



Ranking of Nelore animals in cattle championships: genetic parameters and correlations with production traits

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ABSTRACT. Records of 17,141 Nelore cattle participating in cattle championships, born from 1994-2009, were used to estimate genetic parameters between animal rank in cattle championships, evaluated from weaning to 36 months of age as repeated traits, and growth, fertility, and carcass traits, evaluated at 365 days of age as single traits. Two traits were defined for animal rank in cattle championships: value 1 was attributed to animals ranked from 1st to 3rd place within the age category, and value 0 was assigned to the remaining animals (TOP3). Value 1 was attributed to animals ranked from 1st to 5th place within the age category and value 0 was assigned to the remaining animals (TOP5). The (co)variance components were estimated based on Bayesian inference under a 2-trait threshold-linear animal model. The posterior means of heritability estimated for TOP3 and TOP5 were 0.182 ± 0.010 and 0.260 ± 0.012 , respectively, and their repeatabilities were 0.341 ± 0.007 and 0.400 ± 0.007 , respectively. High-ranking animals generally presented higher breeding values for body weight, height,

body length, and heart girth. The phenotypic correlations indicate that judges of cattle championships primarily rank animals based on weight and heart girth.

Key words: Beef cattle; Categorical trait; Conformation; Production traits

INTRODUCTION

For centuries, domestic animals have been selected based on shape and appearance. Despite the widespread use of animal breeding techniques, emergence of performance tests, and evaluation and selection programs in a large number of herds, cattle judging at championships remains intensively used for selecting beef cattle in Brazil. Although these judgments do not involve the use of modern techniques, such as genetic evaluation, and population samples are not comprehensive in terms of the number of animals evaluated, cattle championships determine the direction of evolution within breeds as the champion animals are rapidly disseminated in the population through semen or oocytes. Cattle championships also help to highlight the phenotypes of a racial breed maintained or sought by breeders of a particular breed. In Brazil, beef cattle championships, particularly the judgment system based on animal appearance promoted by the Association of Brazilian Zebu Breeders (ABCZ), have markedly influenced the commercialization of bull semen (Cyrillo et al., 2000). Currently, commercialization trends of Nelore semen are undergoing major changes. The 2011 results published by a major cattle artificial insemination center in Brazil showed that 80% of semen doses commercialized and 75% of revenues were derived from bulls that had undergone some form of genetic evaluation. This result is a consequence of the increased number of genetic evaluation programs and their coverage in terms of the number of animals evaluated; animals with good expected breeding values are used for production traits with good market value, such as basic growth and fertility traits (Albuquerque et al., 2006).

The ABCZ possesses a database that contains growth, fertility, and carcass trait records, as well as ranking records of animals that have participated in national and international Zebu championships. Genetic parameters for postweaning growth traits of Zebu beef cattle have been reported in many studies (Giannotti et al., 2005), whereas studies investigating genetic parameters for traits related to body measures and ultrasound-measured carcass traits are limited (Cyrillo et al., 2001; Magnabosco et al., 2002; Riley et al., 2007; Yokoo et al., 2008; Pinheiro et al., 2012). Moreover, there have been no studies to examine the genetic parameters of traits related to cattle ranking in championships and the genetic and phenotypic correlations of these traits with production traits, such as body weight at certain ages, scrotal circumference, rib eye area, or fat thickness.

The objective of the present study was to determine the genetic and phenotypic correlations between traits related to the ranking of Nelore animals in cattle championships and growth, fertility, and carcass traits. This study will allow identification of traits that impact these championships.

MATERIAL AND METHODS

Data from Nelore animals born between 1994-2009 provided by the ABCZ were

used. The results of cattle judging were obtained for 26 national or international cattle championships that occurred between 1988-2010 in Uberaba, Minas Gerais, Brazil. Records regarding growth, fertility, and carcass traits were obtained at the time of entry of the animals in the show ring. Only animals that had been submitted to weight gain control or weight gain tests organized and/or monitored by the ABCZ participated in these cattle championships. In addition, a minimum body weight per age was required according to the regulations of each show (ABCZ, 2010).

