

OPPORTUNITIES TO BREED FOR RESISTANCE TO BREECH STRIKE IN MERINO SHEEP IN A MEDITERRANEAN ENVIRONMENT

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SUMMARY

Three lines of Merino sheep that were selected on breech wrinkles, breech cover, dags, urine stain and wool colour from research and industry flocks were exposed to flies from birth to hogget age. Significant differences ($P < 0.01$) existed between lines in breech strike from post-weaning to hogget shearing but not from birth to hogget shearing. The lines differed significantly ($P < 0.05$) for the indicator traits except for dags. Highly significant differences ($P < 0.01$) were found between sire progeny groups for incidence of breech strike. Dags was the dominant predisposing factor for breech strike in one of four years. Breech strike in unmulesed sheep had a heritability of 0.57 ± 0.28 which was genetically positively correlated to all the scored indicator traits but had the strongest relationship with dags ($r_g = 0.86 \pm 0.17$).

INTRODUCTION

Flystrike became a serious disease for Merino sheep with the arrival of *Lucilia cuprina* and the introduction of the extremely wrinkly Vermont Merino from the USA in the late 1800's (Cameron 1999). Breech strike occurs when the wool and skin in the breech area becomes wet from capturing and holding rain, urine or fluid faeces during periods when the blowflies are active. This attracts the fly and creates an ideal environment for the gravid fly to lay its eggs, and for the eggs to hatch. When the hatched maggots develop into the third instar stage, they can cause serious damage and death to sheep, if not detected and treated early. In 1931, Seddon *et al.* (1931) showed that breech folds was a major determining factor. The limited treatment options at that time resulted in the development of the mules operation by Mr JWH Mules in 1931 in which the excess loose caudal skin folds are surgically removed. After healing this artificial extension of the bare skin area reduced breech strike as well as making crutching easier, hence its gradual adoption by the industry. However, changing public values has resulted in the questioning of this method from a welfare position and strong pressure is being applied onto the Australian Industry to phase out mulesing. A number of different alternatives are being pursued, but it is generally agreed that breeding is the only long term sustainable solution.

Many studies have been carried out to identify blowfly resistant animals (Atkins and McGuirk 1979; Mortimer 2001; Scobie *et al.* 2002). A number of studies has shown that wrinkles, wool colour and fibre diameter variability traits (James 2008; Raadsma and Rogan, 1987; Raadsma *et al.* 1997) contribute to body strike, and bare breech and dags (Scobie *et al.* 2002) to breech strike. Edwards *et al.* (2009) have confirmed that the bare breech trait is heritable, while Smith *et al.* (2009) have also shown that wrinkles and dags are correlated with the incidence of breech strikes. However, these indicator traits are generally correlated and confounded, and therefore this approach does not present a clear picture of the relationship between the indicator traits and breech strike on an individual basis. No study has been carried out on unmulesed Merino sheep where the visually scored indicator traits at weaning and hogget fleece traits, were jointly evaluated against breech strike. The aim of this study was to demonstrate the changes in breech strike in a Merino flock by selecting Merino sheep on the known indicator traits, *i.e.* breech wrinkles, breech cover, dags, urine stain and wool colour, to quantify their relative importance in contributing to breech strike in a Mediterranean environment and to determine whether genetic differences exist between sires in breech strike resistance.

MATERIALS AND METHODS

Animals. Three lines of 200 ewes each were established on the Mt Barker research station in Western Australia. This research station has an annual winter rainfall of approximately 700mm. The first line (BSR-A) represents a scenario in which a ram breeder would select both his rams and ewes intensely for the known indicator traits and using any breech strike information. The second line (BSR-B) represents a scenario in which a commercial producer buys rams from a BSR-A rambreeder and only culls replacement ewes using the indicator traits. The third flock consists of an unselected control flock (BSR-con).

To generate more reliable results the above mentioned three lines were selected from representative commercial populations by using existing knowledge on the known indicator traits. The foundation ewe population was established by screening ewe lambs on 10 different medium wool properties in Western Australia in 2005. On each property 22 ewe lambs were selected for each of the three lines at marking as follows. Firstly, ewe lambs were selected randomly for the control flock after which average animals were selected for line 2. As it was only possible to differentiate between lambs for wrinkles at this early age, the plainest lambs on each property were identified for line 1. A similar approach was used to screen mature ewes from three different medium wool research flocks of the Department of Agriculture and Food Western Australia. Potential rams from research and industry flocks were identified based on their performance on the key indicator traits of breech cover, wrinkles and dags. However, very little objective information was available on industry rams and most industry rams were used on the basis of their own wrinkle and breech cover scores.

