

GENETIC PARAMETERS FOR BREECH STRIKE INDICATOR TRAITS AND YEARLING PRODUCTION TRAITS IN MERINOS

A.J. Scholtz^{1,2}, S.W.P. Cloete^{1,3}, J.J.E. Cloete^{3,4}, A.C.M. Kruger¹, J.B. van Wyk⁵ and T.C. de K. van der Linde⁶

¹Institute for Animal Production: Elsenburg, Private Bag X1, Elsenburg 7607, South Africa.

²Centre for Sustainable Agriculture and Rural Development, Faculty of Natural and Agricultural Sciences, University of the Free State, PO Box 339, Bloemfontein 9300, South Africa.

³Department of Animal Sciences, Stellenbosch University, Private Bag X1, Matieland 7599, South Africa.

⁴Cape Institute for Agricultural Training: Elsenburg, Private Bag X1, Elsenburg 7607, South Africa.

⁵Department of Animal, Wildlife and Grassland Sciences, University of the Free State, PO Box 339, Bloemfontein 9300, South Africa.

⁶Department of Zoology and Entomology, University of the Free State, PO Box 339, Bloemfontein 9300, South Africa

SUMMARY

Genetic parameters for breech traits were estimated for 741 to 963 yearling Merino sheep divergently selected for reproduction rate. Breech traits were autumn dag score (ADS), spring dag (SDS) score, breech wrinkle score (BWS), as well as the width and depth of bare area around the perineum (respectively WBA and DBA). All traits exhibited genetic variation, heritability estimates ranging from 0.21 for ADS and DBA to 0.53 for BWS. ADS and SDS were highly correlated on the genetic level (0.67). BWS was positively related to dag scores (0.50 for ADS and 0.46 for SDS) on the genetic level. The only other genetic correlation of significance was a positive correlation (0.72) between DBA and WBA. Genetic correlations of yearling live weight with the breech traits were all in the desired direction, and only the genetic correlation with BWS did not reach significance. The only other genetic correlation of importance suggested that sheep with heavier fleeces would have more wrinkly breeches (0.47).

INTRODUCTION

With moves towards cessation of mulesing internationally, studies have been increasingly directed towards genetic alternatives for the prevention of breech strike. A number of traits, including wrinkle scores, breech cover/breech bareness scores, dag scores, urine stain and wool colour scores were identified as potential indicator traits for the reduction of breech strike. Limited sets of genetic parameters for these indicator traits are available; indicating that they do exhibit additive genetic variation (James 2006; Smith *et al.* 2009; Brown *et al.* 2010). Based on these estimates, genetic change in these traits seems feasible. To establish breeding programs, studies on the relationship of traits associated with breech strike resistance with other traits of economic importance (live weight, fleece traits) are needed. The objective of this study was to determine genetic parameters for some of the indicator traits for breech strike, and to examine genetic and phenotypic correlations with live weight, clean fleece weight and fibre diameter in Merinos.

MATERIALS AND METHODS

Animals and selection procedures. Two lines of Merino sheep were divergently selected from the same base population from 1986 to 2009, using maternal ranking values for number of lambs reared per joining. Details of the procedure for the selection of replacements have been reported elsewhere (Scholtz *et al.* 2010b). Briefly, male and female progeny of ewes that reared more than

one lamb per joining (i.e. reared twins at least once) were preferred as replacements in the High (H) line. Replacements in the Low (L) line were preferably descended from ewes that reared fewer than one lamb per joining (i.e. were barren, or lost all lambs at least once). Selection decisions were mostly based on ≥ 3 maternal joinings, especially in the case of rams. 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.

Location and recordings. The lines were maintained on the Elsenburg Research farm near Stellenbosch in the Western Cape province of South Africa. Scholtz *et al.* (2010b) described the climate at the site and the management of the animals. The animals used were the 2004 to 2008 lamb drops (born June-July). All lambs were unmulesed, tail docked at the third palpable joint at approximately three weeks of age and shorn in September - October as weaners. The animals were scored for dags in April or May (autumn dag score - ADS) as yearlings (10 - 11 months old) and shorn shortly afterwards (with 7 month's wool growth). Midrib wool samples were taken at shearing and analysed for fibre diameter (FD) and clean yield (CY). Information on CY was used to derive clean fleece weight (CFW) from the greasy fleece weight (GFW). After shearing, all the animals were weighed and two measurements of the bare area around the perineum were made in mm with a caliper, namely the width of the bare area (WBA) as well as the depth of the bare areas (DBA). Breech wrinkle scores (BWS) were also determined at this stage using a photographic system similar to the Visual Breech Scoring System (Australian Wool Innovation Limited 2007). However, the BWS scorecard used had six categories (e.g. score of 1 = least expression of the trait; score 6 = most expression of that specific trait), in contrast to the five categories used in the former system. Dags were also scored on all the animals as hoggets prior to being crutched in September (spring dag score - SDS) when they were approximately 15 months old. During the allocation of these scores, provision was made for half scores when dag scores (DS) for specific animals were situated between two of the five fixed categories for dags.

