

## Genetic parameters for resistance to parasites in Nellore cattle through random regression

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**ABSTRACT:** The aim of this study was to obtain genetic parameters for resistance to ticks, gastrointestinal nematodes and *Eimeria* spp. in Nellore cattle using random regression models through Bayesian inference. Animals were classified as resistant or susceptible for each parasite. Heritability estimates ranged from low to high magnitude (0.07 to 0.30 for resistance to ticks, 0.02 to 0.34 for resistance to gastrointestinal nematodes, and from 0.04 to 0.39 for resistance *Eimeria* spp.) In general, the posterior means of genetic correlations between resistance characteristics were low while high density intervals were large, and in many cases included zero. Thus, there is genetic variation in resistance traits in Nellore cattle and these may be included in breeding programs. The selection may increase the frequency of resistant animals in any age evaluated in this study.

**Keywords:** beef cattle; correlation; heritability; resistance

### Introduction

Parasitism adversely affects beef cattle production in the world. Parasites are responsible for productive, reproductive and economic losses in beef chain. The conventional parasite control method is the application of chemicals, which lead to increases in production costs, may leave residues in meat (Spisso et al. (2009)) and result in the selection of resistant parasites to the active principles (Jonsson and Hope (2007); Knox et al. (2012)). In this context, selection of resistant animals could be used as an alternative control method.

Resistance traits can be measured repeatedly during the animal lifetime and are called longitudinal data. Traditionally, these features are evaluated by repeatability models (Burrow (2001); Morris and Amyes (2012)). These models assume unrealistic assumptions, since they consider that measures in the same individual represent a unique feature and that correlations between different observations obtained from the same animal are equal to one. Random regression models are suitable for longitudinal data analysis (Meyer (2005)) because they describe the covariance structure of the random effects of interest during the evaluated interval, provide estimates of genetic parameters for each age and increase the accuracy of evaluation (Meyer (2004)).

Thus, the aim of this study was to identify the most appropriate random regression model for data analysis of resistance to ticks, gastrointestinal nematodes and protozoa of the genus *Eimeria* in Nellore and obtain genetic parameters for these traits through Bayesian inference.

### Materials and Methods

**Sample collection.** The experiment was conducted in a farm located in Uberaba, Minas Gerais, Brazil. The region has an average annual rainfall of 1400 mm, mainly in the months of October to March, and annual average temperatures between 5°C to 39°C. The area of the farm is 4,250 hectares, with a stocking rate of approximately 0.98 AU/ha. The animals used in the experiment were purebred Nellore. The animals were raised on pasture with mineral supplementation throughout the year with water availability of small dams or natural reservoirs in each paddock.

Data collection was conducted between April 2010 and June 2013. Tick counts were performed in cattle (Wharhorn and Utech (1970)) naturally infested and faecal samples were collected for the counts of egg of gastrointestinal nematodes (EPG) and oocysts of *Eimeria* spp (OPG) per gram of feces (Ueno and Gonçalves (1998)) After counting, animals were classified as resistant (counts equal to zero, score = 1) or susceptible (counts exceeding zero, score = 0) separately for each parasite.

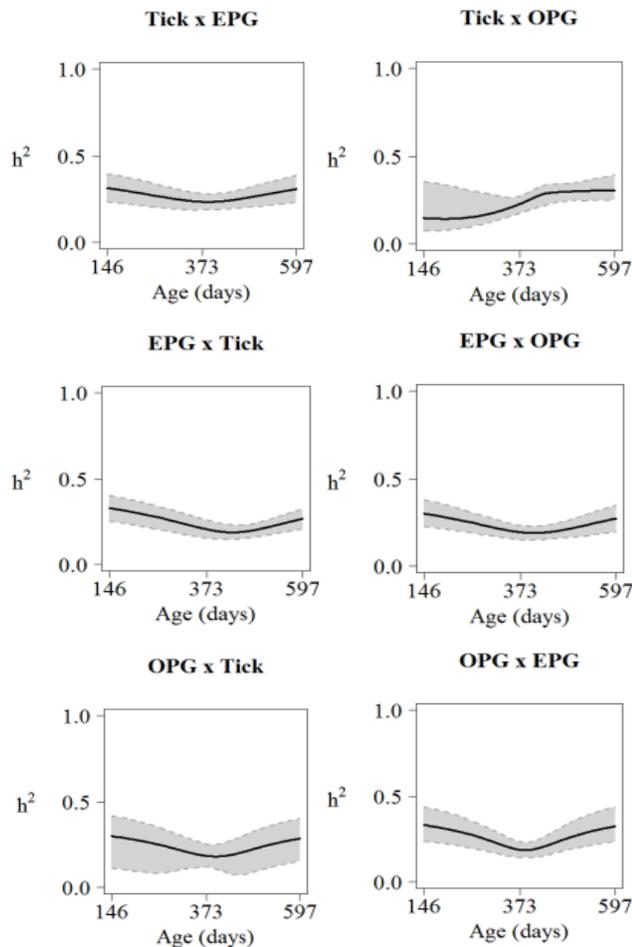
**Data.** The datasets considered only information on the traits of resistance of 146 to 597 days old. In this period up to three measurements were performed in females and up to six in males. Information from animals with less than two observations were disregarded as well as measures whose interval of use of any anti-parasitic product was less than 120 days and, finally, contemporary groups with less than four data and three animals. After these restrictions, three databases were formed - one for each trait. The database of tick resistance was composed of 4,270 observations from 1,188 animals, offspring of 968 cows and 88 bulls. The databases of resistance to gastrointestinal nematodes and *Eimeria* spp. were composed of 3,872 records of 1,142 calves from 933 cows and 88 bulls. The relationship matrix consisted of 15,927 animals, with 5,327 cows and 566 bulls.

