Study of stayability in Nellore cows using a threshold model

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ABSTRACT: The objectives of the current study were to assess the feasibility of using stayability traits to improve fertility of Nellore cows and to examine the genetic relationship among the stayabilities at different ages. Stayability was defined as whether a cow calved every year up to the age of 5 (Stay5), 6 (Stay6), or 7 (Stay7) yr of age or more, given that she was provided the opportunity to breed. Data were analyzed based on a maximum a posteriori probit threshold model to predict breeding values on the liability scale, whereas the Gibbs sampler was used to estimate variance components. The EBV were obtained using all animals included in the pedigree or bulls with at least 10 daughters with stayability observations, and average genetic trends were obtained in the liability and transformed to the probability scale. Additional analyses were performed to study the genetic relationship among stayability traits, which were compared by contrasting results in terms of EBV and the average genetic superiority as a function of the selected proportion of sires. Heritability estimates and SD were 0.25 ± 0.02, 0.22 ± 0.03, and 0.28 ± 0.03 for Stay5, Stay6, and Stay7, respectively. Average genetic trends, by year, were 0.51, 0.34, and 0.38% for Stay5, Stay6, and Stay7, respectively. Estimates of EBV SD, in the probability scale, for all animals included in the pedigree and for bulls with at least 10 daughters with stayability observations were 7.98 and 12.95, 6.93 and 11.38, and 8.24 and 14.30% for Stay5, Stay6, and Stay7, respectively. A reduction in the average genetic superiorities in Stay7 would be expected if the selection were based on Stay5 or Stay6. Nonetheless, the reduction in EPD, depending on selection intensity, is on average 0.74 and 1.55%, respectively. Regressions of the sires’ EBV for Stay5 and Stay6 on the sires’ EBV for Stay7 confirmed these results. The heritability and genetic trend estimates for all stayability traits indicate that it is possible to improve fertility with selection based on a threshold analysis of stayability. The SD of EBV for stayability traits show that there is adequate genetic variability among animals to justify inclusion of stayability as a selection criterion. The potential linear relationship among stayability traits indicates that selection for improved female traits would be more effective by having predictions on the Stay5 trait.

Key words: Bayesian inference, beef cattle, nonlinear model, reproductive trait, survival

INTRODUCTION

The importance of including reproductive traits in the selection objectives for beef cattle has been evidenced in several studies that considered such traits as being of great importance in improving profitability (Newman et al., 1992; Melton, 1995; Phocas et al., 1998). In Brazil, however, with the exception of a single reproductive indicator trait (scrotal circumference), traits generally included in selection indexes refer to growth, such as BW and BW gain. Golden and Bourdon (1999) pointed out that indicator traits such as scrotal circumference do not affect profit directly; they only indicate genetic merit of an animal for economically relevant traits (traits of breeding objectives). These economically relevant traits, on the other hand, are directly associated with profitability of the production system through a relationship with specific costs or income.

Some authors have evaluated reproductive traits that can be measured directly on females, such as heifer
Study of stayability in Nellore cows

Materials and Methods

Animal Care and Use Committee approval was not obtained for this study because the data set utilized was obtained from an existing database (Agro-Pecuária CFM Ltda.).

Data

Data were obtained from 15 herds owned by Agro-Pecuaria CFM Ltda. located in the states of São Paulo, Mato Grosso do Sul, and Goiás, Brazil. The CFM owns close to 17,000 Nellore cows and sells about 2,000 young bulls yearly of 7,000 males weaned.

Hudson and Van Vleck (1981) defined stayability as the probability of a cow remaining in the herd until a specific age given the opportunity to reach this age. In this study, stayability was defined as whether a cow calved every year up to the age of 5 (Stay5), 6 (Stay6), or 7 (Stay7) yr of age or more given that she was provided the opportunity to breed. Records included calving date from 1990 to 2003 of Nellore cows born between 1987 and 1998 for Stay5, from 1987 to 1997 for Stay6, and from 1987 to 1996 for Stay7. The data set used in this study was based on reproductive performance records on CFM cows that were exposed to first breeding beginning at 2 yr of age (1987 to 1994) or at 14 mo of age (1995 to 2003). To increase sexual precocity, in 1995 CFM began exposing all heifers to breeding at 14 mo of age, but from 1987 to 1994, cows were exposed at 2 yr of age. Due to the use of a short breeding season (from 60 to 90 d), however, heifers that did not become pregnant when exposed at 14 mo of age were exposed again at 2 yr of age. Data included identification of the cows, the cows’ dams and sires, their herds, and year of birth and herd of birth of each of their offspring up to the specified ages.

