

GENETIC ANALYSIS OF TEMPERAMENT IN NELORE CATTLE

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INTRODUCTION

Cattle temperament has practical implications, animals with a nervous temperament are more difficult and dangerous to handle and they could present a worsening in performance. Beef cattle producer's should be concerned about cattle temperament since it is related to human and cattle safety and welfare, herd productivity and meat quality (Fordyce et al., 1988; Grandin, 1993). Inversely, it is expected that animals with a calm temperament would have better performance in feedlot trials (Voisinet et al., 1997).

In spite of some confusion over the meaning of the term temperament, in this study we adopted the Fordyce et al. (1982) definition, as follow: "temperament are the reactions of animals in relation to human beings, generally attributed to the fear...". It is possible to assess cattle temperament measuring their flight distance (Fordyce et al. 1985).

Many reports have considered that cattle temperament is heritable, being described as a trait of moderate heritability (Le Neindre et al., 1995; Fordyce et al., 1996; Mourão et al., 1998). Thus, temperament may be considered in selection programs, searching for animals less excitable.

The objective of this study was to estimate the heritability and the expected progeny difference (EPD) of the cattle temperament in a Nelore herd.

MATERIAL AND METHODS

This research was carried out at Mundo Novo ranch, located in Brotas, state of São Paulo, Brazil, where the temperament of Nelore cattle (*Bos taurus indicus*) was routinely assessed. It has been done scoring the cattle reaction when a handler approaches an animal, trying to touch it with one of his hands, characterising the flight distance (FD) measurement. Every measurement was taken in a corral, where there were only the handler and the animal in test. A five-point scale has been used, giving the highest score to those animals which allowed to touch and the lowest to those attack the handler.

The analysis was carried out with 8,800 records (from 4,570 bullocks and 4,230 heifers), born from 1985 to 1998. The absolute and relative frequencies of 1 to 5 FD scores is presented on Table 1. In order to run the statistical and genetic analysis, using method R, the scores were grouped in three levels, adding the frequencies of scores 2 and 4 to scores 1 and 5, respectively.

Table 1. Absolute and relative frequencies of flight distance (FD) scores in a Nelore herd

FD score	Absolute frequencies (N)	Relative frequencies (%)
1	858	9,75
2	410	4,66
3	3712	42,18
4	976	11,09
5	2844	32,32
Total	8800	100

A single-trait animal model was used, including the contemporary group as a fixed effect and the animal as a random effect. It was applied the Method R (Reverter et al., 1994) to estimate heritability. A maximum posteriori probit threshold model (MAP) was used to produce the expected progeny difference (EPD) on the underlying standard normal scale (Gianola and Foulley, 1983; Harville and Mee, 1984). Models considered up to the eighth generation pedigree structure. The Wright's numerator relationship matrix consisted of 28,158 animals. The contemporary groups (N=277) consisted of herd, sex and year of birth + weaning and post weaning management group.

EPD were computed by transforming the MAP solutions for 50% probability values according to the following equation: $EPD_i = [\Phi (MAP_i * 0.50) - 0.50] * 100$, where EPD_i is the Flight Distance EPD of the i^{th} animal on a probability scale, Φ is a standard normal integral, and MAP_i is the prediction genetic value of the i^{th} animal on the underlying scale. On the probability scale, animals with higher EPD have a higher probability of producing animals with shorter FD.

The accuracies (AC), as established by the Beef Improvement Federation (BIF) for all animals in the pedigree, were calculated according to the following equation: $AC_i = 1 - (PEV_i / \sigma_a^2)^{0.5}$ where AC_i is the accuracy of the i^{th} individual's prediction, PEV_i is the error variance of the i^{th} individual's prediction, and σ_a^2 is the estimate genetic variance.

RESULTS

On average the h^2 estimates for FD was $.128 \pm .003$ (mean \pm se), estimated from 178 random 50% sub-samples of the data. All of the heritability estimates were within the parameter space. The distribution of all h^2 estimates is presented as Figure 1. Higher values of heritability were reported by Mourão et al. (1998) for pure and crossed zebu cattle (*Bos taurus taurus* x *Bos taurus indicus*), using linear procedures. The analytical techniques used here are based on non-linear models that seem to be more adequate for the analysis of categorical data.

