PRELIMINARY GENETIC PARAMETERS FOR FLYSTRIKE AND ITS ASSOCIATION WITH PRODUCTION TRAITS IN AUSTRALIAN MERINO SHEEP

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SUMMARY

This study explored the phenotypic and genetic variation in breech flystrike and its relationship with production traits in the Connemara Merino ram breeding flock. Yearling breech strike (struck/non-struck) had a low heritability of 0.09 ± 0.04 when using a binomial model. Heritability estimates for production traits ranged from 0.12 ± 0.04 (for faecal worm egg count) to 0.70 ± 0.07 (for staple length). Genetic correlations between breech strike and production traits varied from negative (-0.25 ± 0.24 for fibre diameter) to high positive (0.70 ± 0.21 for dag score), illustrating both favourable and unfavourable relationships that will have implications for future selection programs incorporating breech strike resistance with production traits.

INTRODUCTION

Flystrike, one of the most significant costs facing the Australian sheep industry, is a parasitic infection caused by the larvae of the sheep blowfly (*Lucilia cuprina*) and can cause production losses, chronic disease, and mortality (Lane *et al.* 2015). Breech flystrike is the most common type of flystrike and is a priority research area for Australian Wool Innovation Ltd (AWI). Australian Sheep Breeding Values (ASBVs) for indicator traits of breech flystrike resistance, such as wrinkle, breech cover, dag and other visual wool traits are available through Sheep Genetics (Brown *et al.* 2010) and provide the industry with tools to improve flystrike resistance through indirect selection. There is also interest in using direct measures of flystrike to further improve the accuracy of selection and also animal welfare. Furthermore, understanding the relationship between flystrike and production traits is also essential for predicting response to selection. Therefore, this study was conducted using an existing Merino sheep industry dataset to explore breech flystrike trait definition, genetic variation and its association with production and visual traits.

MATERIALS AND METHODS

Flystrike dataset. The initial dataset used for this study was 2,692 animals from the Connemara Merino ram breeding flock, located at Tarcutta, NSW, born between 2017 and 2021. There were 3,232 records from 1,364 ewes and 1,328 rams available to check the status of flystrike (including struck and non-struck animals). Routine screening for flystrike is done primarily from birth to crutching time (6-7 months) and mulesing of lambs ceased in this flock in 2018 since then regular monitoring and treatment of flystrike have been undertaken. For this study, all animals were assessed and considered for flystrike from birth to yearling age. Animals who were not affected by flystrike were identified by matching contemporary groups (CG) of affected animals based on wool traits submitted to MERINOSELECT. The contemporary groups (defined as flock, year, sex, date of measurement and management group conducted by Sheep Genetics; Brown *et al.* 2010) of these traits were used as a fixed effect for breech strike. The traits for finding CGs included records for curvature, fibre diameter, fibre diameter CV, and clean and greasy fleece weight traits. The combination of site/flock and year of birth was used to set

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minimum thresholds of 0.05 and 20 for frequency of flystrike and number of animals within each class combination, respectively. Further restrictions were applied to remove contemporary groups within the site/flock-years with less than 5 animals and with no variation. After filtering, 1,941 animals with breech strike phenotypes (Table 1) were retained for analysis where most struck animals were observed in summer and early autumn at an average of 184 days.

Flystrike definition. Breech strike, which is an infection of fly larvae in the breech area of sheep, was defined as "struck" or "not struck", coded as 1 or 0 respectively, within a defined shearing period, in this case, birth to yearling (Table 1). Periods were bounded by shearing events and consequently, recorded animals that fall within shearing intervals were assigned a phenotype.

Production traits. Overall, the number of observed records ranged from 1,536 to 5,732 for production and visual traits recorded at the weaning to yearling stages. These traits included breech wrinkle (BWR), dag score (DAG), clean fleece weight (CFW), fibre curvature (CUV), fibre diameter CV (DCV), fibre diameter (FD), faecal worm egg count (FEC), greasy fleece weight (GFW), staple length (SL), staple strength (SS), weaning weight (WWT) and yearling weight (YWT) that were available and sufficient to analyse. Records for production traits were only included for the birth years where breech strike was observed (2017 to 2021). After adding CGs to the fixed part of the model, a range of systematic effects, including birth and rear type (single and multiple), lamb age and age of dam (linear and or quadratic) were tested for significance for each trait and included in the models for variance component estimation accordingly.

