

EFFECT OF DIFFERENT DATA EXCLUSION POLICIES ON THE HERITABILITY OF FAT DEPTH IN MATERNAL, MERINO AND TERMINAL SHEEP

A.J. McMillan¹ and D.J. Brown¹

¹Animal Genetics Breeding Unit*, University of New England, New South Wales, Australia

SUMMARY

The effect of different data exclusion policies for post weaning fat depth on heritability estimates were examined using industry data for Maternal, Merino and Terminal sheep. The exclusion policies which had the most positive effect on heritability were mean fat depth for the contemporary group (CG), and standard deviation of fat depth for the contemporary group. Exclusion based on mean weight of the CG showed some effectiveness for light animals. Excluding records based on mean age of the CG had no effect on heritability estimates. In order for fat depth to be analysed most appropriately animals should be measured when they have had the opportunity to express the trait. It is appropriate to exclude CGs from the analysis where the variation in fat depth for a CG is low to improve heritability. The impact of these data exclusions on the utility of breeding values would need to be investigated in each analysis before any policies can be implemented.

INTRODUCTION

Data quality and structure impacts heritability estimates, this is particularly evident- when using industry data (Swan *et al.* 2007). Various data quality factors which could have an effect on heritability estimates were examined in this study and include, mean weight of contemporary groups, age of animals in CG, mean fatness of the CG, and variability of fatness in group. In order for an animal to express its true genetic potential for fat depth the animal needs both the physical maturity and environment to deposit sufficient fat. For genetic evaluations to be able to appropriately capture that genetic merit as a breeding value the animal needs also to have contemporaries to contrast those differences.

The aim of this study was to examine the impact of data restriction policies on the heritability of post weaning fat depth using data from Maternal, Merino and Terminal sheep. The intention is also to provide feedback to the sheep industry on best practise for recording post-weaning fat and possible post measurement exclusion policies for the national genetic evaluation.

MATERIALS AND METHODS

Animals. Pedigree and phenotypes were extracted from the Sheep Genetics database (Brown *et al.* 2007). The datasets used includes 10 years (2004-2014) of records with the Terminal analyses being restricted to only Poll Dorset animals due to size constraints, while the Maternal and Merino analyses had no restriction on breed. Sheep Genetics has standard protocols to exclude fat depth records outside of 0.5 mm to 15mm, records more than 4 standard deviations from the CG mean and records with no live weight recorded at the time of measurement.

Alternate Data exclusion policies. Four data exclusion policies were developed to examine their effect on fat depth heritability estimates, and in addition an analysis with current standard data

* AGBU is a joint venture of NSW Department of Primary Industries and University of New England

exclusions was completed to provide a benchmark set of results. The four policies were; 1) excluding CGs where the mean weight was outside of minimum and maximum criteria, 2) excluding CGs where the mean age of the CG at recording was below age criteria and also excluding CGs where the mean age was outside of minimum and maximum criteria, 3) excluding CGs where the mean fat depth of the group was outside of minimum and maximum fat depth criteria and 4) excluding data where the standard deviation of fat depth for the group was outside of minimum and maximum standard deviation of fat depth criteria. The thresholds defined were derived by examining the distributions of these terms across the data sets.

Statistical Analysis. Genetic parameters for fat depth were estimated in univariate animal model analyses using ASReml (Gilmour et al. 2009). The fixed effects of CG and the animal's liveweight at measurement (as quadratic) were fitted. CG was defined as flock, year of birth, sex, date of measurement, management group. Random terms for the direct genetic effects and sire by flock year interactions were fitted.

RESULTS AND DISCUSSION

Heritability estimates for the Maternal, Merino and Terminal datasets are summarised in Table 1. Sheep Genetics currently use heritabilities of 0.30, 0.20 and 0.25 for post weaning fat depths in the routine evaluations for Maternal, Terminal and Merinos respectively. These benchmark heritabilities estimated are slightly lower than the current Sheep Genetics parameters for Maternal and Terminal and this reduction is likely due to the inclusion of sire by flock-year interaction term as shown by Brown et al. (2009).

