

## THE USE OF WEANING WEIGHT TO ADJUST FOR PRE-WEANING ENVIRONMENTAL EFFECTS ON BODYWEIGHT, FLEECE WEIGHT AND FIBRE DIAMETER IN MERINO HOGGETS

**D. J. Brown and A. Reverter**

Animal Genetics and Breeding Unit, University of New England and NSW Agriculture,  
Armidale, NSW 2351, Australia

### INTRODUCTION

The collection of pedigree, environmental and performance information is a major cost in most livestock improvement programs, particularly under extensive conditions such as frequently encountered in the Merino industry. Ideal quality of data is achieved when full pedigree, date of birth, birth type (BT), rearing type (RT), management and performance information is recorded. When this information is missing inaccurate estimates are made of these effects or an incomplete model fitted. Recently Atkins and Ramsay (2001) suggested an alternate approach that would reduce these demands for Merino breeders. Using research station data, the authors illustrated that by using weaning weight as a covariate, breeding values could be estimated with accuracy close to that achieved from a model including all fixed effects. The aim of this study was to examine the accuracy of estimated breeding values (EBVs) produced from industry recorded data for hogget bodyweight, greasy fleece weight and fibre diameter using different models to adjust for pre-weaning environmental effects.

### MATERIAL AND METHODS

**Data.** The industry recorded data from the Merino Genetic Services (an Australian across flock genetic evaluation service) database were extracted for animals with all of weaning weight (WWT), hogget weight (HWT), hogget greasy fleece weight (HGFWT) and hogget fibre diameter (HFD), meeting the following criteria : 1) date of measurement and current owner known, 2) at least sire or dam known, 3) date of birth known, 4) sex known (male or female), 5) BT and RT recorded, 6) pure-bred Merino, and 7) dam age (DA) known and less than 12 years. Observations more than 3 standard deviations from the mean of their contemporaries, and contemporary groups (CG) with fewer than 50 animals were deleted. A pedigree file was built using all available ancestors. These edits resulted in 9624 animals of which 76 %, 20 % and 4% had both parents, only their sire and only their dam known, respectively. There were 249 sires and 2862 dams. Descriptive statistics for the data collected for each trait are shown in table 1.

**Statistical analyses.** The influence of age, birth type, rearing type, and dam age (years) on weaning weight and the three hogget traits was examined using GLM in SAS (1990). Four models were explored : (1) a model including birth type, rearing type and CG (defined as flock, management group, sex and year of measurement) as fixed effects and age nested within sex, dam age and dam age squared as covariates (Standard) ; (2) the standard model with weaning weight as an additional covariate (Combined) ; (3) an alternate model with weaning

weight and CG the only fixed effects (Covariate) and (4) a model with CG the only fixed effect (Simple).

**Table 1. Mean, standard deviation (SD), minimum and maximum for each trait (n = 9624)**

Trait <sup>A</sup>	Mean	SD	Minimum	Maximum
WWT (kg)	27.6	5.2	8.6	49
HAGE (days)	467	26.5	406	532
HWT (kg)	55.7	10.6	28.9	91
HGFWT (kg)	5.4	1.6	1.8	11
HFD (µm)	19.7	2.0	14.7	27.5

<sup>A</sup> WWT = weaning weight, HAGE = hogget age, HWT = Hogget weight, HGFWT = hogget greasy fleece weight and HFD = hogget fibre diameter

Genetic parameters and breeding values were estimated using ASREML (Gilmour *et al.*, 1999) and the model :  $\mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{e}$ , where  $\mathbf{y}$  is a vector of observations,  $\beta$  a vector of fixed effects,  $\mathbf{a}$  and  $\mathbf{m}$  vectors of direct and maternal breeding values,  $\mathbf{X}$ ,  $\mathbf{Z}_1$  and  $\mathbf{Z}_2$  are incidence matrices relating observations and effects, and  $\mathbf{e}$  is the vector of random residuals. Also with  $\text{Var}(\mathbf{a}) = \mathbf{A}\sigma_a^2$ ,  $\text{Var}(\mathbf{m}) = \mathbf{A}\sigma_m^2$ ,  $\text{Cov}(\mathbf{a},\mathbf{m}) = 0$  and  $\text{Var}(\mathbf{e}) = \mathbf{I}\sigma_e^2$ . This analysis was performed using the four models described above with and without the maternal ( $\mathbf{m}$ ) effect.