**Statistical analyses.** Resistance traits were evaluated using random regression models in bivariate analysis. Models with two traits were defined by univariate analysis, in which the Bayesian Information Criteria (BIC) indicated the best fit models for each trait. Statistical models contemplated the fixed effects of the mean trajectory of the population and the contemporary groups (year and month of birth, sex and lot), and as the random effects, the direct additive genetic effect, direct permanent environmental effect and residue. For modeling the average trajectory and the random effects, linear orthogonal Legendre polynomials were considered over the age of calf on the day of collection, in exception for the mean trajectory of resistance to *Eimeria* spp. that considered a cubic polynomial. Samples of the complete conditional

distributions were obtained through the Gibbs sampler using THRGIBBS1F90 program (Tsuruta and Misztal, (2006)). Chains of 410,000 cycles, discarding 10,000 initial samples and sampling interval of 200 cycles were considered. The size and the convergence of the Markov chain were observed in the software R (The R Foundation for Statistical Computing (2009)).

## Results and Discussion

The posterior mean of direct heritability for all traits were similar. In general, the direct heritability described trajectories with high values at the ends of the interval when compared with intermediary values of range for each trait (Figure 1). These ends values may be attributed to the small numbers of records at the beginning and at the end of interval.



**Figure 1: Posterior means and high density interval (95%) of heritability for tick (superior line), gastrointestinal nematodes (EPG, central line) and *Eimeria* spp. (OPG, inferior line) resistance obtained in bivariate analysis**

In general, the heritability ranged from low to high magnitude for all models and traits. Despite Nellore cattle are considered resistant to the studied parasites (Ibelli et al.

(2011)), our results indicated that there are sufficient additive genetic variability to promote genetic and phenotypic changes in this population over the years through selection. Furthermore, genetic evaluations to resistance traits allow to identify genetically superior animals, which are able to combat the parasites and eliminate minor amounts of eggs and oocyst in feces. These aspects reduce pasture contamination and animal exposure to these parasites. Direct heritabilities support the inclusion of resistance traits in Nellore breeding programs.

The posterior means of direct heritability to tick resistance ranged from 0.11 to 0.30 and from 0.11 to 0.24 for tick with gastrointestinal nematodes and tick with *Eimeria* spp., respectively. The results of this study corroborate with those obtained by Fraga et al. (2003), which used repeatability models for genetic evaluation in Caracu cattle and obtained direct heritability of 0.22 for tick counts. These authors concluded that there is sufficient additive genetic variability, thus genetic progress can be achieved through selection.

The posterior means of direct heritability for resistance to gastrointestinal nematodes ranged from 0.08 to 0.33 and from 0.02 to 0.34 for gastrointestinal nematodes with tick and gastrointestinal nematodes with *Eimeria* spp., respectively. Heritability values ranged from low to high magnitude were also described by Burrow (2001) and Morris and Amyes (2012). Considering the high density interval (HDI95%) it would be possible to obtain heritability values equal or greater than 0.3 to 0.4, as recommended by Sonstegard and Gasbarre (2001). These authors emphasized that heritability of this magnitude indicates the possibility of obtaining genetic gain through selection, supporting selection for resistance to gastrointestinal nematodes in some ages for the studied population.

