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PRELIMINARY INVESTIGATION OF THE GENETICS OF SHEDDING IN MATERNAL SHEEP

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SUMMARY

There has been increasing interest from commercial sheep producers to shift to shedding breeds such as the Dorper and Wiltshire Horn, which has triggered the development of shedding composite lines. This study analysed the genetic expression of spring shedding in adult ewes using a single-step animal model, from which potential marker effects could be identified. Early investigations into the genetic architecture of shedding support previous literature which suggests that the trait is highly heritable and controlled by a dominant gene effect. However, further research of major SNP effects within this population and the multi-breed population within the Sheep Genetics LAMBPLAN is required.

INTRODUCTION

The viability of sheep production systems can be impacted by the varying prices of commodities, such as labour and feed, and proceeds from wool and meat (Rose *et al.* 2014). This is evident in self-replacing meat focussed flocks where the value of the high micron wool is outweighed by the increasing cost to remove the wool, shearing and crutching, meaning wool is considered a net loss to the production system. This has resulted in commercial sheep producers shifting to shedding breeds and triggering the development of shedding composite lines throughout the Australian sheep meat industry. In these cases, the breeders are looking to take advantage of desirable 'Terminal' and 'Maternal' genetic characteristics of the major non-shedding breeds/composites while also introducing shedding attributes. Consequently, both the commercial and seedstock sectors are interested in breeding from animals with a known genetic capacity to shed their fleece. Shedding animals are considered easy-care animals with not only the demand for shearing greatly reduced but also a reduction in the need for preventative treatment practices.

Assessed through visual shedding scores, wool-shedding ability exhibited moderate to strong genetic variation in UK, and American flocks (Pollot 2011; Matika *et al.* 2013; Vargas Juardo *et al.* 2019) with heritability estimates ranging from 0.26 to 0.54. Preliminary analysis of an earlier subset of the shedding data utilised within this study, reported similar heritability estimates and showed strong genetic correlations between shedding scored at different ages of recording (Guy *et al.* 2021). This aligned with the findings of Vargas Juardo *et al.* (2019) and Vargas Juardo *et al.* (2016) who showed strong correlations between lamb and adult shedding assessments, and that shedding scores were highly repeatable across shedding events in adult sheep, respectively. This is not surprising with Pollot (2011) reporting that the mode of inheritance in shedding characteristics matches that observed of a dominant major gene effect. Thus, Matika *et al.* (2013) proposed that seasonal fleece shedding should be regarded as the ancestral trait where the dominant nature of the target locus suggests that the derived trait, that is, fleece retention, is caused by the recessive mutation.

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This study continues the analysis of shedding in two composite shedding flocks, previously reported by Guy *et al.* (2021), by analysing spring shedding expression in adult ewes using a single-step animal model, from which potential marker effects were identified.

MATERIALS AND METHODS

Shedding Data. Shedding was scored annually in late spring, between October and December, providing repeat records across 10 years within the two genetically linked composite shedding flocks in western Victoria. The flocks were developed from a composite maternal flock of primarily Coopworth origin, with the shedding characteristics infused via Dorper, Wiltipoll and Wiltshire Horn sires.

As per Guy *et al.* (2021), the wool-shedding score was based on the Sheep Genetics (2019) 1-5 scale. The shedding score refers to the animal's skin area covered in wool at the time of assessment. An animal with a score of 1 does not currently have wool longer than 1cm on any part of the body, it may have grown wool and completely shed, or it may be a hair sheep. An animal with a score of 5 is completely covered in wool (excluding the head and lower limbs). The three middle scores refer to the proportion of the body covered in wool and are independent of the pattern in which shedding is expressed. A score of 2 should reflect ~1-32% wool coverage, score 3 ~33-66% and score 4 ~67-99% wool coverage.

Statistical analysis. The analysed shedding traits were based on the expression of shedding of their first adult fleece (grown over winter) in a spring lambing flock. Three shedding traits were analysed within the study, 1) SS, shedding score (1 to 5 scale); 2) CS, fleece is Completely Shed (score 1 vs. scores 2-5); and 3) FF, No shedding evident (Full Fleece, score 5 vs. scores 1-4). The trait based on the shedding score was also analysed with a repeatability model, where repeat records (Table 1) were available across adult shedding periods (repeat across years).

Variance components and breeding values were estimated from a single-step genomic BLUP model incorporating genomic and pedigree information with a lambda of 0.75 (Legarra *et al.* 2014), using the WOMBAT linear model program (Meyer 2007). Shedding records were available for 6,226 animals, from two flocks, with an associated pedigree of 36,595 animals, with genotypes available for 11,435 animals. Animal information, pedigree and genotypes were sourced from the Sheep Genetics LAMBPLAN database (Brown *et al.* 2007). After the removal of SNPs based on QC checks, a combined imputed SNP genotype for 60,867 markers was constructed for all animals. In this preliminary study, breed effects were not accounted for in the genomic relationship matrix.

The fixed effects model included birth and rearing type (11, 21, 22, 31, 32, 33), sex (M, F), the number of days since the winter solstice (days, indication of days into the shedding period) as a linear covariate, and contemporary group. The contemporary group was defined as a concatenated term that included property, year of birth, year of shedding, and period of scoring (21-day window of recording, Table 1).

Marker effects. Wombat (Meyer 2007) was used to estimate marker effects for the shedding traits. Predicted marker effects were obtained as 'back solved solutions', through a linear transformation of the predicted breeding values 'single step' genomic BLUP, taking advantage of relationships between individuals and information from un-genotyped animals as per Aguilar *et al.* (2019). The derived probabilities were plotted as a Manhattan plot against the genome position of each SNP an arbitrary p-value of equal or less than 1.0×10^{-5} (blue line in figure 1) was considered as a threshold to identify regions of potential significance.