Statistical analyses. Environmental factors considered for the breech traits included year of birth (2004 to 2008), gender (male or female), age of dam (2 to 7+ years) and birth type (single or pooled multiples). The identity of the sire and dam of lambs were known individually. This information enabled linkage back to the line they were born in. The ASREML program (Gilmour *et al.* 2006) was used for the analysis fitting single-trait and multi-trait models. Since heritability estimates did not differ appreciably between single- and multi-trait analyses, (co)variance components and ratios from a five-trait model are reported. As the number of records assessed was fewer than 1000, no attempt was made to partition direct and maternal variances.

RESULTS AND DISCUSSION

Descriptive statistics are given in Table 1. The difference in the numbers available between the SDS and ADS are mostly caused by DS not being recorded in the spring of 2006. All data were distributed normally, but DS had coefficients of variation (CV's) exceeding 50%, as was also reported by Brown *et al.* (2010). The CV of 39% for BWS was also higher than an estimate of 24% (Scholtz *et al.* 2010a), but lower than CV's of >50% (Greeff and Karlsson 2009).

Heritability, genetic correlations and selection response. All traits were heritable with estimates ranging from 0.21 (ADS and DBA) to 0.53 (BWS; Table 2). Recent published heritability estimates for DS ranged from 0.25 to 0.31 (Brown *et al.* 2010; Pickering *et al.* 2010), and from 0.52 to 0.69 for BWS (Brown *et al.* 2010). Subjective scores for breech cover reported in the literature had heritability estimates ranging from 0.27 to 0.32 (Brown *et al.* 2010). The inclusion of live weight (LW) as a covariate for DBA and WBA resulted in a reduction in

heritability for these traits (0.12 ± 0.05 for DBA and 0.22 ± 0.07 for WBA). These results suggested that part of the genetic variation in these traits could be ascribed to size differences between animals. ADS and SDS were genetically highly correlated (0.67). Pickering *et al.* (2010) accordingly reported a genetic correlation of 0.71 between DS at three and eight months. BWS was genetically positively related to DS (0.50 for ADS and 0.46 for SDS). ADS was negatively related to the dimensions of the breech bare areas (-0.61 for DBA and -0.45 for WBA) on the genetic level (Table 2). These relationships also appeared to be size-dependent, as the inclusion of LW as a covariate resulted in the correlations being reduced to respectively -0.15 ± 0.25 and -0.19 ± 0.22 . DBA and WBA were positively genetically correlated (0.72 ± 0.14 without LW as covariate and 0.50 ± 0.24 with LW as covariate). Phenotypic correlations resembled genetic correlations in direction, but were smaller in magnitude.

Mature H line ewes had a lower frequency of breech strike than their L line contemporaries (Scholtz *et al.* 2010b). Line specific averaged breeding values (BV's) from the present study supported this line difference. Respective means (\pm s.e.) for BV's in the H and L lines were -0.46 ± 0.01 and 0.41 ± 0.03 for ADS, -0.43 ± 0.02 and 0.43 ± 0.05 for SDS, -0.51 ± 0.02 and 0.43 ± 0.06 for BWS, 4.84 ± 0.09 and -3.74 ± 0.27 for DBA as well as 3.36 ± 0.08 and -1.85 ± 0.23 for WBA. Reproduction thus seems to be favourably correlated to breech traits.

Table 1. Descriptive statistics for autumn dag score (ADS), spring dag score (SDS), breech wrinkle score (BWS), depth of bare area (DBA) and width of bare area (WBA)

Statistics	Trait				
	ADS (1-5)	SDS (1-5)	BWS (1-6)	DBA (mm)	WBA (mm)
Number of records	963	741	951	948	948
Mean	1.75	1.93	2.60	70.0	46.1
Standard deviation	0.95	0.99	1.02	11.1	9.8
Range	1 – 5	1 – 5	1 – 6	26 – 100	19 – 79
Skewness	1.55	1.55	0.36	-0.03	-0.21
Kurtosis	1.97	1.91	-0.28	0.07	-0.33

Table 2. Phenotypic variances (σ^2_p), genetic correlations (above diagonal), phenotypic correlations (below diagonal) and heritability (mean \pm s.e.) (in bold print on the diagonal) of autumn dag score (ADS), spring dag score (SDS), breech wrinkle score (BWS), depth of bare area (DBA) and width of bare area (WBA) in the breech subjectively scored for Merinos

Variance and traits (σ^2_p)	ADS	SDS	BWS	DBA (mm)	WBA (mm)
	0.725	0.918	0.968	103.2	44.5
ADS	0.21 \pm 0.06	0.67 \pm 0.14	0.50 \pm 0.15	-0.61 \pm 0.19	-0.45 \pm 0.20
SDS	0.28 \pm 0.04	0.45 \pm 0.09	0.46 \pm 0.14	-0.12 \pm 0.20	-0.01 \pm 0.19
BWS	0.28 \pm 0.04	0.14 \pm 0.04	0.53 \pm 0.08	-0.23 \pm 0.19	-0.17 \pm 0.17
DBA (mm)	-0.12 \pm 0.04	-0.06 \pm 0.04	-0.04 \pm 0.04	0.21 \pm 0.06	0.72 \pm 0.14
WBA (mm)	-0.15 \pm 0.04	-0.06 \pm 0.04	-0.09 \pm 0.04	0.48 \pm 0.03	0.28 \pm 0.08

