Genetic Relationships between Indicator Traits for Fly Strike Resistance and Production Traits in Merino Sheep

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Introduction

Fly strike in sheep has been estimated to cost the Australian sheep industry approximately $280m dollars annually (Sackett *et al.* 2006) as a result of sheep losses, cost of treatment and loss of wool and carcase production and value. Historically Australian sheep producers have surgically removed skin from around the tail (mulesing) to help avoid fly strike. Although this has proved highly successful in the past, increasing public concern for animal welfare has forced sheep breeders to search for alternatives. One such alternative is to breed fly strike resistant sheep that do not require mulesing. While the breeding objective is to reduce fly strike, the trait itself if not conducive to measurement and direct selection. Research has revealed a number of indicator traits that are more readily measured and related to fly strike (James 2008; Greeff and Karlson 2009; Smith *et al.* 2009). These traits include wool cover, skin wrinkle, scouring (dags), wool colour and fleece rot. There is now a large data set of these traits in the Sheep Genetic database from both industry and research flocks. A subset of these traits is included in routine analyses to estimate Australian Sheep Breeding Values (ASBVs).

Accurate estimates of the relationships of these traits with key production traits are required to evaluate the impact of including fly strike in the overall breeding objective and using these traits as selection criteria. Due to the diverse nature of the Australian sheep flock and breeding philosophies and the increased use of across flock sires it is possible that the relationships observed across the entire population may be quite different to those within individual flocks. The aims of this study were firstly, to estimate the genetic correlations between the visual traits and production traits within the Sheep Genetics database, and secondly, to attempt to separate within and across flock genetic relationships.

Material and methods

Data. Pedigree and performance data were extracted from the Sheep Genetics MERINOSELECT database (Brown *et al.* 2007). This database consists of pedigree and performance records submitted by Australian ram breeders which are used for genetic evaluation purposes. For the visual traits Sheep Genetics currently utilises two observation ages, early (marking or weaning) and late (the first yearling, hogget or adult record). Data were

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extracted for early breech cover (ebcov), early breech wrinkle (ebwr), late body wrinkle (lbdwr), late wool colour (lcol), late dag (ldag), late fleece rot (lflrot), yearling (ywt), yearling greasy fleece weight (yfgw) and fibre diameter (yfd). A summary of the data is shown in Table 1. The pedigree was built using all available ancestral information. The data originated from 156 flocks across 16 years.

Table 1: Summary of the data used in this study

Trait	Pedigree	Sires	Dams	Records	Ncg*	Mean	SD	Min	Max
ebcov	50,742	2,922	18,991	29,300	305	3.5	1.0	1	5
ebwr	54,834	3,151	20,246	31,963	337	2.6	1.0	1	5
lbdwr	65,922	2,630	16,290	54,421	311	2.4	0.9	1	5
lcol	10,477	1,203	5,391	4,173	59	2.3	0.7	1	5
ldag	30,458	2,458	11,426	17,155	316	1.9	1.1	1	5
lflrot	26,552	1,301	9,981	20,932	121	1.6	1.3	1	5
ywt	160,458	6,331	70,660	90,792	1,298	45.2	5.6	18.1	87.1
ygfw	151,966	6,023	66,317	86,330	1,348	3.5	0.6	0.7	9.2
yfd	222,334	7,246	91,552	138,832	1,480	18.2	1.4	12.6	27.0

* number of contemporary groups

Statistical analyses. Parameters were estimated in bivariate analyses for each trait combination, fitting an animal model in ASReml (Gilmour *et al.* 2006). The full model included direct genetic, maternal genetic and dam permanent environment effects. Maternal genetic effects were only fitted for ywt and ygfw. For all traits the fixed effects of age and age of dam were fitted as covariates. Age of dam was fitted with both linear and quadratic components. Birth and rearing type were fitted as non-interacting fixed effects with levels ranging from 1 to 4 for both. Contemporary group (CG) was defined using flock, year of birth, sex, date of measurement and management group.

Table 2: Phenotypic variance (σ^2_p) and direct heritability (h^2_d) for each trait from each data set and model combination (± se)

	ebcov	ebwr	lbdwr	lcol	ldag	lflrot	ywt	ygfw	yfd
Full data set with normal model									
σ^2_p	0.48±0.01	0.75±0.01	0.55±0.01	0.30±0.01	0.80±0.01	1.16±0.01	35.1±0.66	0.34±0.01	1.68±0.03
h^2_d	0.30±0.02	0.40±0.03	0.39±0.02	0.37±0.05	0.26±0.02	0.18±0.01	0.66±0.06	0.60±0.05	0.67±0.04
Full data set with genetic groups									
σ^2_p	0.50±0.01	0.82±0.02	0.64±0.01	0.32±0.01	0.83±0.01	1.26±0.02	36.8±0.77	0.37±0.01	2.10±0.04
h^2_d	0.31±0.03	0.40±0.03	0.41±0.02	0.29±0.05	0.20±0.02	0.24±0.02	0.44±0.04	0.53±0.05	0.67±0.04
Home- bred progeny only									
σ^2_p	0.46±0.01	0.52±0.02	0.60±0.01	0.63±0.08	0.87±0.02	1.29±0.02	36.7±1.01	0.34±0.01	1.71±0.04
h^2_d	0.39±0.04	0.40±0.05	0.45±0.03	0.20±0.09	0.25±0.03	0.21±0.02	0.69±0.10	0.52±0.07	0.59±0.05

