Reproduction in Domestic Animals

Reprod Dom Anim 47, 313–318 (2012); doi: 10.1111/j.1439-0531.2011.01874.x
ISSN 0936-6768

Heritability Estimate and Genetic Correlations of Reproductive Features in Nellore Bulls, Offspring of Super Precocious, Precocious and Normal Cows Under Extensive Farming Conditions

JB Siqueira[1], E Oba[2], RO Pinho[3], HP Quintino[4], JP Eler[5], T Miranda Neto[6], SEF Guimarães[3] and JD Guimarães[3]*

[1]*Federal University of Espírito Santo (UFES), Alegre, ES;* [2]*Faculty of Veterinary Medicine and Animal Science (FMVZ), UNESP, Botucatu, SP;* [3]*Federal University of Viçosa (UFV), Viçosa, MG;* [4]*Municipal Foundation of Higher Education of Bragança Paulista (FESB), Bragança Paulista, SP;* [5]*College of Animal Science and Foods Engineering, USP, Pirassununga, SP;* [6]*Agro-Pecuária CFM Ltda., São José do Rio Preto, SP, Brazil*

Contents

The present work aimed to estimate heritability and genetic correlations of reproductive features of Nellore bulls, offspring of mothers classified as superprecocious (M1), precocious (M2) and normal (M3). Twenty one thousand hundred and eighty-six animals with average age of 21.29 months were used, evaluated through the breeding soundness evaluation from 1999 to 2008. The breeding soundness features included physical semen evaluation (progressive sperm motility and sperm vigour), semen morphology (major, minor and total sperm defects), scrotal circumference (SC), testicular volume (TV) and SC at 18 months of age (SC18). The components of variance, heritability and genetic correlations for and between the features were estimated simultaneously by restricted maximum likelihood, with the use of the VCE software system vs 6. The heritability estimates were high for SC18, SC and TV (0.43, 0.63 and 0.54; 0.45, 0.45 and 0.44; 0.42, 0.45 and 0.41, respectively for the categories of mothers M1, M2 and M3) and low for physical and morphological semen aspects. The genetic correlations between SC18 and SC were high, as well as between these variables with TV. High and positive genetic correlations were recorded among SC18, SC and TV with the physical aspects of the semen, although no favourable association was verified with the morphological aspects, for the three categories of mothers. It can be concluded that the mother's sexual precocity did not affect the heritability of their offspring reproduction features.

Introduction

There are approximately 70% of Zebu animals and crosses in the Brazilian cattle population, with more than 173 million head of cattle (Anualpec, 2010). In Brazil, among the Zebu breeds, Nellore has been studied with the objective of identifying good selection criteria (Lira et al. 2008). Therefore, it is necessary to identify genetically superior animals, which is a key element in the production process. The selection of young animals can accelerate the genetic progress by reducing the interval between generations. Currently, precocity is a tool that targets at increasing cattle productivity. Cattles with high sexual and fertility precocity present more availability of animals, both for marketing and selection, allowing higher selection intensity and, consequently, higher genetic improvements and higher profitability (Bergmann 1999).

There are few reports related to genetic associations between testicular and seminal features in Zebu bulls, and the most studied include biometric measurements (SC, testicular lengths and widths, TV and testicular shape), physical (progressive sperm motility and sperm vigour) and morphological (major, minor and total sperm defects) features (Sarreiro et al. 2002; Quirino et al. 2004; Silveira 2004; Dias et al. 2006, 2008; Silva 2009).

Several studies considered the importance of estimating heritability and genetic, phenotypic and environmental associations among the breeding soundness features and among these and characteristics of economic interest (Dias et al. 2006). Thus, knowledge of estimates of genetic parameters for seminal, testicular and sexual behavioural features achieved by the breeding soundness evaluation may allow more appropriate guidance for selection for fertility in commercial cattle (Silva 2009).

It is necessary to establish criteria or parameters to evaluate the genetic value of breeders for economically relevant features, which are highly important, such as pregnancy of heifers at the ages of 14, 18 and 24 months and the permanence of a fertile matrix in the cattle for time enough to compensate its costs, which was defined as stayability or ability to remain in the cattle. The current trend is to expose the 14-month-old Nellore heifers to bulls. This exposure to bulls, although reaching average pregnancy rates of approximately 10–20%, increases the frequency of sexually precocious females (Ferraz and Eler 1999) and males in the cattle (Siqueira, 2009).

Therefore, the present work aimed to verify the existence of differences in the heritability and genetic correlations of reproduction features of Nellore bulls, offspring of mothers classified as superprecocious, precocious and normal.