Table 1. Heritability (h^2) and sire by flock-year (s^2) estimates for post-weaning fat using current standard data exclusion policies

Analysis group	Records	CGs	h^2	s^2
Maternal	143866	5609	0.24 (0.01)	0.02 (0.00)
Merino	55028	985	0.21 (0.02)	0.02 (0.00)
Terminal	249866	10014	0.21 (0.01)	0.01 (0.00)

The impact of applying the first data exclusion policy of mean CG live weight is summarised in Table 2. All analyses show a small increase in heritability from the low mean weight groups to the higher weight groups. Applying an exclusion policy solely on weight would result in improved heritability estimates, however this would be at the cost of a large proportion of data being excluded from the analysis. Heritability gains could be made if breeders waited until animals were heavier and fatter rather than measuring at lighter and leaner weight ranges.

For all breed groups the heritability estimates show no increase as age of the CG increases, using both age exclusion policies. Older groups of animals across all breeds did not show increased heritability suggesting that factors other than age are important in allowing the genetic potential for fat depth to be estimated. In all breed groups there was an increase in heritability estimates as the mean fatness of the CGs' increased (Table 3). While it would not be feasible to exclude all groups where fatness of the CG is low, breeders should be encouraged to record animals when higher levels of fatness have been achieved in the CG. Increasing the mean fatness of CG reduces the proportion of measurement error in relation to the mean. Measurement errors in fat depth scanning on average should be less than 1mm as this is a requirement of scanning accreditation (Woolcott *et al*, 2006). Heritability increases achieved through increased fatness of

CGs would allow for genetic evaluations to more accurately separate the genetic and non-genetic effects resulting in more accurate breeding values.

Table 2. Heritability (h^2) estimates for post-weaning fat depth with different contemporary group mean body weight (kg) data exclusion policies

<i>Criteria</i>		<i>Maternal</i>		<i>Merino</i>		<i>Terminal</i>	
Min	Max	%Records	h^2	% Records	h^2	% Records	h^2
30	35	N.A	N.A	9.3	0.15 (0.06)	N.A	N.A
35	40	20.4	0.23 (0.02)	22.4	0.18 (0.03)	3.3	0.06 (0.04)
40	45	25.0	0.19 (0.02)	29.6	0.14 (0.03)	11.7	0.16 (0.02)
45	50	21.2	0.20 (0.02)	19.3	0.26 (0.05)	20.3	0.17 (0.01)
50	55	15.6	0.25 (0.02)	8.4	0.26 (0.07)	21.2	0.19 (0.01)
55	60	8.0	0.32 (0.04)	7.2	0.19 (0.10)	17.0	0.17 (0.02)
60	65	N.A	N.A	1.7	0.43 (0.15)	12.2	0.22 (0.02)

N.A - Insufficient data to estimate

Table 3. Heritability (h^2) estimates for post -weaning fat depth with data exclusion based on mean fat depth of the contemporary group (mm)

<i>Criteria</i>		<i>Maternal</i>		<i>Merino</i>		<i>Terminal</i>	
Min	Max	% Records	h^2	% Records	h^2	% Recs	h^2
1	2	10.3	0.20 (0.03)	28.9	0.15 (0.03)	4.6	0.05 (0.02)
2	3	39.7	0.18 (0.01)	42.5	0.19 (0.03)	29.1	0.17 (0.01)
3	4	32.3	0.28 (0.02)	26.5	0.33 (0.03)	37.6	0.20 (0.01)
4	5	13.6	0.33 (0.03)	N.A	N.A	23.6	0.27 (0.01)

The final exclusion policy investigated was for the level of variability in fat depth within each CG (Table 4). For lower levels of fat depth variability across Maternal, Merino and Terminal analyses groups the heritability estimates were 0.10 or lower. As variability increased for all three breed groups the heritability generally increased. Thus, having greater variability in fat depth within the CGs allowed for better estimation of the genetic differences.