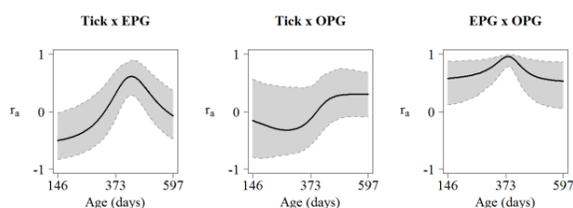
The posterior means of direct heritability for resistance to *Eimeria* spp. ranged from 0.04 to 0.30 and from 0.05 to 0.39 for *Eimeria* spp. with tick and *Eimeria* spp. with gastrointestinal nematodes, respectively. Our data are pioneer in genetic evaluation of this trait in beef cattle.

The posterior means of genetic correlations between resistance to ticks and gastrointestinal nematodes (Figure 2) increased until 436 days of age and decreased since then until 597 days of age. Correlations ranged from low to high magnitude and most values were negative in this interval. The HDI95% from 386 until 491 days of age were positive and did not included zero. Thus, it may infer that in these ages pleiotropic genes regulates mechanisms of defense for resistance to ticks and gastrointestinal nematodes. Therefore, the selection for one of these traits results in genetic gain of the other trait in the same way in this interval.

The posterior means of genetic correlations in resistance to ticks and *Eimeria* spp. ranged from low to medium magnitude associated with a large HDI95% which contains zero all over the interval. This result indicates that there is no association between genetic resistance to ticks and *Eimeria* spp. in the assessed ages.

The posterior means of genetic correlations between resistance to gastrointestinal nematodes and *Eimeria* spp. were high and positive. The HDI95 % did not

include zero in all ages. In this case, it is also possible that pleiotropic effects regulates genetic resistance for both endoparasites studied.



**Figure 2: Posterior means and high density interval (95%) of genetic correlation between resistance for tick and gastrointestinal nematodes (Tick x EPG), tick and *Eimeria* spp. (Tick x OPG) and gastrointestinal nematodes and *Eimeria* spp. (EPG x OPG) in Nellore cattle**

The lack of association between the resistance traits between ticks and endoparasites may be due to the polygenic nature of these traits, in which there are different genes controlling each trait. These results suggest that defense mechanisms involved in tick resistance includes besides the cellular and humoral response, the physical barriers such as a greater skin thickness and hair length.

The positive association between the resistance to gastrointestinal nematodes and *Eimeria* spp. suggests that the defense mechanisms for both traits are similar and should involve the same immune cellular and humoral response.

These results indicate that it is possible to include only gastrointestinal nematode or *Eimeria* spp. resistance as selection criteria because of the high and positive association between these traits. The choice of each of them should consider the incidence of the parasite in the herd.

## Conclusion

Random regression models with Legendre polynomials of low order are efficient to describe genetic variation for resistance to ticks, gastrointestinal nematodes and *Eimeria* spp. in Nellore cattle from 146 to 597 days of age.

It is possible to increase the frequency of genetically resistant animals to ticks, gastrointestinal nematodes and *Eimeria* spp. by selection.

## Literature Cited

- Burrow, H. M. (2001) Livest. Prod. Sci. 70:213-233.
- Fraga, A.B., Alencar, M. M.; Figueiredo, L. A. et al. (2003) Rev. Bras. Zootecn. 32:1578-1586.
- Ibelli, A. M. G., Nakata, L. C., Andréo, R. et al. (2011) Vet. Parasitol. 176:195-200.
- Jonsson, N. N. and Hope, M. (2007) Vet. Parasitol. 137:193-198.
- Knox, M. R., Besier, R. B., Jambre, L. F. et al. (2012) Vet. Parasitol. 186:413-419.
- Meyer, K. (2004) Livest. Prod. Sci. 86:69-83.
- Meyer, K. (2005) Genet. Sel. Evol. 37:473-500.
- Morris, C. A. and Amyes, N. C. (2012) Proc. New. Zeal. Soc. An. 72:236-239.
- Sonstegard, T. S.; Gasbarre, L. C. (2001). Vet. Parasitol. 101:387-403.
- Spisso, B. F., Nóbrega, A. W, Marques, M. A. S. (2009) Cienc. S Col. 14:2091-2106.
- Tsuruta. S. and Misztal, I. Proc 8th WCGALP, volume 8:253-256
- Ueno, H. and Gonçalves, P. C. 1998. Page 14 in ICA: Tokyo: Japan.
- Wharhorn, R.H. and Utech, K. B. W. J. Aust. Entomol. Soc. 9:171-182.