Proc. Assoc. Advmt. Anim. Breed. Genet. 20:110-103

GENETIC CORRELATIONS ACROSS AGES FOR GREASY FLEECE WEIGHT AND FIBRE DIAMETER IN MERINO SHEEP

D.J. Brown[1], A.A. Swan[1] and J.S. Gill[2]

[1]Animal Genetics and Breeding Unit[*], University of New England, Armidale, NSW 2351
[2]Meat and Livestock Australia, University of New England, Armidale, NSW 2351

SUMMARY

While adult wool production is a key determinant of profitability of Merino flocks, much of the on-farm recording through MERINOSELCT is focused on assessments at 12 or 18 months of age. While there have been numerous studies in research flocks examining these relationships these results have not been validated in industry flocks. The aim of this paper was to investigate the genetic correlations between multiple age expressions of fibre diameter and greasy fleece weight using the MERINOSELECT database.

The results support earlier research in that, while the correlations across ages are generally very high they also suggest that at least one adult assessment of fleece weight and fibre diameter would be beneficial for the breeding program. As a result of this work the genetic evaluation for Sheep Genetics will be modified to include annual expressions of adult fleece traits.

INTRODUCTION

The correlations between early age performance (12 and 18 months of age) and adult performance have been examined in numerous research studies (Atkins 1990; Atkins and Mortimer 1987; Coelli *et al.* 1998; Hickson *et al.* 1994; Fozi *et al.* 2012). These studies all suggest that the correlations between early age measurements and adult expression are moderate to high (r_g=0.60 to 0.90). Furthermore correlations between adult expressions are very high and can be treated as repeated expressions of the same trait. This has been the approach currently adopted by Sheep Genetics in the MERINOSELECT analysis (Brown *et al.* 2007), although most industry breeders choose not to record animals at an adult age.

The aim of this study was to evaluate the value of recording fleece weight and fibre diameter throughout the animal's lifetime by estimating genetic correlations between multiple age expressions of these traits from the MERINOSELECT database.

MATERIALS AND METHODS

Data. Pedigree and performance data were extracted from the Sheep Genetics MERINOSELECT database (Brown *et al.* 2007). This database consists of pedigree and performance records submitted by Australian and New Zealand Merino ram breeders which are used for genetic evaluation purposes.

As the complete database was too large for parameter estimation analyses, a subset of 78 flocks were used based on their recording of adult wool traits. These flocks are a mix of industry ram breeders, research and sire evaluation flocks. Within these flocks all animals with at least sire pedigree and born from 1990 and later were included. Data were extracted for all greasy fleece weight (GFW) and fibre diameter (FD) records from these flocks. Records were classified to one of 7 age based traits, yearling (Y, 12 months), hogget (H, 18 months) and 2 year old adult (A2) through to 6 year old adult records (A6). All contemporary groups were transformed to a common mean within each group for both greasy fleece weight and fibre diameter, as is done routinely for

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

Sheep Genetic analyses (Brown *et al.* 2007). A summary of the data used for each trait is shown in Table 1. The pedigree was built using all ancestral information available. This resulted in pedigree files comprising 243,996 and 240,989 animals and data files comprising 337,846 and 338,909 records from 204,540 and 199,663 animals recorded at least once for greasy fleece weight and fibre diameter respectively.

Table 1. Summary of the data used in this study

	Fibre diameter (micron)					Greasy fleece weight (kg)				
Age	**Count**	**Mean**	**SD**	**Min**	**Max**	**Count**	**Mean**	**SD**	**Min**	**Max**
Y	125,810	17.5	1.2	12.6	25.5	127,291	3.5	0.60	0.7	7.0
H	84,610	19.0	1.4	13.1	27.0	71,524	4.5	0.67	1.4	8.0
A2	92,230	19.5	1.4	13.8	29.3	94,988	5.5	0.75	1.9	11.6
A3	17,498	19.5	1.5	14.7	27.5	21,309	5.5	0.82	1.9	10.2
A4	11,312	19.5	1.6	14.5	27.3	13,802	5.5	0.83	2.6	9.4
A5	6,756	19.5	1.6	14.2	27.2	8,680	5.5	0.83	2.4	9.4
A6	693	19.5	1.2	16.5	23.0	252	5.5	0.82	3.5	7.5

In this dataset approximately 47% and 53% of the animals studied had multiple records for fleece weight and fibre diameter respectively (Table 2). On average animals had 1.7 age expressions recorded for each trait. Furthermore 91% and 94% of the sires had progeny recorded across multiple age expressions for fleece weight and fibre diameter respectively.

