### GENETIC AND ENVIRONMENTAL PARAMETERS OF MILK PRODUCTION AND MILK COMPOSITION IN SOUTH AFRICAN MERINOS

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## SUMMARY

Daily milk production, butterfat, protein and lactose contents as well as somatic cell counts were recorded for 1553 repeated lactation records derived from 427 grazing Merino ewes divergently selected for reproduction. Recordings involved the oxytocin technique, and were conducted ~3 or ~12 weeks post lambing. Five-trait heritability estimates were 0.10 for milk yield (MY), 0.37 for butterfat percentage (BF), 0.36 for protein percentage (PP), 0.38 for lactose percentage (LP) and 0.17 for somatic cell count (SCC). Animal permanent environmental effects amounted to 0.12 for MY. On a genetic level, MY was unfavourably related to BF (-0.18) and PP (-0.51), while the latter two traits were positively correlated (0.46). Further studies aim to assess milk traits in relation to offspring growth and ewe reproduction.

## INTRODUCTION

Milk production of ewes is expected to have a determining impact on the growth and survival of their lambs (Sawalha *et al.* 2005). The determination of milk production in grazing ewes is problematic and can only be done indirectly. This led to the application of a milk score in free-ranging ewes, as described by Ercanbrack and Knight (1998) and Sawalha *et al.* (2005). Alternatively, milk production of free-ranging ewes can be determined directly by the oxitocin technique, as described by Snyman and Cloete (2008) and Afolayan *et al.* (2009b), leading to fairly accurate estimates of actual milk production.

The oxytocin technique was used to estimate milk production of lactating, free-ranging Merino ewes in this study. Environmental factors affecting milk yield and milk composition were studied, while genetic parameters were derived for these traits.

### MATERIALS AND METHODS

Data were obtained from two lines of Merino sheep that were divergently selected from the same base population from 1986 to 2009, using maternal ranking values for number of lambs reared per joining. The procedure used for the selection of replacements has been described by Cloete *et al.* (2004). In short, male and female replacements in the High (H) line were descended from ewes that reared more than one lamb per joining (i.e. reared twins at least once). Replacements in the Low (L) line were descendants from ewes that reared less than one lamb per joining (i.e. were barren, or lost all lambs at least once). The reciprocal cross between the H line and L line was also available for the study period.

Once selected, ewes normally remained in the breeding flock for at least five joinings, except when exiting earlier because of death and mouth or udder malfunction. These lines were maintained on the Elsenburg Research farm near Stellenbosch in the Western Cape province of South Africa. The climate at the site and the management of the animals are described by Cloete *et al.* (2004). Ewes that lambed from 2005 to 2010 were used in this study. Based on previous work of Snyman and Cloete (2008), the ewes were evaluated twice during lactation, namely  $\sim$ 3 weeks after lambing (at 21.9±3.8 days) and  $\sim$ 12 weeks after lambing (84.0±4.7 days). Initially, ewes were separated from their lamb(s) before being injected with 10 IU oxytocin. After the

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injection, their udders were stripped by hand to ensure that their udders were empty. The ewes were then left in a pen, where they had access to a hammermilled lucern hay/oat hay mix and water. This procedure was repeated after 3 hours. Milk output were weighed and recorded individually, and representative milk samples were taken for analysis of butterfat (BF), protein (PP) and lactose (LP) percentages, as well as somatic cell counts (SCC). Daily milk yield (MY) was calculated as 3-hour milk yield multiplied by eight.

The ASREML program (Gilmour *et al.* 2002) was used for the estimation of (co)variance components in single-trait repeatability models at first, to be followed with a five-trait analysis to estimate genetic and environmental correlations among traits. Fixed effects (year, stage of lactation, selection line, number of lambs reared and ewe age) and significant interactions were included in operational models. Number of days in milk was included as a linear covariate, but was confounded with stage of lactation and excluded from the final analyses. The random terms of animal and animal permanent environment (PE) were added to analytical models sequentially. Likelihood Ratio tests were performed to assess the significance of the contribution of each random term to improvements in the model of analysis. Animal PE improved the model only in the case of MY. SCC was transformed to natural logarithms to ensure a normal distribution.

### **RESULTS AND DISCUSSION**

Descriptive statistics for the data are summarized in Table 1. The coefficient of variation (CV) for MY approached 50%, whereas the other traits (lactose % in particular) showed lower levels of variation. Comparable CV's ranged from 32 to 55% for MY, from 14 to 24% for BF, from 8 to 20% for PP (Legarra and Ugarte 2001; Othmane *et al.* 2002; Ligda *et al.* 2004; Afolayan *et al.* 2009a) and from 11 to 14% for log transformed SCC in sheep (Othmane *et al.* 2002; Ligda *et al.* 2002; Ligda *et al.* 2004). LP had a CV of 8% in the study of Afolayan *et al.* (2009a).

