Selection criteria for sexual precocity in Guzerat bulls raised under grazing conditions

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ABSTRACT: The objectives of the present study were to obtain posterior densities of genetic parameters for scrotal circumference (SC), testicular volume (TV), BW, and age at puberty, to determine their correlations, and to evaluate the inclusion of these traits as selection criteria for sexual precocity in Guzerat bulls. Two-trait analyses were performed including records of SC, TV, and BW at 365, 450, 550, 650, 730, 850, and 970 d of age with age at puberty of 1,783 Guzerat bulls born between 2000 and 2011. The (co)variance components were estimated using Bayesian methods. Posterior means of heritability ranged from 0.45 to 0.60 for SC, from 0.35 to 0.55 for TV, and from 0.39 to 0.60 for BW. Posterior means of heritabilities for age at puberty using the two-trait analysis with SC ranged from 0.46 to 0.55, those with TV ranged from 0.49 to 0.57, and those with BW ranged from 0.49 to 0.62. The genetic correlation between age at puberty and SC ranged from -0.52 to -0.85, those between age at puberty and TV ranged from -0.33 to -0.66, and those between age at puberty and BW ranged from -0.38 to -0.72. In general, the same trend was observed for the phenotypic correlation between age at puberty and SC, TV, and BW. The selection of the top 10% of young males for SC, TV, or BW caused a decrease in age at puberty, with the most favorable expected correlated response in age at puberty at 650 d of age (-119.95 ± 15.1 d per generation), 730 d of age (~82.20 ± 20.9), and 850 d of age (~93.68 ± 21.5), respectively. In conclusion, SC, TV, and BW can be used as selection criteria to improve early sexual development in Guzerat bulls, and SC measured at 650 d of age is the most advantageous indicative selection criterion for improvement of age at puberty in Guzerat young bulls.

Key words: beef cattle, body weight, genetic parameter, puberty, scrotal circumference, testicular volume

INTRODUCTION

Zebu breeds (Bos indicus) are predominantly used in extensive management systems in most of South America. Unfortunately, Zebu cattle possess several reproductive disadvantages when compared to European breeds (Bos taurus), including later sexual development (Fields et al., 1982; Silva-Mena, 1997; Nogueira, 2004; Aponte et al., 2005).

Direct selection for reproduction traits is often difficult to apply, thus making it necessary to identify reproductive traits that are easily measured and correlated to reproductive events. Scrotal circumference (SC) is easily measurable, highly heritable (Yokoo et al., 2007; Boligon et al., 2010; Boligon et al., 2011), positively correlated with seminal quality (Silva et al., 2002; Kealey et al., 2006; Latif et al., 2009) and BW (Boligon et al., 2010; Yokoo et al., 2010), and favorably correlated with reproductive performance in females (Vargas et al., 1998; Martinez-Velázquez et al., 2003; Forni and Albuquerque, 2005; Meirelles et al., 2009).

Some investigators have suggested including measuring testicular volume (TV) in routine andrological assessments of males participating in genetic breeding programs (Unanian et al., 2000) because...
the two-dimensional measurement of length and width would be a more accurate predictor of TV and weight than the one-dimensional measurement of SC (Bailey et al., 1998). Few studies have estimated the genetic parameters for TV (Boligon et al., 2010; Silva et al., 2011), and the results suggest that a slower genetic gain is therefore expected if this trait is used as a selection criterion (Silva et al., 2011).

Direct selection for male or female sexual precocity traits is not easy. Thus, the objectives of the present study were to obtain posterior densities of genetic parameters for SC, TV, BW measured at different ages and for age at puberty, to determine their correlation, and to evaluate the expected correlated response in age at puberty by the inclusion of SC, TV, and BW in genetic breeding programs for sexual precocity in Guzerat bulls.

**MATERIALS AND METHODS**

All procedures performed in this study were approved by the ethics committee of Universidade Federal de Minas Gerais.

