INDICATOR TRAITS RECORDED EARLY IN LIFE WILL BE USEFUL SELECTION CRITERIA FOR BREECH FLYSTRIKE RESISTANCE IN WEANER MERINO SHEEP

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SUMMARY

This study demonstrated that breechstrike indicator traits such as wrinkle and wool cover are sufficiently variable, heritable and correlated with breech strike incidence to weaner age to be useful indirect selection criteria for breech strike resistance. Further, the indicator traits recorded at birth would be more suitable selection criteria than the same traits recorded at marking or post-weaning. However, birth traits are far more problematic to record, and therefore less likely to be adopted by industry than those recorded at marking, or even later at post-weaning or yearling ages. The relationships between indictor traits and key production traits for Merinos are yet to be evaluated.

INTRODUCTION

Interest in developing alternatives to mulesing in Merino sheep has led to investigations aimed to evaluate the potential of selection for breech flystrike resistance (Greeff *et al*. 2014; Smith *et al*. 2009). For a disease such as flystrike, it is undesirable for economic and animal welfare reasons to challenge animals directly to evaluate their level of resistance. Hence, indirect selection criteria that are variable, heritable, correlated with flystrike and easily recorded in industry flocks early in life are needed. Here, early life indicator traits were explored in the CSIRO Armidale breech flystrike genetic resource flock as potential indirect selection criteria for breech flystrike at weaner age.

MATERIALS AND METHODS

Sheep and data collection. Progeny of the CSIRO breech flystrike genetic resource flock in Armidale, NSW, born between 2005 and 2014 inclusive, were the subject of this study (n = 4,656). The flock structure up to 2010 is detailed in Smith *et al.* (2009). No mating was conducted in 2010 and the design was changed in 2011 to represent a finewool type flock suited to the summer rainfall environment, and incidence of breech flystrike itself became the primary selection criterion. Lambs were born in September and weaner breech flystrike (wBRSTR) was recorded as the count of flystrikes observed during the first challenge season. Struck sheep were treated to kill the infestation and animals could experience more than one strike per season, yielding the count of strikes for the season. The first challenge season occurred approximately from October to April inclusive, when weaners were approximately one to seven months of age. Up to and including 2009, half the lambs from each sire were mulesed and half remained unmulesed. From 2011 onwards, no mulesing was conducted. Neck wrinkle (NWR), body wrinkle (BDWR), breech wrinkle (BRWR), breech wool cover (BCOV) and crutch wool cover (wool coverage in the inguinal area, CCOV) were recorded at birth (b) up to and including 2009. Traits recorded at marking (m, approximately six weeks of age) and post-weaning (p, approximately six months of age), were those recorded at birth (described above) as well as breech bare width (BW, mm), breech bare depth (BD, mm), and tail length (TL, mm, marking only). Here, correlations between indicator traits at birth, marking and post-weaning with wBRSTR were explored to identify breechstrike indicators that can be recorded early in life.

Statistical analysis. Univariate mixed animal models were applied using ASReml (Gilmour *et al.* 2009). No data transformations were performed on any trait data as with the exception of wBRSTR

most were sufficient approximations of statistical normality. Fixed effects tested for individual traits were selection line nested within the two design phases (originally 3 levels prior to 2011; 2 levels post 2011); contemporary group (combined birth year, lambing management flock, and property-of-origin (latter for the 2005 drop only)); mules group (2 levels; mulesed and non-mulesed); sex (2 levels; castrated male and female); birth type (for traits recorded at birth, 2 levels; single and multiple); birth-rearing type (for traits recorded from marking onward, 3 levels; born and reared single (SS), born multiple and reared single (MS), born and reared multiple (MM)); age of dam (2 levels; maiden (2yo at first lambing) and adult); operator (up to 4 levels; scorer or measurer of trait). Age, and age specific cannon bone length (CBL) as an indicator of frame and bodyweight (WT) were fitted as covariates where appropriate. Only significant effects were retained in statistical models. Maternal genetic effects were tested by fitting dam as a random effect and significance determined using likelihood ratio testing. Where the inclusion of the maternal effect was non-significant, it was excluded from the final model. In 2005, foundation ewes purchased from industry were assigned to one of the three genetic groups described by MerinoSelect (Banks and Brown 2009). From then onward, all progeny born into the flock were fully pedigreed. Correlations among breech traits were estimated from multivariate mixed animal models.

RESULTS AND DISCUSSION

Weaner breechstrike ranged from 0 to 6 within the first challenge season. Phenotypic and genetic parameters for indicator traits of breechstrike recorded at birth and their correlations with wBRSTR are shown in Table 1. Breechstrike at weaner age was of low heritability. The heritabilities of indicator traits recorded at birth were of low to moderate heritability. Genetic correlations between wBRSTR and indicator traits range from $r_g = 0.27–0.59$. Genetic correlations between wrinkle traits recorded on different parts of the body (bNWR, bBDWR and bBRWR) were high at birth. Low negative correlations were found between wrinkle traits and CCOV. Phenotypic correlations were low between wrinkle and wool cover traits. In summary, the heritabilities and correlations for indicator traits recorded at birth would be useful for indirect selection for reducing wBRSTR.

