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# Tick resistance genetic parameters and its correlations with production traits in Hereford and Braford cattle

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ABSTRACT

Inclusion of cattle genetic resistance to ticks in selection programs represents an auxiliary method in strategic control of this parasite. This study was conducted to estimate genetic parameters for cattle tick resistance measured by tick counting on the inner hind legs region (TCHL) and on one side of body (TCBS) of Hereford and Braford cattle naturally exposed to ticks in southern Brazil. Records of weight gain from birth to weaning (WG), visual scores of conformation, precocity and muscling at weaning (WC, WP and WM, respectively) and at yearling (YC, YP and YM, respectively), weight gain from weaning to yearling (YG) and scrotal circumference (SC) were also analyzed to obtain correlations among all the traits. Heritability estimates obtained by bivariate analysis were TCHL = 0.13 and TCBS = 0.17 and phenotypic correlation between both methods was 0.09 ($P < 0.05$). Repeatability estimate for TCBS was 0.29. Heritability estimates obtained by multivariate analysis were TCBS = 0.19; WG = 0.35; WC = 0.28; WP = 0.23; WM = 0.26; YG = 0.14; YC = 0.18; YP = 0.18; YM = 0.18; and SC = 0.43. No unfavorable genetic correlations among TCBS and growth traits and visual scores at different ages and scrotal circumference have been identified, indicating that simultaneous selection for improving all the traits is feasible.

## 1. Introduction

The current need of auxiliary strategies to cattle tick control has been stimulating researchers to find more efficient alternatives for the producers, due to the several limitations related to the conventional chemical control (Abbas et al., 2014; Frisch, 1999; Reck et al., 2014). Cattle genetic resistance to *Rhipicephalus (Boophillus) microplus* ticks have been increasingly studied as an alternative, and the occurrence of variability for tick counts within and between herds indicates the possibility of genetic progress by selecting resistant animals and the potential of this tool as a strategy to reduce infestation levels and losses caused by the parasitism (Cardoso et al., 2015; Frisch et al., 2000; Henshall, 2004; Machado et al., 2010).

The traditional evaluation method of cattle tick-resistance consists in counting female ticks with 4.5 mm or more in diameter, on one side of animal's body (Wharton and Utech, 1970). Although the quantification of ticks on the body side is the typical most accurate method for identifying genetically resistant individuals (FAO, 1984; Roberts, 1968; Wharton and Utech, 1970; Wilkinson, 1955), counts in regions with easier access (on inner hind legs, e. g.) could be an alternative to facilitate evaluation of animals in farms with large herds, stimulating application of the selection of resistant individuals in order to reduce the damages caused by parasitism.

Knowledge about genetic correlations among productive traits is essential to the correctly planning and conduct of any breeding program. Some pioneering research that investigated possible correlations between number of ticks and traits as body weight gains indicates that the selection of genetically resistant cattle would not compromise the development of animals (Wharton et al., 1970). The objective of this study was to estimate genetic parameters for tick counts assessed in two body regions of Hereford and Braford cattle naturally exposed to tick *R. (B.) microplus* and genetic correlations with traits related with capacity for growth and fertility of cattle.

## 2. Materials and methods

All animal procedures performed in this research were approved by

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the Committee for Ethics in Animal Experimentation from the Federal University of Pelotas (Pelotas, RS – Brazil; Process CEEA n° 9409).