Materials and Methods

This study was carried out in five cattle groups raised in northwestern São Paulo State and Mato Grosso do Sul State, Brazil. Twenty one thousand hundred and eighty-six animals young Nellore bulls were used, evaluated by breeding soundness evaluation, from June to August, from 1999 to 2008, corresponding to the harvests from 1997 to 2006. The animals were fed pastures, mainly *Brachiaria decumbens* (40%) and *Panicum maximum* (50%), with mineral salt and water *ad libitum*. When the animals were at 18–20 month of age, they were confined and fed corn silage, mineral salt and water *ad libitum*.

*Adviser of the project.

Because of marketing demands related to the presentation of the product (bulls) to be sold, at the ages from 20 to 22 months, the breeding soundness evaluation was carried out. Because all the animals presented genealogical record, their ascendants, date of birth and the due weightings at birth, weaning and yearling were known, excepting the offspring of multiple breeders, which corresponded to the females covered by a group of unknown bulls (fatherhood can only be verified by means of typing of DNA markers). Thus, the father was considered equal to zero.

The reproduction features evaluated from the females were the age at the first parturition (considered as the age in months at the first parturition), which was studied on the basis of three different definitions: superprecocious category with pregnancy at the age of 14 months (average of 12–16.9 months) for heifers between 21 and 25.9 months; precocious category, with pregnancy at 20 months of age (average from 17 to 23.9) for the heifers that gave birth at the age ranging from 26 to 32.9 months; and normal category (non-precocious), with pregnancy at or above 24 months for the heifers that gave birth after 33 months of age.

During the breeding soundness evaluation, after individual restraint of the animals, testicular measurements were performed, including testicular length and width and scrotal circumference (SC). The SC during the breeding soundness evaluation was achieved with the use of a measuring tape, after a slight ventro-caudal traction of the gonads and in the wider region of the scrotum. The SC at 18 months (SC18) of all the animals was measured similarly.

To determine the testicular shape, the criteria described by Bailey et al. (1996) were used, in which the gonads are classified into long, long/moderate, long/ovoid, ovoid/spherical and spherical. To calculate the testicular volume (TV), it was employed the formula recommended by Fields et al. (1979) for cylindrical shape or else the formula recommended by Bailey et al. (1998) for the spherical shape.

The electroejaculation method was used for semen collection, which was performed after individual restraint of the animals. After collection, the physical features of the ejaculate were evaluated. With an aliquot of the semen (10 μl) between the slide and coverslip, previously heated at 37°C, the rectilinear progressive sperm motility (0–100%) and sperm vigour (0–5) were assessed with augmentation of 200–400× in phase contrast microscope.

A sample of semen (sufficient to cloud the solution) was placed and stored in 1 ml of formaldehyde-buffered saline (Hancoch 1957) for sperm morphological analysis. In this evaluation, the methodology recommended by Blom (1973) was adopted, with records of the defects on head, tail and acrosome. The abnormalities were classified into major, minor and total sperm defects (MD, MID and TD, respectively). Four hundred sperm cells per ejaculate were analysed through phase contrast microscopy, at 1250× power.

The determination of age at sexual maturity was carried out according to Garcia et al. (1987), whose definition was based on the fact that the animals presented ejaculates with major defects below 15% and total sperm defects below 30%. Sexual maturity was also classified according to Guimarães (1997), based on the sperm process, pathophysiology of reproduction and physical and sperm morphological features, resulting in four andrological classes: (i) sexually mature animals, suitable for reproduction, (ii) sexually mature animals, with indexes of sperm pathologies that do not harm the fecundation capacity of the ejaculate, classified as suitable for reproduction under natural mating, (iii) sexually immature animals, temporarily unfit for reproduction and (iv) animals discarded because of imperfect spermatogenesis or morphological defects in the genital organs.

The genetic analyses were performed with the results achieved by breeding soundness examinations of 21 186 Nellore bulls that belong to the genetic breeding programme of the Agropecuária CFM Ltda, between 1999 and 2008. This data bank received information about the SC18 and the group of contemporaries of the animals at this measure aiming at increasing the volume of information and consistency of data. Thus, the data bank now has information about 58 716 problems with a matrix with kinship of 114 504 animals.

The contemporary group for SC18 was formed by the farm where the animal was at 18 months, year of birth, gender and management group to which it was submitted during measurement.

File edition started from the initial data base with information related to the animals with some valid measurement, from which the information related to records that presented errors or incomplete information were eliminated. These incomplete information included the following: unknown parents or offspring from multiple breeders; those belonging to contemporary groups with less than five animals with valid measurements; information related to the animals with breed composition incompatible with those of the parents or presenting above 5% of error in one or more fractions of the racial composition; and information outside the acceptable range for each variable.

