

## Estimates of genetic parameters for reproductive traits in Brahman cattle breed<sup>1</sup>

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**ABSTRACT:** This study was designed to estimate genetic parameters for the following traits of Brahman cattle in Brazil: age at first calving (AFC), calving interval (CI), rebreeding (REB), and stayability (STAY). For REB, the value 1 was assigned to heifers that rebred and calved after first calving and the value 0 was assigned to heifers that failed to rebreed after first calving. Likewise, for STAY, the value 1 was assigned to cows that calved at least 3 times by the time they reach 6 yr of age; otherwise, the value 0 was assigned. A bivariate analysis was used to estimate covariances components by using linear animal

model for CI and AFC and threshold animal model for REB and STAY. The mean  $h^2$  were 0.10, 0.02, 0.22, and 0.10 for AFC, CI, REB, and STAY, respectively. The genetic correlations were  $-0.13$  between AFC and CI,  $-0.35$  between AFC and REB,  $-0.57$  between AFC and STAY, and  $0.32$  between REB and STAY, which reveal that cows that remain productive for longer periods in the herd also start breeding younger and present greater chances to REB. The selection of Brahman cattle for reproductive traits, such as AFC, CI, REB, and STAY, will render low magnitude and long-term responses.

**Key words:** calving interval, heritability, rebreeding, stayability

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### INTRODUCTION

Reproductive traits are economically important in beef cattle production systems, because cows consume a large proportion of the feed resources (Malhado et al., 2013; Silva et al., 2003). Therefore, the production efficiency of the herd would be improved, even though minor changes on genetic structure of the population were made, which might lead to greater profitability.

Nevertheless, selection based on reproductive traits is limited, because, in general, beef cattle

production is based exclusively on pasture in tropical systems, which makes data collection and herd measurements more complicated (Eler et al., 2014; Boligon et al., 2008). Additionally, some reproductive traits are threshold type, which does not present continuous phenotypic expression and makes genetic evaluations more difficult.

Therefore, the estimation of genetic parameters is needed to obtain indices to maximize response to selection (Malhado et al., 2009; Araújo et al., 2008). However, estimations of variance components may be compromised by threshold type traits. Furthermore, it is possible to design selection strategies that positively affect production efficiency and genetic progress of animals by estimating heritability values and correlations between the traits evaluated, which are important parameters to perform genetic evaluations. Also, when reproductive traits are con-

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sidered in breeding programs, sires that generate more productive cows are chosen.

Moreover, studies related to estimations of genetic parameters for reproductive traits of Brahman cattle are scarce (Bunter and Johnston, 2014; Johnston et al., 2014a,b; Zhang et al., 2014). Therefore, the objective of this study was to estimate genetic parameters for reproductive traits, such as age at first calving (AFC), calving interval (CI), rebreeding (REB), and stayability (STAY), of Brahman cattle by Bayesian inference in a bivariate analysis using linear-threshold animal model.

## MATERIALS AND METHODS

Animal Care and Use Committee approval was not necessary for this study because the data were obtained from an existing database. The data set was provided by Brazilian Association of Zebu Breeders (Uberaba, Minas Gerais, Brazil) and included Brahman cattle from states of São Paulo, Minas Gerais, Rio de Janeiro, Espírito Santo, Distrito Federal, Mato Grosso, Mato Grosso do Sul, and Goiás that were born between 1994 and 2012.

### Data and Management

The data consistency was checked considering only cows maintained exclusively on pasture, which had pregnancy either originated from AI ( $n = 15,452$ ) or natural service ( $n = 9,440$ ). For AFC, cows not older than 1,530 d (51 mo old) were used, and for CI, a minimum and maximum interval of 320 (10.7 mo) and 1,095 d (36.5 mo), respectively, were used. Furthermore, for REB, the value 1 was assigned to heifers that rebred and calved after first calving and the value 0 was assigned to heifers that failed to rebred after first calving. In addition, for REB, only heifers that became pregnant not older than 1,230 d (41 mo) were considered. As a result, only cows that became pregnant for the second time not older than 1,648 d were considered, as the average CI on the dataset was 418 d. Likewise, for STAY, the value 1 was assigned to cows that calved at least 3 times by the time they reach 6 yr of age; otherwise, the value 0 was assigned.

