



Is selection for resistance and resilience to *Haemonchus contortus* possible in Morada Nova sheep?

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ABSTRACT

Gastrointestinal nematodes (GIN) are a major constraint for sheep production. Selection of animals resistant to GIN infection is an effective and sustainable control strategy. In this study, the possibility of selection for resistance and resilience, as well as potential correlated responses, were evaluated. A total of 256 lambs and 123 ewes were submitted to two consecutive independent artificial infections with 4,000 infective larvae (L_3) of *Haemonchus contortus*. Records of faecal egg count (FEC), packed cell volume (PCV), and body weight (BW) were taken serially until day 42 after infection in both challenges. Estimates of genetic parameters were obtained for individual records (in lambs) and for overall traits (in lambs and ewes) using mixed models. Phenotypic and genetic correlations were estimated between traits in lambs, with genetic correlations being based on estimated breeding values (EBVs). In addition, correlations between FEC in lambs and FEC in ewes, as well as PCV in lambs and ewes, were calculated. Heritability estimates for FEC in the first and second parasite challenge were, respectively, 0.25 ± 0.18 and 0.46 ± 0.19 for lambs, and 0.00 ± 0.09 and 0.20 ± 0.16 for ewes. For PCV, heritability estimates were 0.23 ± 0.14 and 0.32 ± 0.16 for lambs and 0.13 ± 0.11 and 0.37 ± 0.18 for ewes. For the overall daily weight gain (DWG), the heritability estimate was 0.70 ± 0.21 . No significant genetic correlation was found between DWG and the other traits, while there was a negative genetic correlation between FEC and PCV (-0.70 ± 0.03). Genetic correlations of FEC and PCV between lambs and ewes were 0.36 ± 0.08 and 0.42 ± 0.08 , respectively. The results of the present study suggest that selection for low FEC, high PCV and high BW/DWG is possible in Morada Nova lambs. Furthermore, selection for low FEC should have a correlated response on PCV (leading to higher PCV), while no correlated response is expected on DWG. Selection for low FEC in lambs would, in future generations, lead to higher resistance of lambs and also of ewes. Simultaneous selection for all three traits is possible in Morada Nova lambs, which would increase performance, decrease losses due to parasite infection and reduce the need for anthelmintic treatments, with beneficial consequences regarding selection pressure on parasite populations and productivity.

1. Introduction

Haemonchus contortus, along with other gastrointestinal nematodes (GIN), threatens the productivity and sustainability of sheep farming systems. A high dependency of flock holders on the use of anthelmintics and the increasing prevalence of drug-resistant parasites highlight the

importance of alternative control strategies (Eady et al., 2003; Jackson et al., 2009; Veríssimo et al., 2012).

The selection of animals resistant to gastrointestinal nematodes has been successfully implemented in a variety of environments and production systems, with faecal egg count (FEC) being the most commonly used measure of resistance (Bisset et al., 2001; Goldberg

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et al., 2012; Brown and Fogarty, 2017). Animals selectively bred for low FEC require less anthelmintic treatments and have a lower risk of developing clinical nematodiasis (Bisset et al., 2001; Eady et al., 2003; Kemper et al., 2010). Also, reduced larval contamination of pastures can lead to higher weight gain (Bishop, 2012).

For many tropically adapted sheep breeds, high resistance and resilience to GIN infections have been reported (Baker and Gray, 2004). Even though native breeds are often considered to be “unproductive”, they can show a performance superior to that of commercial breeds in highly parasitized environments, due to genotype by environment interactions (Baker et al., 2004). The utilisation of adapted breeds, with concomitant selection for performance traits, could provide a productive and sustainable option for flock holders (Baker and Gray, 2004; Bishop, 2012).

The Morada Nova breed is a naturalized hair sheep breed which constitutes an important resource for smallholder flocks in the North-eastern region of Brazil. It is characterized by its small size, high adaptation to tropical climate, high prolificacy, non-existent reproductive seasonality, good maternal ability and excellent pelt quality, but also by low weight gain and carcass quality (Facó et al., 2008; Lôbo et al., 2011). High levels of resistance and resilience to GIN infections have been consistently related for this breed (Issakowicz et al., 2016; Toscano et al., 2019). Also, its ability as a maternal breed in meat production has been evidenced (Issakowicz et al., 2016). Therefore, the utilisation of this breed could be an option for farmers who face highly contaminated pastures and anthelmintic resistance.