Later, the same data bank was subdivided according to the age of the mother during the third parturition to compare the components of variance and the genetic parameters of this offspring and assess whether there is difference among them: M1: data bank for superprecocious mothers containing 2284 offspring and 8258 animals in the relationship matrix; M2: data bank for precocious mothers containing 7241 offspring and 21 063 animals in the relationship matrix; M3: data bank for normal mothers containing 49 191 offspring and 102 406 animals in the relationship matrix.

The components of variance, heritability and genetic correlation for and between the parameters were estimated simultaneously by restricted maximum likelihood, using the VCE software system vs. 6 (Kovac and Groeneveld 2007).

The genetic analyses were carried out with a multivariate model involving seven features at a time, to estimate the genetic correlations. The model of analysis adopted for the testicular features of SC18, SC and TV, physical aspects of the semen of MOT and VIG and sperm morphology of MD, MID and TD, can be linearly described as:

$$Y = X\beta + Z\alpha + e, \text{in} \quad \text{which:}$$

Y = vector of observations for the features in study, SC18, SC, TV, MOT, VIG, MD, MID and TD; β = vector of fixed effects (contemporary group and age of the animal as covariable); α = vector of additive genetic values corresponding to the animals that present measured data; e = vector of residues; X = matrix of incidence of $n \times p$ order, associating each observation (n), to each contemporary group (p); Z = matrix of incidence of $n \times p$ order, associating each observation (n), to the animal that produced it (p).

It was assumed that:

$$\text{Var}\begin{pmatrix} a \\ e \end{pmatrix} = \begin{pmatrix} A\sigma_a^2 & 0 \\ 0 & R \end{pmatrix}, \text{in which :}$$

A = the relationship matrix among all the animals; R = residual variance ($R = I\sigma_a^2$).

The equations of mixed models under the animal model can be formed as follows:

$$\begin{pmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}\lambda \end{pmatrix} \cdot \begin{pmatrix} \beta \\ \hat{a} \end{pmatrix} = \begin{pmatrix} \boldsymbol{X}'y \\ \boldsymbol{Z}'y \end{pmatrix},$$

in which:

λ = ratio between σ_e^2 and σ_a^2, in other words, $\sigma_e^2/\sigma_a^2 = (1 - h^2)/h^2$, so that h^2 refers to the heritability for the trait.

Results

The estimates of heritability observed for the scrotal circumference measured at 18 months (SC18), SC and TV during the breeding soundness evaluation were considered of high magnitude for the category of superprecocious, precocious and normal mothers (Tables 1, 2 and 3). No variation was observed for the heritability estimate for SC18, SC and TV among the categories of mothers.

The heritability estimates for the semen physical and morphological aspects for the category of superprecocious, precocious and normal mothers are described in Tables 1, 2 and 3. No variation was observed for the heritability estimate for the semen physical and morphological aspects among the categories of mothers.

Table 1. Estimates of components of variance and heritability of the reproduction features of young Nellore bulls, offspring of superprecocious females raised under extensive farming conditions

Variables	σ_a^2	σ_e^2	σ_p^2	h^2 (± |SE|)	|e^2 (± SE)|
SC18	2.5	3.3	5.8	0.43 ± 0.044	0.57 ± 0.056
SC	3.7	2.2	5.9	0.63 ± 0.046	0.37 ± 0.053
TV	17 328.2	14 988.8	32 316.9	0.54 ± 0.049	0.46 ± 0.058
MOT	29.8	134.9	164.7	0.18 ± 0.052	0.82 ± 0.059
VIG	0	0.3	0.3	0.06 ± 0.029	0.94 ± 0.028
MD	0.8	7	7.8	0.10 ± 0.040	0.90 ± 0.040
MID	0.2	4.2	4.4	0.04 ± 0.026	0.96 ± 0.022
TD	0.5	5.3	5.8	0.08 ± 0.038	0.92 ± 0.038

SC18, scrotal circumference at 18 months in centimetres; SC, scrotal circumference during breeding soundness evaluation in centimetres; TV, testicular volume in cubic centimetres; MOT, percentage of cells with rectilinear progressive motility; VIG (0–5), sperm vigour; MD, percentage of sperm cells with major sperm defects; MID, percentage of sperm cells with minor sperm defects; TD, percentage of total sperm cells with sperm defects; SE, standard error; σ_a^2, additive genetic variance; σ_e^2, residual genetic variance; σ_p^2, phenotypic genetic variance; h^2, heritability; e^2 , heritability for environmental effect and residue.

