GENETIC PARAMETERS FOR FAECAL EGG COUNT, FAMACHA© SCORE AND BODY CONDITION SCORE IN A DOHNE MERINO SHEEP FLOCK SUBJECTED TO HIGH LEVELS OF *HAEMONCHUS CONTORTUS*

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INTRODUCTION

Haemonchus contortus causes major losses among sheep in the summer rainfall regions in South Africa. For some areas, farming with animals resistant to nematode infestation seems to be the only solution in the long run. Genetic variation in resistance to nematode infestation in sheep, based on faecal egg count (FEC) as a criterion, has been reported for various breeds (Morris et al., 1996; Mugambi et al., 1997; Morris et al., 2000; Khusro et al., 2004; Yadav et al., 2006; Cloete et al., 2007; Alba-Hurtado & Muñoz-Guzmán, 2013; McManus et al., 2014). Successful breeding programs for resistance have been reported for Australian (Woolaston & Piper, 1996; Greeff et al., 2006) and New Zealand (Bisset & Morris, 1996; Morris et al., 2005) sheep. No reports on active breeding programs for resistance in South African sheep could be found.

The history of and recent selection practices followed in the Wauldby Dohne Merino flock (Fisher & Van Sittert, 2013; Fisher et al., 2015) makes it an ideal resource for research into host resistance to *H. contortus*.

LITERATURE REVIEW OF GENETIC PARAMETERS FOR RESISTANCE INDICATOR TRAITS

A summary of heritability estimates obtained from literature for Famacha© score (FAM), body condition score (BCS), FEC and Log transformed faecal egg count (LFEC) are presented in Table 1. Reported heritabilities estimated for FAM and BCS ranged from 0.08 ± 0.04 to 0.46 ± 0.08 and 0.17 ± 0.05 to 0.33 ± 0.08 respectively. Heritabilities estimated for untransformed FEC in literature ranged from 0.06 ± 0.03 to 0.35 ± 0.02 and from 0.00 ± 0.02 to 0.37 ± 0.00 for LFEC.

Table 1. Literature summary of heritability estimates for Famacha© score, body condition score, faecal egg count and Log transformed faecal egg count

Reference	Model	Species	Infection type	FEC (epg)	Heritability
Famacha© score					
Riley & Van Wyk (2009)	UNI	H. con.	NI	Low	0.13 ± 0.05
				Moderate	0.08 ± 0.04
				Peak	0.20 ± 0.06
Ngere (2015)	UNI	H. con.	NI		0.33 ± 0.03 to 0.37 ± 0.03
Cloete et al. (2016)	UNI	Tela spp. Trich spp.	NI		0.12 to 0.13
Alvarez et al. (2018)	Various	H. con.	NI		0.20 ± 0.07 to 0.35 ± 0.16
Ngere et al. (2018)	UNI & Sire	H. con.	NI	0 to 44000	0.18 ± 0.05 to 0.26 ± 0.08
	UNI & Sire	H. con.	NI	0 to 87000	0.23 ± 0.04 to 0.46 ± 0.08
Body condition score					
Riley & Van Wyk (2009)	UNI	H. con.	NI	Low	0.17 ± 0.05
				Moderate	0.26 ± 0.06
				Peak	0.33 ± 0.08
Vagenas & Bishop (2002)	BV		AI	0 to 1000	0.32 ± 0.02 to 0.35 ± 0.02
Matebesi-Ranthimo et al. (2014)	UNI 1	Tela spp. Trich spp.	NI	0 to 32700	0.10 ± 0.02
Mpetile et al. (2015)	UNI	Tela spp. Trich spp.	NI	0 to 27600	0.06 ± 0.03
Cube root transformed Faecal egg count					
Pollott et al. (2004)	REP	Trich spp. H. con.	NI	110 to 1000	0.28 ± 0.07
	Sire	Trich spp. H. con.	NI	110 to 1000	0.19 ± 0.08 to 0.60 ± 0.17
Mpetile et al. (2015)	UNI	Tela spp. Trich spp.	NI	0 to 27600	0.09 ± 0.04
Huisman et al. (2008)	UNI		NI		0.18 ± 0.07 to 0.40 ± 0.06
Khusro et al. (2004)	UNI		NI	0 to 51895	0.21 ± 0.02
	UNI		NI	0 to 53583	0.38 ± 0.03
Matebesi-Ranthimo et al. (2014)	UNI	Tela spp. Trich spp.	NI	0 to 32700	0.15 ± 0.01
Log transformed Faecal egg count					
Nieuwoudt et al. (2002)	REP	H. con.	NI	4.2 to 9.0 (66 to 8100)	0.24 ± 0.02
Baker et al. (2003)	Sire	H. con.	NI		0.01 ± 0.02 to 0.19 ± 0.07
	REP	H. con.	NI		0.00 ± 0.02 to 0.15 ± 0.05
Morris et al. (2004)	MV	Tela spp. Trich spp.	NI	87 to 3690	0.28 ± 0.02
	MV	Tela spp. Trich spp.	NI	96 to 3964	0.35 ± 0.02