Binary observations, with 0 indicating failure and 1 indicating success, were used for each dam and for each trait. Success was attributed to cows that calved every year up to the specific age or later and failure was attributed to cows that did not meet these prerequisites. It is important to mention that the reproductive management in the herds investigated in the current study prevented the cows that did not become pregnant during the mating season from remaining in the herd. Records concerning the cows that had not yet reached the specific ages studied, and those concerning animals with unknown sire and dam were eliminated. Records of cows in contemporary groups without variation were also eliminated. A summary of the data set is shown in Table 1.

Cattle Management

A detailed description of the herd management can be found in Eler et al. (2004). Cows were maintained on pasture, with salt and mineral supplementation (11% Ca, 6% P, 1% Mg, 4% S, 16% Na, 0.15% Cu, 0.15% Mn, 0.45% Zn, 0.015% I, 0.007% Co, and 0.002% Se). In each year, the mating season began in November and ended in January, with a duration of 60 d for cows and of 90 d for heifers. Artificial insemination and natural service mating were used in lots with 1 sire or multiple sires. The ratio of cows per bull was approximately 35:1. All cows were evaluated for pregnancy by rectal palpation approximately 60 d after the end of breeding season, and nonpregnant cows were culled. Some culling may have also been performed on the basis of poor progeny performance and health. Bulls were selected based on an index including EPD for weaning weight, postweaning gain, scrotal circumference, and muscle score, in proportions of 20, 40, 20, and 20%, respectively. Since 2000, scrotal circumference was replaced by heifer pregnancy EPD in the index for selection purposes, but not for ranking young bulls for selling.

Model

The model used for each trait included contemporary group and animal effects. The contemporary groups were formed by combining the information relative to the cow’s farm and year of birth, and farm and year of birth of each of their offspring up to the specified ages. The assumed single-trait model for the underlying distribution of the liability (Li) for analysis of each stayability trait was

Table 1. Summary statistics of the data set for the stayability traits at 5 (Stay5), 6 (Stay6), and 7 (Stay7) yr of age

<table>
<thead>
<tr>
<th>Item</th>
<th>Stay5</th>
<th>Stay6</th>
<th>Stay7</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of dams with records</td>
<td>47,113</td>
<td>39,527</td>
<td>34,666</td>
</tr>
<tr>
<td>No. of records in the pedigree</td>
<td>78,163</td>
<td>68,688</td>
<td>62,797</td>
</tr>
<tr>
<td>No. of contemporary groups</td>
<td>287</td>
<td>227</td>
<td>228</td>
</tr>
<tr>
<td>No. of successful records</td>
<td>17,464</td>
<td>11,403</td>
<td>8,391</td>
</tr>
<tr>
<td>% success</td>
<td>37.07</td>
<td>28.85</td>
<td>24.21</td>
</tr>
</tbody>
</table>

1Stayability was defined as whether a cow calved every year up to the age of 5 (Stay5), 6 (Stay6), or 7 (Stay7) yr or more given that she was provided the opportunity to breed.
Table 2. Means, SD, modes, medians, and bounds of greatest posterior density (HPD) intervals at 95% of the posterior distributions of heritability for single-trait analysis of stayability of Nellore cows at 5 (Stay5), 6 (Stay6), and 7 (Stay7) yr of age1

<table>
<thead>
<tr>
<th>Item</th>
<th>Mean</th>
<th>SD</th>
<th>Mode</th>
<th>Median</th>
<th>95% HPD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stay5</td>
<td>0.25</td>
<td>0.02</td>
<td>0.25</td>
<td>0.25</td>
<td>0.20 to 0.29</td>
</tr>
<tr>
<td>Stay6</td>
<td>0.22</td>
<td>0.03</td>
<td>0.23</td>
<td>0.22</td>
<td>0.17 to 0.28</td>
</tr>
<tr>
<td>Stay7</td>
<td>0.28</td>
<td>0.03</td>
<td>0.28</td>
<td>0.28</td>
<td>0.22 to 0.34</td>
</tr>
</tbody>
</table>

1Stayability was defined as whether a cow calved every year up to the age of 5 (Stay5), 6 (Stay6), or 7 (Stay7) yr or more given that she was provided the opportunity to breed.

\[ I_f = X\beta + Zu + e, \]

where \( \beta \) is a vector of contemporary group effects; \( u \) is the vector of genetic effects; \( e \) is a vector of residual effects, and \( X \) and \( Z \) are incidence matrices that link contemporary group and genetic effects to liabilities, respectively.

