

Genetic parameters for body weight, worm resistance, packed cell volume and FAMACHA[®] under natural infestation in Corriedale sheep

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Summary

Gastrointestinal parasites (GIP) are one of the main constraints for sheep production worldwide. In Uruguay, the most prevalent and pathogenic parasite is *Haemonchus contortus*. One approach to control parasite infection is to select genetically resistant animals into a breeding program. Faecal egg count (FEC) is the criterion mostly used to evaluate genetic resistance to GIP, although there are alternative indicators that could be used. The aim of the present study was to estimate genetic parameters for body weight, FEC, packed cell volume (PCV) and FAMACHA[®] score. To determine the possibility to include these traits in the genetic evaluation of GIP resistance, as complementary selection criteria to FEC. Data from 15,073 post-weaned lambs, the offspring of 343 rams, were recorded during a 16-year period from 2000 to 2015, from Uruguayan Corriedale stud flocks. A Bayesian analysis was performed to estimate genetic parameters, using a multivariate animal model including post-weaning body weight (BW), FEC, PCV and FAMACHA[®]. Heritabilities for these traits were of low to moderate magnitude (0.14 to 0.35). Genetic correlations (r_g) were close to zero for FAMACHA[®]-BW, low but favourable for FEC-BW (-0.12) and for FEC-PCV (-0.23), and moderate to high between PCV-BW, PCV-FAMACHA[®] and FEC-FAMACHA[®] (0.54-0.73). The high r_g between FEC-FAMACHA[®] estimated in the present study, indicate the possibility to complement both traits in order to select resistant and resilient animal to GIP. There would be an improvement not only at a genetic level but also for the environment and it would curb help to lead with the problematic situation of anthelmintic resistance.

Keywords: Haemonchus contortus, faecal egg count, heritability, genetic correlation

Introduction

Gastrointestinal parasitism is one of the most important diseases in sheep flocks worldwide, causing important economic losses (Perry *et al.*, 2002). *Haemonchus contortus* is the most predominant gastrointestinal parasite (GIP) genus present in Uruguay (Castells, 2009) and is also the most pathogenic, causing high morbidity and mortality rates in sheep flocks. It has been well documented that genetic resistance to GIP is a moderately heritable trait (Safari *et al.*, 2005; Bishop, 2012). In 1994, the National Genetic Evaluation (NGE) for the Corriedale breed was developed in Uruguay. Genetic resistance to GIP was included as a selection objective from the beginning. The selection criterion used as a proxy for parasite resistance is faecal worm egg count (FEC). The evaluation of animals for enhancing resistance to GIP is based on two faecal samples taken under natural mixed-species challenge, as is described by

50 Goldberg *et al.* (2011). As the evaluation of this trait is not mandatory for the
 51 Corriedale NGE, and since the protocol to recollect faecal samples and FEC
 52 measurements are laborious and is expensive for breeders, only approximately 10% of
 53 the stud flocks that participate in the NGE, have FEC expected progeny difference
 54 (EPD).

55 Although FEC has been the most used method to evaluate resistant animals to
 56 GIP, other indicator traits such as packed cell volume (PCV), eosinophil count,
 57 Immunoglobulin A (IgA) activity, fructosamine concentration, pepsinogen activity and
 58 the FAMACHA[®] score can be used; all indicative of resilience to GIP (Davies *et al.*,
 59 2005). FAMACHA[®] score enables clinical identification of anaemic sheep and goats
 60 based on a 5-point scale (Bath *et al.*, 1996).

61 The aim of the present study was to estimate heritabilities for and genetic
 62 correlations among body weight, FEC, FAMACHA[®] and PCV to determine the
 63 possibility to include these traits in the genetic evaluation of GIP resistance, as
 64 alternative selection criteria to FEC.

65

66 **Material and methods**

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68 Records from 15,073 lambs, the offspring of 343 rams, were collected during a 16-year
 69 period from 2000 to 2015, belonging to Corriedale studs flocks participating in the
 70 NGE and taking FEC records. The Rural Association of Uruguay (ARU) provided
 71 pedigree information and the Uruguayan Corriedale Breeders Society the performance
 72 and FEC data.