Reference	Model	Species	Infection type	FEC (epg)	Heritability
Mpetile et al. (2015)	UNI	Tela spp. Trich spp.	NI	0 to 27600	0.10 ± 0.04
Riley & Van Wyk (2009)	UNI	H. con.	NI	8.65	0.19 ± 0.06
Morris et al. (2010)	Various	Tela spp. Trich spp.	NI		0.27 ± 0.01
Matebesi-Ranthimo et al. (2014)	UNI	Tela spp. Trich spp.	NI	0 to 32700	0.16 ± 0.02
Ngere (2015)	UNI	H. con.	NI		0.04 ± 0.02 to 0.05 ± 0.03
Benavides et al. (2016)	UNI	H. con.	NI	3.09 (1773)	0.37 ± 0.00
Cloete et al. (2016)	UNI	Tela spp. Trich spp.	NI		0.12 to 0.14
Mpetile et al. (2017)	MV	Tela spp. Trich spp.	NI	0 to 37200	0.07 ± 0.05
				0 to 14900	0.13 ± 0.04
				0 to 14300	0.19 ± 0.05
Alvarez et al. (2018)	Various	H. con.	NI		0.06 ± 0.08 to 0.23 ± 0.09

FEC = Faecal egg count;
Species: H. con. = *Haemonchus contortus*; Tela spp. = *Teladorsagia* spp.; Trich spp. = *Trichostrongylus* spp.;
Infection type: AI = Artificial infection; NI = Natural infection;
UNI = Univariate model 1; MV = Multivariate model; REP = Repeatability model; Sire = Sire model.

In Table 2, genetic correlations among FAM, BCS, FEC and LFEC obtained from literature are summarised. The correlations among these traits were generally favourable and moderate to high.

Table 2. Literature summary of genetic correlations among Famacha© score (FAM), body condition score (BCS), faecal egg count (FEC) and Log transformed faecal egg count (LFEC)

Trait	BCS	FEC	LFEC	FEC (epg)	Reference
FAM	-0.39 ± 0.22			Low	Riley & Van Wyk (2009)
	-0.55 ± 0.22			Moderate	
	-0.47 ± 0.16		0.85 ± 0.12	Peak	
FAM			0.66		Cloete et al. (2016)
FAM			0.25		Notter et al. (2017)
			0.31		
FAM			0.55 ± 0.05 to 0.79 ± 0.24		Alvarez et al. (2018)
FEC		0.82 ± 0.13			Ngere et al. (2018)
LFEC			0.86 ± 0.02		Morris et al. (2004)
LFEC			0.55 ± 0.30 to 0.89 ± 0.34	0 to 37200	Mpetile et al. (2017)

MATERIALS AND METHODS

The study was done on animals from a Dohne Merino flock kept at the farm Wauldby (27° 37' East, 32° 35' South) in the Stutterheim district in the Eastern Cape Province of South Africa. The selection practices and data collection procedures in the flock have already been documented (Fisher & Van Sittert, 2013; Fisher et al., 2015; Snyman & Fisher, 2018). The available faecal egg count (FEC), Famacha© score (FAM) and body condition score (BCS) data recorded on 1865 lambs over the seven year period from 2012 (2011-born lambs) until 2018 (2017-born lambs) were analysed. Between 9 and 12 two-weekly recordings of FEC were done over the years, which amounted to 20026 individual data records.

