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# INHERITANCE OF WRINKLE IN MERINO SHEEP AT DIFFERENT AGES

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## SUMMARY

The inheritance of wrinkle on the neck and on the tail was investigated in a medium micron Merino flock in a Mediterranean environment from birth to hogget shearing. It was moderate to highly heritable (0.32 to 0.74) at all ages but it was not genetically the same trait at the different ages. Log transforming the data did not generally increase the heritability of the trait. Body wrinkle at birth was genetically moderately to lowly correlated with neck and skin wrinkle at later ages. The best time to score tail wrinkle in a Mediterranean environment is between yearling and hogget age as this is when the heritability and variation of the trait was the highest.

## INTRODUCTION

High breech or tail skin wrinkle is one of the most important predisposing factors for breech strike in Merino sheep (Greeff *et al.* 2014; Smith *et al.* 2009). Morley *et al.* (1952), Brown *et al.* (2010), Greeff *et al.* (2014), Hatcher and Preston (2015) and Smith et al. (2009) showed that skin wrinkle is a heritable trait and Greeff *et al.* (2014) showed that neck wrinkle at yearling age was the best indicator trait to select for reduced wrinkle. Scholtz *et al.* (2010) reported that the correlations between neck wrinkle, body wrinkle and breech wrinkle scored at hogget age were generally high ($r_g > 0.89$), implying that selecting on any trait will result in a correlated response in the other. However, the Mediterranean regions of Australia suffer from large fluctuations in rainfall from hot, dry summers to cold, wet winters. This results in dramatic changes in the feed supply during the year, often requiring animals to be supplementary fed during the dry times of the year. Schlink *et al.* (2000) and Herselman and King (1993) showed that large changes in skin wrinkles and skin weight can occur during the year in Merino sheep on high and low planes of nutrition. Adding the effect of different times of crutching and shearing, growers need to consider a range of environmental and management factors under their specific production system, in selecting the best indicator trait for reduced skin wrinkle at different ages.

## MATERIAL AND METHODS

The Australian Wool Innovation Breech strike flock of the Department of Agriculture and Food Western Australia was used to investigate the inheritance of neck and tail wrinkle during the year up to hogget age, as well as the genetic and phenotypic relationships between neck and tail wrinkle from birth to hogget shearing.

The flock consisted of 3623 lambs born from 1674 dams that were mated to 80 rams over a four-year period (2010 to 2013). The lambs were scored for body wrinkle at birth and for neck wrinkle and tail wrinkle at marking, weaning, early post-weaning, post-weaning, yearling and hogget shearing (16 months), using the visual sheep scoring system (AWI, 2008). As the animals in the flock were relatively plain, and previous studies (Greeff, submitted) have shown that tail wrinkle was a better indicator trait to differentiate between sheep than breech wrinkle, tail wrinkle was used in this study. Skin wrinkle was scored from 1 (plain) to 5 (high wrinkle count), and half scores were allocated where appropriate.

Lambs were born in July/August, and marked in late August. They were weaned at approximately 100 days of age. The lambs were shorn approximately 5 weeks after weaning, and crutched at 12 months of age in July the following year. They were shorn with 12 months wool in early December when the sheep were approximately 18 months of age.

## STATISTICAL ANALYSIS

ASREML (Gilmour *et al.* 2009) was used to analyse the data. A series of univariate analysis were carried out on each of the skin traits (body wrinkle at birth, neck and tail wrinkle at marking, weaning, early post-weaning, post-weaning, yearling, hogget and at post hogget shearing) to obtain estimates of the heritability of skin wrinkle at different ages on the neck and tail. Year of birth (2010-2013), age of the dam (2-7 years), birth status (single or multiple) and sex of the lamb were fitted as fixed effects. All two-way interactions were initially fitted. Statistically non-significant factors were dropped from the final model. This was followed by a bivariate analysis to obtain genetic and phenotypic (co)variances to estimate the phenotypic and genetic correlations between skin wrinkle on the neck and on the tail at different ages. Two analyses were carried out on each trait: one on the raw trait scores and one where the trait had been log transformed (log(wrinkle+10)) to normalise the data as it was skewed distributed in all cases, with low numbers of animals in the higher wrinkle categories.