73 Phenotypes analysed were post-weaning body weight (BW), the first FEC
 74 corresponding to the protocol to evaluate the genetic resistance to GIP mentioned above
 75 (under natural mixed-species challenge), PCV and FAMACHA[®] score. The BW and
 76 FEC were recorded on average at 249±31 and 261±67 days of age, respectively. Blood
 77 extraction from the jugular vein to determine PCV was carried out at faecal sampling
 78 and was only measured in 2010 and 2011. FAMACHA[®] scores were recorded at the
 79 same time. were recorded at the same time. Larvae cultures were made for all samples
 80 and flocks to ensure that *Haemonchus contortus* was the most prevalent parasite.

81 Unlinked flocks, animals with unknown sires, contemporary groups with less than
 82 three observations or with fewer than two sires, and observations with more than three
 83 standard deviations outside the mean of the contemporary group, were deleted from the
 84 data set. For PCV, phenotypic data were discarded if values were <10% or >50%.

85

86 Faecal egg counts were transformed to $\log_e(\text{FEC}+100)$ to produce approximately
 87 normally distributed data. Covariance components were estimated fitting a multivariate
 88 animal model including BW, log transformed FEC, PCV and FAMACHA[®]. A Bayesian
 89 methodology was adopted for inference. The analysis was performed with the
 90 GIBBS2F90 computer package (Misztal *et al.*, 2002). After preliminary analysis, it was
 91 decided to run a single chain of 800,000 iterations. The first 400,000 iterations were
 92 discarded and the sampling interval was 20, so that a total of 20,000 samples were kept
 93 to estimates features of posterior distributions. The posterior mean, posterior standard
 94 deviation and the highest posterior density interval at 95% (95%HPD) of the estimated
 95 marginal posterior distribution were then calculated.

96 The full model was defined as:

$$97 \quad y = Xb + Za + e$$

98 where y is the record of the animal (BW, FEC, PCV or FAMACHA[®]), b , a and e were
 99 the vectors of the systematic effects, direct genetic effects and random residual effects,

100 respectively; and X and Z were the incidence matrices relating the respective effects to
 101 y . The systematic effects are the contemporary group (332 levels defined as flock-year-
 102 sex-management group), birth type (2 levels: single-born and multiple-born), dam age
 103 (3 levels) and age at recording in days as a covariate.

104

105 **Results and discussion**

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107 Summary statistics and data structure for the four traits analysed are presented in
 108 Table 1. The average FEC by FAMACHA[®] level was 443±741, 524±897, 1170±1794,
 109 1862±2786 and 2223±1907 eggs per gram, for score 1 (non-anemic), 2, 3, 4 and 5
 110 (severely anemic) respectively. In case of PCV the average was 37.4±3.4, 36.3±4.2,
 111 35.5±4.8, 33.2±6.0 and 27.1±7.4 %, respectively. The score five (severely anemic)
 112 included only 17 records. The values of PCV were higher than the cited by Bath et al.
 113 (1996) and with smaller differences between scores.

114

115 *Table 1. Descriptive statistics for post-weaning body weight (BW) and worm resistance*
 116 *traits (FAMACHA[®], packed cell volume (PCV) and faecal worm egg count (FEC)).*

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Trait	n	Mean	SD	Min	Max
BW (kg)	13,015	34.42	8.28	15	71
FAMACHA [®]	1,592	2.53	0.84	1.0	5.0
PCV (%)	2,242	35.39	4.71	10	50
FEC (log _e FEC)	14,850	6.61	1.24	4.61	10.13

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120 The estimates of direct heritability (h^2) and genetic correlations for BW, FEC,
 121 PCV and FAMACHA[®] score are shown in Table 2. The h^2 of BW was of moderate
 122 magnitude and similar than estimates reported by Riley & Van Wyk (2009) under
 123 moderate and peak worm challenge (0.35 and 0.32±0.07, respectively). Slightly lower
 124 estimates were reported in the review paper of Safari *et al.* (2005), where the direct h^2
 125 of post-weaning weight for dual-purpose breeds was 0.29±0.03 based on 23 different
 126 publications. They also reported estimates when maternal effects are included in the
 127 model, concluding that generally, a very small reduction in direct h^2 estimates is shown
 128 when maternal effects are included. Pollot *et al.* (2004) also estimated a lower h^2 than
 129 the present study in Merino sheep (0.19 and 0.25 for BW at 236 days and 279 days of
 130 age, respectively).

