Parameter estimates for reproductive and carcass traits in Nelore beef cattle

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ABSTRACT

The aim of this study was to estimate genetic parameters for scrotal circumference at 365 (SC365) and 450 (SC450) days of age, age at first calving (AFC), ribeye area (REA), backfat (BF) thickness, and rump fat (RF) thickness, in order to provide information on potential traits for Nelore cattle breeding program. Genetic parameters were estimated using the Average Information Restricted Maximum Likelihood method in single- and multitrait analyses. Four different animal models were tested for SC365, SC450, REA, BF, and RF in single-trait analyses. For SC365 and SC450, the maternal genetic effect was statistically significant (P < 0.01) and was included for multitrait analyses. The direct heritability estimates for SC365, SC450, AFC, REA, BF, and RF were equal to 0.31, 0.38, 0.24, 0.32, 0.16, and 0.19, respectively. Maternal heritability for SC365 and SC450 was equal to 0.06 and 0.08, respectively. The highest genetic correlations were found among the scrotal circumferences. Testing for the inclusion of maternal effects in genetic parameters estimation for scrotal circumference should be evaluated in the Nelore breeding program, mostly for correctly ranking the animal's estimated breeding values. Similar heritability estimates were observed for scrotal circumference, as well as favorable genetic correlations of this trait with AFC and carcass traits. Thus, scrotal circumference measured at 365 days of age could be a target trait for consideration in the Nelore selection index in order to improve most of the traits herein analyzed.

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1. Introduction

In beef cattle, the reproductive performance of the cows, which is represented by the number of calves born annually, is one of the main economic factors affecting the production system [1]. The genetic improvement of reproductive traits in females is generally challenging due to difficulties in measuring the traits as well as to the low genetic variability, which results in a slow response to selection [2–4]. Thus, breeding programs have been considering reproductive measures taken in males (i.e., scrotal circumference) in the selection criteria due to moderate to high heritability estimates and ease of measurement [5].

Scrotal circumference is indicative of fertility and development in beef cattle, due to favorable genetic correlations with reproductive traits (semen volume, age at puberty in males and related females, and heifer pregnancy) [6–8] and production traits (body weight and longissimus muscle area) [5,9,10].

The carcass traits, such as ribeye area (REA) and fat thickness, are directly related to the quality of meat products, which may influence in the financial revenue received by the producers [11]. Animals with early fat deposition could be in the final stages of development, showing evidence of reproductive maturity. As observed by Foster and Nagatani [12], fat deposition could be assigned to the production of hormones, which triggers the folliculogenesis process. Thus, the aim of our study was to estimate genetic parameters for male and female reproductive traits and carcass traits in order to provide information on potential traits for Nelore cattle breeding program.

2. Material and methods

2.1. Animals and data set

The data used in this study were provided by the Nelore Genetic Improvement Program (Nelore Brazil), coordinated by the National Association of Breeders and Researchers. Animals were raised in an extensive production system and kept on pastures with mineral supplementation. Weaning occurred at around 6 to 8 months of age. The reproductive management consisted of a breeding season lasting from 90 to 120 days, using artificial insemination or controlled natural breeding.

The traits analyzed were scrotal circumference at 365 (SC365) and 450 (SC450) days of age, age at first calving (AFC), REA, subcutaneous backfat (BF) thickness measured between the 12th and 13th ribs, and rump fat (RF). The raw data consist of 23,129 (SC365), 25,431 (SC450), 17,586 (AFC), and 11,578 (REA, BF, and RF) animals with phenotypic information. To measure the REA, BF, and RF, ultrasound images were obtained using the ALOKA 500 V device, with a 3.5 MHz linear probe measuring 17.2 cm and an acoustic coupler, in conjunction with an image capture system (Blackbox, Biotronics Inc., Ames, IA, USA). These images were subsequently interpreted by the laboratory responsible for data quality (Aval Serviços Tecnológicos S/ S). These measurements were carried out at the average age of 546 days.

2.2. Fixed effects

The general linear model procedure of the Statistical Analysis System Software (SAS 9.1 SAS Institute, Cary, NC, USA) was used to define the fixed effects. The significant effects (P < 0.05) were used in the genetic parameters

analyses. Sires with less than three offspring and management groups with less than five animals were excluded from the data set.

For SC365 and SC450, the significant effects (P < 0.05) considered were farm (20 levels), birth year (from 1998 to 2008), birth season (two levels), management group at 365 days of age (for SC365), and management group at 450 days of age (for SC450). For AFC, the significant effects (P < 0.05) considered were animals born in the same year (from 1998 to 2006) and season and at the same farm (21 levels). For the carcass traits (REA, BF, and RF), the effects of sex, birth year (from 2000 to 2008), birth season, and management group at 450 days were statistically significant (P < 0.05). The age of the animal at ultrasound measurement was statistically significant (P < 0.05) and was considered as a linear and quadratic covariate for REA, BF, and RF.

The birth season was defined as rainy season (animals born between October and March) and dry season (animals born between April and September). The number of management groups at 365 and 450 days of age were 187 and 194, respectively. The observations with standardized residuals above 3.5 or below −3.5 were excluded. The final number of records is described in Table 1.

2.3. Genetic parameters

Genetic parameters and standard errors were estimated using the Average Information Restricted Maximum Likelihood method under an animal model (single-trait and multitrait analyses). The total number of animals in the relationship matrix was 81,579. Analyses were conducted using the software WOMBAT [13] considering the convergence criterion of 10^{-9}. The general statistical model was:

$$y = X\beta + Za + Mm + Wpe + e$$

in which y is the vector of observations for each trait; β is the vector of all fixed effects and covariate; a is the vector of random additive genetic direct effect; m is the vector of random maternal genetic effect; pe is the vector of random maternal permanent environment effects; e is the vector of random residual effects; X, Z, M, and W are the incidence matrixes related to β, a, m, and pe, respectively.

Four different models were evaluated for SC365, SC450, REA, BF, and RF in single-trait analyses. The genetic covariance between the direct and maternal effects and the residual covariances between traits measured on opposite sex were not estimated [14].

Table 1
Number of animals, means and standard deviations, minimum and maximum values, and coefficient of variation (CV) for scrotal circumference at 365 (SC365) and 450 (SC450) days of age, age at first calving (AFC), ribeye area (REA), subcutaneous backfat thickness (BF), and rump fat (RF) in Nelore cattle.

Trait	Animals	Sires	Dams	Mean ± standard deviation	Minimum	Maximum	CV
SC365 (mm)	17,542	704	12,338	204 ± 22	127	294	10.89
SC450 (mm)	17,542	704	12,338	236 ± 30	136	354	12.70
AFC (mo)	14,069	858	10,931	35.19 ± 5.03	21.00	49.00	14.29
REA (cm^2)	9776	405	7256	52.47 ± 10.02	22.37	103.55	19.10
BF (mm)	9776	405	7256	2.42 ± 0.82	0.40	6.60	33.88
RF (mm)	9776	405	7256	3.01 ± 1.21	0.40	10.80	40.20