ANALYSIS OF GENETIC AND ENVIRONMENTAL TRENDS FOR STAYABILITY AMONG NELORE COWS

ANÁLISE DA TENDÊNCIA GENÉTICA E AMBIENTAL DA HABILIDADE DE PERMANÊNCIA EM VACAS NELORE

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ABSTRACT: The objective of the present study was to determine the genetic and environmental values for the Stayability (STAY) trait in Nelore cows. STAY was defined as the probability of a cow in a herd to calve at a specific age or after this age when she had calved at an earlier age. The trait has a binary distribution, with 1 indicating success and 0 indicating failure. The specific ages studied were five (STAY5), six (STAY6) and seven (STAY7) years. Data for 53,271, 46,011 and 41,517 animals were analyzed for the respective ages. A maximum a posteriori probit threshold model was applied to obtain the solutions on a normal underlying scale. The genetic trend per year was 0.12 %, 0.06 % and 0.11 %, and the environmental trend was - 0.89 %, - 0.68 % and - 0.11 % for STAY5, STAY6 and STAY7, respectively. The increasing genetic trends suggest that culling policies have had a favorable genetic influence on underlying fertility.

UNITERMS: Longevity, Reproduction Trait, Threshold model

INTRODUCTION

The reproductive traits of females have not been contemplated in genetic breeding programs, mainly because of their low heritability and lack of information. It was only recently that some initiatives were taken to included the prediction of the breeding value of reproductive traits in genetic evaluations in beef cattle, and few are the traits in this category for which the compendia of genetic evaluation publish EPD (Expected Progenies Difference) In Brazil, some of this information is available in the Nelore breed summary (FERRAZ; ELER, 1998; LÔBO; BEZERRA; OLIVEIRA, 1999), along with the growth and conformation traits that had been the main selection objectives on the breed.

Reproductive fails are the main cause of culling beef cattle cows, especially when the animals are reared in range conditions. Assuming that mortality, culling on poor progeny performance and health is very low and other culling causes are not so important, the ability of cows to remain in the herd at a specific age may be considered as an indicative trait for fertility.

Stayability, defined as the probability of surviving to a specific age, given the opportunity to reach that age

(HUDSON; VAN VLECK, 1981), is an important trait in beef cattle. The inclusion of this trait in genetic evaluation would permit the selection of bulls with a higher probability of producing daughters that will remain productive in the herd for a longer period of time.

The objective of the present study was to evaluate the genetic and environmental changes of Stayability in a Nelore herd submitted to a rigid scheme of female culling due to reproductive faults, in order to determine the impact of the use of this trait as a selection criterion in breed improvement programs.

MATERIAL AND METHODS

Records of dams born between 1970 and 1997 belonging to 15 farms of Agropecuária CFM Ltda located in the states of São Paulo, Mato Grosso do Sul and Goiás were analyzed. Agro-Pecuária CFM was a purebred Nelore operation consisting of approximately 17,000 cows and selling an average of 2,000 young bulls per year out of about 7,000 males weaned.

Data included identification of the dams and their herds and year of birth, and the herds and year of birth of

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their calves for all parturitions that occurred during the study period. In the case of twin births, only the records of one calf were used.

The cows were maintained on pasture, with no supplementation. The breeding season starts in October and ends in December, with duration of 60 days, excepted for heifer exposed at 14 months of age for which the breeding season of 90 days. Artificial insemination and natural mating in single- and multiple-sire pastures with bulls selected from within the herd. At the end of each mating season, non-pregnant cows were culled. Some culling was also on the basis of poor progeny performance and health.

Three specific ages were considered for Stayability, i.e., five (STAY5), six (STAY6) and seven (STAY7) years, considering STAY as a different trait at each age. Files were formed with the inclusion of cows that had calved at least once before the age specified for each trait. Binary observa-

tions, with zero (0) indicating failure and one (1) indicating success, were made for each dam and for each trait. Success was attributed to cows that calved at a specific age or later and with at least one calf previously recorded, and failure was attributed to cows that did not satisfy these prerequisites. The reproductive management policy for the herds included in the present study, cows that didn't became pregnant in the breeding season were culled. Thus, if a cow produces a calf at a given age it is because it has been calving regularly during the preceding years.