In the present study, genetic parameters for FEC, packed cell volume (PCV) and weight gain (WG) were estimated in a Morada Nova sheep flock after artificial infection with *H. contortus* in order to investigate the possibility of selection for resistance, and to evaluate the relationship between resistance and performance in lambs.

2. Material and methods

2.1. Experimental animals and phenotypes

The experimental site –Embrapa Pecuária Sudeste (CPPSE) in São Paulo state, Brazil – is characterized by tropical climate, with a dry season typically occurring between May and September each year. Management practices and experimental design have been described in detail by Toscano et al. (2019). Briefly, data of 123 Morada Nova ewes and 256 lambs, born in 2017 and 2018, were recorded during two consecutive parasite challenges. Two age groups of lambs were formed each year, with animals of the same group being weaned and submitted to parasite challenges together. Lambs were kept on pasture with their dams until weaning at approximately 100 days of age, when individual FEC, packed cell volume (PCV) and body weight (BW) were recorded and animals were drenched with monepantel at 2.5 mg/kg body weight, in order to eliminate natural infection (confirmed by two FEC, 7 and 14 days after treatment). Fifteen days later (at day 0 of the first parasite challenge – d0-1) lambs were orally infected with 4,000 infective larvae (L_3) of *H. contortus*. Records of FEC, PCV and BW were taken serially during the first parasite challenge until day 42 after infection, when animals were drenched. After another fifteen days, animals were infected for the second time (d0-2), with subsequent monitoring of FEC, PCV and BW following the exact pattern of the first parasite challenge. Overall, 4 records of FEC (d21, d28, d35, d42), 3 records of PCV (d14, d28, d42), and 2 records of BW (d28, d42) were obtained during each parasite challenge. In 2018, the 123 Morada Nova ewes were also submitted to artificial infections, applying the same protocol used for lambs.

2.2. Statistical analysis

Phenotypic data of FEC and PCV from 256 lambs and 123 ewes were used for analyses. Records of BW were only considered in lambs, given that the ewe’s BWs remained relatively constant during the experiment, as they were not in a growing phase. Descriptive statistics for records of

Table 1

Descriptive statistics for faecal egg counts (FEC), packed cell volume (PCV), body weight (BW) and daily weight gain (DWG) in Morada Nova lambs (n = 256).

trait	recording	minimum	maximum	mean	sd	CV(%)
FEC	weaning	0	71350	6777	9319	137.51
	d21-1	0	19200	1876	3046	162.40
	d28-1	0	28100	5974	6063	101.50
	d35-1	0	46150	9010	8733	96.93
	d42-1	0	56100	8561	9351	109.22
	d21-2	0	22500	1375	2487	180.91
	d28-2	0	40000	3274	5082	155.20
	d35-2	0	81950	4473	7497	167.61
	d42-2	0	44050	4666	6420	137.61
	PCV	weaning	17	45	33.06	4.87
d14-1		29	49	36.60	2.92	7.99
d28-1		22	42	31.38	4.29	13.67
d42-1		20	41	31.20	4.11	13.17
d14-2		26	44	35.49	3.02	8.52
d28-2		19	45	33.09	4.35	13.16
d42-2		18	44	32.66	4.65	14.24
BW	weaning	8.0	24.5	15.83	2.99	18.88
	d28-1	10.9	32.8	20.32	3.83	18.85
	d42-1	10.9	35.3	21.15	4.14	19.57
	d28-2	12.0	40.0	24.17	4.58	18.94
	d42-2	10.0	40.3	24.51	4.74	19.33
DWG	DWG1	-0.04	0.19	0.093	0.037	39.27
	DWG2	-0.05	0.17	0.061	0.032	52.38
	totalDWG	-0.03	0.15	0.078	0.028	35.26

dxx-y = recording at day xx of the y-th parasite challenge; DWG1 = daily weight gain during first parasite challenge; DWG2 = daily weight gain during second parasite challenge; totalDWG = daily weight gain from weaning to the end of the second parasite challenge, CV = coefficient of variance.

