Heritability estimates for slaughter traits in South African terminal crossbred lambs

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Abstract

Data of between 580 and 1160 terminal crossbred lambs bred at three localities were used to estimate genetic parameters for the following slaughter traits: slaughter age, dressing percentage, fat depth at the 13th rib and between the 3rd and 4thth lumbar vertebrae, 25 mm from the midline. Meat quality traits included colour measurements, Warner-Bratzler tenderness and meat pH 24 hours post mortem. The data were derived from crosses between 7 ram breeds and 5 ewe breeds/lines. Six rams were transferred between localities to facilitate genetic ties. The data were assessed by a sire model, with the sire and the permanent environment of the dam as random factors. Direct heritability ($h^2 \pm$ s.e.) were 0.45 ± 0.16 for slaughter age, 0.20 ± 0.09 for dressing percentage, 0.11 ± 0.08 (13th rib) and 0.13 ± 0.08 (between the 3rd and 4th lumbar vertebrae) for fat depths. Estimates of h^2 for meat quality traits amounted to 0.45 ± 0.19 for L*, 0.04 ± 0.10 for a*, 0.21 ± 0.14 for b*, 0.44 ± 0.18 for Warner-Bratzler tenderness and 0.09 ± 0.09 for pH 24 hours post mortem. Dam permanent environment only affected slaughter age (0.06 ± 0.06) and fat depth between the 3rd and 4th lumbar vertebrae (0.04 ± 0.05). Some meat attributes were heritable and worthy of consideration in a selection programme.

Introduction

A lack of stability in the wool price has resulted in meat becoming more important in the South African meat industry (Olivier, 1999). This has lead to a change in the selection strategy of Merinos, as well as other wool and dual-purpose breeds. The same change has taken place in the Australian sheep industry over the past decade (Swan *et al*., 2007). However, despite the importance of meat, little research effort has been focused on the genetic improvement of meat quality traits. In the comprehensive review of Safari *et al*. (2005) on genetic parameters in sheep, meat quality traits were generally represented by five or less heritability estimates in the literature. This situation also seems to apply to the South African sheep industry, as no local papers quoting heritability estimates for meat quality traits could be found. Clearly the lack of reliable estimates of the genetic variation in slaughter traits is unacceptable, and needs to be addressed.

Against this background, analyses were conducted to derive heritability estimates for meat quality traits in crosses between common South African sheep breeds. Since limited data were available for this purpose, estimates should be regarded as preliminary.

Material and methods

Experimental animals used in the study were derived from three terminal crossing experiments involving South African sheep breeds. The experiments were carried out at the Nortier, Langgewens and Tygerhoek research farms in the Western Cape. All experiments were adequately described in the literature, and only brief information pertaining to experimental outlay and the breeds involved will be provided in this paper.

The experiment at Nortier involved the utilisation of the Dorper as ewe line in terminal crosses with Ile de France, Merino Landsheep and SA Mutton Merino rams during the period from 2000 to 2001. Purebred Dorper rams were also used as a control. This experiment are described by Cloete *et al*. (2007), and sought to improve the propensity of purebred Dorpers to lay down fat at an early age by terminal crossbreeding with leaner breeds. At Langgewens, five Merino type ewe lines (SA Mutton Merino, Dohne Merino, SA Mutton Merino x Merino and specialist Merino lines selected either for fleece weight or for reproduction) were evaluated in a terminal crossbreeding situation with Dormer and Suffolk sires. The experiment was conducted during the period from 1999 to 2002, and was described by Cloete *et al*. (2003; 2004). The Tygerhoek study involved the using of Merino ewes as a dam line in a terminal crossbreeding experiment with Dormer, Dorper, Ile de France, Merino

Landsheep and Suffolk rams. Purebred Merino progeny were also produced to serve as a control treatment as described by Cloete *et al*. (2006).

Four common sires with an average (± s.d.) number of progeny of 29 ± 4 linked the Nortier and Tygerhoek localities. Two common sires with respectively 85 and 45 progeny linked the Langgewens and Tygerhoek localities. The difference in the number of progeny between the latter two sires can be ascribed to the fact that one link sire was used for two years at Langgewens, thus yielding more progeny at that locality. The traits that were recorded at all three localities were slaughter age (it was attempted to slaughter animals at a fixed weight at all three locations), dressing percentage, the lightness (L*), redness (a*) and yellowness (b*) colour measurements, instrumental tenderness using the Warner-Braztler test, and fat depth at two sites (at the 13th rib and between the 3rd and $4th^{th}$ lumbar vertebrae, 25 mm from the midline). The tests used were previously described in the literature (Cloete *et al*., 2005).