Championships were carried out for age categories: calf championship, with 4 categories that included animals from 8-12 months of age; junior and young heifer championship, with 4 categories that included animals >12-16 months of age; junior and senior heifer championship, with 3 categories that included animals >16-22 months of age; bull and young female championship, with 3 categories that included animals >22-28 months of age; and senior bull and adult cow championship, with 3 categories that included animals >28-36 months of age (ABCZ, 2010). In one specific cattle championship, there were also 2 baby championships, which included 2 categories of 6.16-7 months of age and 7.27-8 months of age. Each category was allowed to contain up to 30 animals. When the number of animals was more than 30, the category was subdivided into as many subcategories as necessary so that the number of animals in each subcategory did not exceed 30. After judging of the subcategories, ranked animals were assembled and again judged.

Two traits, TOP3 and TOP5, were defined. For TOP3, a value of 1 was attributed to animals ranking 1st, 2nd, or 3rd place within the category, and a value of 0 was assigned to the remaining animals in the category. For TOP5, a value of 1 was attributed to animals ranking 1st to 5th place within the category, and a value of 0 was assigned to the remaining animals in the category. The success (value 1) indicates the animals with the largest number of desired characteristics (such as weight, height, breed characteristics, beauty, etc.). By construction, TOP5 should capture more phenotypic, and potentially genetic, variability than TOP3.

The following traits obtained at 365 days of age were also analyzed: i) growth traits: body weight (BW), hip height (HH), body length (BL), heart girth (HG); ii) fertility trait: scrotal circumference (SC); iii) carcass traits: longissimus muscle area between the 12th and 13th rib measured by ultrasound (LMA), backfat thickness between the 12th and 13th rib measured by ultrasound (BF), and rump fat thickness at the junction of the biceps femoris and gluteus medius muscles measured by ultrasound (RF). HG, SC, LMA, BF, and RF were only measured in males. The dataset analyzed contained 28,279 records of 17,141 animals (5904 males and 11,237 females) born to 764 sires and 9734 cows.

Growth, fertility, and carcass traits were analyzed as single traits at 12 months of age, with an interval of 305-425 days (mean of 361 days for all traits), as most records were obtained during this interval. In addition, this is a well-established standard age for selection programs, and weight at this age shows high genetic correlations with weight at other ages (Mercadante et al., 1995).

For all traits, contemporary groups (CGs) were formed including animals of the same sex (1, 2) and breed group (standard Nellore or hornless Nellore) and participating in the same cattle championship (1, ..., 26) and category of the championship judged (1-19), for a total of 1583 CGs (minimum of 3 and maximum of 131 animals per CG). For TOP3 and TOP5, 65 CGs (321 records) showing no variability, in which all animals presented a value of 0 or 1, i.e., all or no animals were ranked, were eliminated. For growth, fertility, and carcass traits, records from animals that participated in the championship in the category of 12 months of age were

used. If no records of this category were available, the record for the category of 11, 13, 10, or 14 months of age, in this order, was considered. Records that were below or above 3.5 standard deviations of the mean of the CG and CG containing less than 5 animals were eliminated. The pedigree file contained 33,562 animals born to 1928 sires and 16,231 cows, comprising up to the sixth generation of animals with records. The results of descriptive statistics for the traits studied are shown in Table 1.

Table 1. Summary of the data structure and descriptive statistics for cattle championship, growth, fertility, and carcass traits.

Trait	No. of records	No. of sires	Means \pm SD	Minimum	Maximum
TOP3 (%)	28,279	764	19.6 \pm 3.96	0	1
TOP5 (%)	28,279	764	31.7 \pm 4.65	0	1
BW (kg)	7,800	480	460 \pm 63.3	265	700
HH (cm)	7,296	475	144 \pm 5.04	128	163
BL (cm)	7,296	475	140 \pm 6.80	118	164
HG (cm)	2,556	299	184 \pm 9.23	150	220
SC (cm)	2,642	300	27 \pm 3.82	17	39
LMA (cm ²)	1,161	201	80.2 \pm 11.5	68	119
BF (mm)	1,162	200	6.25 \pm 2.39	1.50	20.07
RF (mm)	918	200	8.06 \pm 2.32	2.30	19.30

TOP3 = animals ranked 1st to 3rd place within the category; TOP5 = animals ranked 1st to 5th place within the category; BW = body weight at 365 days; HH = hip height; BL = body length; HG = heart girth; SC = scrotal circumference; LMA = longissimus muscle area; BF = backfat thickness; RF = rump fat thickness.

