodologies and even to a lack of knowledge of such traits. Traits related to longevity have utmost importance in beef cattle evaluation, nevertheless, the main disadvantage of selecting for such traits is the increase in generation interval due to delay in phenotypic data collection (Ducrocq et al., 1988). Therefore, selecting for correlated traits recorded early in lifetime would allow the selection for longevity to be performed without such problems.

The aims of this research were to estimate genetic parameters for reproductive and longevity traits measured in females and also scrotal circumference in order to verify the possibility of using such traits as selection criteria in cattle breeding programs.

Materials and Methods

Data. This study used records of from animals of 37 different farms belonging to the Aliança Nelore dataset (Gensys, 2010), raised in Brazil and Paraguay. The feeding system adopted in these farms consisted basically of tropical pastures, mineral salt and water ad libitum. In general, supplementation was not performed for any category of females.

The breeding season lasted 90 days and its onset was determined by weather and nutrition conditions of each region. In order to identify sexual precocity females, part of the herds adopted two breeding seasons: an anticipated one that, in general, occurs from March to April, the fall season, and the traditional one, usually from November to February, the summer season. The remaining herds adopted only the summer season. Females were mostly inseminated and, if the pregnancy was not detected, they were exposed to a breeding system with more than one sire for a group of cows. The natural mating was controlled, that is, a group of 30 to 50 females were placed together with a single-sire.

Most of the participating herds exposed the primiparous cows to controlled natural mating or breeding groups, thus increasing the pregnancy rate in this category.

Evaluated Traits. The scrotal circumference (SC) previously adjusted for age and long yearling weight, was obtained approximately at 18 months of age, by measurements made transversely in the region of larger diameter of the scrotum, using a specific measuring tape.

The stayability records (STAY) were analyzed categorically, where score “1” was applied for females that remained in the herd up to 76 months and conceived at least three calves till this age, whereas score “0” represented the failure and was applied for those females were discarded for not becoming pregnant in previous breeding seasons. For this trait, the number of calvings could range from 0 to 5 for those cows with first service at 18 months and, for cows with first service at 24 months, the calving could range from 0 to 4.

The trait number of calvings at 53 months (NC53), ranging from 0 to 3, was defined as the number of calvings till 53 months of age, considering the cow had performance records until yearling age and also had the opportunity to reach this age.

Heifers rebreeding (HR) was defined as success (1) or failure (0) for heifers that calved or not, respectively, since they had previously given birth.

For analyses of reproductive traits, a maximum interval of 15 and 24 months between first and second births was considered for females submitted to a normal and an early breeding season, respectively. The editing of dataset was performed using the software SAS® (SAS Inst., Inc., Cary, NC). Investigations concerning to the identifications of animal, sire, dam, sex, season of birth, age and number of calvings were carried out and animals that did not have dates of birth and/or calving were discharged. To study the reproductive traits measured in females, the age at first calving, calving interval, number of births and season of birth were calculated. The season of calving was defined by two classes: raining, between October and March, and dry, from April to September.

Genetic groups based on the season of birth were used so that the genetic merit of each group was predicted and used to correct the genetic value of each animal based...
on their relationship with their respective group (Westeel et al., 1988).

**Model.** For NC53 and STAY, the models included the fixed effects of contemporary groups (CG) defined based on concatenation of season and year of calving, farm of weaning to long yearling and classification of precocity status. To evaluate STAY, the consistency of the dataset was performed similarly as described to NCS53. There were only births up to 76 months. In addition, for STAY analysis, the effects of mating system were included as a covariate in the model, and it may be: artificial insemination, single and multiple sire.

The definition of contemporary groups for SC included year and season of birth, farm and group of management at birth, weaning and long yearling ages, beyond the dates when the animals were weaned and when measurements of scrotal circumference were taken. The covariates included in the models were the linear and quadratic effects of age of dam at calving.

The CG for HR included the classification of being precocious heifers or not, season and year of calving and farm from weaning to long yearling. The age at first calving, the type of service that the female was submitted to and the date of birth, were included in the model, as covariates.

The (co)variance components and genetic parameters were estimated using Bayesian inference by single and bi-trait analyses (for all possible trait combinations) considering a linear animal model using the computer software THRGIBBS2F90 (Misztal, 2010). It was assumed a linear animal model for SC and a threshold model for NC53, HR and STAY.

The linear model for SC considered the CG as fixed effect and additive genetic effect of the animal as random and can be represented in matrix form by:

\[ Y = Xb + Z_1a + Z_2Q_1c + e \]

where:

- \( Y \) is the vector of observations and \( X \) is the incidence matrix associating observations to the fixed effects of CG, \( b \) is the vector of fixed effects, \( Z_1 \) and \( Z_2 \) are the incidence matrices associating observations to direct genetic effect of animal (\( a \)) and fixed effects of genetic groups (\( Q_1c \)) and \( e \) is the vectors of random direct genetic effect of animal, fixed effects of genetic groups and random residuals, respectively.