Table 2. Number (%) of the animals by number of records observed per animal and number (%) of sires by the number of ages at which they have progeny were recorded

		Number of records per animal or per sire						
		1	**2**	**3**	**4**	**5**	**6**	**7**
GFW	**animals**	108,785 (53)	73,650 (36)	11,225 (5)	6,376 (3)	4,442 (2)	62 (<1)	0 (0)
	sires	414 (9)	1,730 (39)	888 (20)	339 (8)	623 (14)	461 (10)	9 (<1)
FD	**animals**	94,022 (47)	86,352 (43)	9,659 (5)	5,467 (3)	3,744 (2)	315 (<1)	104 (<1)
	sires	274 (6)	1,721 (41)	945 (22)	269 (6)	433 (10)	559 (13)	43 (1)

Models of analysis. Parameters were estimated in multivariate animal model analyses including all 7 age expressions for each trait in ASReml (Gilmour *et al.* 2006). For both traits the fixed effects of contemporary group, birth type, rearing type, age of dam, and animal's age at measurement were fitted. Contemporary group was defined as flock, year of birth, sex, date of measurement, management group subclass. A single random term for the direct genetic effects was modelled.

RESULTS AND DISCUSSION

The phenotypic variance for greasy fleece weight increases with age (Table 3) while the heritability increased from 0.37 at yearling to 0.51 at 2 year old adult age and then plateaued thereafter. The genetic correlations between yearling and adult performance were moderate to high ranging from 0.81 at 2 years to 0.62 at 6 years of age. Hogget traits were more highly correlated with adult expressions ranging from 0.88 to 0.73. The results confirm that assessments for greasy fleece weight made on young animals are good predictors of adult performance genetically (0.62

to 0.81) even if the phenotypic correlations are lower (0.44 to 0.61). Adult expressions were all very highly correlated and can be treated as the same trait genetically. The phenotypic correlations were generally moderate to high and also slightly lower than the genetic correlations.

Table 3. Phenotypic variance (σ^2_p), direct (h^2) heritability, genetic (below) and phenotypic (above) correlations for greasy fleece weight (s.e. in parentheses)

	Y	H	A2	A3	A4	A5	A6
σ^2_p	0.32 (0.00)	0.39 (0.00)	0.56 (0.00)	0.63 (0.01)	0.63 (0.01)	0.65 (0.01)	0.72 (0.05)
h^2	0.37 (0.01)	0.48 (0.01)	0.51 (0.01)	0.48 (0.01)	0.50 (0.02)	0.49 (0.02)	0.44 (0.10)
Y	.	0.59 (0.00)	0.61 (0.00)	0.47 (0.01)	0.46 (0.01)	0.44 (0.01)	0.47 (0.05)
H	0.84 (0.01)	.	0.65 (0.00)	0.63 (0.01)	0.63 (0.01)	0.58 (0.01)	0.63 (0.09)
A2	0.81 (0.01)	0.88 (0.01)	.	0.67 (0.00)	0.69 (0.00)	0.66 (0.01)	0.75 (0.03)
A3	0.71 (0.02)	0.82 (0.01)	0.93 (0.01)	.	0.70 (0.00)	0.69 (0.01)	0.66 (0.04)
A4	0.67 (0.02)	0.79 (0.01)	0.92 (0.01)	0.95 (0.01)	.	0.72 (0.01)	0.72 (0.04)
A5	0.66 (0.02)	0.77 (0.02)	0.90 (0.01)	0.94 (0.01)	0.97 (0.01)	.	0.77 (0.03)
A6	0.62 (0.12)	0.73 (0.15)	0.82 (0.09)	0.90 (0.09)	0.96 (0.09)	0.90 (0.08)	.

The phenotypic variance for fibre diameter also increased with age (Table 4) while the heritability increased from 0.60 at yearling to 0.68 at 3 year old adult age and then plateaued thereafter. The genetic correlations between yearling and adult performance were moderate to high ranging from 0.92 to 0.74 at 6 years of age. Hogget traits were more highly correlated with adult traits ranging from 0.91 to 0.79. The results again confirm that assessments of key fleece traits made on young animals are good genetic predictors of adult performance. The adult expressions were all very highly correlated and can be treated as the same trait genetically. The phenotypic correlations were generally moderate to high and slightly lower than the genetic correlations.