Table 1. Arithmetic mean and standard deviation (sd), phenotypic variance (Vp), heritability (bold, diagonal), phenotypic correlations (above diagonal) and genetic correlations (below diagonal) for wrinkle and wool cover traits recorded at birth (b), and weaner (w) breech flystrike (standard error in parentheses)

Trait	bNWR	bBDWR	bBRWR	bCCOV	bBCOV	wBRSTR
Mean, sd	2.57, 0.77	2.18, 0.85	2.30, 0.90	3.55, 0.70	4.49, 0.62	0.181, 0.482
Vp	0.49 (0.02)	0.58 (0.02)	0.72 (0.02)	0.45 (0.02)	0.29 (0.02)	0.21 (0.01)
bNWR	**0.42 (0.06)**	0.65 (0.02)	0.56 (0.02)	-0.02 (0.03)	0.06 (0.06)	0.05 (0.03)
bBDWR	0.91 (0.04)	**0.36 (0.06)**	0.66 (0.02)	-0.03 (0.03)	0.04 (0.03)	0.07 (0.03)
bBRWR	0.82 (0.06)	0.90 (0.4)	**0.37 (0.06)**	-0.05 (0.03)	0.02 (0.03)	0.08 (0.03)
bCCOV	0.04 (0.14)	-0.03 (0.13)	-0.12 (0.13)	**0.38 (0.06)**	0.20 (0.03)	0.01 (0.03)
bBCOV	0.28 (0.17)	0.26 (0.16)	0.11 (0.17)	0.43 (0.15)	**0.22 (0.06)**	0.03 (0.03)
wBRSTR	0.42 (0.15)	0.41 (0.15)	0.47 (0.14)	0.27 (0.14)	0.59 (0.18)	0.18 (0.03)

Genetic and phenotypic parameters for indicator traits recorded at marking and their correlations with wBRSTR are summarised in Table 2. Heritabilities for indicator traits recorded at marking ranged from h^2=0.20-0.43 and were similar to the estimates for the same traits recorded at birth. Tail length at marking had a high heritability. However, the genetic correlations of wBRSTR indicator traits at marking were lower than with the same traits recorded at birth. Favourable genetic correlations

between mBW and mBD and wBRSTR were observed. Phenotypic correlations between wBRSTR and indicator traits recorded at marking were low. Genetic correlations between wool cover, wrinkle, and tail length were also mostly low. The exceptions were high favourable genetic correlations between BCOV and BW, and between BCOV and BD. The primary reason for recording BW and BD was validation of the visual sheep scores for BCOV (Australian Wool Innovation Ltd and Meat and Livestock Australia 2007). The strong genetic relationships between these traits confirm that the BCOV score is indeed a suitable industry method for assessing breech cover. In summary, the genetic correlations between indicator traits and wBRSTR recorded at marking were not as favourable as for the same traits recorded at birth.

Table 2. Arithmetic mean and standard deviation (sd), phenotypic variance (Vp), heritability (bold, diagonal), phenotypic correlations (above diagonal) and genetic correlations (below diagonal) for wrinkle and wool cover traits recorded at marking (m), and weaner (w) breech flystrike (standard errors in parentheses)

Trait	mNWR	mBDWR	mBRWR	mCCOV	mBCOV	mBW	mBD	TL	wBRSTR
Mean, sd	2.72, 0.89	2.37, 0.95	2.38, 1.02	3.50, 0.74	4.39, 0.66	26, 10	36, 19	237, 30	0.18, 0.48
Vp	0.54	0.63	0.73	0.42	0.34	53.4	146.0	601.5	0.21
	(0.02)	(0.02)	(0.02)	(0.01)	(0.01)	(1.5)	(4.3)	(22.4)	(0.01)
mNWR	**0.39**	0.71	0.67	0.06	0.02	0.00	0.00	0.09	0.09
	(0.04)	(0.01)	(0.01)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)
mBDWR	0.93	**0.36**	0.72	0.06	0.02	-0.01	-0.01	0.04	0.10
	(0.02)	**(0.03)**	(0.01)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)
mBRWR	0.93	0.91	**0.43**	0.05	0.02	0.01	-0.01	0.05	0.10
	(0.02)	(0.02)	**(0.04)**	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)
mCCOV	0.04	0.08	0.04	**0.35**	0.20	-0.14	-0.17	-0.10	0.06
	(0.08)	(0.08)	(0.08)	**(0.03)**	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)
mBCOV	-0.03	0.09	-0.04	0.46	**0.20**	-0.37	-0.44	-0.12	0.03
	(0.1)	(0.1)	(0.1)	(0.09)	**(0.03)**	(0.02)	(0.02)	(0.02)	(0.02)
mBW	-0.12	-0.13	-0.02	-0.44	-0.86	**0.23**	0.31	0.16	-0.06
	(0.1)	(0.1)	(0.10)	(0.09)	(0.06)	**(0.04)**	(0.02)	(0.02)	(0.02)
mBD	-0.05	-0.16	-0.03	-0.51	-0.80	0.52	**0.25**	0.17	-0.00
	(0.1)	(0.1)	(0.09)	(0.08)	(0.06)	(0.10)	**(0.04)**	(0.02)	(0.02)
TL	0.08	0.03	0.02	-0.25	-0.37	0.41	0.32	**0.62**	0.03
	(0.07)	(0.07)	(0.07)	(0.07)	(0.09)	(0.09)	(0.09)	**(0.04)**	(0.02)
wBRSTR	0.13	0.23	0.26	0.20	0.09	-0.08	-0.25	0.12	0.18
	(0.11)	(0.1)	(0.10)	(0.11)	(0.13)	(0.13)	(0.13)	(0.10)	(0.03)