- \( a \sim N(0, A\sigma_a^2) \), \( e \sim N(0, I_e\sigma_e^2) \) and \( g \sim N(0, I_g\sigma_g^2) \).

Where \( A \) is the additive genetic relationship matrix, \( I \) is an identity matrix of order equal to the number of observations and \( \sigma_a^2, \sigma_e^2, \sigma_g^2 \) are the additive genetic, residual and between genetic group variances, respectively. For analysis purposes, residual correlations were fixed at zero.

For HR and STAY, only one threshold was used, as these traits had only two phenotypic classes. In this way, the liability \( g \) (Gianola 1979), was modeled as:

\[ g = X_1b + Z_1u + Z_2Q_1c + e \]

where:

- \( X_1, Z_1 \) and \( Z_2 \) represent incidence matrices relating elements in \( b, u \) and \( c \) to \( g \), respectively. \( Q_1 \) is incidence matrix that relates animals to fixed effect of genetic groups. It was assumed that: \( Ef[e] = X_Ab, u \sim N(0, A\sigma_u^2) \) and \( e \sim N(0, I_e\sigma_e^2) \), where \( A \) is the additive genetic relationship matrix and \( I \) is an identity matrix of order equal to the number of observations.

In single and bi-trait analyses, chains with length of 1,000,000 cycles were originated, in which the first 100,000 cycles were discarded (Burn-in). In the single-trait analyses, the samples were stored every 100 cycles and, for bi-trait, every 50 cycles. These values were set randomly in order to verify the convergence of chains.

The convergence of Gibbs Sampling algorithm was verified by graphical visual inspection (sampled values versus iterations), using the BOA package (Smith, 2005). It was assumed convergence when, after a certain point, the data presented behavior considered constant, which could be observed for all traits under study.

Estimates of average posterior heritability and correlations were estimated based on averages of the estimated posterior variances in single and bi-trait analyses. The response in the correlated trait, \( Y \), was estimated by the regression of the genetic value of the trait \( Y \) in the genetic value of \( X \). The response of \( X \), the trait that is under selection, was estimated by \( R_x = \frac{i_h \sigma_{ax}}{\sigma_x} \). It was adopted the criteria described by Falconer and Mackay (1996) that calculates the merit of indirect selection relative to direct selection (\( CR_x/R_x \)).

In order to know the effect of the selection on SC on the other studied traits, it was assumed intensity of selection equal to 2.67 (selection of 1% of the animals) and direct selection for SC. For evaluation longevity in females by analyzing the number of calvings at 53 months, it was adopted selection intensities of 1.16 (selection of 30% of the animals).

**Results and Discussion**

All the traits have reached the stationary phase of the Gibbs chain, indicating that the sampling processes were appropriate. Results for variance components and genetic parameters, obtained in bi-trait analyses, are presented in Table 1. Correlated and direct responses and efficiency of indirect selection for evaluation of longevity in females for SC and HR are presented in Table 2.

Estimates of STAY heritability was moderate and equal to 0.19 ± 0.025 (Table 1). The efficiency of indirect selection values obtained in the present study between NC53 and STAY (1.065), indicated that the selection applied on NC53 will be more efficient to obtain results for longevity of animals compared to the selection applied directly on STAY.

The results found confirm there is an advantage of selecting for NC53, due to its correlation (0.99 ± 0.051) and greater heritability compared to STAY and also higher accuracy and consequently reduction in generation interval for being a trait evaluated earlier in lifetime. The evaluation of STAY implies reducing costs related to replacement of animals due to discard. Furthermore, with a decrease in replacement and consequent increase in selection intensity, there is also an increase in the response to selection.
However, due to the long time needed for evaluation this trait, this practice could lead to an increase in the generation interval. This problem can be minimized by adopting NC53 as an indirect trait of evaluating the longevity of animals.

Table 1. Estimates of marginal posterior distributions of direct additive genetic variance ($\sigma^2_a$), residual variance ($\sigma^2_e$) and heritabilities ($h^2$) for number of calvings at 53 months (NC53), heifers rebreeding (HR), stayability (STAY) and scrotal circumference (SC) of Nellore Cattle.