**Animals and Data**

This study was conducted on three farms located in Brasiliânda de Minas (17°00’36″S, 46°00’32″W), Carlos Chagas (17°41’30″S, 40°45’15″W), and Unaí (16°21’43″S, 46°54’09″W) in the state of Minas Gerais, Brazil. The climate classification in these regions is Aw (tropical rainy climate, Köppen classification), with an average temperature of 18°C in the coldest month. The dry season coincides with fall and winter, principally, and these seasons go from April to September. Spring and summer go from October to March. November, December, January, and February receive approximately 60% of the total yearly rainfall. During the nursing period and after weaning (~7 mo old), all Guzerat males were raised under grazing conditions on palisade grass (Brachiaria brizantha Stapf cv. Marandu) and bluestem (Andropogon gayanus Kunth cv. Planaltina) in the savanna region with water and mineral salt ad libitum. During the dry season the animals were supplemented with salt-type protein or roughage. During the dry season the animals were supplemented with salt-type protein or roughage.

Data from 1,783 Guzerat bulls born from 187 sires and 1,125 cows between 2000 and 2011 were used. The following traits were studied: SC, TV, and BW at 365 (SC365, TV365, BW365), 450 (SC450, TV450, BW450), 550 (SC550, TV550, BW550), 650 (SC650, TV650, BW650), 730 (SC730, TV730, BW730), 850 (SC850, TV850, BW850), and 970 d of age (SC970, TV970, BW970). Scrotal circumference was measured in the region of the greatest diameter of the testes and covered two gonads positioned symmetrically side by side, leaving the skin of the scrotum distended. The length and width of each testis were measured with a caliper, and these measurements were used to estimate testicular volume by the formula proposed by Fields et al. (1979): 

$$TV = 2[(r^2) \times \pi \times L]$$

where $r = 1/2$ testis width (radius), $\pi = 3.141592654$, and $L =$ testis length. Testicular measurements and weight were obtained from bulls 305 to 1,030 d of age at intervals of approximately 3 mo.

Semen collection by electroejaculation was attempted in the animals when they reached 20 cm SC. Twenty centimeters was the threshold SC below which sperm cell collection was always unsuccessful (Torres-Júnior and Henry, 2005). The interval between semen collections was approximately 3 mo, and onset of puberty was considered to be the age when the first mobile spermatozoa were observed in the ejaculate (Garcia et al., 1987; Torres-Júnior and Henry, 2005). When mobile spermatozoa were found 3 mo after an unsuccessful attempt, onset of puberty was estimated by interpolation (half the time between the unsuccessful and successful semen collections). It was impossible to measure age at puberty in all animals because some of them had already reached puberty at the first semen collection or they were sold before the end of measurements. Age at puberty in these types of animals was considered missing information. Because of this, we performed two-trait analysis to avoid culling bias (Mrode, 2005).

**Statistical Model**

General statistical models for SC, TV, and BW could be represented as

$$y_{ijkl} = \mu + CG_i + \text{month}_j + b(\text{age}_k - \bar{\text{age}}) + a_l + e_{ijkl},$$

where $y_{ijkl}$ represents the $y$ variable (SC, TV, or BW) of the $i^{th}$ animal of age $k$, $j^{th}$ contemporary group, and $l^{th}$ month of birth; $\mu$ represent a constant; $CG_i$ represents the fixed effects of the $i^{th}$ contemporary group (farm and year of birth); month$_j$ represents the $j^{th}$ fixed effect of month of birth; $b$ represents the linear regression coefficient of age$_k$ of the animal at measurements (age$_k$); age represents the mean of the age; $a_l$ represents the random additive genetic effect of animal $l$; and $e_{ijkl}$ represents the random residual effects. Contemporary groups with fewer than 2 records were deleted. The statistical model for age at puberty was similar to the previous one with the exclusion of the linear regression coefficient.
Under the matrix form, the general model considered in the two-trait analysis was

$$
\begin{bmatrix}
y_i^1 \\
y_i^2
\end{bmatrix} =
\begin{bmatrix}
x_i^1 & 0 \\
0 & x_i^2
\end{bmatrix}
\begin{bmatrix}
\beta_i^1 \\
\beta_i^2
\end{bmatrix} +
\begin{bmatrix}
Z_i^1 & 0 \\
0 & Z_i^2
\end{bmatrix}
\begin{bmatrix}
a_i \\
e_i
\end{bmatrix} +
\begin{bmatrix}
e_i
\end{bmatrix},
$$

where $y_i$ is a vector with the observations of trait $i$, $\beta_i$ is a vector with the fixed effect solutions (contemporary groups, month of birth, age), $a_i$ is a vector with solutions of the random direct genetic additive effect of trait $i$, $e_i$ is a vector with the solutions of random residual effects, and $x_i$ and $Z_i$ are incidence matrices that relate $y_i$ with $\beta_i$ and $a_i$, respectively.

