

Genetic Association Between Growth Traits And Tick Infestation In Nellore x Hereford Multibreed Cattle Population

D. R. Ayres^{*}, F.S. Baldi^{*}, A.B. Bignardi^{*}, V. M. Roso[†] and L. G. Albuquerque^{*,‡}

Introduction

Infestations by *Rhipicephalus (Boophilus) microplus* have a large negative impact on livestock production, decreasing animals performance, mainly due to loss of appetite, causing loss of weight even when high-quality diet is offered (Seebeck, R.M., Springell, O.H., and O'Kelly, J.C.O. (1971)). Moreover, increase costs associate with chemical control (drugs), management and labor. Also, considering the increasing alertness of chemical residues in meat products, alternate strategies to control external parasites are necessary (Prayaga (2003)). Among tick control methods, a low cost and environmental impact option would be the selection of resistant animals, i.e., those with ability to limit the number of ticks that survive to maturity (Utech, K. B. W., Wharton, R. H. and Kerr, J. D. (1978)). Usually, weight and weight gain are used as selection criteria in most of beef cattle breeding programs. However, little attention has been placed on tick infestation and its relationship with other economically important traits. For selection programs, accurate genetic parameter estimates have to be available. The aim of this study was to estimate genetic parameters for tick count and its association with growth traits in Nellore x Hereford multibreed cattle.

Material and methods

Records from animals belonging to the Braford Breeding Program - Conexão Delta G - were used. Animals were distributed in 19 herds of southern and midwestern Brazil and born from 1993 to 2008. Traits were: ticks count (TC), birth weight (BW), weaning weight (WW) and yearling weight (YW). The TC data were collected using the methodology proposed by Cardoso, V., Fries, L.A. and Albuquerque, L.G. (2000), consisting of tick counts located in groin areas (including the region located between the hind limbs of animals). Ticks count was transformed as: $LTC = \log_{10}(n+1)$, where n is the number of ticks counted on the animal. Contemporary groups for TC were defined as: year, season (December to February, March to May, June to August, and September to November) and herd of birth, sex, management group, and season of tick recording. Contemporary groups (CG) for weights sex. Weight records out of the range given by the mean of CG \pm 3 standard deviations and CG with less than 4 observations were excluded. The general structure of data set is presented in Table 1.

^{*} Department of Animal Science, FCAV/UNESP, Jaboticabal-SP, Brazil

[†] GenSys Consultores Associados S/S Ltda

[‡] CNPq and INCT-CA, São Paulo-Brazil

Table 1: Number of records, sires, dams and contemporary groups

Traits*	Records	Sires	Dams	GC
LTC	6,481	398	5,430	169
BW	42,170	817	22,690	1,532
WW	35,096	784	20,056	1,673
YW	15,260	663	10,761	1,925

* LTC=ticks count transformed; BW= birth weight; WW=weaning weight; YW=yearling weight

For all traits, the model included additive direct genetic effect as random. For BW and WW, maternal genetic and permanent environmental random effects were added. Fixed effects were CG and animal age (linear effect), dam age (linear and quadratic effects) were included as covariables. Moreover, for weights traits, linear effects of animal and maternal breed composition (in proportion of zebu breed, varying from 0 to 0.81) and individual and maternal heterozygosis were also considered. Maternal fixed effects and individual heterozygosis effect were not included in the LTC model. Covariance components were estimated by restricted maximum likelihood using multiple-trait animal model and Wombat package (Meyer (2006)). A pedigree file with a total 60,380 animals in the relationship matrix was used.

Results and discussion

For LTC, linear regression coefficient of animal breed composition was -0.34, indicating that the number of ticks decreased with the increasing in Nellore breed genes. These results agree with those reported by Prayaga (2003), Silva, A.M., Alencar, M.M., Regitano, L.C.A. *et al.* (2004) and D'andrea, L.A.B., Sartor, I.F., Madruga, C.R. *et al.* (2006) that indicated higher resistance of zebu breeds to external parasites such as ticks. Considering that the major problem for cattle production in the tropics is the high incidence of ticks, the resistance observed in Nellore breed is one of the main reasons for the dissemination of the Zebu in the tropics (Albuquerque, L.G., L, Mercadante, M.E.Z. and J.P. Eler (2006)). For weight traits, the maximum expression of individual and maternal heterosis was attained at yearling (34.7kg) and weaning (14.8 kg), respectively. The animal and maternal Nellore breed effects were negative for birth and yearling weight.

The covariance and genetic parameter estimates for LTC, BW, WW and YW, obtained by multiple-trait analysis are shown in Table 2. For LTC, the residual variance estimate was markedly higher than the additive genetic variance estimate, suggesting that the variation in this trait is mainly due to environmental differences. Similar results were described by Silva, A.M., Alencar, M.M., Regitano, L.C.A. *et al.* (2004) for crossbred beef cattle (0.15) in Brazil, counting the number of ticks in one side of animal. Budeli, M.A., Nephawe, K.A., Norris, D. *et al.* (2009), also found similar heritability estimates for tick count in Bonsmara cattle (0.17). The authors concluded that selection to tick resistance is feasible even though genetic progress may be slow. Working with crossbred Nellore x Hereford, Cardoso, V., Fries, L.A. and Albuquerque, L.G. (2000) compared different counting ticks methods (posterior areas, groin areas and one side of the animal), and obtained higher heritability estimates (0.46, 0.32 and 0.47) than those obtained in the present study. Also, Burrow (2001)

in Australia, working with Australian Belmont Red breed, reported high heritability estimates (0.42) for tick counts.