The screened sheep were transported to the Mt Barker research station in December 2005. Mating took place in February/March with lambing in July/August from 2006 to 2008. Half of each sire's progeny were mulesed in the first 3 years, but this practise ceased in 2008. However, only the records of unmulesed sheep were used in this study. The progeny were scored for breech wrinkle (WSB), breech cover (BC), dags (DS), wool colour (WCOL) and urine stain (US) at weaning using the National Visual Sheep Scoring System (AWI 2007). No preventative fly treatments such as crutching and jetting were applied to the young sheep to ensure that the animals were appropriately challenged. Animals were allowed to be struck naturally until hogget shearing. Any struck animal was identified, treated with a short acting chemical and returned to the flock. The total number of fly strikes from birth to post-weaner shearing and from post-weaner shearing to hogget shearing, were recorded per site on all struck animals. Breechstrw (breech strike birth to post-weaning shearing) and breechstrh (breech strike post-weaning to hogget shearing) indicate the total number of flystrikes in the breech over these two periods, respectively. In 2008 the Rylington Merino (RM) flock (Karlsson and Greeff, 2006) was included in this trial because of the relatively small number of unmulesed sheep in this trial. The same traits were recorded and measured in the RM flock as in the BSR flock. However, the RM flock was managed separately to the BSR flock up to weaning, but after weaning the sexes were separated in each flock and combined across flocks.

Data. Two sets of data were used in this study. The first dataset was recorded on the BSR flock that consisted of 1882 records of which 710 animals were mules and 1172 unmulesed sheep. The RM flock contributed 505 records from the 2008 born lambs that were recorded up to December 2008, resulting in a combined dataset of 2387 records from 46 sires and 1061 dams of which 1677 progeny were from unmulesed sheep. The average sire progeny group size was 35 which varied between 11 and 73 animals. No pedigrees were available on animals sourced from industry flocks.

Statistical analysis. The breech strike counts from birth to post-weaning shearing (breechstrw) and from post-weaning shearing to hogget shearing (breechstrh) were pooled into breech strike (breechstr). This trait and the indicator traits on unmulesed sheep of the BSR lines were analysed using ASREML (Gilmour *et al.* 2006). A univariate analysis was carried out by fitting line (3 levels), property of origin (1-12), year of birth (2005, 2006, 2007, 2008), sex (male and female), birth type (singleton/multiple) and age of the dam (7 levels) as fixed factors. As breech strike was a count and the mean and variance was the same, a Poisson distribution with a log link function was fitted to breech strike. A multivariate analysis was then carried out by adding breech cover, breech wrinkle, dags, wool colour and urine stain at weaning and the fleece traits, greasy fleece weight (GFW), clean fleece weight (CFW) fibre diameter (FD), coefficient of variation of fibre diameter (CV), clean yield (YLD) and fibre curvature as covariates to the model to identify their relative contribution to breech strike. As all the traits were not available in every year, this was undertaken separately for each year for the RM flock.

The data from the BSR and RM flocks were then combined and the genetic parameters estimated by using the Gibbs sampling threshold program from the BLUPF90 suite of programs (Misztal *et al.* 2002). An animal model was fitted with flock, property of origin and the significant environmental factors as fixed factors. The sires' solutions were then regressed against the incidence of breech strike of their progeny groups.