Table 2

Descriptive statistics for faecal egg counts (FEC) and packed cell volume (PCV) in Morada Nova ewes (n = 123).

trait	recording	minimum	maximum	mean	sd	CV(%)
FEC	d-14	0	10350	1189	1696	142.74
	d21-1	0	1400	76	183	240.28
	d28-1	0	2600	93	323	349.42
	d35-1	0	10400	220	1060	482.27
	d42-1	0	21300	408	2108	516.30
	d21-2	0	2000	259	440	169.94
	d28-2	0	8400	357	924	258.95
	d35-2	0	9200	632	1398	221.33
	d42-2	0	11800	430	1284	298.47
	PCV	d-14	24	44	34.62	3.70
d14-1		30	44	36.33	2.72	7.49
d28-1		28	43	34.57	3.52	10.18
d42-1		23	43	34.19	3.46	10.11
d14-2		28	44	34.44	3.16	9.18
d28-2		28	43	34.55	3.16	9.16
d42-2		24	44	34.71	3.41	9.82

d-14 = recording under natural infection 14 days before first artificial infection; dxx-y = recording at day xx of the y-th parasite challenge; CV = coefficient of variance.

FEC, PCV, BW and DWG in lambs and FEC and PCV in ewes are presented in Table 1 and Table 2, respectively. FEC data showed very wide distributions and high coefficients of variance, as well as a positive skewness. A log-transformation ($\log_{10}(\text{FEC} + 25)$) was thus performed to achieve more symmetrical distributions. For lambs, daily weight gain (DWG) between weaning and the last day of the second challenge (totalDWG), and individually for each parasite challenge between days 0 and 42 (DWG1, DWG2), were calculated.

Preliminary analyses for model definition were conducted using the "R" software (R Core Team, 2018), applying a significance level of 0.05. Fixed effects were tested in a linear normal model (lm() function) for DWG and for analyses of individual sampling dates of FEC, PCV and BW. A linear mixed model (lme() function of the nlme package) with maximum

likelihood estimation (application of the anova() function on the respective models) was established when fixed effects were tested for analyses of repeated measurements of FEC and PCV. Fixed effects of sex, group (2 age groups per year, totalling 4 groups), birth type (single or twin), age of the dam (1–6), and first-order interactions were tested in lambs. Age at sampling and weight of the dam at birth were tested as covariates. For ewes, age was tested as a covariate. Whenever significant interactions between two fixed effects were detected, contemporary groups including both effects were used in genetic analyses.

For estimation of variance components and genetic parameters, the MTDFREML software was employed (Boldman et al., 1995). Univariate mixed animal models were implemented for analyses of DWG and individual sampling dates of FEC, PCV and BW. They were based on the formula: $y = Xb + Z1a + e$ Where y was a vector of the respective observed traits of animals, b , a and e were vectors of fixed effects, additive genetic effects and residuals, while X and $Z1$ where the respective incidence matrices for fixed and additive genetic effects.

Univariate animal models of repeated measures were applied using FEC and PCV of all sampling dates (AllRepFEC, AllRepPCV), and separately for sampling dates in the first (RepFEC1, RepPCV1) and second (RepFEC2, RepPCV2) parasite challenge using the formula: $y = Xb + Z1a + Z2pe + e$ Where y was a vector of the respective observed traits of animals, b , a , pe and e were vectors of fixed effects, additive genetic effects, permanent environment effects and residuals, while X , $Z1$ and $Z2$ where the respective incidence matrices for fixed, additive genetic effects and permanent environment effects. For ewes, only the repeated measures animal models for FEC and PCV were performed.

Phenotypic and genetic correlations were estimated between traits based on data of lambs and using Pearson's correlation. Genetic correlations were calculated using Estimated Breeding Values (EBVs) from analyses of lamb records, according to Lóbo et al. (2009). Genetic correlations between FEC in ewes and FEC in lambs were also analysed, using EBVs of 146 animals. The same was done for PCV, using EBVs of 147 animals. For most of these animals, EBVs for FEC and PCV as lambs were based on information of progeny, but 37 animals that were born in 2017 had records taken as lambs (in 2017) and as adults (in 2018).

3. Results

Estimates of genetic parameters for FEC, PCV, BW and DWG of lambs and for FEC and PCV of ewes are presented in Table 3 and Table 4, respectively. Heritability estimates for FEC and PCV under natural infection (at weaning in lambs and on day -14 in ewes) did not differ significantly from zero. During the first parasite challenge, estimates for FEC and PCV were low to moderate in lambs, while estimates of heritability in ewes were zero for FEC and low for PCV. During the second parasite challenge, heritability estimates for FEC and PCV were mostly low to moderate. (FEC: 0.31 ± 0.19 ; 0.15 ± 0.14 ; 0.26 ± 0.21 ; 0.29 ± 0.19 ; PCV: 0.27 ± 0.24 ; 0.78 ± 0.23 ; 0.24 ± 0.19). In lambs, the overall heritability estimates for FEC and PCV were higher for the second (FEC: 0.46 ± 0.19 ; PCV: 0.32 ± 0.16) compared to the first parasite challenge (FEC: 0.25 ± 0.18 ; PCV: 0.23 ± 0.14). Heritability estimates of BW and DWG were mostly high (BW: 0.94 ± 0.21 ; 0.89 ± 0.21 ; 0.68 ± 0.22 ; 0.88 ± 0.20 ; 0.80 ± 0.21 ; DWG: 0.70 ± 0.21 ; 0.39 ± 0.18 ; 0.44 ± 0.22). Standard errors for heritability estimates were generally high.