The contemporary groups were composed from farm, type of gestation or natural service, and birth year of dam. In addition, only for STAY, birth season of dam (rainy or dry) was included into the contemporary group. However, contemporary groups containing less than 3 animals as well as contemporary groups for REB and STAY in which all animals presented same response (0 or 1) were not included in the analysis.

The data consistency as well as the tests of significance for environmental effects and formation of

**Table 1.** Number of records ( $n$ ), records assigned as 0 ( $n_0$ ), records assigned as 1 ( $n_1$ ), means, and contemporary groups (CG) represented for each reproductive trait of Brahman cattle

Trait <sup>1</sup>	$n$	$n_0$	$n_1$	Mini- mum <sup>2</sup>	Maxi- mum <sup>2</sup>	Mean <sup>2</sup>	SD	CG
AFC	9,174	–	–	451	1,530	1,129.3	175.32	676
CI	10,225	–	–	320	1,095	519.9	160.54	604
REB	4,516	1,456	3,060	–	–	–	–	361
STAY	4,990	3,598	1,392	–	–	–	–	299

<sup>1</sup>AFC = age at first calving; CI = calving interval; REB = rebreeding; STAY = stayability.

<sup>2</sup>Expressed as days.

contemporary groups were performed by using R software (R Development Core Team, 2011). Also, when significant, calf birth year or calf birth season were included as a separate fixed effects in the model.

### Statistical Models

Number of records, records assigned as 0, records assigned as 1, and contemporary groups included in each analysis are presented in Table 1. A bivariate analysis was used to estimate components of covariance by using linear-animal model for AFC and CI and threshold-animal model for REB and STAY. The mathematical description of the models used can be represented as follows:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{c} + \mathbf{e},$$

in which  $\mathbf{y}$  is the vector of observations;  $\boldsymbol{\beta}$  is the vector of fixed effects;  $\mathbf{a}$  is the vector of random effects that represent additive genetic direct effects of each animal;  $\mathbf{c}$  is the vector of permanent environmental effects, included as random;  $\mathbf{e}$  is the vector of residuals; and  $\mathbf{X}$ ,  $\mathbf{Z}_1$ , and  $\mathbf{Z}_2$  are incidence matrices relating  $\boldsymbol{\beta}$ ,  $\mathbf{a}$ , and  $\mathbf{c}$  to  $\mathbf{y}$ .

With respect to the fixed effects, for AFC and STAY, only contemporary group was included. However, for CI, the fixed effects of contemporary group, calf birth year, calf birth season, and the covariate dam age at calving were included. For the analysis of REB, contemporary group, calf birth year, and calf birth season were included in the model as fixed effects. The permanent environmental effects only were included in the model for CI. Therefore, the incidence matrix  $\mathbf{Z}_2$  and the vector  $\mathbf{c}$  were excluded from the models for REB, STAY, and AFC.

According to Bayesian inference, the vectors  $\boldsymbol{\beta}$ ,  $\mathbf{a}$ , and  $\mathbf{c}$  are location parameters of the conditional distribution  $\mathbf{y}|\boldsymbol{\beta}, \mathbf{a}, \mathbf{c}$ . In the threshold animal model, it was assumed that underlying scale presents normal continuous distribution, represented as follows:

$$\mathbf{U}|\boldsymbol{\theta} \sim N(\mathbf{W}\boldsymbol{\theta}, \mathbf{I}\sigma_e^2),$$

in which  $\mathbf{U}$  is the vector of the base scale of order  $r$ ,  $\boldsymbol{\theta}' = (\boldsymbol{\beta}', \mathbf{a}')$  is the vector of the location parameters of order  $s$  with  $\boldsymbol{\beta}$  (defined, from the frequentist view, as fixed effects) and order  $s$  with  $\mathbf{a}$  (as direct additive genetic random effects),  $\mathbf{W}$  is the known incidence matrix of order  $r$  for  $s$ ,  $\mathbf{I}$  is the identity matrix of order  $r$  for  $r$ , and  $\sigma_e^2$  is the residual variance (Gianola and Foulley, 1983). As REC and STAY variables in an underlying distribution are not observable, parameterization  $\sigma_e^2 = 1$  is usually adopted to identify these variables in the likelihood function (Gianola and Sorensen, 2002). This is a standard assumption for threshold animal model analysis.