### 2.1. Animals and traits

Analysis used a set of 149,781 Hereford and Braford (racial composition between ½ Hereford + ½ Zebu and ¾ Hereford + ¼ Zebu) cattle grazed at pasture in southern Brazil and belonging to the Delta G Connection Genetic Improvement Consortium (Delta G Connection, 2007) and naturally exposed to ticks between 2001 and 2011. Tick counts were performed by manually counting adult female ticks (sized between 4.5 mm and 8.0 mm) on the inner hind legs region (TCHL) or on the left body side (TCBS) of each animal, held in a squeeze chute. Tick counting were performed in late spring and summer. For each animal was conducted one manual counting on TCHL or up to three consecutive counts on TCBS. Evaluations of TCBS were repeated in time, observing a minimum period of 30 days between counts. Total data set analyzed contained 14,769 records of counting conducted in 8459 animals (animal's age at the moment of evaluations was about 18 months): 4096 of these records corresponded to evaluations on TCHL made from 2001 to 2008, and 10,673 records provided counting information on TCBS carried out between 2009 and 2013 in 4363 animals.

Data set also included records of weight gain from birth to weaning (WG); visual scores of conformation (WC), precocity (WP) and muscling (WM) at weaning; weight gain from weaning to yearling (YG); visual scores of conformation (YC), precocity (YP) and muscling (YM) at yearling; and scrotal circumference (SC). Weight gain from birth to weaning was determined by subtracting birth weight from weaning weight and dividing by the number of days since birth (weaning date – birth date). Weight gain from weaning to yearling was determined by subtracting weaning weight from yearling weight and dividing by the number of days since weaning (yearling date – weaning date). Visual scores (WC, WP, WM, YC, YP and YM) from 1 to 5 were attributed to cattle individually by trained technicians at weaning and yearling, with 5 corresponding to the highest expression of the trait and 1 to the lowest expression in relation to the animal contemporaries. For these evaluations, technicians observed each contemporary group and set a relative scale where score 3 is attributed to the animals considered to be at the average performance, and scores 1 and 5 for the animals with poorer and greater expression of the trait within that group, respectively. Therefore, visual scores of each animal were always assigned in relation to its contemporary group. Scrotal circumference was measured with a flexible measuring tape at the greatest horizontal distance around the scrotum after manually forcing the testicles into the base of the scrotum.

The pedigree information was composed of 151,681 records, including base animals with unknown parents.

### 2.2. Data consistency analyses

Data consistency analyses were performed using SAS (Statistical Analysis System, v. 9.1.3). Contemporary groups (CG) met animals from the same farm, sex, year and season of birth, sex and management group and date of phenotypic evaluations. Three birth seasons were considered: April to July, August to November and December to March. Contemporary groups under five observations and animals with phenotypic evaluation standard deviation above or below 3.5 from the CG mean were previously excluded from the analysis. Table 1 presents descriptive statistics of traits analyzed after data consistency.

### 2.3. Statistical analyses

Statistical analyses were performed under two models: bivariate analyses (Model I) and multitrait analyses (Model II). The statistical models included the fixed effect of contemporary groups; the linear covariate effects of zebu breed composition and heterozygosity; the linear and quadratic covariate effects of animal age; and the random additive genetic and permanent environment animal, and residuals effects. Due to lack of adjustment to a normal distribution, before analyses counting records were transformed by applying a base 10 logarithmic function to the observed value + 1001 (this constant was used because $\log_{10}(1.0) = 0.0$ and null values are treated as missing by the used software).

**Table 1**
Descriptive summary of tick counting on inner hind legs region (TCHL), on one side of body (TCBS), weight gain from birth to weaning (WG), conformation (WC), precocity (WP), muscling (WM) at weaning, weight gain from weaning to yearling (YG), conformation (YC), precocity (YP), muscling (YM) at yearling and scrotal circumference (SC) from Hereford and Braford cattle.

| Trait | N records | Mean | SD | Minimum | Maximum |
|---|---|---|---|---|---|
| TCHL | 4096 | 0.94 | 0.45 | 0.0005 | 1.92 |
| TCBS | 10,673 | 1.36 | 0.44 | 0.0004 | 2.73 |
| WG | 135,283 | 145.04 | 32.60 | 41.0 | 329.80 |
| WC | 137,341 | 2.93 | 1.10 | 1 | 5 |
| WP | 128,236 | 3.20 | 1.05 | 1 | 5 |
| WM | 128,229 | 3.10 | 1.05 | 1 | 5 |
| YG | 70,929 | 135.88 | 63.37 | 34.50 | 592.80 |
| YC | 80,719 | 3.06 | 1.01 | 1 | 5 |
| YP | 76,092 | 3.23 | 0.99 | 1 | 5 |
| YM | 75,887 | 3.17 | 1.00 | 1 | 5 |
| SC | 18,361 | 30.47 | 3.72 | 18 | 45 |