The factors used for data exclusion in this study are all positively correlated with each other and thus all expected to influence the level of expression in fatness. However the results confirm that the best factor to influence the heritability of fatness is to the variability of fat depth. Age and body weight provide practical proxies for breeders to assess if animals are in condition for scanning but measured fat depth is a more reliable tool.

CONCLUSIONS

These analyses show that data exclusion policies can have an effect on heritability estimates for post weaning fat depth in Maternal, Merino and Terminal sheep. Using CG based exclusion policies for mean fat depth or standard deviation of fat depth showed increases in heritability, with Maternal and Merino sheep showing the greatest benefit of these policies. Using mean weight of the group resulted in some small increases in heritability, especially when comparing lighter

groups to much heavier CGs, and could be useful for excluding very light CGs. Age at measurement had no effect on heritability estimates. In order for the most appropriate fat depth breeding values to be produced, phenotypic data should be collected for animals in CGs that have high variability for fatness. Increases in variability of CGs are indicative of groups which have exhibited the differences in their genetic potentials and provide meaningful comparisons for genetic evaluation. Excluding CGs below minimum thresholds for fat depth variability during genetic evaluation could be implemented to more accurately estimate breeding values for fat depth. However the impact such data exclusions would have on the utility of breeding values would need to be investigated and an appropriate policy developed for both historical and new data used in these analyses.

Table 4. Heritability estimates for post-weaning fat with data exclusion based on standard deviation of fat depth of each CG

<i>Criteria</i>		<i>Maternal</i>		<i>Merino</i>		<i>Terminal</i>	
Min	Max	% Recs	h^2	% Recs	h^2	% Recs	h^2
0.0	0.3	3.2	0.10 (0.07)	5.3	0.06 (0.08)	2.8	0.06 (0.05)
0.3	0.4	6.3	0.08 (0.04)	16.7	0.12 (0.04)	5.8	0.09 (0.02)
0.4	0.5	15.7	0.16 (0.02)	32.4	0.17 (0.03)	14.5	0.13 (0.02)
0.5	0.6	20.1	0.20 (0.02)	21.2	0.12 (0.04)	17.5	0.13 (0.01)
0.6	0.7	16.0	0.17 (0.02)	10.7	0.23 (0.06)	17.5	0.14 (0.01)
0.7	0.8	11.2	0.19 (0.03)	5.9	0.16 (0.05)	13.4	0.17 (0.02)
0.8	0.9	8.2	0.19 (0.04)	3.7	0.29 (0.08)	10.0	0.23 (0.02)
0.9	1.0	6.2	0.23 (0.05)	1.3	0.60 (0.20)	7.0	0.20 (0.03)

ACKNOWLEDGEMENTS

This research is funded by Meat and Livestock Australia and Australian Wool Innovation, and Sheep Genetics is made possible through the support of the Australian sheep industry. The authors acknowledge the contributions of the Sheep CRC Information Nucleus, the Australia Merino Sire Evaluation Association and industry-funded research flocks.

REFERENCES

- Brown D.J., Huisman A.E., Swan A.A., Graser H-U., Woolaston R.R., *et al.* (2007) *Proc. Ass. Adv. Anim. Breed. Genet.* **17**: 187.
- Brown D.J., Swan A.A., Johnston D.J. and Graser H. (2009) *Proc. Ass. Adv. Anim. Breed.* **18**: 48.
- Gilmour A.R., Gogel B.J., Cullis B.R. and Thompson R. (2009) ASReml User Guide Release 3.0 VSN International Ltd, Hemel Hempstead, HP1 1ES, UK
- Woolcott M., Ball A. (2005) In 'Real-time ultrasound scanning applications in livestock assessment', pp. 33-34, editor M. Woolcott and J. Allen, AGBU, University of New England, Armidale
- Swan A.A., Brown D. J. (2007) *Proc. Ass. Adv. Anim. Breed. Genet.* **17**: 395.