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GENETIC PARAMETERS AND BREED DIFFERENCES FOR OVINE TICK COUNTS ON INDIGENOUS AND COMMERCIAL SHEEP IN AUTUMN AND SPRING

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SUMMARY

This paper reports body-site specific and overall tick counts as assessed during either spring or autumn for Dorper, SA Mutton Merino (SAMM) and Namaqua Afrikaner (NA) ewes maintained on natural pasture in an arid area. There seem to be a shift in the tick population challenging the hosts from autumn to spring, posing the question whether tick count in spring is genetically the same trait as tick count in autumn. The unimproved, fat tailed, indigenous NA breed had lower tick counts on all body sites compared to the two commercial breeds, the exception being tick counts on the tail of NA ewes. The other breeds have docked tails and could thus not be assessed for this site. All body-site specific tick counts were heritable, both in autumn (range 0.26-0.42) and spring (range 0.15-0.41). Ticks counts in autumn and spring were genetically very similar traits (r_g>0.88). Overall and body-site specific tick counts were heritable and should respond to selection.

INTRODUCTION

Sheep farming is very important in the South African agrarian landscape since it allows the sustainable utilization of arid rural environments (Cloete *et al.* 2014). Sheep are parasitized by ticks throughout the world, with many tick species being of veterinary and economic importance. Some ticks introduce toxins that cause paralysis (Fourie *et al*. 1989); other species can be the cause of severe tissue damage, which either results from their longer mouthparts or a tendency to form clusters (Cloete *et al*. 2016). Ticks are also responsible for anemia and production losses (Norval *et al*. 1988). Ticks are also responsible for direct damage, such as skin or hide damage, damage to udders, teats and the scrotum of livestock (Norval 1983). A variety of factors such as host type, host age or tick inter- and intraspecific interactions can affect the preferential feeding sites of ticks.

Host resistance to pathogens can be used as a component in integrated pest control programs (Walker 2011). However, research on the genetics of tick resistance is very limited in sheep. Van Marle-Köster *et al.* (2015) suggested that adapted, indigenous genetic resources have advantages over imported breeds in their response to stressful conditions, including tick infestations.

The objectives of this paper were: 1) to determine whether the tick challenge of sheep differed between seasons (autumn and spring); 2) to derive heritability estimates for body-site specific and overall tick counts within seasons; 3) to estimate genetic and phenotypic correlations between body-sites and overall tick counts; 4) to derive genetic correlations of tick counts in autumn with those in spring to determine whether tick infestation in autumn and spring are genetically similar traits.

MATERIALS AND METHODS

The experiment was carried out at the Nortier Research Farm (32º02'S and 18º20'E) in the West Coast Strandveld area of the Western Cape Province of South Africa, using a genetic resource population described by Cloete *et al*. (2013; 2016). Ewes from the indigenous fat-tailed Namaqua Afrikaner (NA) sheep breed and two commercial breeds, the Dorper and South African Mutton Merino (SAMM), were compared under marginal, extensive conditions. The Dorper is the leading

South African meat breed while the SAMM is the leading South African dual-purpose (meat and wool) breed and both breeds contribute substantial numbers of weaning weight records to the small stock improvement programme (Cloete *et al*. 2014). The NA, in contrast, is characterised by low numbers and is maintained in a few conservation flocks (Qwabe *et al*. 2012). Previous studies suggested that NA ewes were more resistant to ticks than the other breeds (Cloete *et al*. 2013; 2016).

The climate of the experimental site is Mediterranean, with 78 % of the total long-term annual precipitation of 221 mm being recorded during winter (April–September). Dry, warm summers and cool winters with an unpredictable and variable rainfall characterises the study area. The vegetation is classified as Strandveld of the West Coast (Acocks 1988). The Dorper and the SAMM were tail docked as lambs, while the fat tails of the indigenous NA were left intact. Docking was done with rubber rings applied at the third palpable joint when the lambs were approximately three weeks old.

Ticks were counted in a detailed study involving species during autumn (May) and in spring (September) of 2012 (Trial 1). Ewes (n=73) were cast and a total of 2425 ticks were removed from these animals. The detached ticks were preserved in 70% ethanol and identified according to species. Apart from this detailed study on tick species, ticks were also counted in Trial 2 on all available ewes in the autumn of 2012, 2015 and 2016 as well as in the spring of all years from 2012-2016. The total number of repeated records amounted to 914 records of 358 ewes in spring and 535 records of 341 ewes in autumn. These counts were done without considering the tick species present on the animals. Ticks were counted at three locations: the head and front legs (HFL), udder and hind legs (UHL) and perineum, including the tail of NA ewes (PT) as was described by Cloete *et al*. (2013; 2016). These counts were also summed to obtain a total tick count for each animal (TOT). All ewes were maintained in a single flock except for a six week mating period during which the breeds were kept separate. Ewes were also randomly divided into smaller groups during lambing.