The assumptions for the random effects were

$$
\text{Var}(a) = G \otimes A, \text{Var}(e) = R \otimes I,
$$

in which

$$
G =
\begin{bmatrix}
\sigma_{a1}^2 & \sigma_{a1a2} \\
\sigma_{a1a2} & \sigma_{a2}^2
\end{bmatrix},
$$

$\sigma_{i}^2$ is the additive genetic variance for trait $i$ ($i = 1$ or 2), $\sigma_{a1a2}$ is the additive genetic covariance between traits 1 and 2, $A$ is the numerator relationship matrix,

$$
R =
\begin{bmatrix}
\sigma_{e1}^2 & \sigma_{e1e2} \\
\sigma_{e1e2} & \sigma_{e2}^2
\end{bmatrix},
$$

$\sigma_{e}^2$ is the residual variance for trait $i$, $\sigma_{e1e2}$ is the residual covariance between traits 1 and 2, and $I$ is the identity matrix of order equal to the order of $y_i$.

For the composition of the relationship matrix, a recursive algorithm was used to keep only the individuals with data (1,783) and their ancestors on a pedigree file. In addition, individuals that did not have data or were not dams of animals with data, did not have at least one known ancestor, and were linked to only one animal in the database were also excluded from the pedigree record and the descendant’s pedigree. These procedures were repeated until there were no more animals of this type. In this way, a relationship matrix was formed, containing only genealogical data of animals considered to be informative, i.e., 3,095 animals.

The (co)variance components were estimated by the Bayesian method, using the INTERGEN program (Embrapa Pecuaria Sul., www.cppsul.embrapa.br/unidade/servicos/intergen; Cardoso, 2008), in two-trait analysis. Inference was based on Markov chain Monte Carlo methods with chains of 600,000 cycles with a burn-in period of 100,000 cycles and a thinning interval of 500 cycles. The convergence of the chains was evaluated using R software and the BOA package (The University of Iowa, www.public-health.uiowa.edu/boa; Smith, 2005), which generates convergence diagnostics according to Geweke (1992). In the Geweke test, initial values of the Markov chain are compared with final values of the chain to detect convergence failures. $P$-values lower than 0.05 indicate the existence of evidence against the convergence of chains.

The expected correlated response for SC, TV, and BW were calculated as $AG_{x,y} = i \times h_x \times h_y \times r_a \times \sigma_{px}$, where $x$ is the trait indirectly selected, $y$ is the trait under selection, $i$ is the selection intensity considered for trait $y$ (10% of the males), $h_x$ is the square root of the heritability of $x$, $h_y$ is the square root of the heritability of $y$, $r_a$ is the genetic correlation between the $x$ and $y$ traits, and $\sigma_{px}$ is the phenotypic standard deviation of the trait indirectly selected (Falconer and Mackay, 1996).

**RESULTS AND DISCUSSION**

The number of animals evaluated at each age (SC, TV, or BW), the animals measured at this age with puberty information in some age group, the number and percentage of animals that reached puberty in each age group, and the results of descriptive statistics obtained for testicular and body traits are summarized in Table 1. The means (±SD) of SC, TV, and BW obtained in this work were close to values reported by Trocóniz et al. (1991) and Torres-Júnior and Henry (2005) for Guzerat bulls. Age at puberty obtained from 821 bulls in this work was 622.14 ± 139 d and was within the range of age at puberty reported in other studies for Guzerat bulls raised under grazing conditions (Garcia et al., 1987; Trocóniz et al., 1991; Torres-Júnior and Henry, 2005). Because testicular measures and BW obtained in the present study were similar to those obtained in other works, it could be considered that this database is representative for Guzerat bulls raised under grazing condition in South America.

For every Markov chain the results indicated that the size of chain, burn-in period and thinning interval considered was sufficient to reach convergence. Posterior density statistics of the components of variance for growth and testicular traits obtained by two-trait analysis are shown in Table 2.