Table 2. Estimates of components of variance and heritability of the reproduction features of young Nellore bulls, offspring of precocious females raised under extensive farming conditions

Variables	σ_a^2	σ_e^2	σ_p^2	h^2 (± |SE|)	|e^2 (± SE)|
SC18	2.7	3.2	5.9	0.45 ± 0.024	0.55 ± 0.024
SC	2.5	3.0	5.6	0.45 ± 0.023	0.55 ± 0.023
TV	12 581.7	16 025.1	28 606.8	0.44 ± 0.025	0.56 ± 0.025
MOT	13.1	150.7	163.7	0.08 ± 0.021	0.92 ± 0.020
VIG	0.1	0.3	0.4	0.08 ± 0.018	0.92 ± 0.018
MD	0.3	7.8	8.1	0.04 ± 0.014	0.96 ± 0.014
MID	0.0	4.3	4.3	0.01 ± 0.050	0.99 ± 0.005
TD	0.0	6.1	6.1	0.05 ± 0.017	0.99 ± 0.017

SC18, scrotal circumference at 18 months in centimetres; SC, scrotal circumference during the breeding soundness evaluation in centimetres; TV, testicular volume in cubic centimetres; MOT, percentage of cells with rectilinear progressive motility; VIG (0–5), sperm vigour; MD, percentage of sperm cells with major sperm defects; MID, percentage of sperm cells with minor sperm defects; TD, percentage of total sperm cells with sperm defects; SE, standard error; σ_a^2, additive genetic variance; σ_e^2, residual genetic variance; σ_p^2, phenotypical genetic variance; h^2, heritability; e^2, heritability for environmental effect and residue.

Table 3. Estimates of components of variance and heritability of the reproduction features of young Nellore bulls, offspring of normal females raised under extensive farming conditions

Variables	σ_a^2	σ_e^2	σ_p^2	h^2 (± |SE|)	|e^2 (± SE)|
SC18	2.9	4.0	6.9	0.42 ± 0.009	0.58 ± 0.009
SC	2.8	3.5	6.3	0.45 ± 0.009	0.55 ± 0.009
TV	12 793.7	18 700.5	31 494.2	0.41 ± 0.010	0.59 ± 0.010
MOT	15.4	171.2	186.6	0.08 ± 0.011	0.92 ± 0.011
VIG	0.0	0.3	0.4	0.07 ± 0.007	0.93 ± 0.007
MD	0.3	7.6	7.9	0.03 ± 0.010	0.97 ± 0.009
MID	0.1	4.4	4.5	0.02 ± 0.006	0.98 ± 0.006
TD	0.1	5.7	5.8	0.01 ± 0.002	0.99 ± 0.002

SC18, scrotal circumference at 18 months in centimetres; SC, scrotal circumference during the breeding soundness evaluation in centimetres; TV, testicular volume in cubic centimetres; MOT, percentage of cells with rectilinear progressive motility; VIG (0–5), sperm vigour; MD, percentage of sperm cells with major sperm defects; MID, percentage of minor sperm defects; TD, percentage of total sperm cells with sperm defects; SE, standard error; σ_a^2, additive genetic variance; σ_e^2, residual genetic variance; σ_p^2, phenotypic genetic variance; h^2, heritability; e^2, heritability for environmental effect and residue.

The genetic associations reported between all variables are recorded in Tables 4, 5 and 6. The values recorded between SC18 and SC were high for the categories of supreprecocious, precocious and normal mothers (0.83; 0.82 and 0.91, respectively), so that the animals that presented higher PEs at 18 months in the three categories of mothers demonstrated higher PEs during the breeding soundness evaluation when it was carried out in animals with average of 21.29 ± 1.77 months of age. Similarly, associations were also high for the genetic associations recorded for SC18 and SC with TV and were 0.77 and 0.97; 0.71 and 0.92; 0.84 and 0.93, respectively, for the superprecocious, precocious and normal mothers (Tables 4, 5 and 6). Because of the high genetic correlations observed, it can be considered that the selection for SC18 and SC must lead to genetic change in TV.

The genetic correlations among SC, SC18 and TV with the physical aspects of the semen (MOT and VIG)

Table 4. Averages of the genetic correlations between different reproduction features of young Nellore bulls, offspring of superprecocious females raised under extensive farming conditions

Correlations								
Variables	SC18	SC	TV	MOT	VIG	MD	MID	TD
SC18	1.00	0.83	0.77	0.44	0.58	0.09	0.09	−0.06
SC		1.00	0.97	0.31	0.29	0.11	0.19	0.16
TV			1.00	0.35	0.24	−0.16	0.06	0.09
MOT				1.00	0.87	0.67	0.35	0.07
VIG					1.00	0.81	0.27	−0.19
MD						1.00	0.05	0.37
MID							1.00	0.76
TD								1.00

SC18, scrotal circumference at 18 months in centimetres; SC, scrotal circumference during the breeding soundness evaluation in centimetres; TV, testicular volume in cubic centimetres; MOT, percentage of cells with rectilinear progressive motility; VIG (0–5), sperm vigour; MD, percentage of sperm cells with major sperm defects; MID, percentage of sperm cells with minor sperm defects; TD, percentage of total sperm cells with sperm defects.

