

Exploring the genetic architecture of fleece shedding in Australian sheep

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Introduction

Sheep production systems oriented towards meat or milk production often generate coarse wool (25–40µm fibre diameter) as a by-product, which has limited value in high-quality apparel markets. Over the past decade, global prices for coarse wool have declined markedly, while the cost of wool harvesting in Australia has increased by more than 200%. Consequently, producers are seeking alternative strategies to reduce shearing costs, including the introduction of genetic material from breeds that naturally shed their fleeces into established terminal and maternal lines. Prior studies have shown that fleece shedding as a scored trait is highly heritable, with estimates ranging from 0.40 to 0.80 in adults and lambs (Pollott, 2011; Matika *et al.*, 2013; Costilla *et al.*, 2025). Given these high heritability estimates, some effort has been directed towards understanding the inheritance of fleece shedding and assessing the potential existence of major genes as a means of accelerating genetic improvement. Using Mendelian ratios from structured crosses and backcrosses in UK shedding composites, Pollott (2011) suggested an autosomal dominant mode of inheritance with low levels of incomplete penetrance. Matika *et al.* (2013) later found evidence for major genes with dominance effects in a similar flock, as well as additional variation not explained by a single locus. They proposed that there may be several additive effects that modify the rate, extent and pattern of shedding, indicating a more complex genetic architecture. Despite these findings, previous analyses were conducted on relatively small datasets. Therefore, it remains unclear whether the same genetic architecture, particularly the balance between major gene and polygenic effects, applies to Australian shedding populations. This study aimed to identify potential genomic regions and candidate genes associated with fleece shedding using regional heritability mapping and genome-wide association studies (GWAS).

Materials & Methods

Phenotype & SNP information. Fleece shedding was visually scored during peak expression (October–December) on a five-point scale (1 = complete shedding, 5 = fully woolly) on four genetically linked farms in southern Australia, between 2015 and 2025. Shedding genetics were introduced into these predominantly Coopworth-based maternal composite flocks using Dorper and Wiltipol genetics. Shedding expression among lambs (<11 months) and a subset re-scored as adults (ewes only, 1–7 years) were analysed as a separate trait (means (SD): lambs 4.20(0.99); adults 3.11(1.25)). Animals were genotyped using commercially available 50K SNP arrays, with genotypes imputed to the common set of 62K SNPs routinely used for genomic analyses in Australia to unify data across genotyping panels, following Daetwyler *et al.* (2010). Quality control (QC) excluded SNPs with a minor allele frequency < 0.025, deviations from Hardy-Weinberg equilibrium ($P < 1 \times 10^{-8}$), or call rate < 0.95, and individuals with call rates < 0.95. After QC, shedding records were available for 11,690 lambs and 5,912 adults, with 60,349 autosomal SNPs retained in the analysis.

Chromosomal & regional heritabilities. All analyses were performed using GCTA v1.94.1 software (Yang *et al.*, 2011) to estimate variance components, chromosomal and regional heritabilities, and to conduct a GWAS (using MLMA). Regional heritability mapping was based on sliding windows of 100 SNPs, along each chromosome, with 50% overlap. Genomic relationship matrices (GRMs) were constructed using Yang's method for focal chromosomes or genomic windows and a complementary GRM comprising all remaining SNPs. Variance components were estimated using a GREML. Fixed effects included were birth-rearing type (lambs only, 3 levels), contemporary group (defined by flock, year of birth and year of shedding measurement; lambs n=95 and adults n=125), days since winter solstice as a covariate with mean 88days (SD=15) lambs and 149days (SD=22) in adults, and the three major breed components derived from unsupervised breed structure analysis to account for the composite nature of the population. Chromosomal and regional heritabilities were calculated as the proportion of additive variance explained by SNPs assigned to each chromosome or genomic window relative to the overall phenotypic variance. Genomic windows explaining $\geq 2\%$ of the phenotypic variance were defined as key regions.

GWAS & SNP annotation. GWAS were conducted using the same fixed effects model described above. Multiple testing was controlled using a Bonferroni correction based on the number of SNPs retained after QC ($P < 0.05/60,349$), with SNPs considered significant at $-\log_{10}(P) > 6.08$. The most significant SNPs were annotated to nearby genes using the *Ovis aries* v3.1 genome assembly via the NCBI Genome Data Viewer.