Table 1. Percentage of animals that were struck by flies per site from 2005 to 2008 for the different lines. (M = Mulesed; UM = Unmulesed)

Birth Year	Line	Number		Body strike %		Pollstrike %		Breechstrw ^b %		Breechstrh ^c %	
		M	UM	M	UM	M	UM	M	UM	M	UM
2005	BSR_A	106	105	0.0	3.2	0.0	0.0	0.9	0.0	1.1	5.3
	BSR_B	102	102	0.0	3.4	0.0	1.1	0.0	2.9	2.1	10.3
	Control	102	103	0.0	0.0	0.0	0.0	1.0	1.0	4.6	15.9
2006	BSR_A	84	79	1.2	1.3	22.2	23.1	6.0	25.3	3.6	1.3
	BSR_B	63	62	6.3	4.8	38.5	31.8	3.2	24.2	6.3	1.7
	Control	76	74	5.3	9.5	48.1	48.1	7.9	32.4	4.2	11.1
2007	BSR_A	66	62	15.1	12.5	13.2	18.8	1.5	9.7	3.8	16.7
	BSR_B	66	72	18.8	20.9	16.7	18.6	1.5	11.1	4.2	58.1
	Control	56	59	10.7	22.7	10.7	4.5	3.6	6.8	7.1	50.0
2008	BSR_A	0	199		4.0		2.5		25.6		
	BSR_B	0	144		6.9		1.4		20.1		
	Control	0	113		10.6		2.7		40.7		
	RM ^a	0	505		4.0		0.4		23.0		

^a Not comparable with other lines as RM flock was managed separately for most of the time

^b Breech strike up to post-weaning shearing. ^c Breech strike from post-weaning to hogget shearing

RESULTS AND DISCUSSION

The percentage of animals that were struck on the body, poll and breech at weaning and in the breech between weaning and hogget shearing in mulesed and unmulesed sheep in the different lines over four years are shown in Table 1.

The total number of all types of strike gives an indication of the challenge that the animals received from flies. Twelve percent of the 2005 drop, 45% of the 2006 drop, 46% of the 2007 drop

Disease resistance

and 26% of the 2008 drop animals (during first 5 months) were struck. About 65.4 % of all strikes were in the breech, 17.5% on the body and 17.1% on the head. Sixteen percent of the males and 22.1% of females were struck. Of the 1677 unmulesed animals, 356 (21.2%) animals were struck in the breech once, 36 (2.15%) were struck twice and 4 (0.24%) animals were struck 3 times from birth to hogget age. Breechstrw of the BSR-A line was not significantly different between the BSR lines but breechstrh (post-weaning to hogget shearing) was highly significantly ($P<0.01$) different between lines *i.e.* 7.7%, 20.7% vs. 25.6% for the BSR-A, BSR-B and BSR-C lines, respectively.

Table 2. Number of records, means and standard deviation (SD) of breech strike to hogget age and of the indicator traits at weaning for the breech strike (BSR) flock and the Rylington Merino (RM) flock (BSR-A = selection line 1; BSR-B = selection line 2 and BSR-C = control)

Trait	n	Mean	SD	Level of significance
Total number of breech strikes to hogget age				
BSR-A	296	0.22	0.48	NS
BSR-B	240	0.27	0.53	
BSR-C	209	0.32	0.53	
RM ^a	498	0.24	0.47	
Breech wrinkle score (WSB)				
BSR-A	296	1.48	0.75	$P<0.01$
BSR-B	240	1.80	1.09	
BSR-C	209	1.97	1.16	
RM ^a	498	1.03	0.18	
Breechcover (BC)				
BSR-A	296	3.49	0.56	$P<0.05$
BSR-B	240	3.48	0.51	
BSR-C	209	3.55	0.52	
RM ^a	498	3.62	0.43	
Dag score (DS)				
BSR-A	356	2.35	0.56	NS
BSR-B	309	2.39	0.68	
BSR-C	267	2.38	0.71	
RM ^a	498	2.64	0.66	
Wool colour (WCOL)				
BSR-A	296	2.29	0.46	$P<0.01$
BSR-B	240	2.33	0.43	
BSR-C	209	2.41	0.46	
RM ^a	498	2.52	0.32	
Urine stain at weaning (US-wean)				
BSR-A	356	1.51	0.75	$P<0.01$
BSR-B	309	1.60	0.86	
BSR-C	267	1.77	0.92	
RM ^a	498	1.34	0.77	

^a RM line not directly comparable; NS = not significant ($P>0.10$)

Table 2 shows that the average number of total breech strikes from birth to hogget shearing in unmulesed sheep. Although a clear trend exists, the differences between the three BSR lines were not significant by fitting a Poisson model in spite of the fact that the overall incidence of breech strike from post-weaning to hogget shearing differed significantly between lines. The average breech strike incidence of the RM was 0.24 which is not different from the BSR lines.