The posterior means (PM) of heritability for SC at different ages were considered to have a moderate to high magnitude (Fig. 1A) and were larger than estimates reported in the literature for Zebu cattle (Boligon et al., 2007; Yokoo et al., 2007; Frizzas et al., 2009; Boligon et al., 2010, 2011). The PM of heritability for SC650 was greater than those obtained for the other ages. Frizzas et al. (2009) and Boligon et al. (2010) estimated greater heritability for SC measured at 550 d when compared to those obtained at weaning or at 365 d of age in Nellore cattle. In our study, heritability at weaning was not estimated.
Table 1. Number of observations (n) in each age group, mean, and SD for the traits analyzed in Guzerat bulls

<table>
<thead>
<tr>
<th>Trait</th>
<th>Age, d</th>
<th>365 (305 to 425)</th>
<th>450 (426 to 510)</th>
<th>550 (511 to 610)</th>
<th>650 (611 to 710)</th>
<th>730 (711 to 790)</th>
<th>850 (791 to 910)</th>
<th>970 (911 to 1,030)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean of age</td>
<td></td>
<td>365.5</td>
<td>469.0</td>
<td>560.7</td>
<td>657.7</td>
<td>746.4</td>
<td>837.9</td>
<td>963.2</td>
</tr>
<tr>
<td>SD, d</td>
<td></td>
<td>33.59</td>
<td>24.16</td>
<td>29.36</td>
<td>29.27</td>
<td>22.91</td>
<td>31.30</td>
<td>30.71</td>
</tr>
<tr>
<td>Animals measured</td>
<td></td>
<td>851</td>
<td>911</td>
<td>1,035</td>
<td>1,026</td>
<td>809</td>
<td>985</td>
<td>864</td>
</tr>
<tr>
<td>Puberty information</td>
<td></td>
<td>432</td>
<td>531</td>
<td>668</td>
<td>676</td>
<td>532</td>
<td>614</td>
<td>520</td>
</tr>
<tr>
<td>Pubertal bulls</td>
<td></td>
<td>35 (4.1%)</td>
<td>118 (12.9%)</td>
<td>308 (29.7%)</td>
<td>176 (17.1%)</td>
<td>81 (10%)</td>
<td>71 (7.2%)</td>
<td>32 (3.7%)</td>
</tr>
<tr>
<td>Cumulative number</td>
<td></td>
<td>35 (4.3%)</td>
<td>151 (18.7%)</td>
<td>461 (56.2%)</td>
<td>637 (77.6%)</td>
<td>718 (87.5%)</td>
<td>789 (96.1%)</td>
<td>821 (100%)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>SC</th>
<th>n</th>
<th>851</th>
<th>911</th>
<th>1,035</th>
<th>1,026</th>
<th>809</th>
<th>985</th>
<th>864</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean, cm</td>
<td>17.64</td>
<td>19.72</td>
<td>21.64</td>
<td>24.78</td>
<td>27.52</td>
<td>28.75</td>
<td>30.05</td>
<td></td>
</tr>
<tr>
<td>SD, cm</td>
<td>2.34</td>
<td>2.75</td>
<td>3.28</td>
<td>3.73</td>
<td>3.98</td>
<td>3.80</td>
<td>3.51</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>TV</th>
<th>n</th>
<th>485</th>
<th>664</th>
<th>734</th>
<th>667</th>
<th>532</th>
<th>675</th>
<th>525</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean, cm</td>
<td>110.64</td>
<td>152.63</td>
<td>216.72</td>
<td>316.11</td>
<td>437.11</td>
<td>502.02</td>
<td>571.73</td>
<td></td>
</tr>
<tr>
<td>SD, cm</td>
<td>3.34</td>
<td>69.34</td>
<td>76.50</td>
<td>110.31</td>
<td>148.11</td>
<td>180.59</td>
<td>179.55</td>
<td>186.95</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>BW</th>
<th>n</th>
<th>688</th>
<th>716</th>
<th>880</th>
<th>830</th>
<th>619</th>
<th>756</th>
<th>708</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean, kg</td>
<td>189.36</td>
<td>219.87</td>
<td>244.58</td>
<td>281.94</td>
<td>320.80</td>
<td>341.44</td>
<td>376.48</td>
<td></td>
</tr>
<tr>
<td>SD, kg</td>
<td>2.34</td>
<td>33.59</td>
<td>34.29</td>
<td>38.46</td>
<td>45.82</td>
<td>56.01</td>
<td>60.04</td>
<td></td>
</tr>
</tbody>
</table>

1 SC = scrotal circumference; TV = testicular volume.
2 Puberty information = number of animals that were measured in each age group and reached puberty in some age group.
3 Pubertal bulls = number of animals (and percentage) that were measured in that age and reached puberty in that age group.
4 Cumulative number = cumulative number of animals (and percentage) that reached puberty up to each age group during this study.