Phenotypic and genetic correlations between traits in lambs are presented in Table 5. The phenotypic correlation between FEC and BW at weaning was not different from zero, while the overall traits (FEC and DWG) showed a low negative correlation (-0.16 ± 0.06). During the first challenge, no significant correlation between FEC and BW was detected, while a low negative correlation was found for FEC and DWG (-0.17 ± 0.16). For the second parasite challenge, the opposite was found – FEC had a significant negative correlation with BW, but not with DWG. No significant genetic correlation was found between FEC and DWG or BW. The same was true for PCV and DWG or BW. For FEC and PCV, phenotypic and genetic correlations were negative and significant.

Table 3

Estimates (\pm standard error) of additive genetic variance (σ^2a), residual variance (σ^2e), permanent environmental variance (σ^2pe), heritability (h^2) and repeatability (t) for faecal egg count (FEC), packed cell volume (PCV), body weight (BW) and daily weight gain of Morada Nova lambs.

trait	recording	σ^2a	σ^2e	σ^2pe	h^2	t	
FEC	weaning	0.00	0.46		0.00 ± 0.07		
	overall trait	0.10	0.46	0.11	0.15 ± 0.10	0.31	
	challenge 1	0.19	0.26	0.29	0.25 ± 0.18	0.65	
	challenge 2	0.30	0.20	0.16	0.46 ± 0.19	0.70	
	d21-1	0.19	0.37		0.34 ± 0.28		
	d28-1	0.02	0.48		0.03 ± 0.08		
	d35-1	0.02	0.41		0.05 ± 0.09		
	d42-1	0.03	0.42		0.07 ± 0.12		
	d21-2	0.15	0.33		0.31 ± 0.19		
	d28-2	0.07	0.40		0.15 ± 0.14		
	d35-2	0.11	0.31		0.26 ± 0.21		
	d42-2	0.11	0.28		0.29 ± 0.19		
	PCV	weaning	0.87	14.19		0.06 ± 0.10	
		overall trait	2.34	14.29	1.13	0.13 ± 0.08	0.20
challenge 1		3.97	10.21	3.32	0.23 ± 0.14	0.42	
challenge 2		5.10	9.32	1.32	0.32 ± 0.16	0.41	
d14-1		3.07	5.73		0.35 ± 0.22		
d28-1		0.28	12.85		0.02 ± 0.07		
d42-1		1.99	10.98		0.15 ± 0.14		
d14-2		1.98	5.40		0.27 ± 0.24		
d28-2		12.14	3.42		0.78 ± 0.23		
d42-2		2.80	8.83		0.24 ± 0.19		
BW		weaning	7.70	0.45		0.94 ± 0.21	
		d28-1	12.20	1.57		0.89 ± 0.21	
		d42-1	10.34	4.87		0.68 ± 0.22	
		d28-2	17.15	2.42		0.88 ± 0.20	
	d42-2	16.50	4.14		0.80 ± 0.21		
DWG	totalDWG	0.0004	0.0002		0.70 ± 0.21		
	DWG1	0.0005	0.0008		0.39 ± 0.18		
	DWG2	0.0004	0.0005		0.44 ± 0.22		

dxx-y = analysis of records of day xx of the y-th parasite challenge; totalDWG = daily weight gain from weaning to the end of the second parasite challenge; DWG1/DWG2 = daily weight gain during first/second parasite challenge.

Table 4

Estimates (\pm standard error) of additive genetic variance (σ^2a), residual variance (σ^2e), permanent environmental variance (σ^2pe), heritability (h^2) and repeatability (t) for faecal egg count (FEC) and packed cell volume (PCV) of Morada Nova ewes.

trait	recording	σ^2a	σ^2e	σ^2pe	h^2	t
FEC	d-14	0.00	0.48		0.00 ± 0.17	
	overall trait	0.07	0.24	0.09	0.18 ± 0.14	0.40
	challenge 1	0.00	0.10	0.17	0.00 ± 0.09	0.63
	challenge 2	0.10	0.26	0.14	0.20 ± 0.16	0.48
PCV	d-14	0.00	13.93		0.00 ± 0.12	
	overall trait	2.65	7.14	1.68	0.24 ± 0.13	0.38
	challenge 1	1.42	7.14	2.66	0.13 ± 0.11	0.36
	challenge 2	3.98	5.16	1.55	0.37 ± 0.18	0.52

d-14 = analysis of records under natural infection 14 days before first artificial infection.