Table 4. Phenotypic variance (σ^2_p), direct (h^2) heritability, genetic (below) and phenotypic (above) correlations for fibre diameter (s.e. in parentheses)

	Y	H	A2	A3	A4	A5	A6
σ^2_p	1.34 (0.01)	1.70 (0.01)	1.74 (0.01)	1.78 (0.02)	1.98 (0.02)	2.12 (0.03)	2.56 (0.11)
h^2	0.60 (0.01)	0.61 (0.01)	0.65 (0.01)	0.68 (0.02)	0.66 (0.02)	0.66 (0.03)	0.67 (0.08)
Y		0.71 (0.00)	0.67 (0.00)	0.60 (0.01)	0.59 (0.01)	0.56 (0.01)	0.58 (0.02)
H	0.92 (0.01)		0.71 (0.00)	0.67 (0.00)	0.66 (0.01)	0.61 (0.01)	0.59 (0.02)
A2	0.85 (0.01)	0.91 (0.01)		0.76 (0.00)	0.75 (0.00)	0.71 (0.01)	0.71 (0.02)
A3	0.79 (0.01)	0.87 (0.01)	0.96 (0.01)		0.77 (0.00)	0.75 (0.01)	0.74 (0.02)
A4	0.78 (0.01)	0.86 (0.01)	0.94 (0.01)	0.96 (0.01)		0.79 (0.00)	0.80 (0.01)
A5	0.75 (0.01)	0.81 (0.01)	0.91 (0.01)	0.94 (0.01)	0.98 (0.01)	.	0.84 (0.01)
A6	0.74 (0.03)	0.79 (0.03)	0.87 (0.03)	0.92 (0.02)	0.98 (0.02)	0.98 (0.02)	.

These results suggest that measurement of at least one adult expression would improve the accuracy of selection for lifetime wool production and value. A companion paper in these proceedings (Swan and Brown 2013) used the genetic parameters presented here and estimated the trait and economic gains that can be achieved for various combinations of measurements across ages and as well as incorporating genomic selection. These results confirm that recording at least one adult assessment produced significantly greater trait and economic gain for both traits. Furthermore genomic selection also increased the progress in both fleece weight and fibre diameter.

Additional analysis of the breeding values of sires from these analyses shows that despite the very high correlation between traits some sires have breeding values that either increase or decrease over time. Thus breeders with concerns about changes in fleece value across age should be encouraged to record annual fleece value traits. The genetic evaluation for Sheep Genetics will be modified to include annual expressions of adult fleece traits.

These were preliminary analyses, so they ignored maternal effects (genetic and environmental), genetic group effects and the effects of previous and current physiological state which are known to affect wool production (Hinch *et al.* 1996; Huisman and Brown 2009). It is likely that accounting for these effects would further improve the correlations between traits recorded across different ages.

There is also a general lack of recording of liveweight at adult ages in the MERINOSELECT database. With the increasing focus on mature weight of sheep due to maintenance costs, welfare and occupation health and safety concerns this appears to be an opportunity for breeders to record this trait and increase the focus on this trait in the breeding program.

It is significant to note that this industry data set was/is large enough, and contains sufficient recording of fixed effects, to support very accurate genetic parameter estimation.

CONCLUSIONS

These preliminary estimates from industry data are consistent with those in the literature and reconfirm that assessments made on young animals are good genetic predictors of adult performance. However, genetic correlations do support the need for breeders to collect at least one adult assessment. The adult expressions were all very highly correlated and can be treated as the same trait genetically and support the model currently employed by Sheep Genetics. Additional data and analyses are required to investigate other lifetime traits such as live weight, fertility and wool quality traits.

ACKNOWLEDGMENTS

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

Asadi Fozi, M., van der Werf J.H.J. and Swan A.A. (2012) *Anim. Prod. Sci.* **51**: 1019.

Atkins K.D. and Mortimer S.I. (1987) *Proc. Ass. Adv. Anim. Breed. Genet.* **6**: 79.

Atkins K.D. (1990) *Proc. 4th World Cong. on Genet. App. to Liv. Prod.* **15**: 17.

Brown D.J., Huisman A.E., Swan A.A., Graser H-U., Woolaston R.R., Ball A.J., Atkins K.D. and Banks R.B. (2007) *Proc. Ass. Adv. Anim. Breed. Genet.* **17**: 187.

Coelli K.A., Gilmour A.R. and Atkins K.D. (1998) *Proc. of 6th World Cong. on Genet. App. to Liv. Prod.* **24**: 31.

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.

Hickson J., Kinghorn B.P., Swan A.A., and Piper L.R. (1994) *Proc. 5th World Cong. on Genet. App. to Liv. Prod.* **18**: 139.

Hinch G.N., Lynch J.J., Nolan J.V., Leng R.A., Bindon B.M. and Piper LR (1996) *Aust. J. Exp. Agric.* **36:** 129.

Huisman A.E. and Brown D.J. (2009) *Anim. Prod. Sci.* **49**: 289.

Swan A.A. and Brown D.J. (2013) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **20:** 232