The project protocol was approved by the Ethical Committee of the Grootfontein Agricultural Development Institute (GVE/AP2/21). The study complied with relevant Animal Welfare legislation and generally accepted norms regarding animal care and welfare. The study was carried out under the auspices of the state veterinarian from the Queenstown Provincial Veterinary Laboratory, who is registered with the South African Veterinary Council.

Data on FEC were transformed to logarithms to the base of 10 (after adding 10 to each value to account for zero counts; LFEC) to normalise the data. The minimum, maximum, mean, standard deviation (SD), coefficient of variation (CV), as well as the influence of various non-genetic factors on FAM, BCS, FEC and LFEC for this dataset have been discussed by Snyman & Fisher (2018).

The following animal models were fitted using the ASReml program (Gilmour et al., 2014) to estimate variance components and genetic parameters for FAM, BCS and LFEC:

- Univariate models:
  - The average FAM, BCS and LFEC calculated from all recordings on each animal within each year.
  - The average of FAM, BCS and LFEC recorded at the 1st, 6th and 9th recordings calculated for each animal within each year (FAM169, BCS169 and LFEC169).
  - The average FAM, BCS and LFEC including 1 to 12 recordings respectively.

- Multivariate model:
  - Analysis including FAM, BCS and LFEC

- Repeatability models:
  - Dataset including the individual FAM, BCS and LFEC recordings over all the recording dates for each trait.

RESULTS

Variance components and genetic parameters estimated for FAM, BCS and LFEC with the different models are presented in Tables 3 to 5 respectively. The most suitable univariate model of analysis for FAM, BCS and LFEC was Model 1, including only direct additive genetic effects. This is in accordance with other literature findings summarised in Table 1.

Moderate heritabilities were estimated with univariate models for FAM, BCS and LFEC. Heritabilities obtained for FAM, BCS and LFEC averaged for the 1st, 6th and 9th recordings were much lower than the heritabilities obtained under univariate analyses where all available data were included.

Considering the genetic parameters for the resistance traits over 1 to 12 recordings, it is evident that direct heritability increased with 10% to 15% for all the traits when data from all 12 available recordings were included. Direct heritabilities estimated with repeatability animal models for all the traits were lower than those obtained with the univariate models. Repeatability for FAM was very low. Although the repeatability of BCS and LFEC was slightly higher, it was still low. Direct heritabilities estimated with multivariate models for all the traits were also lower than those obtained with the univariate models. Heritabilities estimated in this study are within the ranges reported in literature and summarised in Table 1 for FAM, BCS and FEC.

Table 3. Variance components and genetic parameters for Famacha© score (FAM) (Most suitable model indicated in bold)

Trait	**Model**	**h^2_a**	**h^2_m**	**c^2_{mpe}**	**c^2_{anim}**	**t**	**LogL**
Aver FAM	UNI 1	0.29 ± 0.05					**1997.53**
Aver FAM	UNI 2	0.28 ± 0.06		0.00 ± 0.00			1997.56
Aver FAM	UNI 3	0.25 ± 0.06	0.03 ± 0.02				1998.31
1st	UNI 1	0.06 ± 0.04					
6th	UNI 1	0.06 ± 0.04					
9th	UNI 1	0.09 ± 0.05					
FAM169	UNI 1	0.07 ± 0.03					
Univariate analyses of FAM including 1 to 12 recordings:							
1	UNI 1	0.06 ± 0.04					
2	UNI 1	0.08 ± 0.04					
3	UNI 1	0.10 ± 0.05					
4	UNI 1	0.10 ± 0.05					
5	UNI 1	0.12 ± 0.05					
6	UNI 1	0.08 ± 0.04					
7	UNI 1	0.06 ± 0.04					
8	UNI 1	0.13 ± 0.06					
9	UNI 1	0.14 ± 0.07					
10	UNI 1	0.16 ± 0.07					
11	UNI 1	0.17 ± 0.07					
12	UNI 1	0.21 ± 0.09					
FAM	REP	0.03 ± 0.01			0.07 ± 0.01	0.10 ± 0.01	
Aver FAM	MULTI	0.10 ± 0.01					