The frequencies at which the respective tick species occurred in Trial 1 was compared by Chi^2-procedures. Raw tick counts in Trial 2 were extremely variable (Table 1) and needed to be suitably transformed. Individual counts were therefore transformed to square roots after 0.5 were added to individual records to reduce the difference between counts to between 0 and 1 (Dickson and Sanford 2005). ASReml (Gilmour *et al*. 2015) was used to first identify significant fixed effects (ewe breed and ewe age) then to derive genetic parameters by fitting four-trait models to all available data in the autumn and spring. The same counts in autumn and spring were then analysed together in two-trait analyses to derive genetic correlations between seasonal counts. Animal permanent environmental effects were initially modeled together with animal additive effects. Based on Log likelihood ratios, only direct animal effects were retained in the final analyses. The pedigree file contained 2713 animals, the progeny of 40 sires and 596 dams. Ethical clearance was provided by the Departmental Ethical Committee for Research on Animals (approval number R13/88).

RESULTS AND DISCUSSION

Trial 1: Ticks from the three major species differed in proportions in autumn and summer. When expressed relative to the total number of ticks recovered, the contribution of *Rhipicephalus evertsi evertsi* amounted to 0.38 in autumn and 0.44 in spring (Chi^2=19.7; degrees of freedom=1; $P<0.01$). *R. gertrudae* were recovered at a substantially higher proportion in autumn (0.52) than during spring (0.19; Chi^2=274.1; degrees of freedom=1; $P<0.01$). Corresponding proportions for *Hyalomma truncatum* amounted to 0.11 and 0.37 respectively (Chi^2=249.8; degrees of freedom=1; $P<0.01$). These results suggested that the tick challenge during spring and autumn was different and potentially needed different coping strategies by the host animals.

Trial 2: Raw tick counts on individual ewes were extremely variable with standard deviations often exceeding the corresponding means (Table 1). The square root transformation normalised the distributions in terms of skewness and kurtosis and reduced the observed coefficients of variation to more manageable levels, ranging from 39.5% for TOT in autumn to 66% for HFL in spring.

Table 1. Descriptive statistics for the raw and transformed tick counts analysed on ewes in autumn (n=535) and spring (n=914), namely head-front leg tick count (HFL), udder-hind leg tick count (UHL), perineum-tail tick count (PT) and total tick count (TOT)

Season	Autumn			Spring		
Trait	**Raw mean ± s.d.**	**Range**	**Transformed mean ± s.d.**	**Raw mean ± s.d.**	**Range**	**Transformed mean ± s.d.**
HFL	10.4 ± 11.1	0 – 88	2.96 ± 1.46	5.1 ± 7.4	0 – 54	1.98 ± 1.46
UHL	11.7 ± 16.0	0 – 112	2.97 ± 1.83	8.6 ± 11.4	0 – 89	2.53 ± 1.64
PT	6.7 ± 7.6	0 – 50	2.37 ± 1.26	6.8 ± 7.4	0 – 61	2.39 ± 1.27
TOT	28.8 ± 25.6	0 – 216	5.03 ± 1.98	21.0 ± 17.5	0 – 126	4.23 ± 1.76

Backtransformed means for tick counts at the HFL and UHL sites of the commercial breeds exceeded those recorded in their NA contemporaries by at least a factor of 2 (P<0.01), both during autumn and spring (Table 2). NA ewes had higher (P<0.01) PT tick counts than the Dorper in both seasons, as well as SAMM ewes during spring. Breed differences were previously reported for tick count as well as for attachment site in sheep (Fourie and Kok 1995; Cloete *et al*. 2013; 2016). The latter authors attributed the higher tick counts at the PT site in the NA to the fact that their tails were left intact. Backtransformed means for TOT in the commercial breeds exceeded those of NA ewes by between 43 and 148% (All P<0.01), suggesting a greater resistance in the indigenous breed.