When bivariate analysis included both a continuous and a threshold trait,  $\boldsymbol{\beta}$  was the vector related to systematic effects; however, according to Bayesian inference,  $\boldsymbol{\beta}$  is a vector of random effects in which initial distribution values have uninformative priors and, therefore, uniform likelihood distribution (Everling et al., 2014).

The components of variance or covariance were estimated based on REML by using the software GIBBSF90 and THRGIBBS1F90 from BGF90 (Misztal et al., 2002). The bivariate analysis were performed between the traits REB and STAY (**REB-STAY**), AFC and CI (**AFC-CI**), STAY and AFC (**STAY-AFC**), and REB and AFC (**REB-AFC**). The Gibbs sampler for bivariate analysis was run for 1,000,000 iterations for REB-STAY, 1,000,000 iterations for AFC-CI, 2,000,000 iterations for STAY-AFC (burn-in period of 400,000), and 2,000,000 iterations for REB-AFC (burn-in period of 400,000). Moreover, the convergence of the Markov chains were checked based on tests of Brooks, Gelman, and Rubin (Gelman and Rubin, 2006) and Geweke (1992) and criteria of Heidelberg and Welch (1983) by using the coda package (Plummer et al., 2006) of R software (R Development Core Team, 2011). Based on the results, the (co)variance components were calculated.

## RESULTS AND DISCUSSION

Means and SD of traits evaluated in this study, related to the performance of the animals, are presented in Table 1. The results of variance components estimated are shown in Table 2. Also, heritability, highest posterior density (**HPD**) intervals, and correlations estimated are shown in Table 3. The convergence diagnoses were not satisfactory for the bivariate analysis involving STAY-CI and REB-CI. Based on this fact, results from those analyses were not included in this study.

Estimates of heritability were low for AFC (0.10), CI (0.02), and STAY (0.10) and moderate for REB

**Table 2.** Posterior means and highest posterior density intervals of variance components<sup>1</sup> for age at first calving (AFC), calving interval (CI), rebreeding (REB), and stayability (STAY) of Brahman cattle<sup>2</sup>

Trait	$\sigma_a^2$	$\sigma_e^2$	$\sigma_c^2$
AFC	2,182.8 (1,400.7, 3,000.7)	19,655.9 (18,773.3, 20,470)	–
CI	405.4 (38.6, 774.4)	20,020 (19,310, 20,730)	560.9 (56.27, 1,093)
REB	0.28 (0.06, 0.53)	0.56 (0.54, 0.58)	–
STAY	0.08 (0.02, 0.15)	0.60 (0.57, 0.62)	–

<sup>1</sup> $\sigma_a^2$  = additive genetic variance;  $\sigma_e^2$  = residual variance;  $\sigma_c^2$  = permanent environmental variance.

<sup>2</sup>Limits for the 95% highest posterior density interval are shown in parentheses.

(0.22; Table 3). Among traits evaluated in this study, REB had lower number of observations, and therefore, the amount of information may have been insufficient to generate more reliable results due to the greater amplitude of the HPD interval. Moreover, heritability estimates presented in this study indicated that a low proportion of the phenotypic variance of the traits evaluated in the population of Brahman cattle may be explained by genetic variance. Based on this fact, for the same generation interval, genetic gains by selection will be low in Brahman cattle. This was more evident for CI, in which the estimate of heritability was 0.02.