Aver FAM = The average FAM calculated from all recordings on each animal within each year.
FAM169 = The average of FAM recorded at the 1st, 6th and 9th recordings calculated for each animal within each year.
FAM = Individual FAM recordings.
UNI 1 / UNI 2 / UNI 3 = Univariate model 1 / 2 / 3; MULTI = Multivariate model including FAM, BCS and LFEC; REP = Repeatability model.
h^2_a = direct additive heritability; h^2_m = maternal additive heritability; c^2_{anim} = animal permanent environmental effect; c^2_{mpe} = maternal permanent environmental effect; t = repeatability; LogL = Log likelihood value.

Table 4. Variance components and genetic parameters for body condition score (BCS) (Most suitable model indicated in bold)

Trait	**Model**	**h^2_a**	**h^2_m**	**c^2_{mpe}**	**c^2_{anim}**	**t**	**LogL**
Aver BCS	UNI 1	0.29 ± 0.05					**2848.67**
Aver BCS	UNI 2	0.29 ± 0.02		0.00 ± 0.00			2848.67
Aver BCS	UNI 3	0.27 ± 0.02	0.00 ± 0.00				2848.81
1st	UNI 1	0.09 ± 0.04					
6th	UNI 1	0.20 ± 0.09					
9th	UNI 1	0.16 ± 0.05					
BCS169	UNI 1	0.18 ± 0.04					
Univariate analyses of BCS including 1 to 12 recordings:							
1	UNI 1	0.09 ± 0.04					
2	UNI 1	0.12 ± 0.05					
3	UNI 1	0.15 ± 0.05					
4	UNI 1	0.20 ± 0.06					
5	UNI 1	0.24 ± 0.06					
6	UNI 1	0.21 ± 0.06					
7	UNI 1	0.26 ± 0.06					
8	UNI 1	0.26 ± 0.06					
9	UNI 1	0.28 ± 0.07					
10	UNI 1	0.28 ± 0.08					
11	UNI 1	0.26 ± 0.07					
12	UNI 1	0.22 ± 0.08					
BCS	REP	0.11 ± 0.03			0.23 ± 0.02	0.34 ± 0.01	
Aver BCS	MULTI	0.13 ± 0.02					

Aver BCS = The average BCS calculated from all recordings on each animal within each year.
BCS169 = The average of BCS recorded at the 1st, 6th and 9th recordings calculated for each animal within each year.
BCS = Individual BCS recordings.
UNI 1 / UNI 2 / UNI 3 = Univariate model 1 / 2 / 3; MULTI = Multivariate model including FAM, BCS and LFEC; REP = Repeatability model.
h^2_a = direct additive heritability; h^2_m = maternal additive heritability; c^2_{anim} = animal permanent environmental effect; c^2_{mpe} = maternal permanent environmental effect; t = repeatability; LogL = Log likelihood value.

Table 5 Variance components and genetic parameters for log transformed faecal egg count (LFEC) (Most suitable model indicated in bold)

Trait	**Model**	**h^2_a**	**h^2_m**	**c^2_{mpe}**	**c^2_{anim}**	**t**	**LogL**
Aver LFEC	UNI 1	0.26 ± 0.05					**1173.36**
Aver LFEC	UNI 2	0.26 ± 0.05		0.00 ± 0.00			1173.36
Aver LFEC	UNI 3	0.26 ± 0.05	0.00 ± 0.00				1173.36
1st	UNI 1	0.17 ± 0.05					
6th	UNI 1	0.09 ± 0.04					
9th	UNI 1	0.10 ± 0.04					
LFEC169	UNI 1	0.14 ± 0.04					
Univariate analyses of LFEC including 1 to 12 recordings:							
1	UNI 1	0.17 ± 0.05					
2	UNI 1	0.20 ± 0.05					
3	UNI 1	0.20 ± 0.05					
4	UNI 1	0.20 ± 0.06					
5	UNI 1	0.19 ± 0.05					
6	UNI 1	0.11 ± 0.05					
7	UNI 1	0.12 ± 0.05					
8	UNI 1	0.21 ± 0.05					
9	UNI 1	0.22 ± 0.06					
10	UNI 1	0.23 ± 0.07					
11	UNI 1	0.23 ± 0.07					
12	UNI 1	0.27 ± 0.08					
LFEC	REP	0.11 ± 0.02			0.22 ± 0.02	0.33 ± 0.01	
Aver LFEC	MULTI	0.09 ± 0.01					