Results & Discussion

Heritability of fleece shedding estimated using the full GRM was $0.54 (\pm 0.02)$ in lambs and $0.58 (\pm 0.02)$ in adults. Additive genetic variance was 0.52 and 0.64, and phenotypic variance was 0.98 and 1.12 in lambs and adults, respectively. These estimates are consistent with previous reports (0.39 to 0.52 ± 0.05 ; O'Connell *et al.*, 2012 and Costilla *et al.*, 2024) and from a subset of the current dataset (0.46 to 0.58 ± 0.03 ; Walkom *et al.*, 2015). Partitioning additive genetic variance by chromosome showed broadly similar patterns between lambs and adults, with chromosomal heritabilities ranging from 0.00 to 0.08 (Fig.1). In both analyses, OAR 23 explained a disproportionately large amount of genetic variance relative to chromosome length (above the regression line Fig.1), with heritability estimates of 0.081 ± 0.01 in lambs and 0.077 ± 0.01 in adults. In adults, OAR 3 and OAR 13 also contributed disproportionately to genetic variance ($\sim 0.075 \pm 0.01$ each), with similar but slightly lower contributions observed in lambs ($\sim 0.063 \pm 0.01$). These results indicate that additive genetic variance for fleece shedding is not evenly distributed across the genome, which is consistent with the presence of one or more major loci and additional polygenic effects.

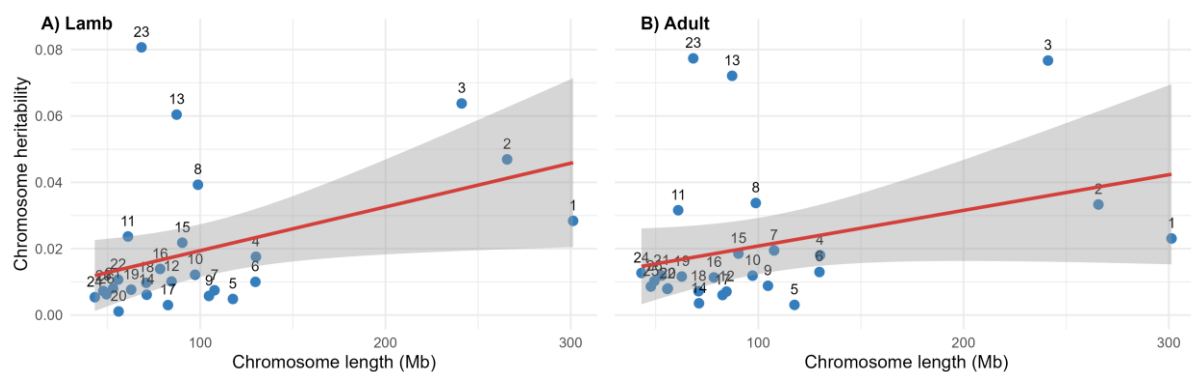


Figure 1. Chromosomal heritability (numbered) of fleece shedding in A) lambs and B) adults. The regression line indicates expected heritability based on chromosome length.

Fig.2 shows regional heritability estimates based on sliding windows of 100 SNPs with 50% overlap. Several regions on OAR 8, 13 and 23 exhibited elevated regional heritability, consistent with the chromosomal partitioning results. Eight key windows ($\geq 2\%$ of phenotypic variance explained) were identified in both analyses. On OAR 23, the top window explained a regional heritability of 0.037 ± 0.01 in adults and 0.067 ± 0.01 in lambs. The top seven windows were common to both lamb and adult traits, suggesting that similar genomic regions contribute to shedding across life stages. However, the overlapping nature of sliding windows may make precise localisation of causal regions difficult. Future analyses using non-overlapping or smaller windows, or regional haplotypes, may provide clearer resolution of the contributing regions.

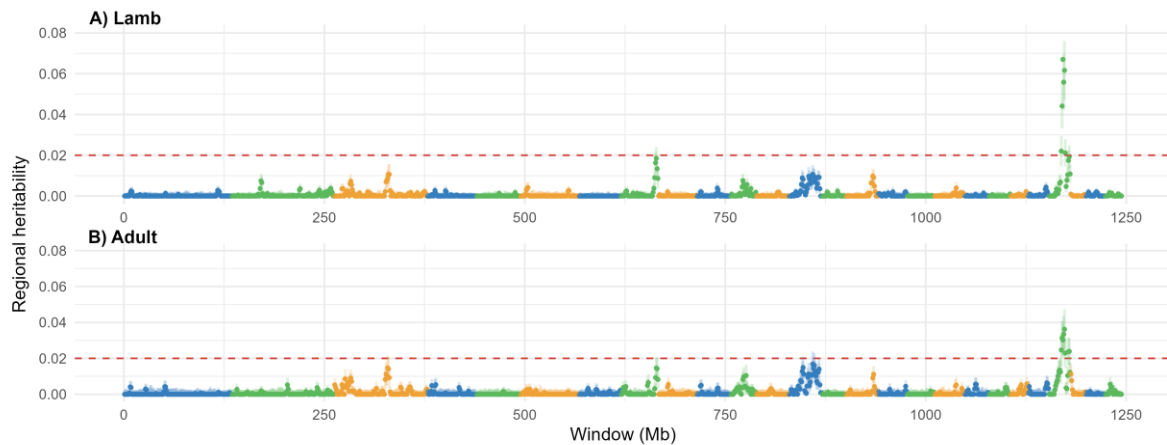


Figure 2. Regional heritability estimates of 100 SNP sliding windows in A) lambs and B) adults, coloured by chromosome number. Key windows are identified above the dashed line.