Table 5. Averages of the genetic correlations between different reproductive features of Nellore young bulls, offspring of precocious females raised under extensive farming conditions

Correlations								
Variables	SC18	SC	TV	MOT	VIG	MD	MID	TD
SC18	1.00	0.82	0.71	0.51	0.53	0.54	−0.24	−0.74
SC		1.00	0.92	0.36	0.38	0.50	−0.55	−0.51
TV			1.00	0.31	0.24	0.44	−0.61	−0.49
MOT				1.00	0.94	0.51	−0.65	−0.10
VIG					1.00	0.31	−0.52	0.02
MD						1.00	−0.52	−0.65
MID							1.00	−0.17
TD								1.00

SC18, scrotal circumference at 18 months in centimetres; SC, scrotal circumference during the breeding soundness evaluation in centimetres; TV, testicular volume in cubic centimetres; MOT, percentage of cells with rectilinear progressive motility; VIG (0–5), sperm vigour; MD, percentage of sperm cells with major sperm defects; MID, per cent of sperm cells with minor sperm defects; TD, percentage of total de sperm cells with sperm defects.

Table 6. Averages of the genetic correlations between different reproduction features of young Nellore bulls, offspring of normal females raised under extensive farming conditions

Correlations								
Variables	SC18	SC	TV	MOT	VIG	MD	MID	TD
SC18	1.00	0.91	0.84	0.68	0.64	0.20	0.38	−0.82
SC		1.00	0.93	0.54	0.48	0.06	0.37	−0.61
TV			1.00	0.55	0.46	0.09	0.38	−0.60
MOT				1.00	0.97	0.57	0.34	−0.81
VIG					1.00	0.41	0.50	−0.86
MD						1.00	−0.56	−0.03
MID							1.00	−0.63
TD								1.00

SC18, scrotal circumference at 18 months in centimetres; SC, scrotal circumference during the breeding soundness evaluation in centimetres; TV, testicular volume in cubic centimetres; MOT, percentage of cells with rectilinear progressive motility; VIG (0–5), sperm vigour; MD, percentage of sperm cells with major sperm defects; MID, per cent of sperm cells with minor sperm defects; TD, percentage of total sperm cells with sperm defects.

presented moderate to high values (0.29–0.68) in the category of superprecocious, precocious and normal females, demonstrating the existence of a positive genetic association and indicating that the genes linked to the expression of SC, SC18 and TV also influenced sperm motility and vigour in the breeding soundness evaluation (average of 21.29 ± 1.77 months of age).

The genetic correlations involving SC, SC18 and SC and sperm morphological aspects (MD, MID and TD) are described in Tables 4, 5 and 6. Low or negative correlations were recorded for the category of superprecocious mothers (Table 4). For the category of precocious mothers (Table 5), negative correlations were recorded between MID and TD with SC18, SC and TVT. Therefore, the selection for these variables is favourable to the decrease of sperm defects in the ejaculate. Positive and high correlations were recorded among SC18, SC and TV with MD. For the category of normal mothers, positive correlations were recorded among SC18, SC and TV with MD and MID and negative with TD.

Discussion

No variation was observed for the estimate of heritability for SC18 and SC among the mother categories. These results are similar to those of other studies with Nellore animals, whose estimates of heritability for SC18 varied from 0.31 to 0.42 (Ortiz Peña et al. 2001; Dias et al. 2003; Silva 2009). However, higher heritability values for SC at 18 months were recorded for Eler et al. (2006) from 0.53 to 0.64; Eler et al. (2004) of 0.57; and Ortiz Peña et al. (2001) of 0.47 adjusted for age and body weight.

Average values at high magnitude for SC were also recorded by Silva (2009), 0.43; Silveira (2004), 0.37; and Sarreiro et al. (2002), 0.30, in Nellore animals with average of 22.5; 21 and 31 months, respectively. Other authors recorded higher values, which is the case of Quirino (1999) – 0.81 (non-adjusted for body weight) and 0.71 (adjusted for body weight) in animals at the age of 2–5 years; Bergmann et al. (1997) – 0.87 in Nellore animals from 19 months of age.

All the values presented, including those of this study, demonstrated the existence of additive genetic variance favourable for the selection of breeders based on SC. Because of the heritability magnitudes achieved, as pointed out in other studies, it is expected that the direct selection both for SC18 and SC results in fast genetic progress for these features.

No variation was observed for the estimate of heritability for TV in the category of mothers (Tables 1, 2 and 3). Quirino (1999) reported high estimate of heritability of 0.50 and moderate of 0.30 for TV, adjusted and non-adjusted to body weight, respectively, for Nellore. In Nellore animals, Silveira (2004) and Silva (2009) recorded values lower than those of this study, of 0.33 and 0.31, respectively.

