

Introduction

Tolerance is a mechanism through which hosts do not reduce parasite infection but alleviate the negative fitness consequences of pathogen burden instead.

Biological mechanisms \times Parasite burden
Parasite type

Spline functions can be used to infer on tolerance, since the solutions for each knot indicate the changes observed on the studied phenotype by the increase of 1 parasite count.

Objective: to study the genetic variability of host tolerance to different parasites and the genotype x parasite load interaction.

Material & Methods



Figure 1. Nellore cattle pasture raised at Mundo Novo farm and evaluated at performance tests.

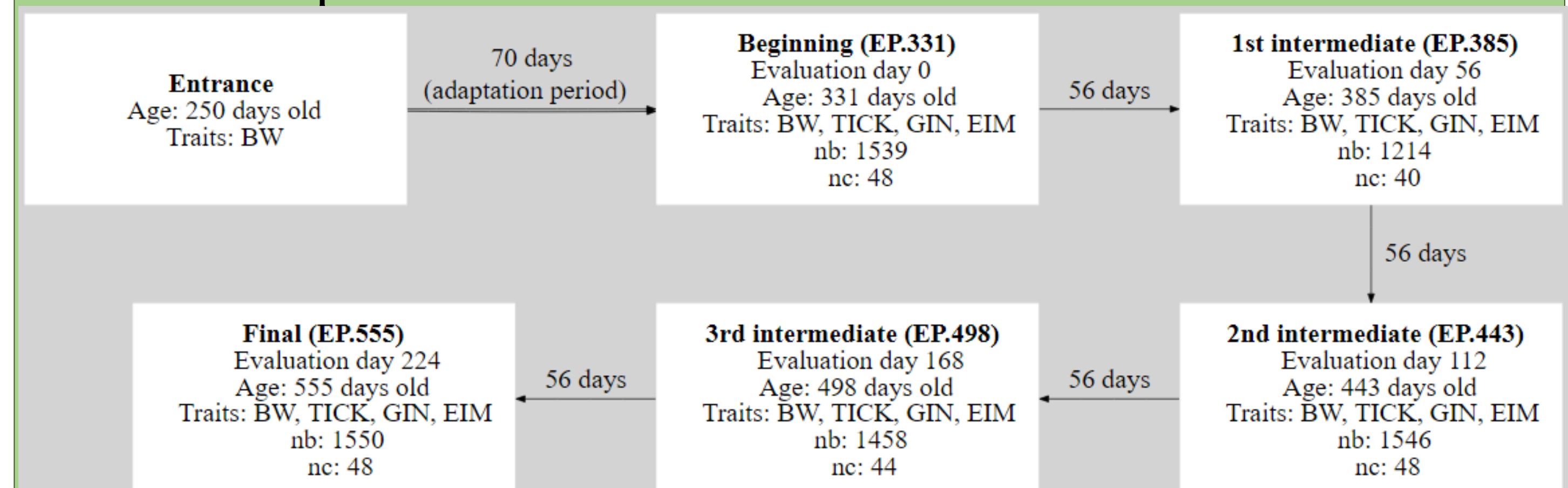


Figure 2. Diagram of data collection at performance tests. Arrows indicates the intervals in days between two evaluations. BW – body weight, and TICK, GIN, and EIM – ticks, gastrointestinal nematodes, and *Eimeria* spp. counts, respectively are the evaluated traits. nb is the number of observations and nc the number of cohorts evaluated in each measurement event.

*information collected at Entrance was not considered in the present study.

Material & Methods

- Median parasite counts per cohorts were used to infer about environmental burden. 2 knots were adjusted at the lower and higher median cohorts, respectively, defining low and high parasite burden environments:

Table 1. Median parasite counts of ticks (TICK), gastrointestinal nematodes (GIN), and *Eimeria* spp. (EIM) used to define low and high environmental parasite burden when animals were evaluated at 331, 385, 443, 498, and 555 days old

Trait	331	385	443	498	555
Low parasite burden					
TICK	0.00	0.00	0.00	0.00	0.00
GIN	0.00	0.00	1.00	0.00	0.00
EIM	0.00	0.00	0.00	0.00	0.00
High parasite burden					
TICK	16.00	33.00	15.00	16.00	18.00
GIN	9.00	11.00	12.00	8.00	8.00
EIM	11.00	10.50	16.50	11.00	7.00

- A model with 7 knots adjusted for age and zero knots adjusted for parasite counts was used as benchmark analysis (independent of infestation).

Model:

$$y_{ijkl} = PTP_j + \sum_{h=1}^7 \phi_h(A_k)b_h + \sum_{h=1}^2 \phi_g(I_l)b_h + \sum_{h=1}^7 \phi_h(A_k)a_{ih} + \sum_{h=1}^2 \phi_g(I_l)a_{ih} + \sum_{h=1}^7 \phi_h(A_k)p_{ih} + \sum_{h=1}^2 \phi_g(I_l)p_{ih} + e_{ijk}$$

where y_{ijk} , represents the weight of the animal; PTP_j is the systematic effect of the performance test; 7 denotes the number of knots adjusted to the ages; $\phi_h(A_k)$, represents the linear spline polynomial h that refers to age k; 2 is the number of knots adjusted in each model; $\phi_g(I_l)$ represents the linear spline polynomial g that refers to parasite count l; b_h denotes the coefficient of regression that is associated with the polynomial h that fits the systematic effect of age k on weight; a_{ih} , represents the coefficient of the additive genetic random effect; p_{ih} , denotes the coefficient of regression associated with the individual permanent environment random effect; and e_{ijk} , represents the error associated with each observation.