To verify the correlations between ticks count methods and analyze tick count as repeated measures on one side of body the repeatability model (Model I) was used:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Z_1a} + \mathbf{Z_2p} + \mathbf{e} \quad (1)$$

where $\mathbf{y}$ is the vector of phenotypic observations; $\boldsymbol{\beta}$ is the vector of fixed effects of contemporary group and covariates; $\mathbf{X}$ is the incidence matrix for fixed effects; $\mathbf{a}$ is the vector of additive genetic random effects; $\mathbf{p}$ is the vector of permanent environmental random effects; $\mathbf{Z_1}$ and $\mathbf{Z_2}$ are the incidence matrices of additive genetic effects and permanent environmental effects, respectively; $\mathbf{e}$ is the vector of residuals, which were assumed to follow a normal distribution with homoscedastic variance (i.e., $\mathbf{e} \sim N(0, \mathbf{I}\sigma^2_e)$, where $\mathbf{I}$ and $\sigma^2_e$ are the identity matrix and residual variance, respectively).

To obtain estimates of genetic correlations among all analyzed traits, a multitrait model (Model II) was employed considering all the effects included in Model I and the maternal effect. The multitrait model is described in matrix form as:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Z_1a} + \mathbf{Z_2m} + \mathbf{Z_3p} + \mathbf{e} \quad (2)$$

where $\mathbf{y}' = [\mathbf{y}_1 \ \mathbf{y}_2 \ \cdots \ \mathbf{y}_n]$ is the vector of phenotypic observations, in which $\mathbf{y}_1$ is the sub-vector of dependent variable 1 (tick counts on one side of cattle body), $\mathbf{y}_2$ is the sub-vector of dependent of variable 2 (body weight gain from birth to weaning), and so on for all $n$ traits; $\boldsymbol{\beta}$, $\mathbf{a}$, $\mathbf{m}$, $\mathbf{p}$ and $\mathbf{e}$ are the vectors for all $n$ traits of fixed effects of contemporary group and covariates, of additive genetic effects, of maternal genetic effects, of permanent environmental effects (individual effect for tick count, and due to the dam effect for body weight gain from birth to weaning), and of residual effects, respectively, partitioned into subvectors for each variable in Eq. (2) similar to that presented for $\mathbf{y}$; $\mathbf{X}$ is the incidence matrix for fixed effects; and $\mathbf{Z_1}$, $\mathbf{Z_2}$ and $\mathbf{Z_3}$ are the incidence matrices of additive genetic effects, maternal genetic effects and permanent environmental effects.

The following assumptions associated with the sampling distribution of the data were considered in the more complete Model II:

$$\mathbf{y}|\boldsymbol{\beta}, \mathbf{a}, \mathbf{m}, \mathbf{p}, \mathbf{R} \sim N(\mathbf{X\beta} + \mathbf{Z_1a} + \mathbf{Z_2m} + \mathbf{Z_3p}, \mathbf{R}) \quad (3)$$

where $\boldsymbol{\beta}$, $\mathbf{a}$, $\mathbf{m}$, $\mathbf{p}$ and $\mathbf{e}$ are the positional parameters of observations conditional distribution; $\mathbf{R} = \mathbf{R}_0 \otimes \mathbf{I}$, where $\mathbf{I}$ and $\mathbf{R}_0\sigma^2_e$ are the identity matrix and residual variance matrix, respectively.