Table 3 shows heritabilities for traits recorded post-weaning and their correlations with wBRSTR. Heritabilities were lower for all traits post-weaning compared to heritabilities for traits recorded at marking and birth. Genetic correlations of indicator traits post-weaning with wBRSTR were low, but higher than with traits recorded at marking. Genetic correlations between post-weaning wrinkle traits were lower than observed at previous recording times. The traits pCCOV and pBCOV had higher genetic correlations than were observed at other times and the correlation for breech measurements with wool cover traits remained negative and high. The genetic parameters for traits recorded post-weaning are generally more favourable than at marking time, but genetic parameters at birth and their relationship with wBRSTR are still the most favourable. It is acknowledged however, that birth traits are far more problematic to record, and therefore less likely to be adopted by industry than those recorded at marking, or even later at post-weaning or yearling ages. Although the heritability of BRWR was lower at post-weaning than marking, the genetic correlation between BRWR and wBRSTR at 0.62 was higher, which makes pBRWR a good alternative to bBRWR.

Table 3. Arithmetic mean and standard deviation (sd), phenotypic variance (Vp), heritability (bold, diagonal), phenotypic correlations (above diagonal) and genetic correlations (below diagonal) for wrinkle and wool cover traits recorded at post-weaning (p), and weaner (w) breech flystrike (standard errors in parentheses)

Trait	pNWR	pBDWR	pBRWR	pCCOV	pBCOV	pBW	pBD	wBRSTR
Mean, sd	2.39, 0.99	2.00, 0.86	2.75, 1.11	3.47, 0.75	3.96, 0.85	39, 14	43, 16	0.18, 0.48
Vp	0.53 (0.01)	0.41 (0.01)	0.63 (0.02)	0.36 (0.01)	0.46 (0.01)	87.4 (2.2)	147.7 (4.0)	0.21 (0.01)
pNWR	**0.24 (0.04)**	0.54 (0.01)	0.38 (0.02)	0.08 (0.02)	0.01 (0.02)	0.00 (0.02)	0.01 (0.02)	0.07 (0.02)
pBDWR	0.82 (0.07)	**0.17 (0.03)**	0.41 (0.02)	0.09 (0.02)	0.02 (0.02)	-0.03 (0.02)	-0.02 (0.02)	0.08 (0.02)
pBRWR	0.66 (0.08)	0.75 (0.08)	**0.30 (0.03)**	0.12 (0.02)	0.05 (0.02)	-0.03 (0.02)	-0.01 (0.02)	0.20 (0.02)
pCCOV	-0.01 (0.09)	0.04 (0.10)	0.15 (0.08)	**0.43 (0.04)**	0.29 (0.02)	-0.24 (0.02)	-0.24 (0.02)	0.09 (0.02)
pBCOV	-0.09 (0.10)	0.10 (0.11)	0.10 (0.09)	0.60 (0.06)	**0.30 (0.03)**	-0.54 (0.01)	-0.64 (0.01)	0.03 (0.02)
pBW	0.05 (0.10)	-0.17 (0.11)	-0.13 (0.09)	-0.55 (0.06)	-0.90 (0.04)	**0.28 (0.03)**	0.43 (0.01)	-0.03 (0.02)
pBD	0.06 (0.10)	-0.11 (0.11)	-0.11 (0.09)	-0.50 (0.06)	-0.94 (0.03)	0.81 (0.05)	**0.30 (0.03)**	0.02 (0.02)
wBRSTR	0.35 (0.13)	0.39 (0.13)	0.62 (0.09)	0.32 (0.10)	0.35 (0.11)	-0.35 (0.10)	-0.34 (0.10)	0.18 (0.03)

CONCLUSION

Traits that can be used early in life and which are correlated strongly with breeding objective traits can help accelerate genetic progress. In this study potential indicator traits for weaner breechstrike resistance measured at early ages, such as wrinkle and wool cover scores, were evaluated and showed potential to be used in the context of breeding for enhanced breechstrike resistance. However, it is acknowledged that trait recording at lambing time is more difficult than during routine husbandry procedures later in life. Once the necessary relationships have been established between these indicator traits and measures of breechstrike at adult ages, and with the other traits of economic importance, incorporation into industry breeding programs can be fully evaluated.

ACKNOWLEDGEMENT

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