The analysis assumed a bivariate linear model for growth, fertility, or carcass traits and the liability for TOP3 or TOP5. A threshold model (Gianola and Foulley, 1983) was used to analyze TOP3 or TOP5 as a binary response variable. The threshold model postulates an underlying continuous random variable, known as liability, λ , so that the observed binary responses (y) are the result of the following relationship:

$$y_i = 0 \text{ if } \lambda_i \leq \tau \text{ and } y_i = 1 \text{ if } \lambda_i > \tau$$

where τ is a fixed threshold and $y_i = 1$ or $y_i = 0$ corresponds to observed TOP or not for observation i . Liability is often assumed to be normally distributed with a mean vector μ and covariance matrix $R = I\sigma_e^2$, where σ_e^2 is the variance in the underlying scale. Because the threshold is not identifiable, this parameter takes an arbitrary value ($\tau = 0$) to denote the origin of measurement.

The general model, in matrix notation, can be written as:

$$y = \begin{bmatrix} \lambda \\ gfc \end{bmatrix} = X\beta + Z\alpha + Wpe + e$$

where λ is a vector of unobservable underlying liability for categorical traits (TOP3 or TOP5) in the threshold model, and gfc is a vector of observations for growth, fertility, or carcass traits in the linear model; β is a vector of systematic effects of CG class and animal age at measurement (linear effect); α is a vector of animal additive genetic effects; pe is a vector of animal permanent environmental effects (only for TOP3 and TOP5); and e is a vector of

random residual effects associated with the observations. X , Z , and W are incidence matrices that link data to their respective effects. The assumptions of the model include $E[y] = X\beta$; $\text{Var}(\alpha) = A \otimes G$; $\text{Var}(pe) = IPE$, and $\text{Var}(e) = I \otimes R$, where A is the relationship numerator matrix among all animals in the pedigree file; G is the (co)variance matrix of additive genetic effects; \otimes is the direct product; I is an identity matrix; PE is the variance of animal permanent environmental effects; R is the (co)variance matrix of residual effects; and vectors b , a , and ep are location parameters of the conditional distribution $y | \beta, \alpha, pe$. A uniform *a priori* distribution of β was assumed, which reflects vague prior knowledge of this vector. A scaled inverted Wishart distribution for the other parameters was assumed *a priori*: $\Sigma \sim IW(S, n)$, in which $S = S^*n$, where S^* plays the role of an expected covariance matrix (known covariance matrix), and n can be interpreted as the degree of belief in S^* . Using $n = -(k + 1)$, with k representing the dimension of the covariance matrix, and assuming S^* as a null matrix, the IW distribution reduces to a k -dimensional improper uniform distribution, which can be directly used as a non-informative prior in Bayesian inference (Sorensen and Gianola, 2002).

Parameters were drawn from the posterior distributions using Gibbs sampling as implemented in the THRGIBBS1F90 program (Tsuruta and Misztal, 2006). Based on the pre-Gibbs diagnosis used (POSTGIBBSF90 program) and on the visual inspection of trace plots, a chain of 200,000 iterations was run, with a burn-in of 20,000 rounds and a thinning interval of 20 samples. These resulting samples were used to compute the posterior means, standard deviations, and the highest posterior density (HPD) region for the variance components.

Analysis was performed including TOP5 at yearling (TOP5_365), with an age interval of 305-425 days, and using only one record per animal. In this dataset, the mean TOP5_365 was 12.4 ± 4.3 for 10,232 animals born to 561 sires. For other traits, the dataset analyzed was the same as that described above. The statistical model used in these analyses was similar to those described above, but did not include permanent environmental effects of the animal.

RESULTS AND DISCUSSION

The mean age of the animals judged was 17.06 ± 7.03 months (range: 6.16-41.93 months). For TOP3 and TOP5, the animals had a maximum of 8 records (i.e., participations in cattle championships), with a mean of 1.65 ± 1.01 records/animal. There was a large concentration of ranks 1-5 in a small number of sires. Approximately 57% of the animals ranked 1st to 5th place were born to 10 sires and 75% were grandsons of 10 paternal grandsires.