A significant genetic correlation was detected between the overall FEC in lambs and ewes (0.36 ± 0.08). For overall PCV between lambs and ewes it was 0.42 ± 0.08 .

4. Discussion

The overall heritability estimates for FEC in lambs (0.15 ± 0.10) and ewes (0.18 ± 0.14) are comparable to those found in the literature, which range from 0.15 ± 0.02 to 0.36 ± 0.09 (Brown and Fogarty, 2017; Aguerre et al., 2018; Li et al., 2019; Snyman and Fisher, 2019). Phenotypic analyses of the Morada Nova flock showed that animals could be categorized into a resistant, intermediate and susceptible group based on individual mean FEC. An increase of resistance parallel to the progression of the

Table 5

Phenotypic (r_p) and genetic (r_g) correlations (\pm standard error) at weaning, for overall traits, per challenge and on individual sampling dates, according to phenotypic values and estimated breeding values (EBVs), between the traits faecal egg count (FEC) and body weight (BW) or daily weight gain (DWG), packed cell volume (PCV) and BW or DWG, and FEC and PCV in Morada Nova lambs.

recordings	FEC and BW or DWG		PCV and BW or DWG		FEC and PCV	
	r_p	r_g	r_p	r_g	r_p	r_g
weaning	-0.00 \pm 0.06	-0.02 \pm 0.05	0.33 \pm 0.06 ¹	0.00 \pm 0.05	-0.39 \pm 0.06 ¹	-0.30 \pm 0.05 ¹
overall traits	-0.16 \pm 0.06 ¹	0.01 \pm 0.05	0.27 \pm 0.06 ¹	-0.05 \pm 0.05	-0.64 \pm 0.05 ¹	-0.70 \pm 0.03 ¹
challenge 1	-0.17 \pm 0.16 ¹	-0.02 \pm 0.05	0.17 \pm 0.06 ¹	-0.01 \pm 0.05	-0.64 \pm 0.05 ¹	-0.79 \pm 0.03 ¹
challenge 2	-0.05 \pm 0.06	-0.02 \pm 0.05	0.08 \pm 0.06	-0.06 \pm 0.05	-0.67 \pm 0.04 ¹	-0.73 \pm 0.03 ¹
d28-1	-0.07 \pm 0.06	0.01 \pm 0.05	0.17 \pm 0.06 ¹	0.00 \pm 0.05	-0.67 \pm 0.04 ¹	-0.85 \pm 0.03 ¹
d42-1	-0.07 \pm 0.06	0.04 \pm 0.05	0.29 \pm 0.06 ¹	0.01 \pm 0.05	-0.51 \pm 0.05 ¹	-0.48 \pm 0.04 ¹
d28-2	-0.14 \pm 0.06 ¹	0.02 \pm 0.05	0.37 \pm 0.05 ¹	-0.05 \pm 0.05	-0.59 \pm 0.05 ¹	-0.51 \pm 0.04 ¹
d42-2	-0.20 \pm 0.06 ¹	0.03 \pm 0.05	0.25 \pm 0.06 ¹	0.01 \pm 0.05	-0.61 \pm 0.05 ¹	-0.68 \pm 0.04 ¹

¹ Correlations significantly different from zero ($P < 0.05$).

experiment was shown in intermediate and susceptible lambs, for which a decrease in FEC was detected in the second compared to the first challenge (Toscano et al., 2019). Estimated genetic parameters indicate that this increase in resistance is based on genetic mechanisms, as the overall heritability of the first challenge (RepFEC1) was lower (0.15 ± 0.10 , 4–5 months old), than that of the second challenge (RepFEC2; 0.45 ± 0.19 , 6–7 months old). A drop in heritability in lambs after weaning (3 months (weaning): 0.20 ± 0.05 ; 4 months: (0.15 ± 0.05), Li et al., 2019); (3 months (weaning): 0.29 ± 0.01 , 8 months: 0.19 ± 0.01 , Brown and Fogarty, 2017) has been reported under natural mixed infection. After two artificial infections with *H. contortus*, however, Assenza et al. (2014) reported an increase in heritability (0.21 ± 0.06 first challenge (3 months) 0.55 ± 0.09 second challenge (4 months)), indicating that the rise in heritability could be due to exposure to the parasite, rather than an effect of age.