The estimates of the means and standard deviations and the range of EPD values for all animals in the pedigree and only for the sires with more than 10 calves, on a probability scale, are presented in Table 2. The EPD values of the sires presented a greater standard deviation and range similar to that observed for the population as a whole, i.e., the limits of the population are given by sires with more than 10 progeny. The values of range and of the standard

deviations reflect the genetic variability of the trait.

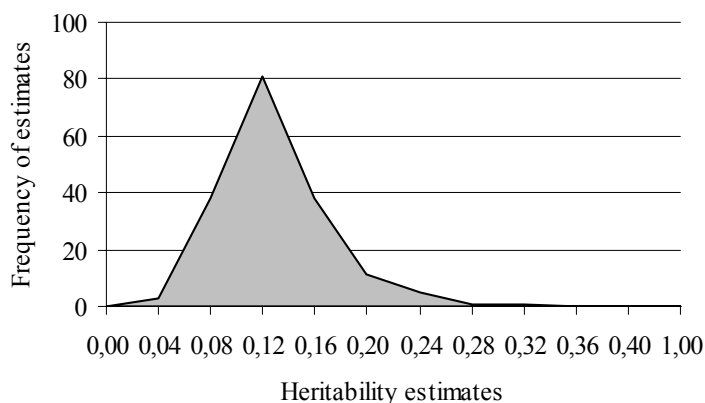


Figure 1. Distribution of heritability estimates (N=178) for flight distance in Nelore

Table 2. Number of animals (N), mean, standard deviation (SD) and range of flight distance EPD for the total data set (Total) and for a restrict data set¹ (Sire) from a Nelore herd

		N	Mean (%)	SD (%)	Min. (%)	Max. (%)
EPD	Total	28,158	0.69	3.62	-10,44	18,01
	Sire	216	1.03	4.46	-9,54	18.01

¹ = only sires with more than 10 progenies

The accuracies were calculated, also with separation into two groups (one with all animals and other only sires with more than 10 progeny) as presented in Table 3. As expected, the sires showed high mean accuracies. The accuracy values demonstrate that the genetic predictions for the sires with more than 10 progeny presented a medium to high level of reliability, indicating that these predicted genetic values can be used as a criterion for sire selection.

Table 3. Number of animals (N), mean, standard deviation (SD) and range of flight distance accuracy (ACC) for the total data set (Total) and for a restrict data set¹ (Sire) from a Nelore herd

		N	Mean	SD	Min.	Max.
ACC	Total	28,158	0.26	0.11	0,00	0,95
	Sire	216	0,72	0.13	0,46	0.95

¹ = only sires with more than 10 progenies

The EPD means and the genetic trend for flight distance, according to the years of birth, are presented in Figure 2. The mean of flight distance EPD increased with time. The mean of annual genetic change, considering all animals analysed, was 0.14%/year. These results indicate that the rate of genetic change may be accelerated by incorporating the flight distance EPD as a criterion for sire selection.

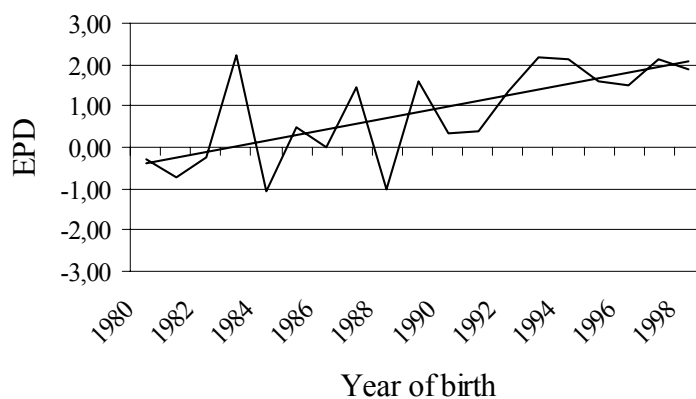


Figure 2. The EPD means and genetic trend for flight distance according to the years of birth in a Nelore herd

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