Heritability estimates for TOP3 obtained by other two-trait analyses were slightly lower (0.106 ± 0.011 to 0.129 ± 0.011 , data not shown) than those shown in Table 2. The lowest heritabilities were estimated by two-trait analysis based on carcass traits (0.101 ± 0.012 to 0.103 ± 0.011). The same was observed for TOP5, whose heritabilities estimated by two-trait analysis with the other traits were lower than those obtained with W_365 (Table 2) and ranged from 0.156 ± 0.014 to 0.189 ± 0.014 . Therefore, heritabilities for the 2 traits related to animal ranking in cattle championships were of low to medium magnitude, demonstrating a marked influence of the environment on these traits. An increase in additive genetic variation was observed from TOP3 to TOP5, but this increase was less pronounced than the increase in heritability estimates. This increase is likely a consequence of the higher percentage of success of TOP5 compared to TOP3 (Table 1), corresponding to a larger number of animals receiving value 1, which increases the scale of variability

observed. Repeatability estimates for animal ranking in cattle championships were of medium magnitude, a fact conferring moderate reliability to the ranking of the same animal judged at different ages.

Table 2. Posterior means, mode, median, and highest posterior density (HPD) region of variance components, heritability and repeatability for animal ranking up to 3rd place (TOP3) and up to 5th place (TOP5), estimated by two-trait analysis with yearling weight (W_365).

Trait	Parameter	Means \pm SD	Mode	Median	95% HPD
TOP3	σ_a^2	0.027 \pm 0.002	0.028	0.027	0.024-0.030
	σ_{ep}^2	0.023 \pm 0.001	0.024	0.023	0.021-0.026
	σ_e^2	0.097 \pm 0.002	0.097	0.097	0.095-0.099
	h^2	0.182 \pm 0.010	0.167	0.183	0.163-0.204
	r	0.341 \pm 0.007	0.333	0.342	0.328-0.356
TOP5	σ_a^2	0.052 \pm 0.003	0.051	0.052	0.046-0.057
	σ_{ep}^2	0.026 \pm 0.002	0.025	0.026	0.022-0.030
	σ_e^2	0.122 \pm 0.001	0.121	0.122	0.119-0.125
	h^2	0.260 \pm 0.012	0.267	0.260	0.233-0.285
	r	0.400 \pm 0.007	0.384	0.390	0.375-0.405

TOP3 = animals ranked 1st to 3rd place within the category; TOP5 = animals ranked 1st to 5th place within the category; σ_a^2 = additive genetic variance; σ_{ep}^2 = permanent environmental variance; σ_e^2 = temporary environmental variance; h^2 = heritability; r = repeatability; SD = standard deviation.

In beef cattle championships, judges evaluate animals based on a set of visual traits. Although rules exist for the judging of Zebu animals, cattle ranking in championships is a subjective trait like other traits used in beef cattle breeding programs in Brazil, e.g., visual scores of conformation, muscling, structure, and navel, among others (Van Melis et al., 2003; Faria et al., 2009; Boligon et al., 2012). For animals ranking in championships, competitions could be structured according to the level (or importance) of the event, i.e., there are more important competitions in which very good animals participate and the level can be considered high, or vice-versa. Recent studies have applied a method that considers the degree of difficulty in evaluating final ranks, including this effect in the probability function of final ranks (Ricard and Legarra, 2010).

In the literature, genetic parameters of visual score traits are available for Nellore herds. These traits are related to the morphology sought in animals during cattle judging at championships. Heritability estimates ranging from 0.07-0.24 for slaughter conformation, from 0.21-0.31 for precocity, and from 0.22-0.38 for muscling have been reported for Nellore animals at 15-18 months of age (Van Melis et al., 2003; Faria et al., 2009; Boligon et al., 2012). Faria et al. (2009) estimated heritabilities of 0.21, 0.46, and 0.36 for scores of breed traits, sacral bone conformation, and naval conformation, respectively. Heritabilities estimated in the present study for TOP3 and TOP5 were lower than those reported for the scores de-

scribed above. This is likely because of the large number of different traits, and consequently, different heritabilities were subjectively evaluated during cattle judging at championships.

The use of certain champion bulls for the production of animals in championships is a common practice in elite herds, as it is believed that the offspring of these bulls have a high chance of success in cattle championships. However, this was not confirmed by heritability estimates for TOP3 and TOP5, which were of low to medium magnitude.