131

132 The h^2 of FEC was lower than most publications in literature, which values are in
 133 the range of 0.2 and 0.4 (Safari *et al.*, 2005). However, in agreement with the present
 134 study, Ciappesoni *et al.* (2010) estimated an h^2 of 0.18±0.02 in Merino sheep, whereas
 135 Cloete *et al.* (2007) estimated an h^2 of 0.18±0.03 for log transformed FEC and
 136 0.17±0.03 for cube root transformed FEC in South African Merinos. Slightly lower
 137 estimates were reported by Castells (2009) for the first FEC recorded according to the
 138 Uruguayan protocol in Corriedale sheep (h^2 0.15) and by Ngere *et al.* (2017) in Dorper
 sheep (h^2 0.10±0.03 and 0.13±0.04).

139 The h^2 of PCV was consistent with the reported of Snyman (2007) (0.17 ± 0.03)
 140 and slightly lower than those reported in most of the literature (Gauly & Erhardt, 2001;
 141 Riley & Van Wyk, 2009; Heckendorn *et al.*, 2017; Ngere *et al.*, 2017). Conversely,
 142 Thomas *et al.* (2016) estimated the h^2 in goats divergently selected for internal parasite
 143 resistance and found that it was close to zero (0.06 ± 0.04).

144 The h^2 of FAMACHA[©] score in the present study was similar to that reported by
 145 Snyman (2007) and by Thomas *et al.* (2016) in sheep and goats, respectively. Higher
 146 estimates were published by Heckendorn *et al.* (2017) in goats (0.22) and by Ngere *et al.*
 147 *et al.* (2017) in Dorper sheep (0.32-0.41). According to Riley & Van Wyk (2009), the
 148 additive genetic control of FAMACHA[©] score is different under different levels of
 149 severity of worm challenge, reporting estimates of h^2 varying between 0.08 ± 0.04 and
 150 0.24 ± 0.05 , obtaining the highest values at peak worm challenge data.

151

152 *Table 2. Estimated marginal posterior distributions statistics for genetic parameters for*
 153 *post-weaning weight (BW) and worm resistance traits (FEC, PCV and FAMACHA[©]).*
 154 *On the diagonal is the heritability, above and below the diagonal are the genetic and*
 155 *phenotypic correlations, with the posterior standard deviation in parenthesis () and the*
 156 *highest posterior density interval at 95% in brackets [].*

Trait	BW	FEC	PCV	FAMACHA [©]
BW	0.35 (0.03) [0.29;0.41]	-0.12 (0.08) [-0.26;0.03]	0.54 (0.18) [0.16;0.85]	-0.06 (0.19) [-0.41;0.31]
FEC	-0.04 (0.02) [-0.09;-0.002]	0.18 (0.02) [0.15;0.22]	-0.23 (0.17) [-0.56;0.08]	0.70 (0.12) [0.48;0.92]
PCV	-0.06 (0.06) [-0.17;0.05]	-0.24 (0.04) [-0.31;-0.17]	0.17 (0.05) [0.08;0.29]	-0.73 (0.08) [-0.87;-0.58]
FAMACHA[©]	-0.04 (0.05) [-0.15;0.05]	0.01 (0.04) [-0.07;0.08]	-0.20 (0.04) [-0.28;-0.12]	0.14 (0.04) [0.08;0.21]

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159 Body weight was favourably genetically correlated with FEC and PCV, while the
 160 genetic correlation (r_g) with FAMACHA[©] was close to zero and the 95% HPD interval
 161 included a wide range of possible values. In the review of Safari *et al.* (2005) the r_g
 162 between BW-FEC was higher than that reported in the present study (-0.24). Higher
 163 values were also reported by Pollot *et al.* (2004) and Castells (2009) (-0.32 ± 0.19 and
 164 -0.35 ± 0.06 in Merino and Corriedale sheep, respectively). Riley & Van Wyk (2009)
 165 published higher estimates than the present study for the r_g between FAMACHA[©]-BW.
 166 Under moderate worm challenge, r_g amounted to between -0.23 and -0.32, and under
 167 the peak worm challenge it was -0.43.