The values verified in this study were high, demonstrating that the selection for this trait, and for SC and SC18, results in fast genetic progress and can also be used as a selection criterion in Nellore animals, when the goal is the achievement of animals with larger testicular volumes, because TV is related to sperm production. However, the high correlation of this trait with PE must be emphasized. The latter is a simpler and faster measurement to be achieved in the field, and is, therefore, the most appropriate. Besides, for the achievement of the measurements required for TV calculation, it is necessary to obtain the width and length of both testicles, which requires a careful measurement procedure (with the help of a caliper ruler) and ability from the technician.

The heritability estimates for the semen physical (MOT and VIG) and morphological (MD, MID and TD) aspects recorded in this study were of low magnitudes, indicating small additive genetic component. In Brazilian literature, there are few reports on estimates of genetic parameters for features of Zebu semen. For most works, the estimates of heritability (of low magnitude) corroborate those recorded in this study (Bergmann et al. 1997; Sarreiro et al. 2002; Silveira 2004; Dias et al. 2006, 2008; Silva 2009). According to Mascioli et al. (1996), heritability estimates are affected by differences in the environments to which the animals were submitted in the several samples of data analysed, genetic differences among the cattle groups and differences in the samples and in the mathematical models used by several authors.

Some authors still disagree about heritability of sperm pathologies and seminal maturity. It must be considered that some sperm anomalies may be inherited (Barth and Oko 1989) or caused by the effects of the environment on males, tending to normalize when the stressing factor is removed (Barth and Bowman 1994). Another complicating fact in the analysis of sperm pathologies is the presence of the same anomaly under different conditions. Barth and Oko (1989) mention that the knobbed sperm pathology might have genetic origin. However, Barth and Bowman (1994) also verified increased frequency of this pathology when they submitted the bulls to scrotal insulation, or in very young animals, in adolescence or puberty (Guimarães 1993).

High values recorded for genetic correlation between SC18 and SC determined that the two variables are mainly determined by the same genes. These findings corroborate that the selection for higher SC18 would result in higher PEs during the andrological examination and, consequently, would allow the phenotypical expression of higher daily sperm production (Kastelic et al. 2001) and seminal quality (Siddiqui et al. 2008). Considering the estimates of heritability of SC18 and the favourable genetic correlations of SC18 with SC during the breeding soundness evaluation (average of 21.29 ± 1.77 months), it is suggested that the most appropriate age to select bulls may be 18 months.

Similar results were recorded by Silva (2009) for genetic correlation between SC18 and SC (0,84). According to the author, considering that the PE18 is measured in animals in average 4 months younger than the PE (at the first andrological examination), and that it can be measured in all the animals at yearling and not only in the males destined to andrological evaluation, this measurement (SC18) may present more advantages to be used as selection criterion.

Because of the high genetic correlations observed, it can be considered that the selection for SC18 and SC must lead to genetic change in TV. These findings corroborate those achieved by Silveira (2004), who recorded a genetic correlation of 0.88 between SC and TV. Similarly, Quirino (1999), Dias et al. (2008) and Silva (2009) observed values of 0.97, 0.99 and 0.78, respectively, in Nellore bulls, for genetic correlation between TV and SC, indicating that advances in the increase of SC strongly affect the increase of the cattle TV. Favourable genetic correlations of high magnitude between TV and SC indicated that these two variables were highly influenced by the action of the same additive genes, and that SC is the adequate parameter to be used in selection programmes for the prediction of testicle dimensions in Nellore animals.

There are several reports of genetic correlations between SC and the physical aspect of semen in literature, generally presenting favourable values of high magnitude, which demonstrates the importance of SC for these features and the common genetic base between them. For SC and sperm motility, the results varied from 0.13 to 1.00, while the results of genetic correlations between SC and sperm vigour varied from 0.69 to 0.99 (Bergmann et al. 1997; Quirino et al. 1999; Sarreiro et al. 2002; Silveira 2004; Dias et al. 2006, 2008). The authors report that this variation in the results is mainly due to the subjectivity of the evaluations and the influence of residual factors.

Silveira (2004) recorded values of −0.05, −0.48 and −0.09 for the genetic correlation of SC with MD, MID and TD, respectively. Higher and negative values were recorded by Quirino et al. (1999) (−0.50, −0.86 and −0.52, respectively, for MD, MID and TD with SC) demonstrating that there is higher genetic correlation between MID and SC, indicating that bovine with larger SC was more genetically likely to present lower MID values in the ejaculate. Silva (2009) recorded values of −0.16, −0.23 and −0.24 among SC18 with MD, MID and TD. According to these results, the increase for the direct selection of SC in a long term will provide, as a correlated response, reduced sperm defects and, consequently, an improvement in the seminal quality of bulls.