**Validation.** The resulting EBVs from each model were compared according to three criteria : (1) The correlation between EBVs ; (2) The significance of the fixed effects on the data and the EBVs and (3) The predictive ability of the EBVs obtained from the regression of progeny performance on sire EBV after removing a random 10 % of the animals in the data file (repeated 20 times).

## RESULTS AND DISCUSSION

The solutions for the fixed effects are presented in table 2. Under the standard model and for weaning weight and all three hogget traits, all effects were significant ( $P < 0.05$ ) except for rearing type on HFD and the quadratic component for dam age on HFD. Under the Covariate model, dam age was not significant ( $P > 0.05$ ) for any trait but age was significant ( $P < 0.05$ ) for all traits. Birth type also significantly increased HWT and HFD while rearing type significantly increased HWT and reduced HGFWT using the Covariate model. CG was significant ( $P < 0.05$ ) in all models. The  $R^2$  for the Simple models were 0.70, 0.80 and 0.48 for HWT, HGFWT and HFD respectively indicating that the addition of the pre-weaning fixed effects only explained a very small amount of the variation in these traits and/or confounding exists between the pre-weaning effects and hogget CG. All effects were smaller in the Combined model compared to the Standard model. Estimates of genetic parameters using each model were very similar for HFD (table 3). All variances for HWT were lower in the Covariate model compared to the Standard model. Using the Simple model the direct heritabilities were lower and the maternal heritabilities were higher than those from the standard model for HWT and HGFWT. Heritability was higher for HGFWT in the weaning weight model.

**Table 2. Summary of solutions fitting the Standard (S), Combined (C) and Covariate (Cov) models**

Model	WWT				HWT <sup>B</sup> (kg)			HGFWT <sup>B</sup> (kg)			HFD <sup>B</sup> (µm)		
	S	S	C	Cov	S	C	Cov	S	C	Cov	S	C	Cov
Age (F)	0.14*	0.08*	-0.06*	-	0.01*	0.00*	-	0.01*	0.01*	-	0.01*	0.01*	-
Age (M)	0.16*	0.13*	-0.04*	-	0.02*	0.01*	-	0.02*	0.01*	-	0.02*	0.01*	-
BT <sup>A</sup>	-2.38*	-0.70*	1.10*	-	-0.15*	0.00	-	0.18*	0.25*	-	0.18*	0.25*	-
RT <sup>A</sup>	-2.43*	-1.18*	0.65*	-	-0.20*	-0.06	-	0.06	0.02	-	0.06	0.02	-
DA <sup>B</sup>	2.05*	1.60*	-0.01	-	0.13*	0.01	-	0.11*	0.04	-	0.11*	0.04	-
DA <sup>2</sup>	-0.21*	-0.16*	0.00	-	-0.01*	-0.00	-	-0.01	0.00	-	-0.01	0.00	-
WWT	-	-	0.78*	0.69	-	0.06*	0.07	-	0.03*	0.03	-	0.03*	0.03
Model R <sup>2</sup>	0.43	0.72	0.80	0.79	0.82	0.84	0.84	0.49	0.49	0.48	0.49	0.49	0.48

\* Effect significant at P &lt; 0.05

<sup>A</sup> Birth type (BT) and rearing type (RT) are the differences between twins and singles<sup>B</sup> WWT = weaning weight, HWT = Hogget weight, HGFWT = hogget greasy fleece weight, HFD = hogget fibre diameter and DA = dam age

The maternal genetic component was significant (P < 0.05) for HWT and HGFWT with the Standard and Simple models and HGFWT for the Covariate model. The mean and range in EBVs were slightly larger from HWT using the Standard model compared to the Covariate model however they were very similar between the two models for HGFWT and HFD.