In general, it is well documented in the Brazilian literature that cows from different breeds, especially Nellore, presented low estimates of heritability for AFC, CI, REB, and STAY as well (Eler et al., 2014; Mello et al., 2014; Caetano et al., 2013; Yokoo et al., 2012; Boligon and Albuquerque, 2010; Buzanskas et al., 2010; Van Melis et al., 2010; Martinez et al., 2004). However, those traits should still be included in animal breeding programs of Brahman cattle in Brazil, because even small alterations may positively impact production efficiency of the herd.

The genetic correlation estimate of  $-0.13$  observed in this study shows a weak relationship between decreased AFC and increased CI. However, because the HPD interval varies from  $-0.60$  to  $0.39$ , no reliable conclusion can be drawn about the relationship and indirect response between those traits in this population of Brahman cattle. Additionally, further studies in this population are needed to provide more convincing results about this correlation. Berry and Evans (2014) reported genetic correlation of  $0.22$  between AFC and CI for *Bos taurus* cattle; however, Mercadante et al. (2000) reported  $-0.06$  for Nellore cattle. This may be explained by differences between populations with respect to the

**Table 3.** Heritability estimates, highest posterior density intervals, and correlations for age at first calving (AFC), calving interval (CI), rebreeding (REB), and stayability (STAY) of Brahman cattle<sup>1,2,3</sup>

	AFC	CI	REB	STAY
AFC	<b>0.10</b> (0.06, 0.14)	-0.13 (-0.60, 0.39)	-0.35 (-0.75, 0.04)	-0.57 (-0.88, -0.25)
CI	-0.05 (-0.08, -0.01)	<b>0.02</b> (0.002, 0.04)	-	-
REB	-0.18 (-0.29, -0.06)	-	<b>0.22</b> (0.09, 0.35)	0.32 (-0.20, 0.90)
STAY	-0.38 (-0.43, -0.33)	-	0.18 (0.12, 0.23)	<b>0.10</b> (0.04, 0.16)

<sup>1</sup>Heritability estimates are bold on main diagonal.

<sup>2</sup>Limits for the 95% highest posterior density interval are shown in parentheses.

<sup>3</sup>Genetic correlations among traits are above diagonal and residual correlations among traits are below diagonal.

age of heifers at first exposition to reproduction and imprecision of collection of phenotypic data.

Despite moderate genetic correlation between AFC and REB (-0.35), the response to selection of animals that are younger at first calving may lead to selection of females that are successful in breeding after first calving as well. These results are not normally expected because of the physiological challenges imposed to heifers (e.g., energy expenses related to maintenance plus growth, and calving difficulty). However, the most part of Brahman heifers in the population evaluated in this study were first exposed to reproduction when they were about 2 yr old, which indicates that challenges due to first calving might have been minimized.

The negative genetic correlation between AFC and STAY (-0.57) is desirable, because the selection of females that are younger at first calving may lead to selection of animals that stay productive for longer periods in the herd as well. Buzanskas et al. (2010) and Mello et al. (2014) reported genetic correlations between AFC and STAY of -0.63 and -0.35, respectively, for Canchim cattle (five-eighths Charolais and three-eighths Nelore), which is in agreement with genetic correlation observed in this study. Likewise, the positive genetic correlation (0.32) between REB and STAY is desirable, because females that become pregnant for the second time at not older than 55 mo old may calve 3 times before reaching 6 yr of age. In general, the genetic correlations presented in Table 3 show that females that stay productive for longer periods in the herd are younger when they first reproduce and also present greater possibility of REB. However, heifers that are too young at first calving may present problems that may increase CI.

The genetic modifications of the reproductive traits evaluated in this study, in breeding programs,

are feasible only if indirect responses are generated by direct selection of an economically important trait that presents higher heritability. Therefore, further studies to estimate genetic correlations between reproductive and productive traits are needed, given its importance for the genetic improvement of Brahman cattle.

## Conclusions

The selection of Brahman cattle for reproductive traits, such as AFC, CI, REB, and STAY, will render low magnitude and long-term responses.

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