Fixed Effects. Within the BSR lines, year of birth affected all traits significantly while property of origin had a significant effect on WCOL, WSB and BC. Females had significantly ($P<0.01$) higher breech cover scores while rams had significantly ($P<0.01$) more dags.. Significant differences ($P<0.05$) were found between the BSR lines for WSB, BCVR, WCOL and US (Table 2) while no significant differences were found between lines for DS. In general there was a progressive increase in all the indicator traits from BSR-A to BSR-B to the BSR-C line. The average scores and standard deviation of WSB, BC, DS, WCOL and US at weaning are shown in Table 2 for the different lines. The amount of variation for WSB was quite large ($>50\%$) in the BSR line while the RM line showed much less variation because it was much plainer.

Table 3. Regression coefficients and standard errors (SE) of total number of breech strikes against the independent variables in different years for the BSR and RM flocks.

Covariate	2005	2006	2007	2008 ^a	2008
	BSR	BSR	BSR	BSR	RM
Mu	0.72 (4.492)	-1.73 (5.359)	4.80 (7.543)	-0.10 (0.168)	0.00 (0.207)
WSB	0.09 (0.309)	-0.02 (0.227)	0.17 (0.287)	0.43 (0.489)	0.28 (0.235)
BC	0.07 (0.207)	0.23 (0.453)	0.72 (0.404)	0.05 (0.169)	0.00 (0.154)
DS	0.09 (0.523)	0.25 (0.196)	0.26 (0.227)	0.36 (0.114)	0.24 (0.109)
WCOL	0.13 (0.243)	--	--	0.01 (0.135)	0.10 (0.168)
US	0.11 (0.387)	--	--	0.12 (0.112)	0.16 (0.114)
GFW	-0.30 (1.271)	-0.11 (1.320)	-0.08 (2.197)	--	--
CFW	0.33 (1.734)	0.11 (1.889)	-0.02 (2.901)	--	--
FD	-0.00 (0.066)	0.03 (0.078)	-0.03 (0.071)	--	--
CV	0.00 (0.032)	0.02 (0.037)	-0.05 (0.063)	--	--
YLD	-0.01 (0.056)	0.01 (0.061)	-0.02 (0.096)	--	--
CRV	0.00 (0.007)	-0.00 (0.011)	-0.02 (0.012)	--	--
Deviance	-13.3	-21.1	-13.2	-57.0	-55.6
Degrees of freedom	217	122	72	429	456

Coefficients in bold are significant ($P<0.05$)

Table 3 shows the association between the incidence of breech strike and the indicator traits in different years and flocks. The models fitted the data reasonably well as shown by the deviance. In 2008 only DS was significantly ($P<0.01$) related to the incidence of breech strike in both the BSR and the RM flock, while only BC was significant ($P<0.05$) in 2007. No trait was significant in 2005 and 2006, and none of the wool traits contributed significantly to breech strike in any year.

Previous studies (Seddon, 1931) have shown a relationship between wrinkle score and breech strike and between dags and breech strike (Scobie *et al.* (2002). This study shows that in this environment dags is the most important predisposing factor, and it appears that under different conditions other traits may be more important.

Table 4 shows that breech strike and the indicator traits all have moderate heritability estimates, but the results are not very precise due to the large standard errors. Except for the negative phenotypic relationship between US and DS all the other indicator traits are genetically and phenotypically positively correlated with each other, and with breech strike. WCOL had the strongest phenotypic relationship with breech strike followed by DS, WSB. US and BC. Genetically the strongest relationship exists between DS and breech strike followed by US and breech strike. However the standard errors are again relatively large.