The GWAS results in Fig.3 identified 55 and 24 SNPs exceeding the genome-wide significance threshold in lambs and adults, respectively, with 20 SNPs common to both analyses. The top-associated variant on OAR 23 explained $\sim 2.1\%$ of the phenotypic variance in lambs and $\sim 1.8\%$ in adults. Additionally, 17 SNPs in lambs and 13 SNPs in adults explained more than 1% of the phenotypic variance, suggesting several loci of moderate- to large effect contribute to fleece shedding. These findings differ from those of Matika *et al.* (2013), who identified significant regions for fleece shedding on OAR2 and OAR5 in an adult Dorper-Katahdin flock. However, their analysis included only 48 genotyped animals and suggested that dominance effects, rather than additive effects, were the primary drivers of shedding. Here, the dominance effect was not tested; however, the results indicate that significant additive genetic effects are present in this population, aligning with Walkom *et al.* (2025), who used a subset of the current dataset and identified significant regions on OARs 23, 13, and 8. Future work could explicitly model both additive and dominance effects to clarify the genetic architecture of fleece shedding further and investigate the difference between treating the trait as binary or linear, which may help to clarify the presence of dominance effects.

Several lead SNPs were located within or in close proximity to candidate genes, including *SETBP1*, *PIEZO2*, *RAB31* and *HNRNPA2B1*, which are involved in transcriptional regulation, mechanosensory signalling and cellular regulatory processes (Wang *et al.*, 2015; Becker *et al.*, 2025). Notably, *PIEZO2* has been implicated in mechanotransduction in skin and sensory tissues, suggesting a biologically plausible role in structural or follicle-related phenotypes (Wang *et al.*, 2015). *SETBP1* encodes a transcriptional regulator and has been associated with wool production and quality and the development of early-onset androgenetic

alopecia in humans (Li *et al.*, 2012; Becker *et al.*, 2025). While these associations do not imply causality, they highlight candidate genes and functions through which genetic variation may influence phenotypic expression of shedding.

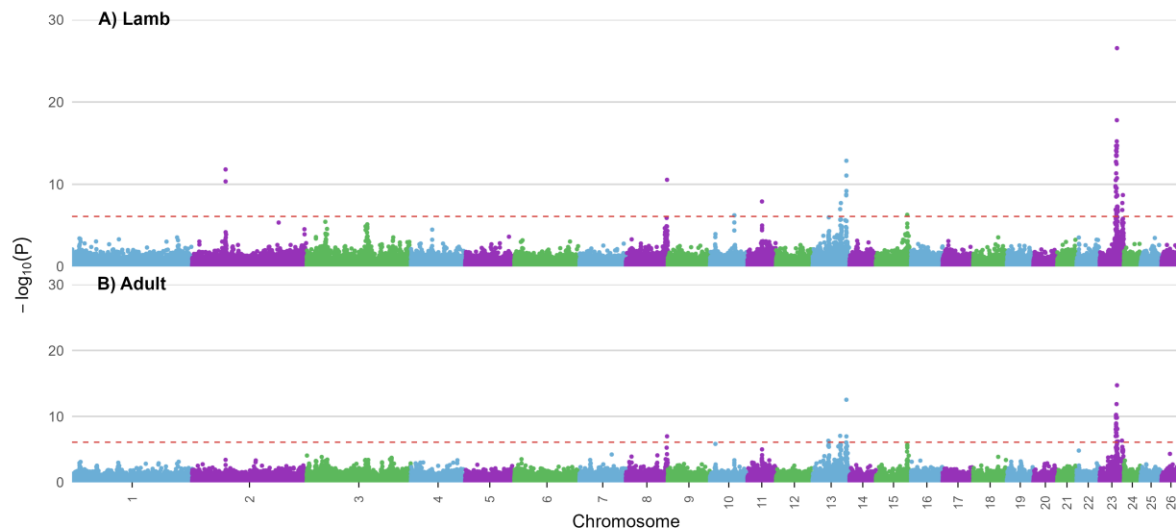


Figure 3. Marker effect for A) lamb and B) adult shedding, dashed line indicates the Bonferroni threshold.

Conclusions

Genetic variation in fleece shedding has been observed in Australian maternal composite sheep and appears to be polygenic, with many moderate-effect loci distributed across the genome. Although OAR 23 harbours regions with disproportionately high genetic variance, it is unlikely to provide sufficient predictive power on its own. Therefore, genomic selection using estimated breeding values that capture the polygenic architecture, potentially via weighted genomic relationship matrices, may be the most effective approach for industry evaluation of fleece shedding in Australian sheep.

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