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GENETIC EVALUATION OF TAIL LENGTH IN AUSTRALIAN SHEEP

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SUMMARY

Sheep tail docking is common practice to reduce the incidence of flystrike and stained fleece, yet it is associated with poor animal welfare. This study aims to explore genetic variation in tail length, which may offer the potential to reduce sheep tail length via genetic selection. Tail length is moderate to highly heritable (0.35±0.01-0.67±0.03) with low (0.14±0.01) to moderately high (0.37±0.01) genetic correlations with body weight. These results indicate tail length may be reduced via genetic selection, offering a welfare-friendly alternative to tail docking.

INTRODUCTION

Flystrike cost the Australian sheep industry in excess of $300 million in 2022 (Shephard *et al.* 2022). Tail length is a key indicator of breech flystrike, as long tails are associated with faecal- and urine-stained fleece which attract the sheep blowfly (James 2006). Currently, sheep producers dock tails at marking using either a hot knife or rubber ring (Grant 2004). However, both methods are associated with poor animal welfare and can negatively impact lamb growth rates. Whist retaining an appropriate tail length (approx. third or fourth tail joint) prevents rectal prolapse and cancer (Woodruff *et al.* 2023), public expectations of sheep welfare may result in tail docking being banned. Therefore, exploring welfare-friendly, cheaper alternatives like genetic selection to reduce sheep tail length, with minimal health and production impacts is important.

Past research found tail length to be moderate to highly heritable (0.38 – 0.68; Greeff *et al.* 2015; Johnson *et al.* 2023; Oberpenning *et al.* 2023; Teubes *et al.* 2023). Strong positive genetic correlations between tail length and body length, tail length and body weight at marking (Greeff *et al.* 2015; Teubes *et al.* 2023). However, these studies were focussed on single flocks of Merino sheep. Past studies also used varied in their method of phenotyping, hence, it is also unclear whether a subjective tail length score (1-5) is adequate, or whether an objective measurement (cm) may be more appropriate to define the tail length phenotype. This study investigated tail length across multiple flocks and breeds to quantify genetic variation in tail length in mixed breeds of sheep and phenotyping protocols, and its correlation with body weight.

MATERIALS AND METHODS

Phenotypes. Tail length and body weight records on 57,760 lambs from the Information Nucleus and MLA Resource Flock (van der Werf *et al.* 2010) and industry flocks were sourced from the Sheep Genetics database. Breeds represented in industry flocks included commercial shedders and a maternal composite from a Coopworth base. The dataset included phenotypes measured two ways – 1) assessed as a 1 to 5 score of tail length relative to the hock, or 2) measured in cm from the tip of the tail to the base (Greeff *et al.* 2015). Data editing removed sites with low numbers of animals phenotyped (n<500), animals with non-genetic influences on tail length performance (i.e., tail bitten off), where the average age of the contemporary group was <14 days and >85 days (to align with commercial sheep marking periods). Further data was removed including tail length records taken

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at birth due to low record counts and when measured tail length records were outside of 4 standard deviations (SD) from the mean. The final dataset included animals from 6 flocks, measured across 12 years comprising 35,383 records for assessed tail length score and 8,964 records for measured tail length (Table 1). Where an animal had multiple body weights taken, the weight measured closest to the date of tail measurement (n=44,347) was used for the bivariate analysis.

Table 1. Summary statistics of tail length phenotypes used in the analysis

Trait	Assessed (score 1-5)	Measured (cm)	Scaled trait (1-5)
Flocks	6	2	6
Animal count	35,383	8,964	44,347
Sire breeds	12	25	27
CGs	344	74	416
Mean age at tail (SD)	29.17 (17.58)	30.76 (8.51)	45.45 (17.77)
Mean tail length (SD	2.82 (0.69)	24.77 (0.411)	2.94 (0.71)
Mean age at weight (SD)	51.04 (19.77)	31.39 (9.06)	47.32 (19.79)

Statistical analysis. To evaluate whether tail length can be adequately phenotyped using a subjective assessment (score 1-5) only (i.e., no measured (cm) trait), a third tail length trait was created (n=44,347) based on all records with both an assessed score and measured tail length. To create the scaled trait, the distribution of measured and assessed data was first evaluated, then a normalisation formula was applied to transform measured tail data to a scaled score (1-5) value that followed a normal distribution. A univariate animal model using a pedigree of 100,648 animals over 18 and 22 generations on the dam and sire side, respectively, was performed using ASReml (version 4.2) (Gilmour *et al.* 2021) for the three tail length traits. Fixed effects included lamb contemporary group (defined as site of measurement, sex, year of birth, and date of measurement), birth type (n=3), age in days at tail measurement (n=123), and age of the dam was fit as a categorical variable (n=12). A second univariate analysis was performed with all prior noted effects, as well as body weight as a covariate. The full model fit for each tail trait was

$$y = \mathrm{X}b + \mathrm{Z}a + e$$

where y, b, a, and e are the vectors of observed traits of animals, fixed effects, direct additive genetic effects, and residual effects, respectively, and X and Z are the incidence matrixes for the fixed and direct additive genetic effects, respectively. Bivariate analysis was performed between the tail traits and body weight. The fixed effects previously defined were fitted with additional fixed effects for body weight (age at body weight measurement (n=138), rear type (n=3), and a random maternal genetic effect). Maternal permanent environment and sire breed effects were found to be low and not significantly different from 0, respectively, (results not reported) and excluded from the model.