The records were on 53,271, 46,011 and 41,517 animals and from 315, 281 and 299 contemporary groups for STAY5, STAY6 and STAY7 traits, respectively. The data were used to obtain the solutions for all animals. Table 1 shows the descriptive statistics for the rates of success per year of cow's birth for the traits STAY5, STAY6 and STAY7.

Table 1. Rate of success per year of cow's birth for the STAY5, STAY6 and STAY7 traits.

Year	STAY5		STAY6		STAY7	
	N	% Success	N	% Success	N	% Success
1984	6,331	0.49	5993	0.41	6284	0.37
1985	5,248	0.46	5481	0.39	5389	0.28
1986	6,410	0.53	6001	0.37	4895	0.19
1987	7,274	0.38	4836	0.25	4818	0.17
1988	3,925	0.30	3847	0.20	3931	0.15
1989	4,899	0.28	4918	0.22	4833	0.18
1990	4,744	0.27	4955	0.26	4295	0.19
1991	5,118	0.29	4622	0.27	4078	0.26
1992	3,519	0.23	2975	0.35	2994	0.27
1993	2,401	0.46	2383	0.37		
1994	3,402	0.35				
Total	53,271	0.38	46011	0.31	41517	0.24

The contemporary groups for the traits were formed by concatenation of farm and year of birth for the cow and farm for each of calves up to the ages specified. When the calf of a cow was not registered for a given year, the farm of the calf was replaced with the farm of the preceding calf and when no calf was born, the farm was replaced with the farm of birth of the cow.

Models used the different eighth generation pedigree structure. The numerator relationship matrix consisted of 81,373, 71,881 and 65,548 animals for STAY5, STAY6 and STAY7, respectively. Of cows studied, all of them with a know dam and daughters of multiple sire were considered to be from unknown sires.

A single-trait animal model was used, including the contemporary group as a fixed effect and the animal as a random effect. A maximum a *posteriori* probit threshold model (MAP) (GIANOLA; FOULLEY, 1983; HARVILLE; MEE, 1984) was applied to obtain the solutions on a normal underlying scale.

Predictions breeding values (PBV) were computed by transforming the MAP solutions for 50% probability values according to the following equation:

$$PBV_{i} = [F (MAP_{i}) - 0.50]*100,$$

where PBV, is the prediction breeding value of the ith animal

on a probability scale, F is a standard normal integral, and MAP_i is the prediction breeding value of the ith animal on the underlying scale. On the probability scale, animals with higher PBV have a higher probability of producing females with the specified stayability.

The accuracies (AC), as established by the Beef Improvement Federation (BIF) for all animals in the pedigree, were calculated according to the following equation:

$$AC_i = 1 - (PEV_i / s_a^2)^{0.5}$$

where AC_i is the accuracy of the ith individual's prediction, PEV_i is the error variance of the ith individual's prediction, and s₂² is the estimate genetic variance.

The predictions of breeding values were used to calculate genetic trends for the population as the regression of the breeding values over the year of birth of the animal. The mean breeding values per year of birth and the genetic trend are presented graphically for all the animals in the pedigree. The genetic trend was also calculated on the basis of the mean breeding value of the bulls used each year. In this case, the predictions breeding values of the bulls were weighted by their effective contribution in terms of the number of calves per year of birth as follows:

$$BVB_{j} = \sum_{i} \frac{n_{ij}GV_{i}}{n_{i}},$$

where BVB_j = mean breeding value of the bulls in the j^{th} year of birth of the products, i.e., value of bull contribution; BV_i = predicted breeding value for the i^{th} bull; n_{ij} = number of calves of the i^{th} bull born in the j^{th} year, and n_{j} = total number of calves born in the j^{th} year.

The environmental trend was obtained by regression of contemporary group solutions over animal's year of birth.

The additive genetic variances used to obtain the solutions were 0.134, 0.139 and 0.206 for STAY5, STAY6

and STAY7, respectively, while the residual variance was always equal to 1. These values were obtained by Silva et al. (2003).