Statistical analyses. Results presented in this study were analysed in ASReml (Gilmour *et al.* 2015) using a binomial model with a probit link function for the trait breech "struck" (BRS), and a continuous model for all production traits. Models included random effects for direct genetic and maternal genetic effects, and maternal permanent environmental effects were fitted where they were significant, as shown in Table 2. The univariate models were tested and compared using likelihood ratio tests (LRT) between the full and reduced models. The best models were used for bivariate models between breech strike and other traits.

RESULTS AND DISCUSSION

Breech strike incidence across years of birth indicates that 2020 and 2021 were the lowest (8.0%) and highest (33.7%) flystrike challenge years in this flock, respectively (Table 1). New South Wales had its 6th wettest year on record (720.6mm overall) in 2021, with rainfall 30% above average since 2010 based on the annual climate summary for New South Wales 2023.

Table	1.	Descriptive	statistics	of	breech	strike	across	years	of	birth.	%Struck	is is	the
percen	itag	ge of animals	s with the	pre	sence of	breech	struck	(1 vs 1	non	-struck,	, 0) from	birt	h to
the year	arli	ng shearing											

Year of birth	Ν	SD	Min	Max	%Struck
2017	402	0.46	0	1	30.1
2018	389	0.35	0	1	14.6
2019	399	0.43	0	1	24.6
2020	451	0.27	0	1	8.0
2021	300	0.47	0	1	33.7

The heritability of breech strike for this dataset was estimated as 0.09 ± 0.04 on the probit scale (Table 2) and 0.13 from a threshold model using a Gibbs sampling method (Tsuruta and Misztal 2006; results not shown in Table 2). These estimates were lower than values reported in other studies. Early breech strike heritability (up to 8 months of age) was reported to be 0.32 ± 0.11 (Smith *et al.* 2009) from a linear model on the logarithm-transformed breech strike, and 0.57 ± 0.13

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from a threshold model using the Gibbs sampling method (Greeff *et al.* 2014). However later, Greeff *et al.* (2021) reported a heritability of 0.07 ± 0.01 using the linear model on the logarithm-transformed breech strike counts and a heritability of 0.51 ± 0.10 on the logistic underlying scale in adult Merino ewes from the same flock. They also found the heritability of 0.44 ± 0.07 and 0.69 ± 0.18 for Merino ewes at hogget age on the normal and logistic underlying scale respectively, both using a binomial model (Greeff *et al.* 2021). Bird-Gardiner *et al.* (2013) observed heritability of 0.33 ± 0.15 for breech strike using a sire linear model in Merinos and 0.30 ± 0.10 across breeds. These differences may be related to the models applied (the binomial model in this study) and scales (the probit underlying scale in this study), and differences between the environmental conditions and management practices across sites contributing to varying levels of expression.

Another aspect to consider is the collection and accuracy of the data, particularly inferences about unaffected animals. In this study, unaffected animals were determined from their contemporary groups (described in the material and method section) recorded for wool traits. Using wool traits is currently the only method for identifying unaffected animals in each group since there is no 'roll-call' as such to identify all animals that were present and the infection by flystrike usually occurs when the animal is in wool. However, this inference may miss animals that disappear and are not recorded for wool traits.

Table 2. Descriptive statistics of traits and direct heritability (h²), maternal heritability (m²), and the proportion of maternal permanent environmental to the total variance (Pe²) using a univariate animal model. Standard errors are in parentheses

Trait ¹	Unit	Ν	Mean	SD	h ²	m ²	Pe ²
BRS ²	1/0	1941	0.21	0.41	0.09 (0.04)		
BWR	1-5 score	3896	2.46	0.78	0.27 (0.06)	0.05 (0.03)	
CFW	Kg	4399	1.96	0.51	0.36 (0.06)	0.04 (0.03)	
CUV	Degree/mm	5399	86.73	20.03	0.42 (0.05)		
DAG	1-5 score	1536	1.75	0.84	0.37 (0.08)		
DCV	%	5727	18.38	2.37	0.27 (0.06)	0.06 (0.03)	
FD	μm	5732	15.45	1.40	0.52 (0.07)	0.07 (0.03)	
FEC	Eggs/gm	2851	7.13	4.13	0.12 (0.04)		
GFW	Kg	5711	2.92	0.77	0.39 (0.06)	0.02 (0.02)	
SL	mm	1914	84.97	11.51	0.70 (0.07)		
SS	N/Ktex	2100	30.02	10.05	0.18 (0.05)		
WWT	Kg	3125	19.04	4.09	0.16 (0.06)	0.02 (0.03)	0.12 (0.04)
YWT	Kg	2024	36.71	9.21	0.40 (0.12)	0.01 (0.05)	

¹Traits are ordered alphabetically and their abbreviations are explained in the text. ² Breech strike was fitted in the binomial model on the probit scale.