Despite a considerable level of infection (mean FEC of 6777), heritability of FEC at weaning was zero (0.00 ± 0.07). Given that significant heritability estimates of resistance were found in other breeds at three months of age (Brown and Fogarty, 2017; Li et al., 2019), it seems unlikely that Morada Nova lambs did not mount any genetically determined immunity at a similar age. A response that was equal to all individuals and therefore did not possess any genetic variation could be an explanation (Bishop et al., 1996)

Heritability estimates of PCV in lambs increased during the experiment, following a pattern similar to that of FEC, suggesting common underlying mechanisms of FEC and PCV. Estimates ranging from 0.12 to 0.39 were reported in literature (Vanimisetti et al., 2004; Lôbo et al., 2009; Oliveira et al., 2018). At weaning, under natural infection, when there was no genetic variation in FEC, estimates for heritability of PCV was also close to zero, indicating that genetic variation in PCV is caused by the animal's responses to parasites.

FEC and PCV heritability estimates in ewes increased over time, with estimates not being different from zero under natural infection. Higher estimates were found in the second, compared to the first challenge, similar to the situation in lambs. This is remarkable because adult animals are continually exposed to natural infection on pastures and show high levels of resistance and resilience in the face of this continuous exposure (Toscano et al., 2019). Rams artificially infected with *H. contortus* also had a higher heritability in a second ($0.35 \pm$

0.08) than in a first (0.14 ± 0.04) parasite challenge (Aguerre et al., 2018), but these animals were housed indoors, and had probably had little exposure to the parasite before the artificial infection. We conclude that there are response mechanisms to parasites in Morada Nova ewes under natural infection, but that they are largely common to all individuals and therefore do not show genetic variability. The artificial infection probably triggers an additional response, which is differently expressed among the animals.

The low precision of most estimates in this study could be explained by the relatively low number of animals evaluated, compared to other studies (Brown and Fogarty, 2017; Li et al., 2019; Snyman and Fisher, 2019). Other authors estimated genetic parameters using animal numbers comparable to those of the present study ($n = 200$ (Bishop et al., 1996); $n = 386$ (Vanimisetti et al., 2004); $n = 119$ (Lôbo et al., 2009)), one of which found high standard errors as well (Bishop et al., 1996), while Vanimisetti et al. (2004) reported p-values lower than 0.05. Lôbo et al. (2009) did not give standard errors or p-values. Using repeated measures models had a favourable effect on precision, with slightly lower standard errors.

The negative phenotypic correlations between FEC and PCV found in this study were stronger than those reported by Oliveira et al. (2018; -0.27 ± 0.03) and Lôbo et al. (2009; 0.28; positive correlation due to the use of transformed values for FEC values, which inverted the scale of data). Lôbo et al. (2009) and Aguerre et al. (2018) did not detect a significant genetic correlation between FEC and PCV, while Oliveira et al. (2018) found a correlation of -0.57 ± 0.12 . The negative genetic correlations found in the present study suggest that mechanisms controlling FEC and PCV under *H. contortus* challenge are predominantly the same.

Phenotypic and genetic correlations of resistance with performance should be accessed prior to selection, in order to estimate phenotypic effects of resistance on performance, as well as possible correlated responses. Phenotypic correlations estimated in this study showed that animals with high FEC had lower DWG during the first artificial infection (-0.17 ± 0.06). The subsequent negative correlation between FEC and BW during the second parasite challenge was most likely a result of the lower weight gain during the first challenge. In the second parasite challenge, however, DWG was not significantly influenced by FEC. An increased level of resilience could have occurred in the second compared to the first challenge, with lambs being able to maintain their growth rate despite infection levels. Genetic correlations between FEC and BW or DWG were not significantly different from zero, indicating that no correlated response on performance is to be expected in the case of selection for resistance.

The significant genetic correlation of FEC in lambs and ewes (0.36 ± 0.08) indicates that selection of animals based on FEC in lambs would not only lead to lower FEC in lambs of future generations, but also in future ewes. A similar situation was found for PCV, with a genetic correlation of 0.42 ± 0.08 between PCV of lambs and ewes. While Vanimisetti et al. (2004) found no significant genetic correlation of FEC between lambs and ewes, Goldberg et al. (2012) reported a high correlation of 0.81 ± 0.11 . One reason for these diverging results could be the physiological status of the animals: the study by Goldberg et al. (2012) was conducted on periparturient ewes, while Vanimisetti et al. (2004) used ewes infected 70 days after lambing. The correlation between FEC or PCV in lambs and ewes in the Morada flock investigated in the present study might be stronger during the periparturient phase of ewes.