All sires were from different, unrelated flocks, while pedigree information was not known for at least some ewes at all three localities. Without adequate familial linkages, it did not seem advisable to fit the traditional animal model for the computation of direct and maternal heritability estimates. ASREML software (Gilmour *et al*., 2006) was used to fit a sire model to the data, while the permanent environmental effect of the dam was added as an additional random factor. Log Likelihood ratios were used to test the respective models for significance, and only significant random effect were retained in the final analyses. Seeing that the data structure did not allow the partitioning of the direct genetic component from the permanent environment of the dam, the former variance component was subtracted from the latter when significant (Gilmour *et al*., 2006). Heritability was estimated as four times the sire variance, expressed as a ratio of the overall phenotypic variance (Gilmour *et al*., 2006).

Results and Discussion

The number of observations ranged from 580 to 1160 for the respective traits (Table 1). Most traits had coefficients of variation (CV) that exceeded 10%, as was also reported by Greeff *et al*. (2005). The exceptions were dressing percentage (CV = 9.9%), instrumental lightness (CV = 7.3%) and pH (CV = 2.7%). The distribution of most traits was normal. In cases where the distributions deviated from normality, it was due to skewness rather than kurtosis. Analysis was thus continued, as suggested by Glass *et al*., (1972).

Table 1. Descriptive statistics and direct and maternal heritability estimates for slaughter traits of crossbred lambs born at the Langgewens, Nortier and Tygerhoek experimental farms

Trait	Descriptive statistics				Variance ratios	
	Number of observations	Mean (s.d.)	Skewness	Kurtosis	Direct	Dam PE
Slaughter age (days)	1160	203 ± 77	0.64	-0.59	0.45 ± 0.16	0.06 ± 0.06
Dressing percentage (%)	1144	40.4 ± 4.0	0.21	0.06	0.20 ± 0.09	n.a.
Quality traits:						
Lightness (L*)	580	36.9 ± 2.7	0.73	1.70	0.45 ± 0.19	n.a.
Redness (a*)	580	13.0 ± 2.3	2.00	6.58	0.04 ± 0.10	n.a.
Yellowness (b*)	580	8.88 ± 1.54	1.30	5.50	0.21 ± 0.14	n.a.
Shear force (Newton)	586	99 ± 41	0.44	-0.62	0.44 ± 0.08	n.a.
pH_{48h}	672	5.59 ± 0.15	0.46	1.37	0.09 ± 0.09	n.a.
Fat depth (mm)						
13th rib	1042	1.77 ± 1.20	1.78	5.27	0.11 ± 0.08	n.a.
6th Lumbar vertebrae	1042	2.29 ± 1.44	1.32	2.11	0.13 ± 0.08	0.04 ± 0.05

n.a. – not applicable

The size of the data set did not support the estimation of accurate genetic parameters with low standard errors. However, there were significant genetic variation (estimates larger than twice the corresponding standard errors)

for slaughter age, dressing percentage, lightness and tenderness. The dam permanent environmental variance ratio was below 0.10 for cases where it was significant.

Comparable heritability estimates averaged by Safari *et al*. (2005) from the literature were 0.42 for dressing percentage (three literature values), 0.16 for lightness, 0.04 for redness, 0.05 for yellowness and 0.18 for pH (all based on two literature values). The heritability of carcass fat depth was 0.30 at the C site (six literature values) and 0.32 at the GR site (three literature values). Subsequent heritability estimates reported by Greeff *et al*. (2005) were 0.04 for lightness, 0.03 for redness, 0.02 for yellowness, 0.18 for pH, 0.41 for fat depth at the C site and 0.27 for fat depth at the GR site. The latter authors contended that sustained genetic progress in pH (low phenotypic variation) and colour traits (low heritability) was unlikely in their population of Merino rams.

Conclusions

The preliminary heritability estimates reported here suggest that some meat quality traits may indeed respond to selection. However, the size of the data set precluded the estimation of accurate genetic parameters. Further research on the genetic basis of meat traits is therefore indicated.

Acknowledgements

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