Table 2. Least-squares means (±s.e.) depicting breed[1] differences between the breeds assessed for head-front leg tick count (HFL), udder-hind leg tick count (UHL), perineum-tail tick count (PT) and total tick count (TOT) recorded either in the autumn or spring with backtransformed means in brackets

Season and breed	N	Trait			
		HFL	**UHL**	**PT**	**TOT**
Autumn		**	**	**	**
NA	204	2.15 ± 0.09 (4.1)	2.15 ± 0.10 (4.1)	2.79 ± 0.08 (7.3)	4.21 ± 0.10 (17.3)
Dorper	238	2.96 ± 0.08 (8.3)	3.33 ± 0.09 (10.6)	1.95 ± 0.07 (3.3)	5.03 ± 0.09 (24.8)
SAMM	76	4.39 ± 0.14 (18.8)	3.88 ± 0.16 (14.5)	2.77 ± 0.12 (7.2)	6.59 ± 0.16 (43.0)
Spring		**	**	**	**
NA	330	1.45 ± 0.07 (1.6)	1.73 ± 0.09 (2.5)	2.88 ± 0.07 (7.8)	3.72 ± 0.09 (13.3)
Dorper	451	2.46 ± 0.06 (5.6)	3.15 ± 0.08 (9.4)	2.00 ± 0.06 (3.5)	4.69 ± 0.08 (21.5)
SAMM	133	1.98 ± 0.11 (3.4)	3.32 ± 0.15 (10.5)	2.63 ± 0.11 (6.4)	4.82 ± 0.15 (22.7)

[1] Namaqua Afrikaner (NA), Dorper and South African Mutton Merino (SAMM)
** P<0.01

Significant genetic variation was detected for all body-site specific tick counts in four-trait analyses conducted in autumn and spring (Table 3). Genetic parameters were quite similar across seasons, except for PT tick counts, where the heritability was lower in spring. These results compared well with previous heritability estimates of 0.26 for HFL, 0.53 for UHL, 0.19 for PT and 0.43 for TOT (Cloete *et al*. 2016). Grøva *et al.* (2014) accordingly reported heritability estimates of 0.37-0.52 for TOT in Norwegian lambs under conditions where another tick species, namely *Ixodes ricinus*, prevails. HFL and UHL tick counts were highly correlated to TOT on the genetic level, as would be expected for traits in a part-whole relationship. These results were also consistent with those previously reported by Cloete *et al.* (2016). Genetic correlations between tick counts recorded in autumn and spring approached, and in some cases exceeded, unity for body-site specific values (Table 3). These preliminary results suggest that resistance to ticks in autumn and spring are

genetically very similar traits. Phenotypic correlations among traits were similar in sign as genetic correlations, but generally smaller in magnitude.

Table 3. (Co)variance ratios (± s.e.) for head-front leg tick count (HFL), udder-hind leg tick count (UHL), perineum-tail tick count (PT) and total tick count (TOT) recorded either in the autumn or spring based on four-trait or two-trait analyses

Component and trait	Trait			
	HFL	**UHL**	**PT**	**TOT**
(Co)variance ratios in autumn*				
HFL	**0.26 ± 0.07**	0.61 ± 0.15	0.17 ± 0.18	0.88 ± 0.08
UHL	0.20 ± 0.05	**0.39 ± 0.06**	-0.40 ± 0.14	0.81 ± 0.06
PT	0.04 ± 0.05	-0.19 ± 0.05	**0.30 ± 0.06**	0.18 ± 0.14
TOT	0.68 ± 0.05	0.68 ± 0.03	0.32 ± 0.04	**0.42 ± 0.06**
(Co)variance ratios in spring*				
HFL	**0.26 ± 0.04**	0.28 ± 0.11	0.10 ± 0.16	0.64 ± 0.08
UHL	0.20 ± 0.04	**0.41 ± 0.04**	-0.23 ± 0.14	0.85 ± 0.04
PT	0.07 ± 0.04	-0.11 ± 0.04	**0.15 ± 0.04**	0.17 ± 0.15
TOT	0.56 ± 0.03	0.74 ± 0.02	0.42 ± 0.03	**0.34 ± 0.04**
Correlations between tick counts in autumn and spring				
Genetic	0.89 ± 0.09	1.01 ± 0.02	1.00 ± 0.08	1.01 ± 0.04
Phenotypic	0.27 ± 0.05	0.48 ± 0.04	0.24 ± 0.04	0.45 ± 0.04

* Heritability in bold on the diagonal, genetic correlations above the diagonal and phenotypic correlations below the diagonal

CONCLUSIONS

The species composition of the tick challenge at the experimental site differed appreciably in species composition between autumn and spring. Notwithstanding this result, appreciable genetic variation in body site specific and total tick counts was present in both seasons. Moreover, genetic correlations between autumn and spring tick counts suggested that these traits were likely to be controlled by largely the same genes, a finding that needs to be verified in further studies.

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