

## **EXPRESSION OF BODY WEIGHT, FLEECE WEIGHT AND FIBRE DIAMETER IN ACROSS FLOCK GENETIC EVALUATION**

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### **SUMMARY**

Historically, estimated breeding values (EBVs) for body weight, fleece weight and fibre diameter of Australian sheep were produced using two different models. With the forming of the Sheep Genetics Australia (a national sheep genetic evaluation system) it was necessary to identify the most appropriate method. This paper compares the two most common methods: data analysed on the observed scale and percentage-transformed data. The results indicate that transforming observed data to a proportion of the contemporary group mean has beneficial outcomes for genetic evaluation. Transformed data have a slightly higher heritability and the resultant EBVs better reflect phenotypic differences in different production environments.

**Keywords:** Liveweight, wool, EBVs, sheep, genetic evaluation

### **INTRODUCTION**

Different analysis methods have historically been used in Australia to estimate breeding values for body weight, fleece weight and fibre diameter. Recently the major genetic evaluation service providers in Australia joined forces to form a national genetic evaluation system for Australian sheep producers. The result is the Australia Sheep Genetics Database (ASGD). Consequently only one approach will remain in operation but must be suitable for the wider industry.

Data used for genetic evaluation of Merino sheep in Australia originate from a vast array of genotypes and environments. As a result there are large differences in the level of production and therefore contemporary group (CG) means within the data. This has implications for within CG variance of the data and results in scale effects on the estimated breeding values (EBVs). Consequently groups with higher means have more variance and, without adjustment, animals from these groups have greater variation in their EBVs. This also leads to EBVs not predicting progeny performance reliably across different production environments.

There are a number of methods for accommodating heterogeneous residual variance across groups that do not remove heterogeneous genetic variance across groups. Heterogeneous genetic variance across groups can occur when genetic differences are expressed more in better environments than in poorer environmental conditions. Expressing traits as a proportion of their contemporary group mean is one method used to avoid these problems.

The aim of this project was to identify an appropriate method for analysis of body weight, fleece weight and fibre diameter for future ASGD analyses.

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## MATERIALS AND METHODS

Pedigree and performance records were obtained from the Merino Genetic Services (MGS) database. This database consists of pedigree and performance records from Australian and New Zealand Merino studs and is used for genetic evaluation purposes. As MGS dataset is greater than 500,000 animals, data were only extracted for all animals from 10 representative studs across Australia. Data included animals with a yearling body weight (Ywt), yearling fibre diameter (Yfd), yearling greasy fleece weight (Ygfw), hogget body weight (Hwt), hogget fibre diameter (Hfd) or hogget greasy fleece weight (Hgfw). These traits were then expressed to a proportion of their contemporary group (CG) means and given a suffix of “P” to their abbreviation. CG was defined by breed, flock, year, sex and management group.

Only data that met the following criteria were used: 1) date of measurement and current owner recorded, 2) at least sire or dam known, 3) date of birth known, 4) sex identified as male or female, 5) pure-bred Horn or Poll Merino, 6) management grouping defined by the breeder, and 7) age of dam less than 12 years. To remove possible outliers, observations more than three standard deviations outside the mean of their contemporaries were deleted, and CGs with fewer than 10 animals were also deleted. The pedigree was built using all available ancestors in the MGS database. After these edits the pedigree consisted of between 20,286 and 31,554 animals (Table 1) and records on between 15,043 and 27,672 animals. There were up to 575 sires and 7,592 dams across 15 years and 251 CGs.

There was a large range in the CG means for all traits (Table 2). The data were divided into low, medium and high subsets based on CG means for each trait. The cut-offs between production levels were established using 0.75 standard deviations either side of the mean of all CGs. Approximately 50% of the data fell into the medium classification with the remaining CGs evenly spread between the low and high production levels.

**Table 1. Summary of the data**

	<b>Animals With Data</b>	<b>Total Pedigree</b>	<b>Dams</b>	<b>Sires</b>	<b>Flocks</b>	<b>Years</b>	<b>Years</b>	<b>Mean</b>	<b>SD</b>	<b>Min</b>	<b>Max</b>
<b>Ywt (kg)</b>	15,043	22,173	5,678	402	10	9	9	42.1	12.6	14.7	87.0
<b>YwtP (%)</b>								100.0	12.6	49.2	153.2
<b>Hwt (kg)</b>	25,700	30,465	6,478	526	9	15	15	48.3	10.2	20.4	93.5
<b>HwtP (%)</b>								100.0	10.9	59.2	141.8
<b>Yfd (kg)</b>	21,600	29,940	7,592	442	10	12	12	16.6	1.4	11.7	23.9
<b>YfdP (%)</b>								100.0	6.2	79.0	128.8
<b>Hfd (kg)</b>	27,672	31,554	6,078	575	9	15	15	18.8	1.6	13.3	27.4
<b>HfdP (%)</b>								100.0	6.5	76.5	124.0
<b>Ygfw (kg)</b>	20,117	28,445	7,378	424	10	12	12	3.0	1.1	0.7	11.4
<b>YgfwP (%)</b>								100.0	16.6	36.3	172.5
<b>Hgfw (kg)</b>	17,247	20,286	3,788	356	8	15	15	4.7	1.0	1.0	9.2
<b>HgfwP (%)</b>								100.0	13.3	42.4	163.3

Breeding values were estimated using the standard MGS analysis. The analysis was then repeated using transformed data and genetic parameters. Genetic parameters were estimated for each trait using an animal model in ASREML (Gilmour *et al.* 1999). The fixed effects of age, birth type, rearing type, dam age and CG were fitted for all traits. Direct and maternal genetic effects were fitted with their covariance fixed at 0. Within each production level progeny phenotype was regressed on sire EBVs. The regression analysis was conducted using PROC GLM in SAS (SAS 1990) fitting CG as a fixed effect and, age, birth type, rearing type, dam age and sire EBVs as covariates.