## RESULTS AND DISCUSSION

Table 1 shows that the highest expression of wrinkle was recorded for body wrinkle at birth. This is contrary to eastern state results which show that the highest expression of skin wrinkle was at weaning (Dun and Eastoe, 1970). In this study, the average neck and tail wrinkle then reduced by more than one unit score at marking, weaning, early and post weaning. This trend can be explained as it is difficult to score wrinkle on sheep with long wool. However, at yearling and at hogget age, tail wrinkle increased and was higher than neck wrinkle. This was probably due to the fact that tail wrinkle was scored post shearing in order to be able to better differentiate between animals. In addition, the scoring system may have also contributed as half scores were also used to capture as much of the differences as possible.

**Table 1. Average skin wrinkle scores (± SD) and the number of records in different ages**

| | Birth | Marking | Wean | Early post weaning | Post weaning | Yearling | Hogget |
|---|---|---|---|---|---|---|---|
| Body wrinkle | 2.86 | | | | | | |
| SD | 1.04 | | | | | | |
| Neck wrinkle | | 1.73 | 1.68 | 1.85 | 1.63 | 1.26 | 1.43 |
| SD | | 0.55 | 0.52 | 0.50 | 0.37 | 0.58 | 0.53 |
| Tail wrinkle | | 1.39 | 1.28 | 1.47 | 1.02 | 2.11 | 2.12 |
| SD | | 0.42 | 0.45 | 0.41 | 0.09 | 0.95 | 0.94 |
| No. of records | 3623 | 2782 | 3585 | 1944 | 3501 | 1709 | 1680 |

Body wrinkle at birth showed the highest amount of phenotypic variation, followed by tail wrinkle at yearling age. The lowest amount of phenotypic variation was found for post weaning wrinkle score. The heritability estimates of neck (Table 2) and tail wrinkle (Table 3) in general agreed with previously published results (Morley, 1952). However, it differed at different ages. The highest estimate on the raw data was at yearling age (0.74) which decreased to 0.37 when log transformed. Transformation of wrinkle sometimes increased the heritability estimate but in other cases it decreased it. It appears that the accuracy of selection is higher for untransformed skin wrinkle score data in this flock.

The phenotypic correlations between the neck wrinkle traits varied from 0.27 to 0.65. Traits closer together had higher correlations than traits further apart. However, neck wrinkle at yearling age appears to be less strongly correlated with the neck wrinkle traits scored at other times.

The genetic correlation between neck wrinkle, and between tail wrinkle at different ages, were higher than the phenotypic correlations. Tail wrinkle and neck wrinkle were genetically highly correlated when scored at the same age ($r_g > 0.085$) (estimates not shown). However, the genetic correlations between body wrinkle at birth, and neck or with tail wrinkle was generally low. Body wrinkle at birth was most correlated with neck wrinkle ($r_g = 0.54$) and tail wrinkle ($r_g = 0.58$). This indicates that body wrinkle at birth is not genetically the same trait as neck or skin wrinkle later in life.

**Table 2. Phenotypic variances (Vp), heritability (on diagonal), phenotypic correlations (above diagonal), and genetic correlations (below diagonal) of body wrinkle at birth (BBDWR) and neck (NKWR) at marking (M), weaning (W), early post weaning (E), post weaning (P), yearling (Y) and hogget (H) shearing**