Table 1. Description of the raw data for daily milk yield, butterfat percentage, protein percentage, lactose percentage and the natural logarithm of somatic cell count

Trait	Number of records	Mean $\pm$ s.d.	Coefficient of variation
Milk yield (ml)	1553	$1128 \pm 544$	48.2
Butterfat %	1545	$7.94 \pm 1.86$	23.4
Protein %	1545	$4.93 \pm 0.85$	17.2
Lactose %	1545	$4.96 \pm 0.37$	7.5
Log of somatic cell count (n)	1545	$5.24 \pm 1.36$	26.0

Analysis of variance indicated that year significantly affected all traits, with the exception of LP (Table 2). Year effects depend on climate, husbandry and management influences, and are common in breeding research. However, such effects are unpredictable and transient, and are thus not presented or discussed in detail. MY recorded 3 weeks into lactation was 68% higher than 12 weeks into lactation, but BF and PP amounted only to 90% and 78% of those 12 weeks into lactation (all P < 0.01). In contrast, LP was higher after 3 weeks compared to 12 weeks into lactation. MY of sheep were shown to decline with test days in Chios dairy sheep, while BF and PP increased (Ligda *et al.* 2004). MY accordingly decreased by 21.2 g/day in crossbred ewes evaluated by Afolayan *et al.* (2009b). A reduction in MY with an increase in lactation length appeared to be fairly robust across genotypes and environments (Snyman and Cloete 2008). Selection line affected only MY, where H line ewes had a 17% higher MY than L line ewes, and a 15% higher MY than L x H line ewes (P < 0.05). H x L line ewes resembled H line ewes in this respect. The higher MY in H line ewes was not unexpected, as several studies related subjective milk score or an improved milk production to the number or weight of lamb weaned in sheep

(Ercanbrack and Knight 1998; Sawalha *et al.* 2005; Afolayan *et al.* 2009a). Multiple-rearing ewes produced 21% more milk than single-rearing ewes, but their BF concentration amounted to only 94% of that of single-rearing ewes (P < 0.01). Othmane *et al.* (2002) similarly reported a higher MY, lower BF and an unchanged PP and SCC in ewes rearing multiple lambs. MY, BF and PP as well as SCC generally increased with ewe age (P < 0.05). Othmane *et al.* (2002) similarly reported increases in milk production as well as BF and PP with age.

Table 2. Least squares means (±s.e.) depicting the effects of year, stage of lactation, selection group, number of lambs weaned and ewe age on milk yield (MY), butterfat percentage (BF) protein percentage (PP), lactose percentage (LP) and the natural logarithm of somatic cell count (SCC)

Effects and level			Traits		
	MY (ml)	BF (%)	PP (%)	LP (%)	SCC (n)
Year	**	**	**	0.12	**
Stage of lactation	**	**	**	**	0.15
3 weeks	1417±43	7.68±0.26	4.38±0.09	5.16±0.04	5.39±0.15
12 weeks	841±43	8.51±0.26	$5.59 \pm 0.09$	$4.69 \pm 0.04$	5.31±0.15
Selection group	*	0.54	0.63	0.87	0.99
H line	1218±49	8.16±0.30	5.06±0.10	4.94±0.05	5.37±0.17
L line	1040±67	7.80±0.41	4.87±0.14	4.91±0.07	5.32±0.22
L x H line	1057±60	8.27±0.34	5.02±0.12	4.91±0.06	5.37±0.19
H x L line	1200±59	8.17±0.32	4.97±0.11	4.95±0.05	5.32±0.19
Number of lambs weaned	**	**	0.21	0.45	0.85
Single	1021±40	8.33±0.25	5.01±0.09	4.93±0.04	5.34±0.14
Multiple	1237±47	7.87±0.27	4.96±0.09	4.92±0.05	5.36±0.16
Ewe age	**	**	*	0.24	**
2 years	970±49	7.79±0.29	4.86±0.10	4.91±0.05	5.12±0.16
3 years	1082±45	7.70±0.27	4.92±0.09	4.93±0.05	5.14±0.15
4 years	1187±46	7.87±0.27	4.94±0.09	4.95±0.05	5.22±0.15
5 years	1148±47	8.38±0.27	5.04±0.09	4.90±0.05	5.36±0.16
6 years	1204±52	8.39±0.28	5.05±0.10	4.94±0.05	5.49±0.17
7+ years	1182±61	8.47±0.31	5.07±0.11	4.93±0.06	5.75±0.19