In young animals, the size of the testicles is directly related to semen quality, mainly during the period from puberty to sexual maturity, with the occurrence of the lamination of the seminiferous tubules and the organization of spermatogenesis for the production of normal spermatozoa in the ejaculate. Therefore, animals that reach puberty with larger testicles have higher chances of presenting lower percentages of sperm defects in the ejaculate. However, in the present study, when the genetic correlations between SC and sperm defects were evaluated in the data banks separately by categories of mothers, this fact was not observed. It is important to point out that the threshold of sperm pathologies that divide the animals into fit or unfit for reproduction (sexually mature and immature) at this stage is very low, which can explain these results.

Besides, it must be also considered that certain sperm abnormalities can be inherited or be caused by unfavourable environmental, nutritional and climatic conditions on males. Therefore, there must be caution, even for selected animals, because even bulls with large PE may present some type of sperm pathology.

Conclusion

Mothers' precocity does not affect the heritability of the reproduction features of their offspring. The genetic correlations among the variables of testicular biometry (SC18, SC and TV) among themselves and with the semen physical aspects (MOT and VIG) were high, demonstrating that SC at 18 months and SC during the breeding soundness evaluation can be used as features of choice in the evaluation and selection of Nellore bulls, with average of 21.29 ± 1.77 months of age, and that the use of TV instead of SC in selection programmes cannot be justified.

Conflict of interest

None of the authors have any conflict of interest to declare.

Author contributions

Siqueira and Pinho have designed the study; Oba was an adviser; Guimarães were co-advisers and analysed statistical analysis; Miranda neto contributed to financial support; Quintino and Eler analysed genetic correlations.