Aver LFEC = The average LFEC calculated from all recordings on each animal within each year.
LFEC169 = The average of LFEC recorded at the 1st, 6th and 9th recordings calculated for each animal within each year.
LFEC = Individual LFEC recordings.
UNI 1 / UNI 2 / UNI 3 = Univariate model 1 / 2 / 3; MULTI = Multivariate model including FAM, BCS and LFEC; REP = Repeatability model.
h^2_a = direct additive heritability; h^2_m = maternal additive heritability; c^2_{anim} = animal permanent environmental effect; c^2_{mpe} = maternal permanent environmental effect; t = repeatability; LogL = Log likelihood value.

Genetic and phenotypic correlations of average FAM, BCS and LFEC recorded over the entire recording period with FAM169, BCS169 and LFEC169 estimated with bivariate animal models, are summarised in Table 6. All genetic correlations between the corresponding traits were high and positive, ranging from 0.97 ± 0.10 for FAM to 0.98 ± 0.03 for BCS and LFEC. Moderate positive phenotypic correlations were obtained among the corresponding traits. Similar high positive genetic correlations ranging from 0.55 ± 0.30 to 0.89 ± 0.34 among various FEC and LFEC recordings of the same animals are reported in literature (Table 2).

Table 6. Genetic and phenotypic correlations of average FAM, BCS and LFEC with FAM169, BCS169 and LFEC169

	FAM169	**BCS169**	**LFEC169**
Genetic correlations			
FAM	0.97 ± 0.10		
BCS		0.98 ± 0.03	
LFEC			0.98 ± 0.04
Phenotypic correlations			
FAM	0.42 ± 0.02		
BCS		0.41 ± 0.02	
LFEC			0.45 ± 0.02

Covariance components and correlations among average FAM, BCS and LFEC estimated with multivariate analysis are summarised in Table 7. High favourable genetic correlations and moderate phenotypic correlation were estimated between FAM and LFEC, while moderate significant genetic correlations were estimated between BCS and LFEC. Similarly moderate to high positive genetic correlations ranging from 0.25 to 0.85 between FAM and FEC were reported in literature (Table 2).

Table 7. Genetic and phenotypic correlations among FAM, BCS and LFEC

	BCS	**LFEC**
Genetic correlation		
FAM	-0.39 ± 0.09	0.62 ± 0.08
BCS		-0.46 ± 0.09
Phenotypic correlation		
FAM	-0.15 ± 0.01	0.22 ± 0.01
BCS		0.05 ± 0.01

DISCUSSION

In this study, ongoing first stage selection was done by identifying animals unsuitable for selection on the basis of FAM and BCS. Identifying animals that required anthelminthic treatment according to FAM will ensure that only truly susceptible animals are identified and destined to be culled. Resilient as well as resistant animals will not be targeted and will remain untreated and available for final stage selection.