**Table 3. Genetic parameters (± s.e.) from the Standard (S), Covariate (Cov) and Simple (Sim) models**

Model	HWT <sup>A</sup>			HGFWT <sup>A</sup>			HFD <sup>A</sup>		
	S	Cov	Sim	S	Cov	Sim	S	Cov	Sim
Direct	16.34	10.83	15.15	0.21	0.23	0.20	1.51	1.54	1.54
Maternal	1.93	0.73	2.65	0.06	0.04	0.08	0.03	0.03	0.04
Residual	14.99	12.29	16.76	0.23	0.18	0.27	0.58	0.58	0.58
Phenotypic	33.25	23.85	34.60	0.50	0.45	0.55	2.13	2.15	2.16
	(0.75)	(0.52)	(0.77)	(0.01)	(0.01)	(0.01)	(0.05)	(0.05)	(0.05)
h <sup>2</sup>	0.49	0.45	0.44	0.42	0.51	0.36	0.71	0.71	0.71
	(0.05)	(0.05)	(0.04)	(0.04)	(0.04)	(0.04)	(0.04)	(0.04)	(0.04)
m <sup>2</sup>	0.06	0.03	0.08	0.12	0.10	0.15	0.01	0.01	0.02
	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)

<sup>A</sup> HWT = Hogget weight, HGFWT = hogget greasy fleece weight and HFD = hogget fibre diameter

The EBVs from the Standard and Covariate models were highly correlated (P < 0.01) for all traits, 0.89, 0.92 and 0.99 for HWT, HGFWT and HFD, respectively. All effects in the Standard model, except CG, did not significantly affect the EBVs that were generated using the Standard model. The R<sup>2</sup> using this model were 0.06, 0.04 and 0.10 for HWT, HGFWT and HFD respectively. The R<sup>2</sup> for the Standard model fitted to the EBVs from the Covariate model were 0.08, 0.04 and 0.10 for HWT, HGFWT and HFD respectively. Age had a very small (-0.01 to 0.01), significant effect (P < 0.05) on all traits when EBVs were generated using the

Covariate model. BT significantly ( $P < 0.05$ ) influenced HWT (the HWT EBV was 0.43 kgs higher for twin versus singles) and HFD (the HFD EBV for twins was 0.13  $\mu\text{m}$  higher than for singles). The EBVs for HWT using the Covariate model were significantly over adjusted while the EBVs for HFD were significantly under adjusted for the BT effect.

The regressions of progeny performance on sire EBV also showed that the Standard and Covariate models predicted progeny performance accurately. The regression coefficients were 0.49, 0.53 and 0.54 for the Standard model and 0.57, 0.53 and 0.54 for the Covariate model for HWT, HGFWT and HFD, respectively. For HWT the relationship using the Standard model was slightly closer to expectation (0.50) than that for the Covariate model. Furthermore, the average standard error for the regression coefficient was higher (0.05 to 0.07 and 0.05 to 0.09 for the Standard and Covariate models respectively) and there was greater variation in the relationship between replicates for the Covariate model (0.06 to 0.07, 0.06 to 0.08 for the Standard and Covariate models respectively). These results suggest that the EBVs from the Standard model provide a more reliable prediction of progeny performance for HWT.

As reproductive performance has a significant impact on the profitability of all sheep productions systems the collection of birth type and rearing type has significance for the genetic evaluation of these traits. The use of the information for this purpose is likely to be justification alone for its collection and using it to more accurately adjust other traits for their effects is likely to be an additional benefit.

#### **CONCLUSION**

The results observed in this study indicate that weaning weight can be used to replace age at measurement, birth type, rearing type and dam age for the genetic evaluation of fleece weight. However, for the traits of hogget body weight and fibre diameter it appears that there may be some effects of birth type that are being over corrected. The collection of birth type and rearing type is also very beneficial in evaluating the reproductive performance of the females in the flock. While pre-weaning effects do not explain a large proportion of the variation in these hogget traits they have a significant influence on the genetic parameters estimated. It would also be worthwhile to repeat this research using these traits measured at yearling ages and body weight and carcase traits in terminal sire and maternal breeds of sheep.

#### **REFERENCES**

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