Table 2. Posterior density statistics of genetic, environmental, and phenotypic variance for scrotal circumference (SC), testicular volume (TV), and BW obtained by two-trait analysis with age at puberty in Guzerat bulls

<table>
<thead>
<tr>
<th>Trait</th>
<th>Age, d</th>
<th>365 (305 to 425)</th>
<th>450 (426 to 510)</th>
<th>550 (511 to 610)</th>
<th>650 (611 to 710)</th>
<th>730 (711 to 790)</th>
<th>850 (791 to 910)</th>
<th>970 (911 to 1,030)</th>
</tr>
</thead>
<tbody>
<tr>
<td>SC, cm</td>
<td>σ²a</td>
<td>1.99</td>
<td>5.16</td>
<td>6.07</td>
<td>5.56</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>HPD (90%)</td>
<td>[1.12:2.83]</td>
<td>[1.69:4.24]</td>
<td>[1.99:5.58]</td>
<td>[4.36:8.39]</td>
<td>[3.03:7.27]</td>
<td>[3.82:8.08]</td>
<td>[3.33:7.58]</td>
</tr>
<tr>
<td></td>
<td>σ²e</td>
<td>2.30</td>
<td>4.76</td>
<td>4.14</td>
<td>5.73</td>
<td>4.53</td>
<td>5.37</td>
<td>5.65</td>
</tr>
<tr>
<td></td>
<td>HPD (90%)</td>
<td>[1.66:2.95]</td>
<td>[2.45:4.65]</td>
<td>[3.05:6.04]</td>
<td>[2.61:5.75]</td>
<td>[3.85:7.50]</td>
<td>[2.92:6.29]</td>
<td>[2.71:6.10]</td>
</tr>
<tr>
<td></td>
<td>σ²p</td>
<td>4.30</td>
<td>8.64</td>
<td>10.58</td>
<td>10.89</td>
<td>9.60</td>
<td>9.93</td>
<td>10.06</td>
</tr>
<tr>
<td>TV, cm³</td>
<td>σ²a</td>
<td>1,006.42</td>
<td>4,277.63</td>
<td>8,385.52</td>
<td>8,385.52</td>
<td>10,789.22</td>
<td>13,432.87</td>
<td>8,181.92</td>
</tr>
<tr>
<td></td>
<td>HPD (90%)</td>
<td>[431.98:1,669.43]</td>
<td>[1,287.41:3,349.93]</td>
<td>[2,241.06:6,083.02]</td>
<td>[4,688.25:12,313.46]</td>
<td>[4,996.45:15,990.45]</td>
<td>[7,930.69:20,333.51]</td>
<td>[8,87:10.92]</td>
</tr>
<tr>
<td></td>
<td>σ²e</td>
<td>1,841.29</td>
<td>5,991.28</td>
<td>9,499.66</td>
<td>7,885.88</td>
<td>10,675.60</td>
<td>15,677.62</td>
<td>15,677.62</td>
</tr>
<tr>
<td></td>
<td>HPD (90%)</td>
<td>[1,236.23:2,420.97]</td>
<td>[4,743.68:7,620.21]</td>
<td>[9,222.88:11,388.33]</td>
<td>[16,062.90:19,917.70]</td>
<td>[5,681.57:15,347.65]</td>
<td>[20,861.16:26,795.23]</td>
<td>[20,981.23:26,777.93]</td>
</tr>
<tr>
<td></td>
<td>σ²p</td>
<td>2,847.70</td>
<td>10,218.91</td>
<td>17,885.48</td>
<td>23,667.56</td>
<td>23,859.54</td>
<td>24,108.67</td>
<td>25,522.88</td>
</tr>
<tr>
<td>BW, kg</td>
<td>σ²a</td>
<td>365.22</td>
<td>789.01</td>
<td>997.32</td>
<td>1,342.87</td>
<td>13,432.87</td>
<td>8,181.92</td>
<td>1,534.77</td>
</tr>
<tr>
<td></td>
<td>HPD (90%)</td>
<td>[365.22:789.01]</td>
<td>[789.01:997.32]</td>
<td>[997.32:1,342.87]</td>
<td>[13,432.87:18,737.97]</td>
<td>[8,181.92:15,347.65]</td>
<td>[1,534.77:2,037.84]</td>
<td>[1,534.77:2,037.84]</td>
</tr>
<tr>
<td></td>
<td>σ²e</td>
<td>1,129.53</td>
<td>3,484.33</td>
<td>6,859.63</td>
<td>10,675.60</td>
<td>15,677.62</td>
<td>20,861.16</td>
<td>24,108.67</td>
</tr>
<tr>
<td></td>
<td>HPD (90%)</td>
<td>[719.56:2,037.84]</td>
<td>[1,287.41:3,349.93]</td>
<td>[2,241.06:6,083.02]</td>
<td>[4,688.25:12,313.46]</td>
<td>[4,996.45:15,990.45]</td>
<td>[7,930.69:20,333.51]</td>
<td>[8,87:10.92]</td>
</tr>
<tr>
<td></td>
<td>σ²p</td>
<td>927.43</td>
<td>17,885.48</td>
<td>17,885.48</td>
<td>23,667.56</td>
<td>23,859.54</td>
<td>24,108.67</td>
<td>25,522.88</td>
</tr>
</tbody>
</table>