RESULTS AND DISCUSSION

The heritability of shedding score (1-5) within this population was moderate to high at 0.58 ± 0.03 (Table 1). This aligns with the previous literature estimates from pedigree-based animal models for populations of shedding composite sheep. Estimates ranged from 0.80 in UK Easycare sheep

(Matika *et al.* 2013), 0.47 to 0.59 in a US Romanov, White Dorper and Katahdin composites in the US (Vargas Jurado *et al.* 2020) and 0.54 in a NZ Wiltshire and Wiltshire-composite flock (Costilla *et al.* 2024). In support of the previous findings by Vargas Juardo *et al.* (2016), the shedding score was moderate to highly repeatable across adult shedding events, 0.54 ± 0.02 (Table 1). The heritability of the binary CS trait was lower at 0.17 (Table 1), which suggests that there may still be genetic variation in shedding beyond just that associated with a single dominant gene effect. The FF trait was explored to test the Matika *et al.* (2013) proposal that the fleece retention is caused by a recessive mutation and thus the threshold between scores 4 and 5 would be triggered by the dominant gene. However, whilst convergence was achieved the linear multifactorial model has limitations for this trait, where the low proportion of expression (4%, Table 1) exacerbates the binary nature, producing a heritability of 0.13 ± 0.02.

Table 1. Data summary and parameter estimates from the univariate analysis of spring shedding traits in composite shedding sheep

	First winter shedding			**Repeat adult shedding**
Trait	Full Fleece (1/0)	Completely Shed (1/0)	Shedding Score (1-5)	Shedding Score (1-5)
Animals	4,345	4,345	4,345	6,226
Records	4,345	4,345	4,345	10,629
CGs	31	31	31	147
Trait mean	0.04	0.26	2.46	2.55
Phenotypic Variance	0.03 ± 0.00	0.17 ± 0.00	1.12 ± 0.03	1.10 ± 0.02
Heritability	0.13 ± 0.02	0.46 ± 0.03	0.58 ± 0.03	0.45 ± 0.02
Repeatability				0.54 ± 0.02

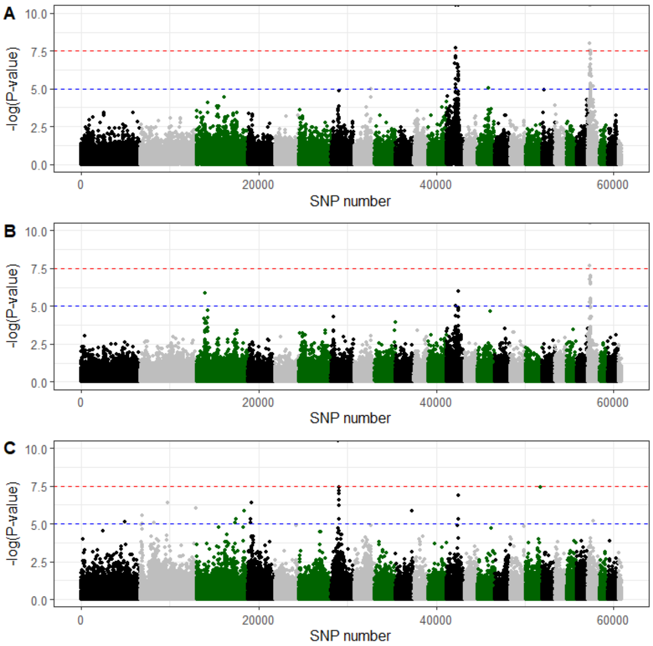

Figure 1. Significance of marker effects from back solved solutions from single-step univariate analysis for Shedding traits recorded on the animal's first adult fleece (A; Shedding score (SS, 1-5), B; Completely Shed (CS, 1/0), C; Full Fleece (FF, 1/0)

Estimates of the significance of marker effects back-solved from the single-step G-BLUP are presented in Figure 1. When shedding was analysed using the SS trait, regions of interest were identified on chromosomes 7, 8, 13, 15, 19 and 23. Marker effects from the CS trait reduced the significance of regions on chromosomes 13 and 23. A peak on chromosome 3 was also observed for the CS trait. A GWAS study of 200 Easycare-shedding sheep (Matika *et al.* 2013) noted a significant SNP on chromosome 3 but discounted it due to the low allele frequency. The small proportion of fully fleeced animals in this study limited the ability to describe the genetics of shed vs. fleeced animals. However, a noticeable peak was observed on chromosome 7 for the FF trait.

Early investigations into the genetic architecture of shedding in these composite shedding flocks align with the previous literature proposals for a dominant major gene effect, with several potential chromosomal regions identified. However, as with the study by Matika *et al.* (2013), the shedding gene in this population has been infused via a limited number of sire lines, thus noticeable regions of significance may reflect breed effects not necessarily the causative shedding gene. Additional analysis regarding the location of significant SNPs along the genome within this population and the multi-breed population within the Sheep Genetics LAMBPLAN are required, but also whether different chromosomal regions are associated with shedding in the wool breeds like the Wiltipol compared to the more hair breeds such as the Dorper.

CONCLUSION

Early investigations into the genetic architecture of shedding in an Australian composite shedding population support previous literature that suggests that the trait is highly heritable and controlled by a dominant gene effect. Consequently, genetic selection can proceed effectively even though marker effects are yet to be identified. Further research on the impact of significant SNPs for shedding within the Australian sheep population is required.

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