\*\* - P < 0.01; \* - P < 0.05; Actual significance level for P > 0.05

Genetic parameters from the five-trait analysis are presented in Table 3. The heritability (h<sup>2</sup>) estimates derived from single-trait analyses were similar to those reported in Table 3 for BF, PP and LP, while yielded a marginally lower estimate of  $0.16\pm0.03$  for SCC. The magnitude of h<sup>2</sup> and c<sup>2</sup> was reversed in the single-trait analysis on MY, being respectively  $0.12\pm0.05$  and  $0.10\pm0.04$ . Estimates of h<sup>2</sup> ranged from relatively low for MY (0.10) and SCC (0.17) to high (> 0.35) for the percentage traits. The h<sup>2</sup> of MY in grazing ewes was accordingly estimated at 0.10 by Afolayan *et al.* (2009a). Afolayan *et al.* (2009b) reported the h<sup>2</sup> of MY in crossbred ewes at 0.10 after 21 days in lactation and at 0.24 after 90 days of lactation. Higher h<sup>2</sup> estimates, ranging from 0.20 to 0.35 for MY, were found in dairy sheep (Legarra and Ugarte 2001; Othmane *et al.* 2002; Ligda *et al.* 2004). Estimates of h<sup>2</sup> for BF were variable, ranging from 0.10 to 0.21 (Legarra and Ugarte 2001; Othmane *et al.* 2002; Ligda *et al.* 2004; Afolayan *et al.* 2009a). Corresponding h<sup>2</sup> estimates for PP (0.26 to 0.38) are in good agreement with the present estimate, while Afolayan *et al.* (2009a) reported a h<sup>2</sup> of 0.23 for LP. The present estimate of h<sup>2</sup> for SCC (0.17) is marginally higher than previous estimates of 0.11 (Othmane *et al.* 2002) and 0.14 (Ligda *et al.* 2004).

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Table 3. Estimates of the phenotypic variance  $(\sigma_p^2)$ , heritability  $(h^2)$ , animal permanent environment  $(c^2)$ , genetic correlations  $(r_g)$  and environmental correlations  $(r_e)$  for milk yield (MY), butterfat percentage (BF) protein percentage (PP), lactose percentage (LP) and the natural logarithm of somatic cell count (SCC)

Component, ratios			Trait			
and traits	MY (ml)	BF (%)	PP (%)	LP (%)	SCC (n)	
$\sigma_{p}^{2}$	22798	3.315	0.4067	0.0931	1.809	
$h^2$	0.10±0.05	0.37±0.03	0.36±0.03	0.38±0.03	$0.17 \pm 0.03$	
$c^2$	0.12±0.04	-	-	-	-	
Correlations ( $r_g$ above the diagonal and $r_e$ below the diagonal)						
MY (ml)		-0.18±0.15	-0.51±0.16	0.07±0.15	0.35±0.18	
BF (%)	-0.06±0.03		$0.46 \pm 0.07$	-0.27±0.08	0.03±0.11	
PP (%)	-0.16±0.03	0.26±0.03		-0.43±0.07	$0.15 \pm 0.11$	
LP (%)	0.22±0.03	-0.38±0.02	-0.51±0.02		-0.49±0.09	
SCC (n)	-0.10±0.03	0.01±0.03	0.14±0.03	-0.33±0.03		

The genetic correlation of MY with PP was negative (Table 3). Corresponding correlations with MY ranged from -0.35 to -0.56 for BF, and from -0.10 to -0.64 for PP (Legarra and Ugarte 2001; Othmane *et al.* 2002; Ligda *et al.* 2004). PP was positively correlated with BF, which is consistent with corresponding correlations ranging from 0.41 to 0.85 in the literature (Legarra and Ugarte 2001; Othmane *et al.* 2002; Ligda *et al.* 2004). Both BF and PP was negatively correlated with LP. SCC tended to be positively related to MY, while the correlation of SCC with LP was negative. Genetic correlations of milk traits with SCC were correspondingly low in the literature (Legarra and Ugarte 2001; Othmane *et al.* 2002). Phenotypic correlations generally resembled genetic correlations in sign, but were mostly smaller in magnitude.

#### CONCLUSIONS

Lactation traits of grazing Merino ewes were heritable and variable. The relationships of these traits with lamb weight and ewe reproduction traits still need to be ascertained in South African flocks. The higher MY of H line ewes compared to their L line contemporaries (which is known to have a markedly poorer reproduction) may suggest a favourable genetic relationship of MY with reproduction, as was reported in literature cited.

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