1σ²a = mean additive genetic variance; σ²e = mean environmental variance; σ²p = mean phenotypic variance; HPD = highest posterior density interval (90%).
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because there were few records for this age. In contrast, Yokoo et al. (2007) reported greater heritabilities at 450 (0.53) than at 550 d of age. Similarly, in the present study, PM of heritability for SC365 and SC450 were greater than those obtained for SC550. Because of the magnitude of heritability, Silva et al. (2011) suggested that direct selection for SC at 550 d of age in Nellore cattle could result in rapid genetic progress for this trait; however, PM of heritability obtained for SC at 550 d was lower than that obtained for the same age in the present study.

Yokoo et al. (2007) indicated the possibility to select animals with greater testicular size using only SC measured at 450 d of age because this trait will provide greater response to selection. Heritability estimates by Yokoo et al. (2007) for SC450 were within the 90% highest posterior density (HPD) interval obtained for this trait. In the present study, the heritability estimate at 650 d was markedly greater than that obtained at other ages; hence, this finding and the phenotypic variances obtained suggest that considering the same intensity of selection at all ages, the response to selection for SC in Guzerat bulls should be greater at 21 mo. Coulter et al. (1987) suggested that precocious beef breeds have high SC heritability at young ages and that the age when optimum response to selection for testicular size occurs will vary with breed. This could explain the differences in SC heritability reported in the literature for Nellore bulls (Yokoo et al., 2007; Boligon et al., 2010; Silva et al., 2011) and those obtained in this study for Guzerat bulls.

Posterior means of heritability estimates for TV were of moderate to high magnitude and increased from 365 to 850 d of age (Fig. 1A). The PM of heritability for TV obtained in the present study was greater than that reported by Toelle and Robinson (1985), Lunstra et al. (1988), Quirino et al. (1999), Boligon et al. (2010), and Silva et al. (2011). Pachymeter is (Digimess, São Paulo, SP, Brazil) the most widely used tool to measure the width and length of both testes, and these measurements are necessary to obtain TV. However, the inaccuracies of the measurements and the complicated equations could be associated to errors in the measurements of this trait.

Posterior means of heritability for BW remained constant between 365 and 450 d of age (0.39) and between 550 and 650 d of age (0.45) and increased from 730 to 970 d of age (Fig. 1A). Heritability estimates for BW in this study were larger than those reported by Forni and Albuquerque (2005) and Boligon et al. (2010) for Nellore bulls but were less than those reported by Yokoo et al. (2007) for BW365, BW450, and BW550.

Posterior density statistics of the components of variance for age at puberty obtained by two-trait analysis are shown in Table 3. Wolf et al. (1965) defined puberty as the age when a bull first produces an ejaculate containing $5 \times 10^9$ sperm of which ≥10% are progressive, and Garcia et al. (1987) used the first mobile spermatozoa observed in the ejaculate as the onset of puberty. Thus, frequent attempts of seminal collection are necessary to identify the onset of puberty in bulls. Posterior means of heritability estimates for age at puberty in this study were of moderate to high magnitude (0.46 to 0.62) and are shown in Fig. 1B. The heritability obtained by two-trait analysis for age at puberty with testicular traits (SC and TV) increased at 365 and 450 d of age and decreased at 550 d. At 650 d of age the heritability of age at puberty increased in the two analyses. The greater heritability obtained for age at puberty in two-trait analyses with BW was observed at 365 d, followed by a decline to 970 d of age. However, the HPD (90%) were overlapping in all the analyses. References for heritability for age at puberty in bulls were not found, and possibly, this is the first work that reports this information. The high heritability of age at puberty in bulls found in the present study indicated that this trait will respond to selection. However, puberty is a trait difficult to measure in large herds because of the need for frequent semen collections; therefore, more easily measurable traits seem to be a more feasible alternative to use as selection criteria for early sexual development.
After 650 d of age, the genetic correlation between SC were negative and strong and were greater at 650 d of age compared to other ages (Fig. 2B). The phenotypic correlations were also negative and greater than at other ages (Fig. 2B). The negative and high genetic correlation observed between SC and age at puberty in this study suggests that the expression of these traits is mainly influenced by the same genes and that the selection for greater SC could produce a decrease in age at puberty.