RESULTS AND DISCUSSION

Heritability. Variance components for the tail length traits with and without body weight fitted as a co-variate are shown in Table 2. Heritability estimates ranged from 0.34 to 0.67 which are similar to those reported in the literature (Greeff *et al.* 2015; Johnson *et al.* 2023; Oberpenning *et al.* 2023). The heritability of measured tail length was significantly higher than both the 1-5 score estimates. This is likely due to different progeny- and sire-breeds and phenotyping protocol (Table 1), as well as any reduced accuracy resulting subjective assessment compared with objective measurement. As more sire breeds were represented in the progeny with measured tail length, there was greater variation in measured tail length which may explain its higher heritability. Both the 1-5 assessed and scaled traits were associated with a lower heritability compared to the measured trait (Table 2). The scaled trait also had a high number of sire breeds represented therefore, it may be possible that the lower associated heritability for both assessed and scaled (1-5) tail length is a result of the reduced variation from a subjective assessed score compared to an objective measured trait. Greeff *et al*. (2015) reported similar heritability estimates for both tail length and reported no significant influence of maternal permanent environmental effects. Further, when body weight at lamb marking was fit as a covariate the tail length heritability was reduced.

Table 2. Genetic parameter estimates and standard errors (± SE) for tail length traits

Tail measurement	Weight fit as covariate	Phenotypic variation ± SE	Genetic variation ± SE	Heritability ± SE
Assessed (1-5 score)	No	0.44±0.00	0.18±0.01	0.41±0.01
Measured (cm)		9.59±0.16	6.46±0.36	0.67±0.03
Scaled trait (1-5)		0.37±0.00	0.13±0.01	0.35±0.01
Assessed (1-5 score)	yes	0.43±0.00	0.18±0.01	0.41±0.01
Measured (cm)		8.56±0.15	5.56±0.32	0.65±0.03
Scaled trait (1-5)		0.37±0.00	0.13±0.01	0.34±0.01

Genetic correlations. Phenotypic correlations ranged from 0.24 to 0.51, and genetic correlations ranged from 0.14 to 0.37, depending on the method of tail length phenotyping (Table 3). Correlations reported in the present study align with Oberpenning *et al.* (2023), however are lower than those reported by Greeff *et al.* (2015). This may be due to Greeff *et al.* (2015) measuring body weight and tail length measurement on the same day compared to the present study where this was not necessarily the case. Age at phenotyping (both tail length and body weight) was fit in the model to try to account for this. While the present study did not have enough records to evaluate the relationship between tail length and body length, past research by Greeff *et al.* (2015) noted body weight and body length adjustments at lamb marking removed any genetic correlation between tail and body length. Hümmelchen *et al.* (2025) reported small differences in body weight between short and long tailed groups. Genetic correlations between assessed and measured tail length measurement (cm) were able to be estimated in the present study due to singularities resulting from insufficient data. This warrants further investigation.

Table 3. Genetic and phenotypic correlations (± SE) for tail length and body weight

Body weight	Assessed (1-5 score)	Measured (cm)	Scaled trait (1-5)
Genetic correlation ±SE	0.14±0.01	0.37±0.01	0.16±0.01
Phenotypic correlation ±SE	0.24±0.03	0.51±0.04	0.31±0.03

Recommendations. Reducing tail length via genetic selection may be a viable, welfare friendly alternative to tail docking as it is moderate to highly heritable. However, the heritability of assessed tail length was approximately 20% lower than measured tail length. Given there was no significant difference the heritability estimates of assessed tail length and the scaled trait, it may be a viable option to develop breeding values based on assessed tail length in industry flocks (enabling greater levels of trait recording due to simplicity) and the scaled traits based on measured tail length in resource flocks. Despite the unfavourable genetic correlation between tail length and body weight, sheep producers may make gains in both traits by identifying and selecting animals which perform favourably for both traits or using a selection index appropriately weighting both traits. The relationship between tail length, body length, and carcase structure requires further investigation, as past studies have reported carcase abnormalities in shorter tailed sheep (James 2006). Assessment of tail length as a 1-5 score, with tail length relative to the hock (Table 4) as recommended by Greeff *et al.* (2015) could be a viable option for industry sheep flocks to genetically reduce tail length.

Further, it would be worthwhile assessing and measuring tail length in MLA research flocks to allow for future investigation into the relationship between both traits. While the dataset used in this study is larger than past studies, it is still relatively small, and it would therefore be worthwhile re-estimating genetic parameters following the collection of more tail length measurements according to the protocol suggested. It would therefore be worthwhile recommending measuring body weight at the same time as phenotyping for tail length for any future re-estimates of genetic parameters.

Table 4. Recommended scoring guide for measuring tail length

Score	Tail length
1	Tail is half way from the base of the tail to the hock
2	Tail is three quarters of the way from the base of the tail to the hock
3	Tail is at the hock
4	Tail is longer than the hock
5	Tail is towards the pasterns/very long

CONCLUSION

The moderate to high heritability of assessed and measured tail length indicates that genetic selection offers a welfare friendly alternative to tail docking. However, the unfavourable genetic correlation with liveweight needs to be accounted for in breeding programs. Phenotyping tail length using an assessment (1-5 score) provides a simple, quick measure of tail length for sheep breeders interested in genetically reducing tail length. Further work is required to estimate genetic correlations between tail length and additional important to sheep production traits like carcase composition and quality, wool quality and production, and reproduction.

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