Correlations between breech traits and yearling production traits. Genetic correlations of hogget LW with the recorded breech traits were all in the desired direction, and only the genetic correlation with BWS failed to reach significance (Table 3). Heavier animals tended to be less daggy, with larger bare areas and a suggestion of a lower BWS than lighter animals, as was also reported by Brown *et al.* (2010). Heavier cutting sheep tended to have higher BWS's than those with lower fleece weights. Comparable genetic correlations reported by Brown *et al.* (2010)

Genetic Parameters II

ranged from 0.14 to 0.44. Genetic correlations between the dag and breech traits and FD were mostly inconclusive, because it failed to reach statistical significance. However, the absolute direction of these correlations was unfavourable for DS and BWS, suggesting that finer sheep would also have more dags and more wrinkly breeches. Brown *et al.* (2010) reported genetic correlations of FD with BWS that were mostly negative (-0.27 to 0.10) while correlations with DS were positive (0.04 to 0.12). It is noted that the correlations between LW and DBA and WBA were very high (respectively 0.86 and 0.70).

Table 3. Genetic and phenotypic correlations of live weight (LW), clean fleece weight (CFW) and fibre diameter (FD) with autumn dag score (ADS), spring dag score (SDS), breech wrinkle score (BWS), depth of bare area (DBA) and width of bare area (WBA) in the breech

Trait and type of correlation	Trait				
	ADS	SDS	BWS	DBA (mm)	WBA (mm)
LW (kg)					
Genetic	-0.69 ± 0.14	-0.55 ± 0.15	-0.18 ± 0.14	0.86 ± 0.07	0.70 ± 0.12
Phenotypic	-0.13 ± 0.04	-0.09 ± 0.04	-0.04 ± 0.04	0.54 ± 0.03	0.40 ± 0.03
CFW (kg)					
Genetic	-0.01 ± 0.18	-0.03 ± 0.16	0.47 ± 0.12	0.28 ± 0.17	0.31 ± 0.16
Phenotypic	0.12 ± 0.04	0.05 ± 0.05	0.33 ± 0.04	0.27 ± 0.04	0.22 ± 0.04
FD (µm)					
Genetic	-0.24 ± 0.14	-0.14 ± 0.14	-0.21 ± 0.12	0.10 ± 0.16	0.21 ± 0.14
Phenotypic	-0.05 ± 0.04	-0.04 ± 0.05	-0.11 ± 0.04	0.15 ± 0.04	0.19 ± 0.04

CONCLUSIONS

The data used were at the minimum required for genetic analysis. However, results were consistent with comparable results in the literature. All the breech traits exhibited genetic variation. Genetic correlations of breech traits with production traits were mostly favourable or small in magnitude and not significant. The notable exception was the positive genetic correlation between clean fleece weight and BWS, suggesting that heavier cutting sheep were likely to be more wrinkly. Selection of Merino sheep for favourable breech traits is thus likely to require application of an appropriate selection index to accommodate the latter unfavourable genetic correlations.

REFERENCES

- Australian Wool Innovation Limited (AWI) (2007). Online: www.wool.com.au/publications.
- Brown D.J., Swan A.A. and Gill J.S. (2010) *Anim. Prod. Sci.* **50**:1060.
- Gilmour A.R., Gogel B.J., Cullis B.R. and Thompson R. (2006). ASReml User Guide. Release 2.0. (VSN International Ltd, Hemel Hempstead, HP1 1ES: UK)
- Greeff J.C. and Karlsson L.J.E. (2009). *Proc. Assoc. Advmt. Anim. Breed. Genet.* **18**:272.
- James P.J. (2006). *Aust. J. Exp. Agric.* **46**:1.
- Pickering N.K., Dodds K.G., Blair H.T., Hickson R.E., Johnson P.L. and McEwan J.C. (2010) *Proc. World Cong. Gen. Appl. Livest. Prod.*, Leipzig, Germany. ISBN 978-3-00-031608-1. Available at: <http://www.kongressband.de/wcgalp2010/assets/pdf/0294.pdf>.
- Scholtz A.J., Cloete S.W.P., van Wyk J.B., Misztal I., du Toit E. and van der Linde T.C.deK. (2010a). *Anim. Prod. Sci.* **50**:203.
- Scholtz A.J., Cloete S.W.P., van Wyk J.B., Kruger A.C.M. and van der Linde T.C.deK. (2010b). *Anim. Prod. Sci.* **50**:210.
- Smith J.L., Brewer H.G. and Dyall T. (2009). *Proc. Assoc. Advmt. Anim. Breed. Genet.* **18**:334.