Table 3 shows the results of descriptive statistics for variance and heritability estimates of growth, fertility, and carcass traits obtained by two-trait analysis with TOP5. For some traits, heritability estimates were higher than those reported for Nellore herds, whereas heritability for HH was similar (Cyrillo et al., 2001; Magnabosco et al., 2002; Giannotti et al., 2005; Yokoo et al., 2010; Pinheiro et al., 2012). However, heritability for BW was much higher than estimates reported in previous studies. In addition to the fact that these animals suffered strong pre-selection in their herds of origin before weaning, it is likely that the environment offered to animals is the best possible in all herds. As a result, environmental variation in this trait is minimal. Another explanation for the high heritability for BW is that the analysis models did not include factors such as age of dam at calving or maternal effects (genetic and permanent environmental). However, previous analyses showed that these effects are negligible since most of these animals were derived from embryo transfers and are commonly fed differently at an early age as preparation for championships. In addition, the concentration of offspring of few sires and few parental grandparents, i.e., the small number of families, may also explain why the heritability for BW was outside of the expected range. As expected, the results of descriptive statistics for variance and heritability estimates of the growth, fertility, and carcass traits obtained by two-trait analysis with TOP3 were very similar.

Estimates of genetic and phenotypic correlations between TOP5 and growth, fertility, and carcass traits are shown in Table 4. Genetic correlations between the traits related to animal rank in championships and growth traits were high, whereas the phenotypic correlations between the same traits were of medium to low magnitude. The highest phenotypic correlations were observed between TOP5 and BW (0.535 ± 0.009), followed by the phenotypic correlations with HG (0.377 ± 0.018), demonstrating that judges are most influenced by these 2 traits when awarding prizes. However, the best animals according to the rank in championships generally presented higher breeding values for BW and HG, as well as for HH and BL, as the genetic correlations of TOP3 (results not shown) and TOP5 with these traits were high.

The use of high-ranked animals as bulls may promote genetic gain in growth traits obtained at 365 days of age. This may be beneficial because these traits show a favorable genetic and phenotypic correlation with carcass weight (Bonilha et al., 2008). However, genetic gain in HH, which is also genetically correlated with TOP3 and TOP5, may be undesirable as there is evidence of a negative, but relatively low, genetic correlation between HH and carcass traits of finishing cattle (Yokoo et al., 2010; Pinheiro et al., 2012). The medium genetic correlation between SC and TOP3 (0.439 ± 0.072) and TOP5 (0.382 ± 0.067) may be improved through the use of high-ranked animals as bulls. The genetic correlations of TOP3 and TOP5 with the carcass traits measured by ultrasound should be interpreted with caution as they showed high standard deviations and wide HPD regions because of the small number of available records for these traits. The phenotypic and genetic correlations estimated in this study (Table 4) reflect the current trend of selection employed in cattle judging at championships, i.e., an emphasis on the choice of large and heavy animals.

Table 3. Posterior means, mode, median, and highest posterior density (HPD) region of variance components and heritability for growth, fertility and carcass traits estimated by two-trait analysis with animal ranking up to 5th place (TOP5).

Trait	Parameter	Mean ± SD	Mode	Median	95% HDI
BW	σ_a^2	1025 ± 47.8	1021	1027	932-1118
	σ_e^2	352 ± 57.2	363	350	298-412
	h ²	0.745 ± 0.024	0.755	0.746	0.696-0.788
HH	σ_a^2	7.58 ± 0.600	7.09	7.55	6.50-8.82
	σ_e^2	5.51 ± 0.40	5.51	5.53	4.70-6.26
	h ²	0.578 ± 0.036	0.530	0.578	0.512-0.650
BL	σ_a^2	13.7 ± 1.20	13.6	13.6	11.5-16.1
	σ_e^2	12.5 ± 0.823	12.3	12.5	10.8-14.0
	h ²	0.522 ± 0.037	0.500	0.521	0.454-0.596
HG	σ_a^2	15.8 ± 3.0	16.3	15.8	10.6-22.1
	σ_e^2	19.7 ± 2.28	19.4	19.7	15.0-24.0
	h ²	0.443 ± 0.073	0.500	0.446	0.309-0.593
SC	σ_a^2	4.39 ± 0.73	4.79	4.37	3.05-5.90
	σ_e^2	3.35 ± 0.54	3.29	3.36	2.27-4.37
	h ²	0.566 ± 0.079	0.552	0.565	0.412-0.720
LMA	σ_a^2	23.6 ± 7.81	20.5	23.1	7.61-41.8
	σ_e^2	53.8 ± 6.44	54.4	53.9	40.0-67.0
	h ²	0.303 ± 0.092	0.333	0.301	0.104-0.508
BF	σ_a^2	2.08 ± 0.670	1.56	2.01	1.09-3.72
	σ_e^2	2.71 ± 0.500	3.15	2.75	1.57-3.55
	h ²	0.430 ± 0.120	0.254	0.421	0.241-0.704
RF	σ_a^2	2.22 ± 0.730	1.87	2.17	0.95-3.89
	σ_e^2	2.29 ± 0.55	2.08	2.30	1.05-3.30
	h ²	0.487 ± 0.137	0.556	0.486	0.229-0.788

For abbreviations, see legends to Tables 1 and 2.