Phenotypic and genetic correlations of breech strike (BRS) with most traits were consistent with Bird-Gardiner *et al.* (2013), except that of Greeff *et al.* (2014) who estimated low and non-significant correlations with wool traits. However, the result of this study was more in line with their later research (Greeff *et al.* 2021). DAG, FEC, and BWR had the highest genetic correlations (>0.60) with BRS supporting the value of these traits as indirect selection criteria in this flock, which is also supported by the other two studies. Among wool traits, clean and greasy fleece weights and fibre diameter CV had moderate positive correlations ($r_g\approx0.50$) with BRS, and SL had a low positive correlation ($r_g=0.27$) with BRS, all of which were stronger than other studies (Table 3). The antagonism between fleece weight and breech strike incidence is problematic given the importance of fleece weight in industry breeding objectives and profit. Low, negative genetic correlations for FD, SS, CUR, and YWT (-0.09 to -0.25; P> 0.05) with breech strike indicate that

selection for resistance to breech strike may have lower impacts on wool quality and growth traits.

Table 3. Phenotypic (r_p) and genetic (r_g) correlations between breech strike and production traits estimated in this study and in the literature

Trait	This s	study	Bird-Gardine	r <i>et al</i> . (2013)	Greeff et al (2014) 1		
ITall	rp	rg	rp	rg	rp	r_{g}	
BWR	-0.01 (0.03)	0.64 (0.21)	0.17 (0.03)	0.65 (0.22)	0.20	0.18 (0.17)	
CFW	0.04 (0.03)	0.50 (0.18)	0.03 (0.04)	0.28 (0.26)	0.01	0.05 (0.12)	
CUV	0.02 (0.03)	-0.09 (0.22)	-0.02 (0.04)	-0.07 (0.28)	-0.08	-0.04 (0.12)	
DAG	0.09 (0.04)	0.70 (0.21)	0.08 (0.03)	0.84 (0.49)	0.45	0.81 (0.15)	
DCV	0.06 (0.03)	0.59 (0.20)	0.08 (0.03)	0.45 (0.27)	0.05	-0.27 (0.13)	
FD	-0.04 (0.03)	-0.25 (0.24)	-0.04 (0.03)	-0.05 (0.19)	0.04	0.14 (0.12)	
FEC	0.05 (0.03)	0.69 (0.29)	0.06 (0.03)	0.60 (0.30)	0.01	0.27 (0.12)	
GFW	0.05 (0.03)	0.49 (0.18)	0.07 (0.03)	0.32 (0.22)	0.02	0.06 (0.11)	
SL	0.02 (0.03)	0.27 (0.22)	-0.09 (0.04)	-0.10 (0.20)	-0.05	0.02 (0.14)	
SS	-0.07 (0.03)	-0.21 (0.29)	-0.03 (0.03)	-0.05 (0.30)	-0.01	0.15 (0.16)	
WWT	0.04 (0.03)	0.07 (0.28)					
YWT	-0.03 (0.14)	-0.15 (0.28)					

¹ Standard errors are in parentheses except those that are not published. Figures are presented only in stages similar to the present study.

CONCLUSIONS

Breech strike had a low heritability while its correlation with production and visual traits varied depending on the trait. Although indirect selection on indicator traits is of value to improve flystrike resistance, direct selection on the trait itself may help to increase response, particularly in combination with genomic information. The results of this study can be used to predict changes in flystrike resistance and production traits in response to selection for a range of breeding objectives in industry ram breeding programs. Further analysis has commenced combining data from this flock, the Sheep CRC Information Nucleus Flock (INF), the AWI Breech Flystrike Genetics flocks, sire evaluation flocks and other available research and industry flocks.

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