Posterior means of expected correlated responses to selection are shown in Table 4. The selection for 10% of the young males with high SC is expected to provide a decrease in age at puberty, and the most favorable expected correlated response between these two traits was at 650 d of age. Boligon et al. (2010) and Silva et al. (2011) suggested that the selection of males based on SC can be made between 12 and 18 mo of age, and SC at 18 mo used as a selection criterion may promote favorable correlated responses in TV, semen quality, and satisfactory breeding soundness evaluation in Nellore bulls (Silva et al., 2011). However, in these works the genetic parameters for SC at 650 d were not estimated.

In Guzerat bulls, faster testicular growth rate ranged between 13 and 16 mo of age (Garcia et al., 1987; Lunstra and Echternkamp, 1982). After 650 d of age, the genetic correlation between SC and age at puberty decreased, possibly because Guzerat bulls in this study reached puberty at 622.14 d of age. The genetic correlations were also negative and greater between 450 and 650 d than at other ages (Table 4). The negative and high genetic correlation observed between SC and age at puberty in this study suggests that the expression of these traits is mainly influenced by the same genes and that the selection for greater SC could produce a decrease in age at puberty.

Table 3. Posterior density statistics of genetic, environmental, and phenotypic variance for age at puberty obtained by two-trait analysis with scrotal circumference (SC), testicular volume (TV), and BW in Guzerat bulls

<table>
<thead>
<tr>
<th>Trait</th>
<th>Age, d</th>
<th>365</th>
<th>450</th>
<th>550</th>
<th>650</th>
<th>730</th>
<th>850</th>
<th>970</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pub-SC, d</td>
<td>605.09</td>
<td>6,164.03</td>
<td>5,648.17</td>
<td>6,822.90</td>
<td>6,802.90</td>
<td>6,331.65</td>
<td>6,507.03</td>
<td></td>
</tr>
<tr>
<td>Pub-TV, d</td>
<td>6,333.78</td>
<td>6,405.34</td>
<td>5,803.86</td>
<td>6,682.20</td>
<td>6,583.24</td>
<td>6,158.00</td>
<td>6,778.55</td>
<td></td>
</tr>
<tr>
<td>Pub-BW, d</td>
<td>7,470.47</td>
<td>7,067.32</td>
<td>6,893.45</td>
<td>6,682.77</td>
<td>6,337.23</td>
<td>5,754.37</td>
<td>6,012.60</td>
<td></td>
</tr>
</tbody>
</table>

1Pub = age at puberty; $\sigma^2_a$ = mean additive genetic variance; $\sigma^2_e$ = mean environmental variance; $\sigma^2_p$ = mean phenotypic variance; HPD = highest posterior density interval (90%).
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useful for describing pubertal status in groups of young bulls, regardless of breed. Brito et al. (2004), working with Nellore and Canchim bulls, suggested the use of yearling SC to select bulls for sexual precocity.

Posterior means of genetic correlation between TV and age at puberty were negative and strong and greater for TV750 compared to those obtained at yearling and other ages (Fig. 2A). The phenotypic correlation was greater at 450 d and decreased to 970 d of age. According to Silva et al. (2011) and as shown in the present study, TV could be used in routine andrological assessments of males participating in genetic breeding programs. However, great care must be taken when measuring width and length of both testes because some structures surrounding the testicle can interfere with the accuracy of the measurements.