168 FEC was moderately and highly genetically correlated with PCV and
 169 FAMACHA[©], respectively. As expected, the r_g between PCV-FAMACHA[©] was also
 170 high. Riley & Van Wyk (2009) reported a r_g between FAMACHA[©]-PCV near to
 171 negative unity (-0.96 to -0.98). The r_g for FAMACHA[©]-FEC was also high (0.73 to
 172 0.85). However, these authors found a higher estimate for the r_g between FEC-PCV
 173 than that reported in the present study (between -0.80 and -0.83). Conversely, Thomas
 174 *et al.* (2016) using a trivariate repeated-records model and a small number of animals

175 (n=686), reported lower values for the r_g between FEC-FAMACHA[©] in goats
 176 (0.46±0.11), a r_g between FEC-PCV equal to zero but with a high standard error
 177 (0.00±7.71) and a very low r_g between FAMACHA[©]-PCV (-0.09±0.04). Heckendorn *et al.*, 2017)
 178 *et al.*, 2017) evaluated the potential of FAMACHA[©] and PCV to replace FEC as
 179 phenotypes for selecting goats resistant to GIP. Unfortunately, they showed low to zero
 180 genetic correlations with FEC concluding that at least, in situations with medium
 181 proportions of *Haemonchus spp.*, FAMACHA[©] scores and PCV are not suitable to serve
 182 as auxiliary traits to select for GIP resistance. The overall mean prevalence of
 183 *Haemonchus spp.* was approximately 50%, which might explain the rather weak
 184 relation of FAMACHA[©] with PCV and with FEC in their work.

185 As is shown in Table 2, phenotypic correlations (r_p) between traits were close to
 186 zero for most of the traits with the exception of the r_p between FEC-PCV and
 187 FAMACHA[©]-PCV which were low to moderate. Various authors found similar results
 188 for the r_p between BW and FEC (Pollot *et al.*, 2004; Safari *et al.*, 2005 and Castells,
 189 2009) (values between -0.05 to -0.10). Moreover, Heckendorn *et al.* (2017) estimated
 190 the r_p between FEC-PCV and FAMACHA-PCV close to those reported in the present
 191 study (-0.27±0.02 and -0.17±0.02 respectively). Conversely, Riley & Van Wyk (2009)
 192 published higher values for the r_p FAMACHA[©]-PCV (-0.58 to -0.64), FAMACHA[©]-
 193 FEC (0.75-0.80) and PCV-FEC (-0.56).

194

195 **Conclusions**

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197 The results of the present study indicate that there is considerable genetic variation in
 198 the four traits analysed, indicating the potential to make genetic progress in all traits.
 199 The FAMACHA[©] system offers a practical and low-cost phenotype as long as
 200 *Haemonchus contortus* predominates. The high r_g between FEC-FAMACHA[©] estimated
 201 in the present study, suggested the possibility to use both traits in order to select
 202 resistant and resilient animal to GIP. Since the reticence of sheep breeders in Uruguay
 203 to record this trait is low due to the laborious protocol that requires repeated measures,
 204 one option could be to record only one FEC and measure FAMACHA[©] score.

205 Nowadays, some studies are developed to evaluate a new protocol in Corriedale breed.
 206 In this way, it would be an improvement not only at a genetic level but also will have a
 207 greater impact in the environment and epidemiology of GIP. In addition, selection for
 208 resistance and resilience, would help deal with the problematic situation of anthelmintic
 209 resistance. Drenching only animals showing some grade of anaemia, could delay the
 210 development of anthelmintic resistance for new drugs or for those that yet have some
 211 percentage of efficacy, besides decreasing costs associated with treatment. Animals that
 212 require more frequent treatments should be culled from the flock.

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