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Genetic Analysis of Adult Body Weight and Condition Scores in Merino Sheep

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ABSTRACT: Adult body weight (WT) and condition score (CS) are important traits in sheep production systems. This study aimed to estimate the correlations between these traits across time points within year and across ages.

WT was highly correlated both phenotypically and genetically within and across years and with and without adjustment for previous and current physiological state. These results suggest that one assessment of adult weight is sufficient for selection purposes and this assessment can be made at any time within the year.

CS, on the other hand, while highly correlated between ages was not as highly correlated between times within year of recording. Furthermore the phenotypic variation and heritability varied throughout the year with more genetic variance apparent at weaning time.

WT and CS were also moderately correlated with each other suggesting that they are different traits genetically and further research is required to identify optimum measurement timing and to determine the importance of condition score in the breeding program.

Keywords: Sheep; Body weight; Condition Score

Introduction

Mature body weight and condition score are economically important traits in sheep production systems. Currently Sheep Genetics (Brown et al. 2007) uses only one expression of adult body weight in its national genetic evaluation for Australian meat and wool sheep. The ongoing selection for early growth has led to a correlated increase in mature size, which a number of breeders now wish to limit due to concerns about both occupational health and safety and carrying capacity for larger animals. The increase in mature size occurs in spite of negative economic values for the trait in most selection indexes, firstly because positive economic values for early growth are more dominant in relative terms and secondly because of limited recording of adult weights by industry.

Condition scoring sheep is a subjective method of estimating the condition or 'nutritional well-being' of sheep (Thompson and Meyer 1994), and hence may be used to indicate energy balance of the ewe. The importance of maintaining high condition scores to increase commercial sheep productivity has been recommended in recent times (Young et al. 2011), but at present there is no information on the genetic variability of the trait, and few ram breeders are including it in their breeding programs.

The objective of this research was to estimate genetic parameters for adult body weights and condition score recorded at various ages and times within the annual production cycle.

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 sheep breeders which are used for genetic evaluation purposes. Data from the Sheep CRC Information Nucleus Flock (Fogarty et al. 2007) is also included in this database. Data were extracted for adult body weights (WT) and condition scores (CS). CS records were scored on a scale from 1 (thin) to 5 (fat) (at increments of 0.25). The 124,986 records (Table 1) from 84,620 animals originated from 102 flocks across 22 years with 85% of the animals having sire known and 28% having dam known.

Table	1.	Summary	of	data	available	for	adult	body
weight	(W	VT) and con	dit	ion sc	ore (CS).			

Trait Age ^{&}		animals	records	rec/animal	Mean	SD
WT	A2	75,626	84,006	1.11	47.34	13.04
	A3	10,641	20,777	1.95	59.25	12.38
	A4	5,210	6,782	1.30	59.28	12.32
	A5+	4,861	6,068	1.25	56.79	11.66
CS	A2	4,952	13,924	2.81	2.96	0.50
	A3	3,409	13,017	3.82	3.05	0.53
	A4	1,265	2,902	2.29	3.01	0.55
	A5+	1,016	2,360	2.32	2.98	0.54
$^{\&}$ A 2 = 1.5 to 2.5 common A 2 = 2.5 to 2.5 common A 4 = 2.5 to 4.5 common and A.5						

A2 = 1.5 to 2.5 years, A3 = 2.5 to 3.5 years, A4 = 3.5 to 4.5 years and A5 = 4.5 to 5.5 years

Model. Parameters were estimated in bivariate analyses for each trait combination of WT and CS, fitting an animal model in ASReml (Gilmour et al. 2009). The model included a direct genetic effect as a random term. The fixed effects of age and age of dam were fitted as covariates while birth type, rearing type, sire breed, dam breed, number of lambs weaned in the previous calendar vear (nlwp) and number of lambs born for the current calendar year (nlbc) were all fitted as non-interacting fixed effects. Contemporary group (CG) was also fitted and was defined using flock, year of birth, sex, date of measurement

and management group. Approximately 32% (39,943) of the records had information available about the reproductive status at recording and all other animals received an unknown class effect. These observations on animals with lambing information were allocated to stages throughout the reproductive cycle such that 6,791 were recorded in the dry period between weaning and joining, 12,380 of the records were taken around joining, 10,056 during pregnancy, 6,112 pre-lambing and 4,604 around weaning time. The analyses to examine the physiological status effects were performed using 2 data sets; 1) all data where these effects were known and 2) only these observations recorded 50 days either side of the commencement of joining.

The correlations between WT and CS were estimated at each time of recording. These analyses included records across all ages treated as repeated records.

These analyses were repeated with and without the physiological status fixed effects. As these effects had little impact on the variance components and correlations only the results from the models with physiological status fixed effects are reported here.

Results and Discussion

The physiological status effects of previous and current number of lambs were highly significant for both traits (Table 2). The effect for previous lambs weaned was up to 4.20kg for WT and 0.17 for CS of ewes who weaned triplets compared to ewes which were dry in the previous year. These effects were greater when only analyzing data around joining. The number of lambs for the current parity had a positive effect on WT but negative effect on CS. Despite these significant effects their inclusions in the model had little impact on the variance components and correlations estimated. This suggests that while they may improve the accuracy of breeding values the recording of these effects should not be reasons to exclude WT and CS from the genetic evaluation.

Table 2. Solutions for litter size effects on adult body weight (WT) and condition score (CS) using records taken at joining (n=22,769) or at any time of the year (n=39.943) (expressed relative to dry ewes).