The response in stayability was modeled with a probit approach:

\[
 f(y_i | I_f) = \prod_{i=1,n} f(y_i | I_i) = \prod_{i=1,n} 1(I_i < t)1(y_i = 0) + 1(I_i > t)1(y_i = 1),
\]

and

\[
 f(I_f | \beta, u, \sigma^2_e) = N(X\beta + Zu, I\sigma^2_e),
\]

where \( t \) is the threshold that defines the categories of the response, \( n \) is the total number of data points, \( \beta, u, X, \) and \( Z \) are as described above, and \( \sigma^2_e \) is the residual variance (set to 1).

The following prior distributions were assumed:

\[
p(u | \sigma^2_u) \sim N(0, A\sigma^2_u),
\]

where \( A \) is the numerator relationship matrix, \( \sigma^2_u \) is the additive genetic variance, \( u \) is as defined above, and \( 0 \) is a vector of zeros. Flat distributions were assumed for \( \beta \) and \( \sigma^2_u \).

Statistical Procedures

Bayesian analyses of the single-trait models were carried out with the Gibbs sampler algorithm (Geman and Geman, 1984; Gelfand and Smith, 1990; Tanner, 1993) to obtain samples from the joint posterior density (and consequently from the marginal posterior densities) of all the unknowns in the model. These analyses were performed using the MTGSAM software (Van Tassell et al., 1998) for threshold model.

The Gibbs sampler analysis was carried out through a single chain of 550,000 iterations with a conservative burn-in period of 50,000 iterations. All remaining iterations of the Gibbs sampling were used to compute features of the marginal posterior distributions. The analysis of convergence followed the approach of Raftery and Lewis (1992), using the Gibanal software (Van Kaam, 1997).

The EBV was computed using a maximum a posteriori probit threshold model (Gianola and Foulley, 1983; Harville and Mee, 1984). Solutions obtained from the underlying scale were transformed to the standard cumulative distribution and multiplied by 100. In the probability scale, animals with greater EBV have a greater probability of remaining productive in the herd for a longer period of time.

Estimates of average genetic trends, by year, were obtained in the observed scale with solutions from the underlying scale. The EBV was used to calculate the genetic trend for the population as a regression of the breeding values over the year of birth of the animal. Phenotypic means of each trait were used to obtain critical values (\( T_\alpha \)) in the standardized probability density functions. Average genetic trend estimates on the observed scale were obtained as the angular coefficients from the regression of EBV on the underlying scale within years of birth of animals and with \( T_\alpha \).

Additional Analyses to Examine the Genetic Relationship Among the Stayability Traits

Because the bivariate analyses of pairs of stayability traits were not possible because of the nature of the traits considered, the comparison between the single-trait analyses to study the genetic relationship among the stayability traits was performed by comparing the EBV and the average genetic superiority as a function of the selected proportion of sires.

**RESULTS AND DISCUSSION**

Analysis of Convergence of the Gibbs Sampler

The required length of the burn-in or initialization period was always less than 5,000 iterations. Thus, 550,000 iterations of the sampler were run with a conservative chain of 50,000 iterations discarded as burn-in. The remaining 500,000 iterations were retained for the postGibbs analysis. Effective sample sizes for heritabilities were 80, 79, and 170 cycles for Stay5, Stay6, and Stay7 analysis, respectively. In spite of the appar-
Table 3. Number of records, mean of estimated breeding values (EBV), SD, and minimum and maximum values for all animals (total) and for sires (sires) included in the pedigree for stayability at 5 (Stay5), 6 (Stay6), and 7 (Stay7) yr of age1

<table>
<thead>
<tr>
<th>Item</th>
<th>No. of records</th>
<th>Mean EBV, %</th>
<th>SD, %</th>
<th>Minimum, %</th>
<th>Maximum, %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stay5</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>78,163</td>
<td>50.66</td>
<td>7.98</td>
<td>15.13</td>
<td>86.59</td>
</tr>
<tr>
<td>Sires</td>
<td>330</td>
<td>49.96</td>
<td>12.95</td>
<td>15.13</td>
<td>81.09</td>
</tr>
<tr>
<td>Stay6</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>68,688</td>
<td>50.41</td>
<td>6.93</td>
<td>16.83</td>
<td>77.60</td>
</tr>
<tr>
<td>Sires</td>
<td>266</td>
<td>49.75</td>
<td>11.38</td>
<td>16.83</td>
<td>75.17</td>
</tr>
<tr>
<td>Stay7</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>62,797</td>
<td>50.46</td>
<td>8.24</td>
<td>15.55</td>
<td>86.49</td>
</tr>
<tr>
<td>Sires</td>
<td>226</td>
<td>50.89</td>
<td>14.30</td>
<td>15.55</td>
<td>82.68</td>
</tr>
</tbody>
</table>

