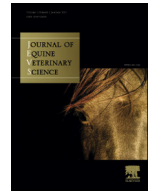




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Original Research

Genetic Parameters for Racing Performance of Thoroughbred Horses Using Bayesian Linear and Thurstonian Models



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ABSTRACT

The objective of this study was to estimate genetic parameters for rank in Thoroughbred horses using a Bayesian linear model (BLM) and a Thurstonian model (TM) to provide data that contribute to the selection and consequent genetic improvement of the breed in Brazil. Data were provided by the company Turf Total Ltda and consisted of 250,809 records for rank obtained from 40,300 horses and from 34,316 Thoroughbred races (distances of 1,000, 1,300, 1,600, and 2,000 m) that occurred between 1992 and 2011 on six tracks. The rank records at each distance were considered different traits and were submitted to single-trait analysis using BLM and TM. Fixed effects included sex, age, post-position, race, and level of difficulty. The heritability estimates for rank ranged from 0.228 to 0.032 when BLM was used and from 0.293 to 0.047 when TM was used. These estimates tended to decrease with increasing race distance in the two analyses. The TM estimated higher heritability for rank than BLM, indicating the possible use of this model in selection programs of Thoroughbred racehorses in Brazil.

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1. Introduction

In Brazil, the selection of Thoroughbred horses is based on the performance of the animal and of its parents. The pedigree plays an important role in the choice of parents of the next generation. Racing time, that is, the performance of the animal, is the main trait taken into consideration to evaluate and choose an animal as a reproducer.

Furthermore, the animal's performance is directly related to its earnings.

In addition to earnings and racing time, the final rank of the animal in a race is one of the most common performance measures of Thoroughbred racehorses. The use of rank traits may better adjust the information collected during Brazilian races because the ranks of all animals of the competition are recorded, whereas racing time and earnings are not always available for all horses competing in a race. The use of ranks permits to compare animals that participate in the same race with those of another race. However, in this case, the level of difficulty of a race should be determined and included in the analysis model [1].

Rank corresponds to differences in the level of the animals of that competition but does not evaluate velocity

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itself. This criterion eliminates some of the problems associated with the assessment of performance for different distances and track conditions, atypical inferior performance, and problems with abnormal performance criteria [2–8]. Rank is a good selection criterion for genetic improvement programs because it is heritable, according to genetic parameter estimates [9]. In two different studies, genetic parameter estimates for rank ranged 0.07–0.10 and 0.07–0.12, respectively [5,9]. These heritabilities were 0.18 in French Thoroughbreds and 0.06 in racehorses from the United Kingdom and Ireland [8], 0.14 in Thoroughbreds [10], 0.13 in Quarter horses [11], and 0.12 [5] and 0.25 in Arab horses [12]. In view of the above considerations, the aim of the present study was to the estimate genetic parameters for rank using a Bayesian linear model (BLM) and a Thurstonian model (TM) in Thoroughbred breeding programs in Brazil.

2. Material and Methods

2.1. Origin and Description of the Data

The database used was provided by Turf Total Ltda and consisted of 272,277 records for rank obtained from 40,300 different Thoroughbreds horses participating in races that occurred from 1992 to 2011 on tracks in Gávea (Rio de Janeiro State), Campos (Rio de Janeiro State), Cidade Jardim (São Paulo State), Tarumã (Paraná State), Cristal (Rio Grande do Sul State), and São Vicente (São Paulo State). The contemporary groups were defined using animals that participated in the same race (combination of day, hour, and city where the race occurred).

The database initially contained 30 different distances, which were restricted to four in the present study because they are the most traditional and most important distances in the country and therefore accounted for most observations in the data file. Table 1 shows the number of races, number of animals and observations per sex, and mean number of animals per race according to distance. There was a larger number of observations for 1,300-m races because many breeders decide whether their horses will participate in longer distance races based on the results of the animals obtained at this distance. The choice of distance and level of difficulty is made by the breeder based on the animal's performance at shorter distances and in previous races.

The pedigree file contained 58,694 animals, which were used in all analyses. As can be seen in Table 1, the mean number of animals per race was always about seven and the participation of females tended to decrease with increasing race distance and was only higher at 1,000 m.

For the genetic analysis of rank, races performed at different distances were considered different traits. This strategy was adopted because studies investigating other performance traits [13] demonstrated that races at different distances show genetic correlations less than unity, indicating that the addition of this effect as fixed effect alone would not be sufficient to describe all differences between animals. Thus, single-trait analysis was performed for each trait using BLM and TM.

2.2. Analysis of Rank Using a Bayesian Linear Model

The BLM model can be written in matrix form as:

$$y = X\beta + Za + Wc + \varepsilon \quad (1)$$

where y , β , a , c , and ε are vectors of observations and fixed (sex, age, postposition, race, and level of difficulty), direct additive genetic, permanent environmental, and residual effects, respectively, and X , Z , and W are incidence matrices that associate β , a , and c with the observations. Uniform and Gaussian a priori distributions were assumed for the fixed and random effects, respectively:

$$\beta \propto \text{constant} \quad (2)$$

$$a | \sigma_a^2 \sim N[0, (A\sigma_a^2)] \quad (3)$$

$$c | \sigma_p^2 \sim N[0, (I_n \sigma_p^2)] \quad \varepsilon | \sigma_r^2 \sim N[0, (I_n \sigma_r^2)] \quad (4)$$

where A and I_n are relationship and identity matrices, respectively, and σ_a^2 , σ_p^2 , and σ_r^2 are the additive genetic, permanent environmental, and residual variance, respectively. A priori distributions derived from inverted chi-square distributions were used for the variance components. Thus:

$$\sigma_a^2 | S_a, v_a \sim \chi^{-2}[S_a v_a, v_a] \quad (5)$$

$$\sigma_p^2 | S_p, v_p \sim \chi^{-2}[S_p v_p, v_p] \quad (6)$$

$$\sigma_r^2 | S_r, v_r \sim \chi^{-2}[S_r v_r, v_r] \quad (7)$$

where S_a and v_a , S_p and v_p , and S_r and v_r are a priori values and degrees of freedom for direct additive,

Table 1

Number of races, observations per sex, number of animals per sex, and mean number of animals per race according to distance.

Distance [m]	No. of Races	No. of Male Observations	No. of Males	No. of Female Observations	No. of Females	Mean Number of Animals/Race
1,000	6,793	23,915	8,007	28,847	9,375	7.76
1,300	15,282	63,270	14,610	47,606	12,692	7.25
1,600	9,133	46,523	10,339	20,002	6,627	7.28
2,000	3,108	14,051	4,640	7,540	2,677	6.95

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