The highest heritability and repeatability of the resistance traits were recorded for BCS, but BCS had a moderate genetic and a low phenotypic correlation with LFEC. In this study, BCS of the lamb, in combination with FAM, was considered in the decision whether to treat the lamb or not. However, due to the low phenotypic correlation between BCS and faecal egg count, BCS of an animal by itself is not an accurate indication of the existing level of *H. contortus* infection. This confirmed the findings of Vatta et al. (2002) and Burke et al. (2007). By the time BCS is affected by *H. contortus per se,* the animal would have shown other clinical signs of Haemonchosis. This is in contrast to the positive role that body condition score can play as a practical and effective management tool for Targeted Selective Treatment (TST) strategies where *Trichostrongylus* spp. and *Teladorsagia circumcincta* are the main parasites (Cornelius et al., 2014). Furthermore, the role of BCS as selection criterion for resistance to *H. contortus* in growing lambs as used in the current study is not the same when compared to BCS as management tool for TST in adult ewes (Cornelius et al., 2014; Cornelius et al., 2015). The low phenotypic correlation estimated between BCS and LFEC in this study is also an indication that other factors apart from worm load influence BCS in growing lambs. Similar results were obtained by Burke et al. (2007). BCS had a moderate genetic correlation with LFEC, while a moderate favourable genetic correlation of -0.39 ± 0.09 was estimated between FAM and BCS in this study, which is in accordance with the correlations reported in Table 2.

The balance between the levels of resistance and resilience required in a specific flock depends on the level of anthelmintic resistance on the specific farm. On farms where anthelmintic resistance is already a severe problem and no anthelmintic susceptible strain exists, resistant animals would be preferable in an attempt to keep pasture contamination as low as possible. Resilient animals would just contaminate the pasture with worms resistant to anthelmintics. On farms with less severe anthelmintic resistance, it is important that a population of susceptible *H. contortus* be maintained. To achieve this, FAM could be used as management tool for identification of susceptible animals in the adult ewe flock for treatment, which will leave resilient animals untreated and thus contributing to maintain a population of susceptible worms in refugia (Burke et al., 2007). FAM has been used successfully as management tool for the identification of animals that need anthelmintic treatment (Kaplan et al., 2004; Burke et al., 2007; Molento et al., 2009; Arece-García et al., 2014; Pereira et al., 2016; Traoré et al., 2017). This practice reduces the number of animals that needs to be treated and subsequently saving anthelmintic treatment cost.

As far as the application of FAM as criterion for the selection of resilient or resistant sires and dams is concerned, it should be used in combination with other resistance indicators such as LFEC. Burke & Miller (2008) indicated that resilient/resistant sires can be identify by monitoring FAM of their offspring. During the high challenge summer rainfall period FAM will be recorded weekly or bi-weekly, therefore more FAM recordings will be available for inclusion in a final selection protocol. This will compensate for the low repeatability of FAM and the low heritability of FAM169.

Due to its favourable genetic correlations with FEC and the production traits, and the fact that BCS of the Not dosed lambs in this study was higher than BCS of the Dosed lambs (Snyman & Fisher, 2018), BCS could be included in the selection protocol to be used for selection against resistance to *H. contortus*. BCS and LFEC can be recorded at the beginning (January), at the peak (middle to end of March) and towards the end of the *H. contortus* season (June). Lambs that did not require any anthelmintic treatment up until selection age could be selected on the basis of a selection protocol incorporating these LFEC and BCS recordings, together with all the recorded FAM. The genetic parameters estimated for this flock will be used to design the most suitable selection protocol incorporating FAM, BCS and FEC for the selection of sires and dams resistant to *H. contortus* in Dohne Merino lambs.

As in the case of FAM and BCS, univariate model analysis of the average LFEC over the available number of recordings will be the most suitable model to apply when considering LFEC for inclusion in the final stage of selection for resistance against *H. contortus*.

CONCLUSIONS

Moderate heritabilities and genetic correlations were estimated for and among FAM, BCS and FEC in this study in a Dohne Merino flock subjected to high levels of anthelmintic resistant *H. contortus*. Except for the unfavourable genetic correlation with fibre diameter, no detrimental genetic correlations between the resistance and production traits were estimated. The genetic parameters estimated for this flock will be used to design the most suitable selection protocol incorporating FAM, BCS and FEC to be used for the selection of sires and dams resistant to *H. contortus* under South African conditions.

ACKNOWLEDGEMENTS

The authors wish to convey their sincere appreciation to Mr Robbie Blaine of the farm Wauldby for making his animals available for this project, and for him and the personnel at Wauldby for their valuable contribution in the execution of the project.

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