We also performed two-trait analysis considering TOP5 at yearling (TOP5_365), with an age interval of 305-425 days, and using only one record per animal. The mean heritability for TOP5_365 obtained in 8 analyses with the other traits evaluated at 365 days was 0.238. This estimate is similar to that obtained for TOP5 based on repeated records (Table 2) in two-trait analysis with BW, showing a higher consistency of heritability estimates in analyses including TOP5_365 rather than TOP5, most because of the difficulty in modeling the permanent environmental variance of binomial repeated measures. The heritability estimates for all traits (BW, HH, BL, HG, SC, LMA, BF, and RF) obtained in two-trait analysis with TOP5_365 were 0.599 ± 0.034, 0.498 ± 0.040, 0.471 ± 0.038, 0.533 ± 0.082, 0.443 ±

0.073, 0.325 ± 0.089 , 0.489 ± 0.125 , and 0.502 ± 0.121 , respectively. In general, genetic and phenotypic correlations estimated in the second series of analysis ranged from negative low to high magnitude. Comparison with the first analysis showed that the correlations between TOP5_365 with SC and carcass traits continued to be moderate to low. Thus, the criteria used for judging of Zebu cattle should be revised because these traits are of economic importance due to their association with male fertility, heifer sexual precocity, and carcass quality.

Table 4. Posterior means and highest posterior density (HPD) regions of genetic and phenotypic correlations of TOP5 with growth, fertility and carcass traits.

Traits	Genetic correlation		Phenotypic correlation	
	Means \pm SD	95% HPD	Means \pm SD	95% HPD
TOP5 x BW	0.943 ± 0.014	0.910-0.970	0.535 ± 0.009	0.520-0.550
TOP5 x HH	0.739 ± 0.034	0.670-0.800	0.298 ± 0.012	0.270-0.320
TOP5 x BL	0.754 ± 0.037	0.680-0.830	0.309 ± 0.012	0.280-0.330
TOP5 x HG	0.535 ± 0.098	0.340-0.710	0.377 ± 0.018	0.340-0.410
TOP5 x SC	0.382 ± 0.067	0.250-0.510	0.132 ± 0.021	0.090-0.170
TOP5 x LMA	0.341 ± 0.114	0.090-0.540	0.149 ± 0.031	0.090-0.210
TOP5 x BF	0.255 ± 0.131	0.010-0.540	0.116 ± 0.033	0.050-0.180
TOP5 x RF	0.281 ± 0.122	0.050-0.520	0.170 ± 0.033	0.100-0.240

For abbreviations, see legend to Table 1.

The selection of young Nellore animals for higher body weight is justifiable and recommended because in Brazil animals are still slaughtered at a lighter weight and produce lighter carcasses than in some of the large meat-producing countries such as the United States, Australia, and Canada (faostat.fao.org). By contrast, selection for higher body weight at younger ages results in correlated responses in the mature weight of cows (Boligon et al., 2013) and increases maintenance requirements. The latter can be a problem in tropical environments with prolonged dry seasons, and may result in reduced pregnancy rates. In addition, the results suggest that important traits such as SC, BF, and RF are not considered in the evaluation criteria of Nellore bulls at cattle championships. Because of its favorable genetic correlation with semen quantity and quality (Silva et al., 2011), heifer sexual precocity (Eler et al., 2004), and its medium heritability (0.42), SC should be an important trait for judging bulls at cattle championships. Genetic variation in BF and RF has been reported for Nellore cattle (Yokoo et al, 2008; Pinheiro et al., 2012), which may be explored for selection. Furthermore, these traits are important for the commercialization of bovine carcasses and should also be considered when judging cattle at championships.

In conclusion, traits related to the ranking of animals in cattle championships have low to medium genetic variability in Nellore cattle. Repeatability estimates are of medium magnitude, a fact conferring moderate reliability to the rank of animals judged at different ages. There is evidence that judges of agricultural shows rank animals based on weight, body length, and heart girth.

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