Results

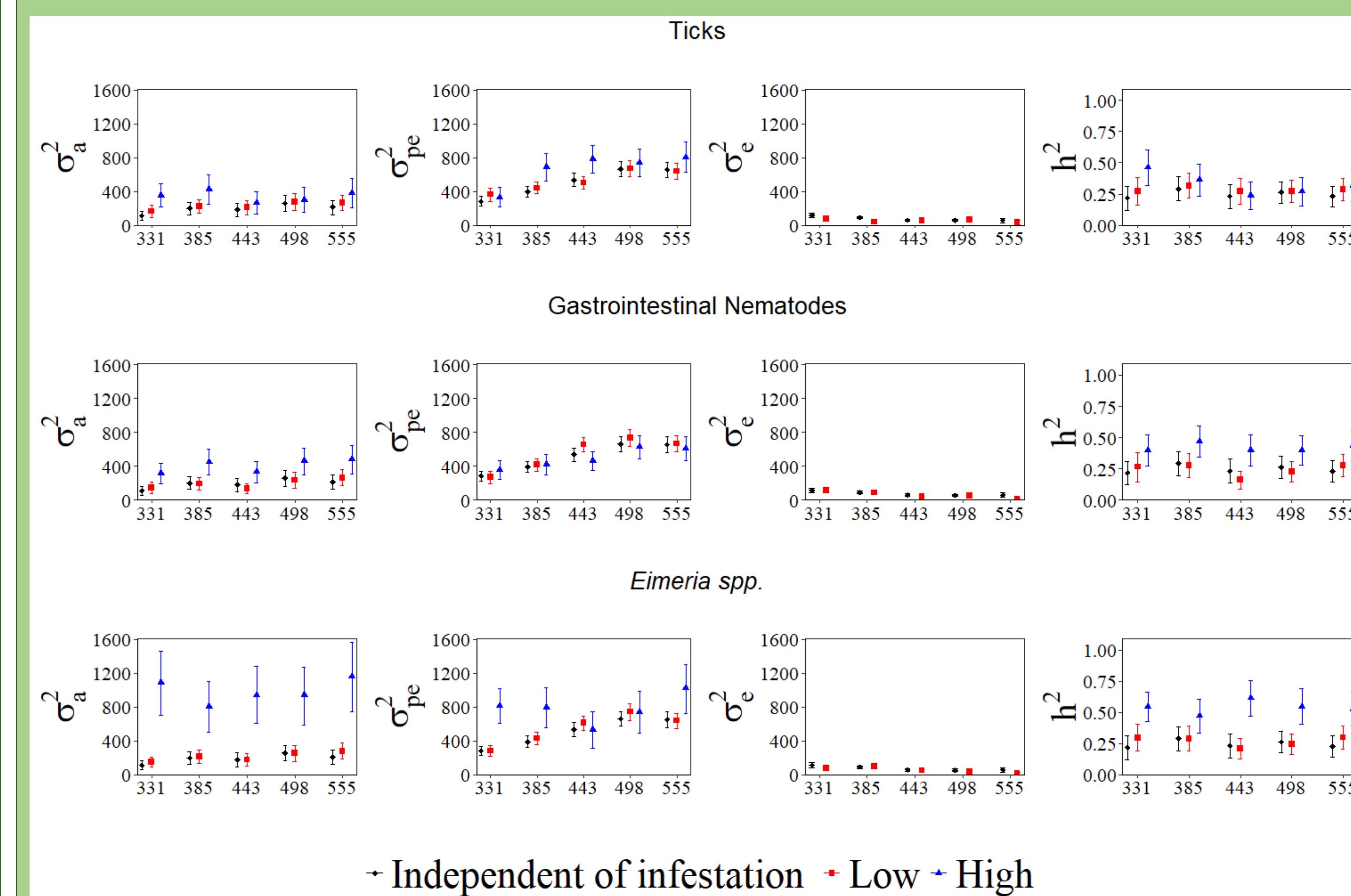


Figure 3. A posteriori means (points) and high-density intervals with 90% of samples (bars) for the genetic additive (σ_a^2), permanent environment (σ_{pe}^2) and residual (σ_e^2) variances and heritabilities (h^2) for body weight at different ages (331, 385, 443, 498 and 555 days old) of Nellore young bulls pasture raised.

- Overlapping of the high density intervals of the genetic parameter between the analysis that considered low parasite burden and the benchmark analysis indicates good fit of models that considered tolerance effects;

- Additive variance estimates for tolerance increase with pathogen burden trajectory, ranging from 63.67 ± 16.68 to 296.89 ± 75.97 for ticks, from 58.13 ± 16.68 to 206.80 ± 46.50 for nematodes and from 57.19 ± 16.29 to 648.25 ± 141.76 for *Eimeria* spp., revealing significant additive variance for parasitic load tolerance;

- Low genetic correlation of 0.20 for ticks; 0.16 for nematodes and -0.03 for *Eimeria* spp. between low and high infestation.

Conclusion

Variation in tolerance can induce genotype re-ranking, contributing to environment-dependent genetic responses to selection.