| | BBDWR | MNKWR | WNKWR | ENKWR | PNKWR | YNKWR | HNKWR |
|---|---|---|---|---|---|---|---|
| *Raw wrinkle scores* | | | | | | | |
| Vp | 1.01 | 0.31 | 0.27 | 0.25 | 0.14 | 0.33 | 0.28 |
| BBDWR | **0.53** | 0.37 | 0.26 | 0.24 | 0.14 | 0.17 | 0.19 |
| MNKWR | 0.54 | **0.66** | 0.48 | 0.51 | 0.30 | 0.27 | 0.40 |
| WNKWR | 0.36 | 0.77 | **0.42** | 0.54 | 0.39 | 0.42 | 0.38 |
| ENKWR | 0.34 | 0.78 | 0.77 | **0.55** | 0.47 | 0.39 | 0.47 |
| PNKWR | 0.20 | 0.59 | 0.64 | 0.78 | **0.37** | 0.35 | 0.39 |
| YNKWR | 0.25 | 0.55 | 0.69 | 0.71 | 0.64 | **0.32** | 0.65 |
| HNKWR | 0.33 | 0.64 | 0.68 | 0.82 | 0.74 | 0.90 | **0.47** |
| SE range | 0.04-0.07 | 0.02-0.08 | 0.02-0.07 | 0.02-0.08 | 0.02-0.08 | 0.02-0.05 | 0.02-0.02 |
| *Log transformed wrinkle score (+10)* | | | | | | | |
| Vp | 0.006 | 0.002 | 0.002 | 0.002 | 0.001 | 0.002 | 0.002 |
| BBDWR | **0.53** | 0.36 | 0.26 | 0.24 | 0.14 | 0.16 | 0.19 |
| MNKWR | 0.52 | **0.62** | 0.50 | 0.47 | 0.31 | 0.27 | 0.39 |
| WNKWR | 0.39 | 0.79 | **0.38** | 0.61 | 0.39 | 0.48 | 0.37 |
| ENKWR | 0.37 | 0.80 | 0.82 | **0.48** | 0.49 | 0.39 | 0.46 |
| PNKWR | 0.21 | 0.61 | 0.64 | 0.83 | **0.39** | 0.36 | 0.37 |
| YNKWR | 0.23 | 0.45 | 0.77 | 0.59 | 0.62 | **0.37** | 0.66 |
| HNKWR | 0.36 | 0.67 | 0.66 | 0.85 | 0.77 | 0.92 | **0.43** |
| SE range | 0.04-0.10 | 0.02-0.08 | 0.02-0.07 | 0.02-0.10 | 0.02-0.06 | 0.02-0.07 | 0.02-0.05 |

## CONCLUSIONS

Neck and tail wrinkle were moderately to highly heritable traits and log transforming the data did not appear to improve the accuracy of selection. Body wrinkle at birth and neck and tail wrinkle at marking, was not strongly genetically correlated to skin wrinkle at later ages. This study shows that the best time to measure skin wrinkle on the tail or neck was after crutching at yearling age or after shearing at hogget age in a Mediterranean environment as this is when the heritability and phenotypic variation was highest. This time also coincided with the fly season in this environment.

**Table 3. Phenotypic variances (Vp), heritability (on diagonal), phenotypic correlations (above diagonal), and genetic correlations (below diagonal) of body wrinkle at birth (BBDWR) and tail wrinkle (TAWR) at marking (M), weaning (W), early post weaning (E), post weaning (P), yearling (Y) and hogget (H) shearing**

| | BBDWR | MTAWR | WTAWR | ETAWR | YTAWR | HTAWR |
|---|---|---|---|---|---|---|
| *Raw wrinkle scores* | | | | | | |
| Vp | 1.01 | 0.16 | 0.19 | 0.16 | 0.52 | 0.17 |
| BBDWR | **0.54** | 0.39 | 0.19 | 0.25 | 0.16 | 0.16 |
| MTAWR | 0.58 | **0.56** | 0.40 | 0.48 | 0.26 | 0.33 |
| WTAWR | 0.28 | 0.52 | **0.43** | 0.51 | 0.35 | 0.21 |
| ETAWR | 0.42 | 0.67 | 0.80 | **0.46** | 0.55 | 0.48 |
| YTAWR | 0.37 | 0.58 | 0.71 | 0.87 | **0.74** | 0.66 |
| HTAWR | 0.27 | 0.55 | 0.40 | 0.79 | 0.90 | **0.47** |
| SE range | 0.05-0.08 | 0.02-0.07 | 0.02-0.07 | 0.02-0.06 | 0.02-0.05 | 0.02-0.05 |
| *Log transformed wrinkle score (+10)* | | | | | | |
| Vp | 0.006 | 0.001 | 0.001 | 0.001 | 0.002 | 0.001 |
| BBDWR | **0.54** | 0.37 | 0.19 | 0.24 | 0.15 | 0.17 |
| MTAWR | 0.56 | **0.58** | 0.41 | 0.43 | 0.23 | 0.35 |
| WTAWR | 0.31 | 0.55 | **0.35** | * | 0.39 | 0.21 |
| ETAWR | 0.38 | 0.65 | * | **0.42** | * | * |
| YTAWR | 0.35 | 0.47 | 0.72 | * | **0.37** | 0.66 |
| HTAWR | 0.28 | 0.59 | 0.41 | * | 1.01 | **0.48** |
| SE range | 0.04-0.10 | 0.02-0.10 | 0.02-0.08 | 0.02-0.07 | 0.03-0.06 | 0.02-0.06 |

* Not estimable

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