The ABTK – Animal Breeder's Tool Kit software (GOLDEN; SNELLING; MALLINCKRODT, 1992) was used for data processing.

RESULTS AND DISCUSSION

The estimates of the means and standard deviations and range of the predicted breeding values for all animals in the pedigree and only for the bulls with more than 10 calves, on a probability scale, are presented in Table 2. The breeding values of the bulls presented a greater standard deviation and range similar to that observed for the populations as a whole, i.e., the limits of the population are given by bulls with more than 10 progeny. The values of range and of the standard deviations reflect the genetic variability of the trait. The differences between the breeding values of the animals analyzed indicate differences in the probability of remaining in the herd up to the age considered. Thus, if the difference between the highest (23.5%) and lowest (-20.5%) predicted breeding values for bulls at STAY5 is 44%, the daughters of the former will have a 22% higher chance to remain in the herd than the daughters of the latter if the bulls are mated to females of average breeding value.

The accuracies were calculated for each trait, also with separation into two groups: all animals and only bulls with more than 10 progeny (Table 3). As expected, the bulls showed high mean accuracies. However, the higher genetic variance for STAY7 did not result in a higher mean accuracy for the bulls for this trait, a result attributed to the lower number of daughters per bull for this last trait. The accuracy values demonstrate that the genetic predictions for the bulls with more than 10 progeny presented a medium to high level of reliability, indicating that these predicted breeding values can be used as a criterion for bull selection.

Table 2. Number of animals (N), mean breeding value, standard deviation (SD), minimum and maximum values for the total data set (Total) and for the bulls¹ (Bull) for the STAY5, STAY6 and STAY7 traits.

Traits		N	Mean (%)	SD (%)	Minimum (%)	Maximum (%)
STAY5	Total	81,373	0.22	3.72	-20.50	23.57
	Bull	181	-0.75	7.02	-20.50	23.57
STAY6	Total	71,881	0.09	3.73	-20.46	19.96
	Bull	150	-0.49	7.92	-20.46	19.34
STAY7	Total	65,551	0.14	4.69	-23.47	28.38
	Bull	131	0.30	9.41	-23.47	22.15

¹ – only bulls with more than 10 progeny

Table 3. Number of animals (N), mean accuracies, standard deviations (SD), minimum and maximum values for the total data set (Total) and for the bulls¹ (Bull), for the STAY5, STAY6 and STAY7 traits.

Traits		N	Mean	SD	Minimum	Maximum
STAY5	Total	81,373	0.06	0.06	0.00	0.90
	Bull	181	0.57	0.11	0.40	0.90
STAY6	Total	71,881	0.06	0.06	0.00	0.89
	Bull	150	0.57	0.12	0.40	0.89
STAY7	Total	65,551	0.05	0.05	0.00	0.86
	Bull	131	0.56	0.12	0.40	0.86

¹ – only bulls with more than 10 progeny

Figures 1 to 3 show the mean values for the years of birth of the animals under study and the genetic and environmental trends for Stayability at five (STAY5), six

(STAY6) and seven (STAY7) years. The mean breeding value for the Stayability traits increased with time at the three ages studied.

Figure 1. Environmental trend (A, - 0.87%/year), genetic trend for the total data set (B, 0.12%/year) and genetic trend for bulls (C, 0.02%/year), per year of birth, for stayability at five years.

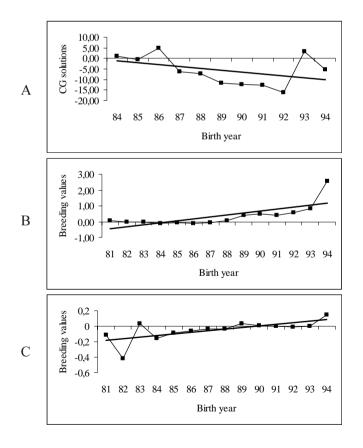


Figure 2. Environmental trend (A, -0.68%/year), genetic trend for the total data set (B, 0.06%/year) and genetic trend for bulls (C, 0.01%/year), per year of birth, for stayability at six years.