Because of the very low heritability estimates of most FEC records taken during the first parasite challenge, the conduction of two parasite challenges is considered necessary for estimation of breeding values for FEC in the Morada Nova sheep flock. Furthermore, EBVs obtained from records of the second challenge (RepFEC2) are more informative than FEC of the overall model (AllRepFEC).

5. Conclusion

Although precision was low for estimates of genetic parameters in the present study due to restricted animal numbers, the estimates found were

in accordance with literature and our findings are therefore genuine. Selection for FEC, PCV and DWG under parasite challenge should thus be possible in lambs of the Morada Nova flock investigated. Selection for low FEC in lambs would lead to higher resistance of lambs and ewes in future generations. No evidence of a favourable or unfavourable correlated response of selection for FEC on BW or DWG was found. Thus, the genetic potential for performance would not be compromised. However, lower infection levels should be favourable to performance due to negative phenotypic correlations between these traits. Selection of animals more resistant and resilient to GIN would decrease the need for treatments and thus slow down the development of resistant parasites, while reducing costs, facilitating management and promoting sustainable production.

Ethical approval

All procedures were approved by the Embrapa Pecuária Sudeste Ethics Committee on Animal Experimentation (process no. 04/2017) and are in accordance with national and international principles and guidelines for animal experimentation adopted by the Brazilian College of Experimentation (CONCEA).

Declaration of Competing Interest

The authors declare that they have no conflict of interest.