To examine the impact of across flock effects a series of bivariate analyses were completed with different models and data selection strategies; 1) complete data set with normal models, 2) complete data set with genetic groups (defined by flock), and 3) progeny of home-bred sires only with normal models.

Results and discussion

All traits studied had moderate to high heritabilities (Table 2). Significant maternal effects were observed for ebcov, ebwr, lbdwr, ywt and ygfw (not shown). The large level of genetic variation that exists for these fly strike indicator traits shows that genetic progress can be achieved. Heritabilities were similar between the models and data sets investigated.

The correlations between the fly strike indicator traits and production traits (Table 3) range from moderately unfavourable (eg yfd and ebwr of -0.38) to moderately favourable (eg ywt and ebcov of -0.33). The results also indicate that dag is less related with production traits than cover and wrinkle. These results clearly indicate that selection for reduce fly strike through these indirect selection criteria needs to be carefully applied through appropriate selection indexes which improve fly strike resistance and production simultaneously.

Table 3: Genetic correlations and flock mean EBV correlations with production traits from each data set and model combination (± se)

		Genetic Correlations			Correlation of flock means EBVs	
Trait1	Trait2	Full data set normal model	Full data set genetic groups	Home-bred progeny only	Full data set normal model	Full data set genetic groups
ywt	ebcov	-0.33±0.07	-0.16±0.08	-0.21±0.10	-0.43	-0.33
	ebwr	-0.13±0.06	-0.29±0.06	0.22±0.09	-0.47	-0.41
	lbdwr	-0.28±0.04	-0.28±0.04	-0.20±0.05	-0.36	-0.33
	lcol	0.65±0.11	0.59±0.12	0.23±0.36	0.34	0.04
	ldag	0.10±0.08	0.06±0.08	0.11±0.12	-0.02	0.05
	lflrot	0.10±0.07	0.01±0.08	0.13±0.07	0.20	0.25
ygfw	ebcov	-0.09±0.07	-0.06±0.07	n.e.	-0.15	-0.10
	ebwr	0.21±0.06	0.12±0.06	0.30±0.11	-0.18	-0.15
	lbdwr	0.11±0.04	0.16±0.04	0.15±0.05	0.07	0.08
	lcol	0.31±0.14	0.34±0.13	0.13±0.47	0.20	0.03
	ldag	0.10±0.10	0.04±0.12	0.13±0.18	0.07	0.00
	lflrot	0.22±0.06	0.11±0.07	0.22±0.07	0.00	0.17
yfd	ebcov	-0.19±0.05	-0.15±0.05	-0.07±0.09	-0.50	-0.47
	ebwr	-0.38±0.04	-0.36±0.04	-0.27±0.08	-0.51	-0.49
	lbdwr	-0.15±0.02	-0.14±0.02	-0.07±0.02	-0.51	-0.52
	lcol	0.31±0.08	0.32±0.09	0.48±0.20	0.31	0.33
	ldag	0.05±0.05	0.06±0.05	0.03±0.09	0.06	0.11
	lflrot	0.02±0.04	-0.09±0.04	0.02±0.04	0.13	0.17

* average genetic correlation ± average se

Sub-setting and modeling the data to separate the within and across flock genetic effects generally led to slightly smaller within flock relationships (Table 3) although the differences were not conclusive. The similarity of the genetic correlations between data sets and models also suggests that the current data structure is adequate to partition flock effects from the additive genetic effects.

The correlations between genetic group effects for different traits were generally in the same direction as genetic correlations, but were higher in magnitude. For example the correlation between the genetic group solutions for ywt, ygfw and yfd with lbdwr were -0.74, -0.50 and -0.39 respectively compared to the average correlations from the other models of -0.25, 0.14 and -0.12 respectively. The correlations between flock mean EBVs between these same traits were approximately -0.35, 0.08 and -0.50 respectively. Thus sire selection strategies across the population will have a significant impact on both the progress made for the fly strike resistance indicator traits and the achievable response in production traits. In the extreme case of selecting sires from across the entire population there would be a lot larger changes in the production traits compared to selecting only within a flock.

Conclusion

Susceptibility to fly strike in Australian Merino sheep populations can be reduced through selection on a number of indicator traits. However this should only be applied using an index selection approach to maximise simultaneous improvement in production traits. Selection response and correlated effects on production will change significantly with breeders individual sire selection strategies.

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