<table>
<thead>
<tr>
<th>Traits</th>
<th>Parameters</th>
<th>Mean ± SD</th>
<th>Mode</th>
<th>Median</th>
</tr>
</thead>
<tbody>
<tr>
<td>NC53</td>
<td>$\sigma^2_a$</td>
<td>0.029 ± 0.001</td>
<td>0.029</td>
<td>0.029</td>
</tr>
<tr>
<td></td>
<td>$\sigma^2_e$</td>
<td>0.102 ± 0.002</td>
<td>0.101</td>
<td>0.102</td>
</tr>
<tr>
<td></td>
<td>$h^2$</td>
<td>0.22 ± 0.009</td>
<td>0.200</td>
<td>0.200</td>
</tr>
<tr>
<td>HR</td>
<td>$\sigma^2_a$</td>
<td>0.175 ± 0.028</td>
<td>0.177</td>
<td>0.174</td>
</tr>
<tr>
<td></td>
<td>$\sigma^2_e$</td>
<td>1.002 ± 0.009</td>
<td>1.003</td>
<td>1.002</td>
</tr>
<tr>
<td></td>
<td>$h^2$</td>
<td>0.15 ± 0.021</td>
<td>0.130</td>
<td>0.140</td>
</tr>
<tr>
<td>STAY</td>
<td>$\sigma^2_a$</td>
<td>0.229 ± 0.037</td>
<td>0.228</td>
<td>0.228</td>
</tr>
<tr>
<td></td>
<td>$\sigma^2_e$</td>
<td>1.002 ± 0.007</td>
<td>1.002</td>
<td>1.002</td>
</tr>
<tr>
<td></td>
<td>$h^2$</td>
<td>0.19 ± 0.025</td>
<td>0.200</td>
<td>0.190</td>
</tr>
<tr>
<td>SC</td>
<td>$\sigma^2_a$</td>
<td>3.602 ± 0.169</td>
<td>3.599</td>
<td>3.600</td>
</tr>
<tr>
<td></td>
<td>$\sigma^2_e$</td>
<td>3.306 ± 0.116</td>
<td>3.305</td>
<td>3.306</td>
</tr>
<tr>
<td></td>
<td>$h^2$</td>
<td>0.52 ± 0.019</td>
<td>0.500</td>
<td>0.520</td>
</tr>
</tbody>
</table>

The heritability estimated for HR was low (0.15 ± 0.021), confirming the influence of environmental effects on this trait. However, the high genetic correlation estimated between HR and STAY (0.97 ± 0.021) and between HR and NC53 (0.99 ± 0.007), combined with heritabilities of these traits obtained in bi-trait analyses, suggest an improvement on HR rates if selection were applied for traits related to longevity. This result can be confirmed by analyzing the value obtained for efficiency of indirect selection between NC53 and HR (1.199). This value indicates that, if selection on NC53 is applied in order to achieve improvements in HR, the results would be more favorable than if directly selection on HR were performed.

The values estimated for genetic variance (3.602) and heritability (0.52 ± 0.019) for SC, indicates the possibility of good responses when selection is applied to this trait. Weak genetic correlations were estimated between SC and NC53, HR and STAY (0.07 ± 0.019, 0.11 ± 0.069 and 0.12 ± 0.058, respectively). Thus, genetic response in those traits through SC selection is not expected to be effective. These results indicate the need to include reproductive traits measured directly in females to obtain improvements in sexual precocity, in a more effective way, instead of considering only the inclusion of scrotal circumference.

The NC53, as a way of measuring the ability of the cow to stay productive in herd, was more efficient than the usual definition of STAY at 76 months. The estimates for genetic correlations between NC53 and STAY (0.99 ± 0.007), when combined with results obtained for correlated responses and indirect selection, confirm that selection performed earlier in life could be more advantageous for evaluation of longevity and animal breeding purposes.

The estimated heritability for NC53 shows that a considerable important part of the variation is determined by additive genes action. Considering the correlations between STAY and NC53, correlated responses and indirect selection efficiency, there are possibilities that the NC53 could be used as an alternative criterion to evaluate the STAY of the cow. Thus, it would have an anticipation on the genetic evaluation of bulls based on the performance of their daughters to 53 months, instead of 76 months, as it has been practiced by breeding programs.

Table 2. Correlated response (C.R.), Direct response (D. R.) and Indirect selection efficiency I.S.E) of direct selection on scrotal circumference (SC) and the response on number of calvings at 53 months (NC53), on heifers rebreeding (HR) and stayability (STAY) of Nellore females.

<table>
<thead>
<tr>
<th>SC</th>
<th>NC53</th>
<th>C.R.</th>
<th>D.R.</th>
<th>I.S.E.</th>
<th>C.R.</th>
<th>D.R.</th>
<th>I.S.E.</th>
</tr>
</thead>
<tbody>
<tr>
<td>NC53</td>
<td>0.022</td>
<td>0.093</td>
<td>0.241</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>HR</td>
<td>0.089</td>
<td>0.188</td>
<td>0.471</td>
<td>0.261</td>
<td>0.242</td>
<td>1.065</td>
<td></td>
</tr>
<tr>
<td>STAY</td>
<td>0.112</td>
<td>0.242</td>
<td>0.457</td>
<td>0.226</td>
<td>0.188</td>
<td>1.199</td>
<td></td>
</tr>
<tr>
<td>SC</td>
<td>0.070</td>
<td>3.654</td>
<td>0.019</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 2. Correlated response (C.R.), Direct response (D. R.) and Indirect selection efficiency I.S.E) of direct selection on scrotal circumference (SC) and the response on number of calvings at 53 months (NC53), on heifers rebreeding (HR) and stayability (STAY) of Nellore females.

The inclusion of reproductive traits measured directly in females as selection criteria in animal breeding programs can be an alternative to gradually improve sexual precocity and length of productive life of cows in the herds studied.

Literature Cited


Acknowledgements

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