1Sires with at least 10 daughters with stayability observations. Stayability was defined as whether a cow calved every year up to the age of 5 (Stay5), 6 (Stay6), or 7 (Stay7) yr or more given that she was provided the opportunity to breed.

Heritabilities

Posterior mean, median, mode, and SD, as well as greatest posterior density intervals at 95% for heritability in single-trait analysis of stayability in Nellore cows at 5, 6, and 7 yr of age are presented in Table 2. Posterior mean and SD for heritability were 0.25 (0.02), 0.22 (0.03), and 0.28 (0.03) for Stay5, Stay6, and Stay7, respectively. These results indicate that the use of stayability as a selection criterion can contribute to increase dam fertility. Differences between posterior mean, mode, and median of heritabilities were not greater than 0.01.

Previous studies using linear models reported heritability estimates for stayability at 6 yr of age of less than 0.10 (Hudson and Van Vleck, 1981; Van Doormaal et al., 1985; Short and Lawlor, 1992). Martínez et al. (2004) estimated genetic parameters for length of productive life (with 6 opportunity groups) and found heritability estimates between 0.05 and 0.15. DeLorenzo and Everett (1986), using the nonlinear approaches described by Gianola and Foulley (1983) and Harville and Mee (1984) obtained heritability estimates of 0.12 and 0.15 for stayability at 41 and 54 mo without correction for the underlying scale, and of 0.28 and 0.26 with correction by the method of Van Vleck (1972). Snelling et al. (1995)

Figure 1. Average breeding values on each year for a population of Nellore cattle for stayability at 5 (Stay5), 6 (Stay6), and 7 (Stay7) yr of age, in the original scale, and their respective genetic trends [linear (Stay5), linear (Stay6), and linear (Stay7)] as regressions of the breeding values over the birth years. Stayability was defined as whether a cow calved every year up to the age of 5, 6, or 7 yr or more given that she was provided the opportunity to breed.
Figure 2. Average genetic superiority for stayability at 7 yr of age (AGS7) given that the sires were selected on stayability at 5 (Stay5), 6 (Stay6), and 7 (Stay7) yr of age, according to the percentage of selection. Stayability was defined as whether a cow calved every year up to the age of 5, 6, or 7 yr or more given that she was provided the opportunity to breed.

Figure 3. Regressions of the sires’ EBV for stayability at 5 (Stay5) and 6 (Stay6) yr of age on the sires’ EBV for stayability at 7 (Stay7) yr of age. Stayability was defined as whether a cow calved every year up to the age of 5, 6, or 7 yr or more given that she was provided the opportunity to breed.
estimated heritabilities below (stayability at 2 and 8 yr of age) and above (stayability at 5 yr of age) 0.10 depending on age endpoints. These results suggest that nonlinear approaches may have a better ability to detect genetic variation in stayability traits than linear methods (Ducrocq et al., 1988).

Snelling et al. (1995) compared linear and nonlinear methods for estimating genetic parameters for stayability, using the REML (Patterson and Thompson, 1971) and the marginal maximum likelihood (MML; Hoeschele et al., 1987) methods for analysis of data related to 2 Angus herds. They reported REML heritability estimates not differing from 0 and MML estimates equal to 0.21 and 0.30 for the 2 herds considered. The authors suggested that MML might be a more appropriate analytical method for categorical data. Also using nonlinear models, Silva et al. (2003a,b) reported heritability estimates between 0.12 and 0.21 for stayability in Nellore cattle. Doyle et al. (2000), working with Angus beef cattle, found a heritability estimate and SD of 0.15 (0.08).

These moderate heritability estimates of stayability suggest that response to selection and genetic gain can be achieved by selection. The EPD of stayability used for bull selection are mainly a prediction of the ability of their daughters to conceive and produce calves when reaching a mature age. Another point to be observed is that stayability encompasses other traits (together with their economic values), which contribute to the selection response for a given production and commercialization system. The unit of genetic change in an economically pertinent trait has a direct impact on the profitability of the future enterprise. The indicator traits of stayability include calving records (cow’s parturition during a given year), cow’s weight, days to calving (or calving interval), and milk yield (maternal weight at weaning). Thus, when the EPD of stayability are used as selection criteria, these indicator traits are somehow incorporated by indirect selection, with favorable effects on the genetic gain (Silva et al., 2003a).