Posterior means of expected correlated response in age at puberty from selection for TV are shown in Table 4. The selection of 10% of the males for high TV is predicted to provide a decrease of age at puberty, and the most favorable expected correlated response was at 730 d age. In contrast, Boligon et al. (2010) suggested that the best age to measure this trait as a selection criterion is between 365 and 550 d of age, but in that work, correlations of testicular traits with age at puberty were not estimated. In the present work, the PM of genetic correlations between TV and age at puberty were lower than those obtained for SC and age at puberty for all ages. In addition, the expected correlated responses for age at puberty were greatest with SC.

Posterior means of genetic correlation between BW and age at puberty ranged from moderate to high and remained constant until 450 d of age. From 550 to 850 d of age, the genetic correlation increased (Fig. 2A). The phenotypic correlations between BW and age at puberty were of moderate magnitude (-0.30 to -0.38). The greatest favorable estimated correlated response for age at puberty by BW selection was at 850 d of age.

These results indicate that more favorable correlated responses for age at puberty can be obtained when testicular traits are used as selection criteria. Also, SC is the trait that produced the most favorable expected correlated response at the youngest age.

**Implications**

The reproductive and growth traits evaluated in this study show genetic and phenotypic variability that supports the inclusion of these traits in selection programs for South American Guzerat cattle. The genetic correlations between SC, TV, and BW with age at puberty in males suggest that these traits can be used as selection

**Table 4.** Posterior density statistics of expected correlated responses per generation for age at puberty by the scrotal circumference (SC), testicular volume (TV), and BW selection in Guzerat bulls

<table>
<thead>
<tr>
<th>Trait</th>
<th>Age, d</th>
<th>SC, d</th>
<th>HPD (90%)</th>
<th>TV, d</th>
<th>HPD (90%)</th>
<th>BW, d</th>
<th>HPD (90%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>365</td>
<td>-63.08</td>
<td>[-105.18, -24.26]</td>
<td>-52.16</td>
<td>[-97.51, -8.18]</td>
<td>-56.36</td>
<td>[-102.24, -8.38]</td>
</tr>
<tr>
<td></td>
<td>450</td>
<td>-85.35</td>
<td>[-127.22, -49.42]</td>
<td>-74.73</td>
<td>[-118.97, -36.26]</td>
<td>-55.72</td>
<td>[-104.36, -1.09]</td>
</tr>
<tr>
<td></td>
<td>550</td>
<td>-73.39</td>
<td>[-115.49, -35.76]</td>
<td>-60.83</td>
<td>[-100.02, -18.73]</td>
<td>-48.55</td>
<td>[-97.03, -0.10]</td>
</tr>
<tr>
<td></td>
<td>650</td>
<td>-119.95</td>
<td>[-154.37, -84.47]</td>
<td>-80.06</td>
<td>[-116.79, -37.77]</td>
<td>-58.86</td>
<td>[-97.03, -0.10]</td>
</tr>
<tr>
<td></td>
<td>730</td>
<td>-90.93</td>
<td>[-128.05, -51.17]</td>
<td>-82.20</td>
<td>[-121.00, -39.77]</td>
<td>-80.59</td>
<td>[-108.28, -13.79]</td>
</tr>
<tr>
<td></td>
<td>850</td>
<td>-86.04</td>
<td>[-124.50, -50.85]</td>
<td>-44.07</td>
<td>[-94.32, -0.49]</td>
<td>-93.68</td>
<td>[-129.64, -34.72]</td>
</tr>
<tr>
<td></td>
<td>970</td>
<td>-84.95</td>
<td>[-122.49, -46.14]</td>
<td>-42.22</td>
<td>[-87.71, -0.434]</td>
<td>-86.92</td>
<td>[-135.26, -53.59]</td>
</tr>
</tbody>
</table>

1HPD = highest posterior density interval (90%).

**Figure 2.** Posterior means and highest posterior density intervals (90%) for (A) genetic and (B) phenotypic correlation between scrotal circumference (SC), testicular volume (TV), and BW with age at puberty (Pub) in Guzerat bulls.
criteria for sexual precocity. However, in view of the difficulty in measuring TV and the favorable association between SC and age at puberty, SC seems to be the most suitable trait to use as a selection criterion for sexual precocity, and therefore, measuring TV seems not to be necessary. The use of scrotal circumference at 650 d of age as a selection criterion should promote a favorable correlated response for age at puberty.

LITERATURE CITED


Mrode, R. A. 2005. Linear models for the prediction of animal breeding values. 2nd ed. CABI Publ., Wallingford, UK.