Table 4. Heritability of (diagonal), and genetic (below diagonal) and phenotypic (above diagonal) correlations between the indicator traits and incidence of breech strike

	WSB	BC	DS	WCOL	US	Breechstr
Vp	0.67	0.35	0.49	0.23	0.85	0.25
WSB	0.45 (0.28)	0.18	0.18	0.35	0.35	0.22
BC	0.19 (0.51)	0.42 (0.32)	0.06	0.15	0.25	0.17
DS	0.07 (0.53)	0.27 (0.65)	0.55 (0.30)	0.15	-0.35	0.23
WCOL	0.31 (0.18)	0.66 (0.25)	0.09 (0.55)	0.49 (0.32)	0.10	0.26
US	0.44 (0.22)	0.23 (0.23)	0.33 (0.18)	0.00 (0.10)	0.49 (0.32)	0.19
Breechstr	0.23 (0.63)	0.17 (0.19)	0.86 (0.17)	0.25 (0.24)	0.53 (0.22)	0.57 (0.28)

Figure 1 shows the raw incidence of breech strike of progeny groups of different sires over three years. Highly significant differences ($P < 0.01$) were found between sires for incidence of breech strike that varied from about 2% to 55% animals struck per progeny group. The sire solutions from the Gibbs analyses were regressed against the raw breech strike incidence of the progeny groups. The relationship is shown in Figure 2 and the traits had a correlations of 0.64..

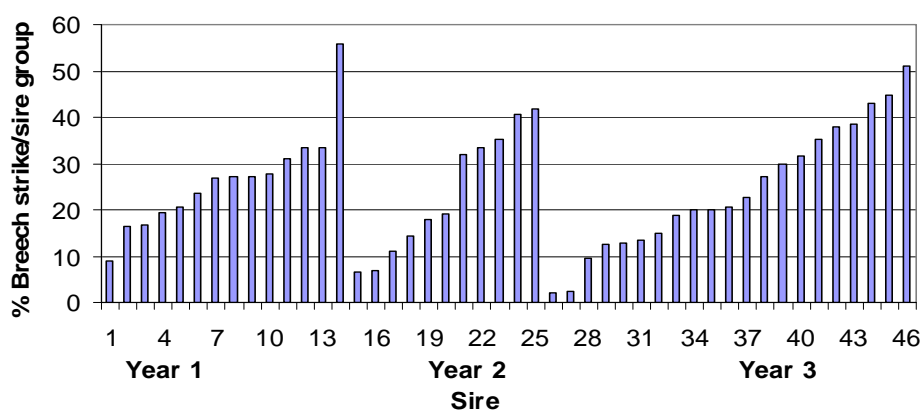


Figure 1 Differences in breech strike resistance between the progeny of 46 sires over 3 years.

CONCLUSIONS

The results show that considerable variation exists amongst sires that can be exploited to improve resistance to breech strike through breeding. While all the visually scored indicator traits are genetically correlated with breech strike, dags followed by breech cover were the most important indicator trait of breech strike in this environment. It appears that the relationships between the “known” indicator traits and breech strike are more complex and that these may vary between years. This indicates that environmental factors will be the key determining factor and more information is needed to elucidate these relationships and to estimate robust genetic and phenotypic parameters for the design of efficient breeding programs.

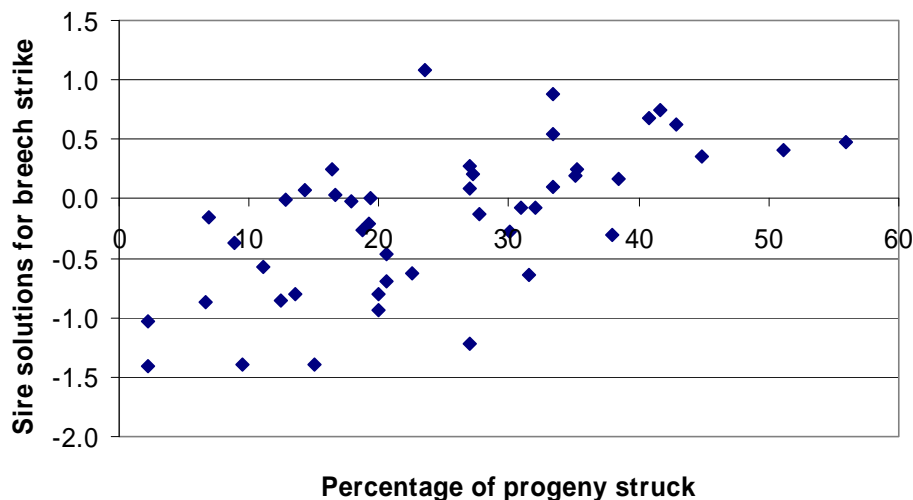


Figure 2. Relationship between sire solution and percentage progeny struck per sire progeny group

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