The direct heritability estimates for BW, WW and YW were moderate to high (Table 2), and agree with those from the literature (Burrow (2001); Meyer, K., Carrick, M.J. and Donnelly, B.J.P. (2003) and Boligon, A.A., Albuquerque, L.G., Mercadante, M.E.Z. *et al.* (2009)) indicating that these traits respond rapidly to individual selection. The genetic correlation estimates between weights at different ages and LTC were low and negative, suggesting long-term selection for increasing weight, after weaning, may result in a reduction of tick count. Burrow (2001) reported genetic correlation estimates between weights at different ages with LTC, and obtained correlation estimates close to zero. In dairy cattle, Jonsson, N.N., Matschoss, A.L., Pepper, P. *et al.* (2000) observed that selection to increase tick resistance in a Holstein–Friesian crossbred cattle population did not affect milk production.

Table 2: Estimates of variance, direct heritability (main diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal)

Traits*	LTC	BW	WW	YW
LTC	0.13±0.03	-0.12±0.12	-0.22±0.11	-0.20±0.12
BW	0.01±0.02	0.22±0.01	0.58±0.03	0.57±0.03
WW	0.005±0.02	0.26±0.00	0.40±0.02	0.94±0.01
YW	0.02±0.02	0.26±0.00	0.66±0.05	0.46±0.02
σ_a^2	0.02	3.50	183.23	376.26
σ_m^2	-	0.60	14.88	-
σ_p^2	-	0.11	54.84	-
σ_e^2	0.12	10.20	196.02	443.98

* birth weight = BW; weaning weight = WW; yearling weight = YW; ticks count = TC; σ_a^2 = direct additive genetic variance; σ_m^2 = maternal genetic variance, σ_p^2 = variance due to permanent environmental; σ_e^2 = residual variance.

The genetic correlation estimates between weights at different ages, (BW x WW), (BW x YW) and (WW x YW), were from moderate to high. Our results agree with most of the estimates reported in the literature for zebu breeds (Mercadante, M.E.Z., Lobo, R.B. and Reyes, A. (1995); Lôbo, R.B., Madalena, F.E. and Vieira, A.R. (2000) and Boligon, A.A., Albuquerque, L.G., Mercadante, M.E.Z. *et al.* (2009)).

Conclusion

Increasing the proportion of Nellore breed genes also increases animal tick resistance. Selection for tick resistance, using tick counts estimated breeding values, is feasible, even though genetic progress may be slow. Despite the genetic association between growth traits at different ages with LTC were low, favorable long-term correlated responses are expected.

Acknowledgements

This study was supported by the National Council of Technological and Scientific Development (CNPq – Brazil).

References

- Albuquerque, L.G., L, Mercadante, M.E.Z. and J.P. Eler (2006). In *Proc 8th WCGALP*, Brazil, Cd-Room.
- Boligon, A.A., Albuquerque, L.G., Mercadante, M.E.Z. *et al.* (2009). *Rev. Bras. Zootec.*, 37:596-601.
- Budeli, M.A., Nephawe, K.A., Norris, D. *et al.* (2009). *Sou. Afri. J. of Anim. Sci.*, 39:321-329.
- Burrow (2001). *Livest. Prod. Sci.*, 70:213-233.
- Cardoso, V., Fries, L.A. and Albuquerque, L.G. (2000). In *Proc 5th SBMA*, Brazil, Cd-Room.
- D'andrea, L.A.B., Sartor, I.F., Madruga, C.R. *et al.* (2006). *Pesqui. vet. Bras.*, 26:74-78.
- Jonsson, N.N., Matschoss, A.L., Pepper, P. *et al.* (2000). *Vet. Parasit.*, 89:297-305.
- Lôbo, R.N.B., Madalena, F.E. and Vieira, A.R. (2000) *Anim. Breed. Abstr.*, 68:433-462.
- Mercadante, M.E.Z., Lobo, R.B. and Reyes, A. (1995) *Arch. Lat-Amer. Prod. Anim.*, 3:45-89,.
- Meyer, K., Carrick, M.J. and Donnelly, B.J.P. (2003). *J. Anim. Sci.*, 71:2614-2622.
- Meyer, K. (2006). In *Proc 8th WCGALP*, Brazil, Cd-Room.
- Prayaga, K.C. (2003). *Aust. J. Agric.Res.*, 54:1027-1038.
- Seebeck, R.M., Springell, O.H., and O'Kelly, J.C.O. (1971). *Aust J Biol Sci* 24:839-50.
- Silva, A.M., Alencar, M.M., Regitano, L.C.A. *et al.* (2004). In *Proc 6th SBMA*, Brazil, Cd-Room.
- Utech, K. B. W., Wharton, R. H. and Kerr, J. D. (1978). *Aust. J. Agric. Res.*, 29:885-895.