**Table 2. Summary of the observed contemporary group means and counts by production level**

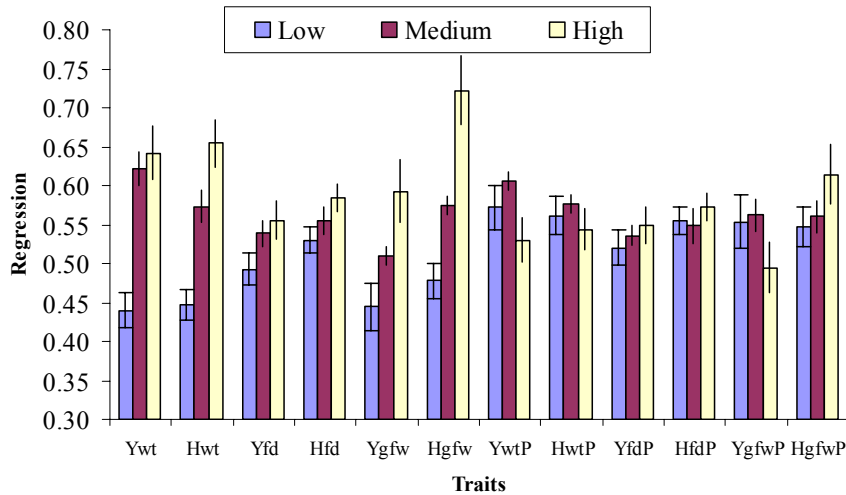
	Contemporary Group Summary					Contemporary Group Counts		
	Count	Mean	SD	Min	Max	Low	Medium	High
<b>Ywt (kg)</b>	103	42.5	11.6	21.6	66.2	29	40	31
<b>Ygfw (kg)</b>	145	2.8	0.9	1.6	8.1	30	94	18
<b>Yfd (µm)</b>	152	16.6	1.0	14.2	19.7	30	91	28
<b>Hwt (kg)</b>	151	48.7	8.3	31.3	69.8	33	79	36
<b>Hgfw (kg)</b>	108	4.7	1.0	2.3	7.0	27	57	21
<b>Hfd (µm)</b>	185	18.6	1.1	16.1	22.5	43	100	39

## RESULTS AND DISCUSSION

The genetic parameters estimated for each trait (Table 3) are very similar to those previously estimated from the SGA data set. Transforming data to a proportion of their CG mean generally resulted in a slightly (but not significantly) higher direct heritability; the exception was a significant increase in the direct heritability for yearling body weight and a significant reduction in the maternal heritability for yearling greasy fleece weight. This is likely a result of the lower quality data structure for estimating maternal effects in yearlings, as only 5% of progeny have a dam record for these traits compared to 20% at the hogget stage. This may also be a function of dams and their progeny being evaluated in similar production environments, leading to an environmental covariance that may be inappropriately partitioned by the model as maternal genetic variance when estimated on the original scale. While the expectation of the regression coefficients in Figure 1 is 0.5, for most traits the regressions are slightly greater than 0.5. This is likely a result of the regression analysis not fully accommodating the maternal genetic and maternal environmental effects on these traits.

**Table 3. Phenotypic variance ( $\sigma_p^2$ ), direct heritability ( $h^2$ ) and maternal heritability ( $m^2$ ) (se)**

Trait	Observed Scale			Percent Transformed		
	$\sigma_p^2$	$h^2$	$m^2$	$\sigma_p^2$	$h^2$	$m^2$
<b>Ywt</b>	32.1(0.50)	0.33(0.03)	0.15(0.01)	165.1(2.52)	0.48(0.03)	0.03(0.01)
<b>Hwt</b>	29.6(0.36)	0.36(0.02)	0.05(0.01)	123.8(1.51)	0.37(0.02)	0.05(0.01)
<b>Yfd</b>	1.1(0.01)	0.62(0.03)	0.01(0.01)	41.0(0.54)	0.63(0.03)	0.00(0.01)
<b>Hfd</b>	1.6(0.02)	0.60(0.02)	0.00(0.00)	44.1(0.49)	0.60(0.02)	0.00(0.00)
<b>Ygfw</b>	0.3(0.00)	0.43(0.02)	0.19(0.01)	278.2(3.64)	0.45(0.03)	0.04(0.01)
<b>Hgfw</b>	0.4(0.01)	0.35(0.02)	0.13(0.01)	193.2(3.31)	0.39(0.03)	0.11(0.01)



**Figure 1. Regression of progeny performance on sire EBV (on the observed and transformed scales) for each trait at low, medium and high levels of production.**

For traits analysed on the observed scale, there was a significant trend in regression coefficients from low through to high levels of production for all traits. This trend was most apparent for body weight and fleece weight traits but still substantial for fibre diameter traits. Analysing the traits on the percentage scale largely removed the trends in regression coefficients, and produced EBVs that were more reliable across different production environments.

**CONCLUSIONS**

Transforming data for these traits to a proportion of their contemporary group mean has beneficial outcomes for genetic evaluation. Transformed data had a slightly higher heritability and the resultant EBVs were more robust in terms of predicting progeny performance across different production environments. That is, on average a 2% difference in EBVs for body weight will produce a 1% change in body weight differences in the progeny, regardless of the production level of the environment. Such EBVs can still be transformed back into kilogram units for reporting, using a standard mean. For example a 2% EBV would equate to 1 kilogram EBV against a mean of 50kg.

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