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References

- Aguerre, S., Jacquet, P., Brodier, H., Bournazel, J.P., Grisez, C., Prévot, F., Michot, L., Fidelle, F., Astruc, J.M., Moreno, C.R., 2018. Resistance to gastrointestinal nematodes in dairy sheep: genetic variability and relevance of artificial infection of nucleus rams to select for resistant ewes on farms. *Vet. Parasitol.* 256, 16–23.
- Assenza, F., Elsen, J.M., Legarra, A., Carré, C., Sallé, G., Robert-Granié, C., Moreno, C.R., 2014. Genetic parameters for growth and faecal worm egg count following *Haemonchus contortus* experimental infestations using pedigree and molecular information. *Genet. Sel. Evol.* 46, 1–9.
- Baker, R.L., Gray, G.D., 2004. Appropriate breeds and breeding schemes for sheep and goats in the tropics. In: Sani, R.A., Gray, G.D., Baker, R.L. (Eds.), *Worm Control for Small Ruminants in Tropical Asia*. ACIAR Monograph 113, Canberra, Australia, pp. 63–95.
- Baker, R.L., Mugambi, J.M., Audho, J.O., Carles, A.B., Thorpe, W., 2004. Genotype by environment interactions for productivity and resistance to gastro-intestinal nematode parasites in Red Maasai and Dorper sheep. *Anim. Sci.* 79, 343–353.
- Bishop, S.C., 2012. Possibilities to breed for resistance to nematode parasite infections in small ruminants in tropical production systems. *Animal* 6, 741–747.
- Bishop, S.C., Bairden, K., McKellar, Q.A., Park, M., Stear, M.J., 1996. Genetic parameters for faecal egg count following mixed, natural, predominantly *Ostertagia circumcincta* infection and relationships with live-weight in young lambs. *Anim. Sci.* 63, 423–428.
- Bisset, S.A., Morris, C.A., McEwan, J.C., Vlassof, A., 2001. Breeding sheep in New Zealand that are less reliant on anthelmintics to maintain health and productivity. *N. Zeal. Vet. J.* 49, 236–246.
- Boldman, K., Kriese, L.A., Van Vleck, L.D., Van Tassel, C.P., Kachman, S.D., 1995. *A Manual for Use of MTDFREML: A Set of Programs to Obtain Estimates of Variance and Covariances (Draft)*. USDA, ARS, Lincoln, NE.
- Brown, D.J., Fogarty, N.M., 2017. Genetic relationships between internal parasite resistance and production traits in Merino sheep. *Anim. Prod. Sci.* 57, 209–215.
- Eady, S.J., Woolaston, R.R., Barger, I.A., 2003. Comparison of genetic and nongenetic strategies for control of gastrointestinal nematodes of sheep. *Livest. Prod. Sci.* 81, 11–23.
- Facó, O., Paiva, S.R., Alves, L.R.N., Lôbo, R.N.B., Villela, L.C.V., 2008. Raça Morada Nova: origem, características e perspectivas. *Embrapa Caprinos, Sobral, Brazil* 43 pp. <https://www.infoteca.cnptia.embrapa.br/bitstream/doc/191266/1/doc75.pdf>. (in Portuguese).
- Goldberg, V., Ciappesoni, G., Aguilar, I., 2012. Genetic parameters for nematode resistance in periparturient ewes and post-weaning lambs in Uruguayan Merino sheep. *Livest. Sci.* 147, 181–187.
- Issakowicz, J., Issakowicz, A.C.K.S., Bueno, M.S., Costa, R.L.D., Katiki, L.M., Geraldo, A. T., Abdalla, A.L., McManus, C., Louvandini, H., 2016. Parasitic infection, reproductive and productive performance from Santa Inês and Morada Nova ewes. *Small Rumin. Res.* 136, 96–103.
- Jackson, F., Bartley, D., Bartley, Y., Kenyon, F., 2009. Worm control in sheep in the future. *Small Rumin. Res.* 86, 40–45.
- Kemper, K.E., Palmer, D.G., Liu, S.M., Greeff, J.C., Bishop, S.C., Karlsson, L.J.E., 2010. Reduction of faecal worm egg count, worm numbers and worm fecundity in sheep selected for worm resistance following artificial infection with *Teladorsagia circumcincta* and *Trichostrongylus colubriformis*. *Vet. Parasitol.* 171, 238–246.
- Li, L., Brown, D.J., Swan, A.A., van der Werf, J.H.J., 2019. Genetic parameters for faecal worm egg count at different ages in Australian sheep under natural challenge. *Anim. Prod. Sci.* 59, 1201–1208.
- Lôbo, R.N., Vieira, L.S., Oliveira, A.A.D., Muniz, E.N., Silva, J.M.D., 2009. Genetic parameters for faecal egg count, packed-cell volume and body-weight in Santa Inês lambs. *Genet. Mol. Biol.* 32, 228–294.
- Lôbo, R.N.B., Pereira, I.D.C., Facó, O., McManus, C.M., 2011. Economic values for production traits of Morada Nova meat sheep in a pasture based production system in semi-arid Brazil. *Small Rumin. Res.* 96, 93–100.
- Oliveira, E.J., Savegnago, R.P., Freitas, L.A., Freitas, A.P., Maia, S.R., Simili, F.F., Faro, L., Costa, R.L.D., Santana Júnior, M.L., Paz, C.C.P., 2018. Estimates of genetic parameters and cluster analysis for worm resistance and resilience in Santa Inês meat sheep. *Pesqui. Agropec. Bras.* 53, 1338–1345.
- R Core Team, 2018. *R: a Language and Environment for Statistical Computing*. URL: R Foundation for Statistical Computing, Vienna, Austria. <https://www.R-project.org/>.
- Snyman, M.A., Fisher, A.D., 2019. Genetic parameters for traits associated with resistance to *Haemonchus contortus* in a South African Dohne Merino sheep flock. *Small Rumin. Res.* 176, 76–88.
- Toscano, J.H.B., Santos, I.B., Haehling, M.B., Giraldeho, L.A., Lopes, L.G., Silva, M.H., Figueredo, A., Esteves, S.N., Chagas, A.C.S., 2019. Morada Nova sheep breed: resistant or resilient to *Haemonchus contortus* infection? *Vet. Parasitol.* X 2, 100019.
- Vanimisetti, H.B., Andrew, S.L., Zajac, A.M., Notter, D.R., 2004. Inheritance of fecal egg count and packed cell volume and their relationship with production traits in sheep infected with *Haemonchus contortus*. *J. Anim. Sci.* 82, 1602–1611.
- Veríssimo, C.J., Niciura, S.C.M., Alberti, A.L.L., Rodrigues, C.F.C., Barbosa, C.M.P., Chiebao, D.P., Cardoso, D., Silva, G.S., Pereira, J.R., Margatho, L.F.F., Costa, R.L.D., Nardon, R.F., Ueno, T.E.H., Curci, V.C.L.M., Molento, M.B., 2012. Multidrug and multispecies resistance in sheep flocks from São Paulo state, Brazil. *Vet. Parasitol.* 187, 209–216.