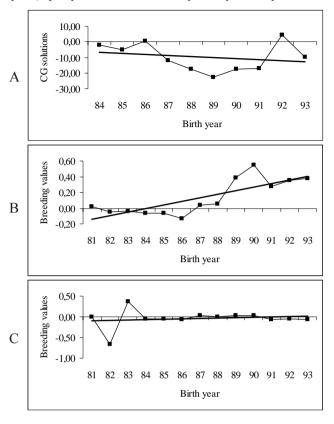
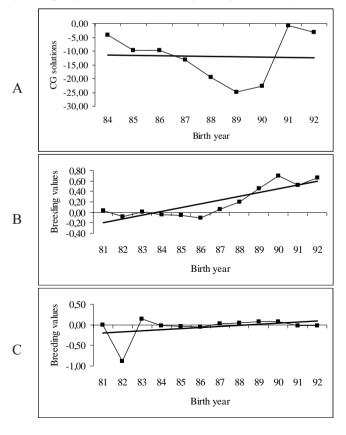


Figure 3. Environmental trend (A, - 0.11%/year), genetic trend for the total data set (B, 0.11%/year) and genetic trend for bulls (C, 0.02%/year), per year of birth, for stayability at seven years.



Mean annual genetic change considering all animals analyzed was 0.12%/year for STAY5, 0.06%/year for STAY6 and 0.11%/year for STAY7. The genetic trends detected in the present study were close to the values obtained by Snelling, Golden e Bourdon (1995) in a study on two herds of the Angus and Red Angus breeds, with estimates ranging from 0.018%/year (for STAY at two years in Red Angus cows) to 0.305%/year (for STAY at five years in Angus cows). Analysis of Figures 1 to 3 shows that the genetic contribution of bulls to the improvement of this trait was small or even negative, demonstrating that the genetic progress was the result of female culling. These results indicate that incorporating the PBV for Stayability as a criterion for bull selection may accelerate the rate of genetic change.

Environmental trend presented negative mean values, -0.89%/year, -0.68%/year and -0.11%/year, for the STAY5, STAY6 and STAY7 traits, respectively. The annual changes in environment of an irregular pattern are difficult to explain since they correspond to animals from various farms, each presenting its own difficulties and improvements over the years. However, when these values are considered together with genetic trends and phenotypic means (Table

1), there was a reduction in the time of permanence of cows in the herd, perhaps a result of more rigid selection criteria. The environmental trends for the three traits showed similar variation in annual mean values, although some discrepancy was observed in the last years.

IMPLICATIONS

The range of the breeding values for Stayability at the three ages studied, i.e., five, six and seven years, shows that there is sufficient genetic variability among the animals for the trait to be included as a selection criterion.

The genetic and environmental trends suggest that the use of these traits as a criterion of bull selection may accelerate the genetic process of these traits.

ACKNOWLEDGEMENTS

The authors gratefully acknowledged the financial support of the FAPESP, CNPq, CAPES and Agro_Pecuária CFM Ltda, and support from the people at the Department of ZAB at FZEA/USP.

RESUMO: O objetivo do presente estudo foi determinar os valores da tendência genética e ambiental para a característica Habilidade de Permanência (STAY) em vacas Nelore. STAY foi definida como a probabilidade da vaca parir a uma idade específica ou depois desta idade, dado que teve uma parição em data anterior. A característica tem distribuição binária, com 1 indicando sucesso e 0 indicando fracasso. As específicas idades estudadas foram cinco (STAY5), seis (STAY6) e sete (STAY7) anos. Dados de 53.271, 46.011 e 41.517 animais foram analisados para as respectivas idades. Um modelo de limiar *maximum a posteriori* foi aplicado para obter as soluções numa escala normal subjacente. A tendência genética por ano foi 0,12%, 0,06% e 0,11%, e a tendência ambiental foi -0,89%, -0,68% e -0,11% para STAY5, STAY6 e STAY7, respectivamente. Os valores das tendências genéticas sugerem que o critério de descarte tem exercido influência genética favorável na fertilidade subjacente.

UNITERMOS: Característica reprodutiva, Longevidade, Modelo Limiar.

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