References

Anuário da Pecuária Brasileira, 2010: Anualpec, 16ª edn. FNP, São Paulo, p. 360.
Bailey TL, Monke D, Hudson RS, Wolff DF, Carson RL, Riddell DF, 1996: Testicular shape and its relationship to sperm production in mature Holstein bulls. Theriogenology **46,** 881–887.
Bailey TL, Hudson RS, Powe TA, Riddelli MG, Wolff DF, Carson RL, 1998: Caliper and ultrasonographic measurements of bovine testicles and a mathematical formula for determining testicular volume and weight in vivo. Theriogenology **49,** 581–594.
Barth AD, Bowman PA, 1994: The sequential appearance of sperm abnormalities after scrotal insulation or dexamethasone treatment in bulls. Can Vet J **35,** 93–102.
Barth AD, Oko RJ, 1989: Abnormal Morphology of Bovine Spermatozoa. Iowa State University Press, Ames, IA, p. 258.
Bergmann JAG, 1999: Seleção de zebuínos para precocidade sexual. In: I Simpósio de produção de gado de corte. Viçosa. Proceedings... SIMCORTE, Viçosa, pp. 51–64.
Bergmann JAG, Quirino CR, Vale Filho VR, Andrade VJ, Fonseca CG, 1997: Herdabilidades e correlações genéticas entre medições testiculares e características espermáticas em touros Nelore. Archivos Latino Americanos de Produção Animal **5,** 473–475.
Blom E, 1973: The ultrastructure of some characteristic sperm defects and a proposal for a new classification of the bull spermiogram. Nord Vet Med **53,** 383–391.
Dias LT, El Faro L, Albuquerque LG, 2003: Estimativas de herdabilidade para perímetro escrotal de animais da raça Nelore. Revista Brasileira de Zootecnia **32,** 1878–1882.
Dias JC, Andrade VJ, Fridrich AB, Salvador DF, Vale Filho VR, Corrêa AB, Silva MR, 2006: Estimativas de parâmetros genéticos de características reprodutivas de touros Nelores, de dois e três anos de idade. Arq Bras Med Vet Zootec **58,** 388–393.
Dias JC, Andrade VJ, Martins JAM, Emerick LL, Vale Filho VR, 2008: Correlações genéticas e fenotípicas entre características reprodutivas e produtivas de touros da raça Nelore. Pesqui Agropecu Bras **43,** 53–59.
Eler JP, Silva JAIV, Evans JL, Ferraz JBS, Dias F, Golden BL, 2004: Additive genetic relationships between heifer pregnancy and scrotal circumference in Nellore cattle. J Anim Sci **82,** 2519–2527.
Eler JP, Ferraz JBS, Balieiro JCC, Mattos EC, Mourão GB, 2006: Genetic correlation between heifer pregnancy and scrotal circumference measured at 15 an 18 months of age in Nellore cattle. Genet Mol Res **5,** 565–570.
Ferraz JBS, Eler JP, 1999: Seleção de zebuínos para características produtivas. In: I Simpósio de produção de gado de corte. Viçosa. Proceedings… SIMCORTE, Viçosa, pp. 29–50.
Fields MJ, Burns WE, Warnick AC, 1979: Age, season and breed effects on testicular volume and semen features in young beef bulls. J Anim Sci **48,** 1289–1304.
Garcia JM, Pinheiro LEL, Okuda HT, 1987: Body development and semen physical and morphological characteristics of young Guzerá bulls. Ars Veterinária **3,** 47–53.
Guimarães JD, 1993: Puberdade e maturidade sexual em touros da raça Gir, criados em condições semi-extensivas. Dissertação (Mestrado) Escola de Veterinária da Universidade Federal de Minas Gerais, Belo Horizonte, 85f.
Guimarães JD, 1997: Avaliação andrológica e estudos quantitativos e qualitativos da espermatogênese de touros mestiços F1 Holandês × Zebu e Red Angus × Zebu. Tese (Doutorado) – Escola de Veterinária da Universidade Federal de Minas Gerais, Belo Horizonte, 186f.
Hancoch JL, 1957: The morphology of boar spermatozoa. J R Microsc Soc **76,** 84–97.
Kastelic JP, Cook RB, Pierson RA, Coulter GH, 2001: Relationship among scrotal and testicular characteristics, sperm production, and seminal quality in 129 beef bulls. Can J Vet Res **65,** 111–115.
Kovac M, Groeneveld E, 2007: VCE-6 User's Guide and Reference Manual Version 6. University of Ljubljana, Slovenia, p. 75.
Lira T, Rosa EM, Garnero AV, 2008: Parâmetros genéticos de características produtivas e reprodutivas em zebuínos de corte (revisão). Ciência Animal Brasileira **9,** 1–22.
Mascioli AS, Alencar MM, Barbosa PF, Novaes AP, Oliveira MCS, 1996: Estimativas de parâmetros genéticos e proposição de critérios de seleção para pesos na raça Canchim. Revista Brasileira de Zootecnia **25,** 72–82.
Ortiz Peña CDO, Queiroz SA, Fries LA, 2001: Comparação entre critérios de seleção de precocidade sexual e a associação destes com características de crescimento em bovinos Nelore. Revista Brasileira de Zootecnia **30,** 93–100.
Quirino CR, 1999: Herdabilidades e correlações genéticas entre medições testiculares, características seminais e libido em touros Nelore. Tese (Doutorado) – Escola de Veterinária da Universidade Federal de Minas Gerais, Belo Horizonte, 104f.
Quirino CR, Bergmann JAG, Vale Filho VR, Andrade VJ, Pereira JCC, 1999: Evaluation of four mathematical functions to describe scrotal circumference maturation in Nellore cattle. Theriogenology **52,** 25–34.
Quirino CR, Bergmann JAG, Vale Filho VR, Andrade VJ, Reis SR, Mendonça RM, Fonseca CG, 2004: Genetic parameters of libido in Brazilian Nellore bulls. Theriogenology **62,** 1–7.
Sarreiro LC, Bergmann JAG, Quirino CR, Pineda NR, Ferreira VCP, Silva MA, 2002: Herdabilidade e correlação genética entre perímetro escrotal, libido e características seminais de touros Nelore. Arq Bras Med Vet Zootec **54,** 602–608.
Siddiqui MAR, Bhattacharjee J, Das ZC, Islam MM, Islam MA, Haque MA, Parrish JJ, Shamsuddin M, 2008: Crossbred bull selection for bigger scrotum and shorter age at puberty with potentials for better quality semen. Reprod Domest Anim **43,** 74–79.
Silva MR, 2009: Estudo Genético das características andrológicas de touros jovens da raça Nelore. Tese (Doutorado). Universidade Estadual de São Paulo, Jaboticabal, 93f.
Silveira TS, 2004: Estádio de maturidade sexual e estimativas de parâmetros genéticos e fenotípicos de características reprodutivas e ponderais, em touros da raça Nelore. Dissertação (Mestrado) – Universidade Federal de Viçosa, Viçosa, 137f.
Siqueira JB, 2009: Maturidade sexual de touros da raça Nelore, filhos de vacas superprecoces, precoces e normais, criados em condições extensivas (*Doutorado em Medicina Veterinária*). Thesis, Universidade Estadual Paulista, Botucatu.

Submitted: 2 Mar 2011; Accepted: 25 Jun 2011

Author's address (for correspondence): Rogério Oliveira Pinho, Universidade Federal de Viçosa/UFV–PH Rolfs Avenue, 36570–000 Viçosa City, MG, Brasil. E-mail: rogerio_op@yahoo.com.br