Improving stayability helps reduce costs as the number of replacements may be reduced. It also enables a greater selection response because fewer animals must be replaced, and thus, greater selection intensity of females is possible. This procedure may cause a greater generation interval. Use of EBV for stayability as a criterion of male and female selection may improve selection effectiveness, leading to an increase in mean time of permanence in the herd. Economic values for 2 reproductive traits (heifer pregnancy and stayability at 6 yr of age) were estimated by Formigoni et al. (2005) using simulated bioeconomic modeling data for a cow-calf production system. The economic importance of stayability at 6 yr of age compared with heifer pregnancy increases as the heifer’s replacement costs increase and may reach values as high as 3.27 times the value of heifer pregnancy.

### Estimated Breeding Values

Estimates of means and SD and the amplitude of variation of the EBV, for all animals in the pedigree or for bulls with at least 10 progeny, on the probability scale, are presented in Table 3. The EBV of bulls presented a larger SD. However, the greatest EBV refer to females. For example, there were only 3 sires (all of them with more than 10 progeny with stayability data) among the top 10 animals. Moreover, among animals in the top 0.1%, only 12.8% were sires with more than 10 progeny, and the remaining 87.2% are females. This result could be explained by the fact that stayability was not used as a selection criterion for sires in this population, so that the greatest EBV were likely associated with females. Differences between the breeding values of the animals analyzed indicate the variability on the probability of remaining in the herd up to the ages considered. For example, the difference between the greatest (81.09%) and lowest (15.13%) predicted genetic values for bulls at Stay5 indicate that daughters of the former were expected to have a 32.98% greater chance to remain in the herd than the daughters of the latter if the bulls were mated with females of equal average breeding values.

### Genetic Trends

The average genetic trends, by year, for Stay5, Stay6, and Stay7 are presented in Figure 1. The average breeding value for the stayability traits increased with time for the 3 ages studied. Mean annual genetic changes considering all animals analyzed were 0.51, 0.34, and 0.38% per year for Stay5, Stay6, and Stay7, respectively. The genetic trends detected in the current study were greater than the values obtained by Snelling et al. (1995) in a study with 2 herds of the Angus and Red Angus breeds, with estimates ranging from 0.018% per yr (for stayability at 2 yr of age in Red Angus cows) to 0.305% per yr (for stayability at 5 yr of age in Angus cows), and greater also than the values reported by Silva et al. (2003b), in which the average genetic trend estimate was 0.14% per yr (for stayability at 6 yr of age) in the Nellore population.

The trend for an increase in breeding values occurring after 1992 (Figure 1) is indicative of the selection criteria applied to the cows which, through indirect selection on correlated traits, contributed with the best performance of stayability. These results indicate that the rate of genetic change may be enhanced by incorporating the EPD for stayability as a criterion for bull selection because the observed genetic progress was only result of female culling.

### Additional Analyses to Examine the Genetic Relationship Among the Stayability Traits

Considering Stay7 analysis as a standard, a comparative graph was elaborated (Figure 2) to verify whether there would be any loss in terms of mean EPD if sire
selection were based on EPD for Stay5 or Stay6. A reduction in the average genetic superiorities in Stay7 would be expected if the selection were based on Stay5 or Stay6. Nonetheless, the reduction in EPD, depending on the fraction selected, is on average just 0.74 and 1.55%, respectively. This indicates, for example, that when the mean of the selected animals by Stay7 is approximately 24.2% (Table 1), selecting by Stay5 and Stay6 would be 24.0 and 23.8% in the response in the observed scale. Regressions of sires' EBV for Stay5 and Stay6 on sires' EBV for Stay7 support these results, as shown in Figure 3.

The choice of a specific age to evaluate stayability depends on considerations of an economic order, such as determining the point of return of the investment in the production system (the number of calves needed to amortize the cost of heifers). Nevertheless, stayability at the age of 5 yr may be suggested to be an adequate trait because it presents a heritability similar to that of stayability at the age of 6 and 7 yr. It also contains a larger number of observations in the records (which permits better accuracy in the prediction of genetic merit), and it is obtained earlier than other stayability traits, and it presents an apparent positive additive genetic relationship with other stayability traits.

**LITERATURE CITED**