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	Litter	Joining Only	All stages		
	size	nlwp	nlbc	nlwp	
WT	1	-3.23 (0.14)	1.88 (0.13)	-2.07 (0.13)	
	2	-4.10 (0.14)	2.16 (0.09)	-2.66 (0.13)	
	3	-4.20 (0.71)	2.85 (0.25)	-2.60 (0.67)	
CS	1	-0.14 (0.01)	0.04 (0.01)	-0.12 (0.01)	
	2	-0.17 (0.01)	-0.01 (0.01)	-0.14 (0.01)	
	3	-0.13 (0.05)	-0.03 (0.02)	-0.14 (0.05)	

nlwp: previous years number of lambs weaned

nlbc: number of lambs born for the current year

The phenotypic variance for WT increased to three years of age and then declined slightly thereafter (Table 3) with the heritability following a similar pattern. The high heritability observed is likely to be due to the fact that 59% of the data used in this study originates from sire evaluation and research flocks which generally have more genetically diverse sires represented. The genetic correlations between ages were very high ranging from 0.97 to 0.99 and not significantly different to 1. The phenotypic correlations between ages were lower ranging from 0.36 to 0.64. These results suggest that one adult weight record is sufficient for selection for mature size.

Table 3. Phenotypic variance (σ^2_p) , heritability (h^2) , genetic correlations (below diagonal) and phenotypic correlations (above diagonal) within adult body weight and condition score records from different ages (using data from any time of the year, n=124,986).

	A2 ^{&}	A3	A4	A5
Body	Weight			
$\sigma^2_{\ p}$	26.85 (0.16)	39.36 (0.55)	38.51 (0.83)	35.43 (0.86)
h^2	0.52 (0.01)	0.66 (0.03)	0.61 (0.04)	0.48 (0.04)
A2		0.64 (0.01)	0.51 (0.01)	0.36 (0.02)
A3	0.98 (0.01)		0.69 (0.01)	0.57 (0.02)
A4	0.97 (0.02)	0.98 (0.01)		0.53 (0.02)
A5	0.99 (0.05)	0.98 (0.03)	0.98 (0.04)	
Cond	ition Score			
$\sigma^2_{\ p}$	0.14 (0.01)	0.15 (0.01)	0.14 (0.01)	0.16 (0.01)
h^2	0.28 (0.02)	0.21 (0.02)	0.22 (0.04)	0.13 (0.06)
A2		0.32 (0.01)	0.18 (0.02)	0.13 (0.04)
A3	0.98 (0.02)		0.26 (0.02)	0.13 (0.03)
A4	0.80 (0.11)	1.00 (0.06)		0.08 (0.08)
A5	0.75 (0.34)	0.99 (0.33)	0.69 (0.71)	
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& see Table 1

The phenotypic variance for CS also increased slightly with age (Table 3) however the heritability declined with age. The heritability observed in this study is slightly higher compared to that of 0.13 to 0.15 observed by Borg et al. (2009) in Western range sheep. The genetic correlations between ages were moderate to high ranging from 0.69 to 1.00. The phenotypic correlations between ages were low ranging from 0.08 to 0.32.

The phenotypic variance for WT varied depending on the time of year the animals are measured. More variation was apparent at lambing and weaning than at joining or during pregnancy (Table 4). However the heritability remained relatively constant across time points. The genetic correlations between times of the year were very high ranging from 0.96 to 1.00. The phenotypic correlations between times of year were also high ranging from 0.72 to 0.80. These results agree with those of Borg et al. (2009) who also estimated very high genetic correlations of 0.93 to 0.99 between WT measured at lactation, gestation and weaning. These results suggest that assessment of WT can be made at any time throughout the year.

Table 4. Phenotypic variance (σ_p^2) , heritability (h^2) , genetic correlations (below diagonal) and phenotypic correlations (above diagonal) for adult body weight and condition score recorded at different times of the year (using data from all ages where physiological status was known, n=40,360).

	Dry ^{&}	Join	Preg	Lamb	Wean	
Body Weight						
$\sigma^2_{\ p}$	39.39	36.26	35.61	42.77	46.39	
h^2	0.71	0.78	0.79	0.73	0.71	
Dry		0.79	0.77	0.73	n.e	
Join	0.99		0.80	0.74	0.76	
Preg	1.00	0.99		n.e	0.75	
Lamb	1.00	1.00	n.e		0.72	
Wean	n.e	0.98	0.96	0.97		
Conditio	n Score					
$\sigma^2_{\ p}$	0.02	0.08	0.11	0.11	0.16	
h^2	0.42	0.15	0.22	0.24	0.21	
Dry		0.18	0.11	0.12	0.11	
Join	0.75		n.e	n.e	0.19	
Preg	0.38	n.e		n.e	0.18	
Lamb	0.42	n.e	n.e		0.24	
Wean	0.43	0.90	0.81	0.90		

 $\overline{n.e} = Not \text{ estimable}$ [&] Dry = records during the period without pregnancy or lactation, Join = records around joining, Preg = records during pregnancy, Lamb = records close to lambing time and Wean = records close to weaning of lambs and Unk = records for animals without physiological status known.

The phenotypic variance and heritability of CS varied significantly throughout the year. The phenotypic variance increased from the dry period through to a maximum at weaning. In contrast the heritability was highest in the period when the ewe was dry and was generally similar at all other times. The genetic variance was at its highest at weaning and at this time was 4 times the magnitude compared to measurements from the dry period. The genetic correlations between measurement times were moderate to high ranging from 0.38 to 0.90. These results are lower than those of Borg et al. (2009) who also estimated very high genetic correlations of 0.93 to 0.96 between CS assessed at lactation, gestation and weaning. The phenotypic correlations between times of the year were also low ranging from 0.11 to 0.24.

These results suggest that multiple assessments of CS may be required throughout the year. Furthermore adult WT and CS were moderately correlated with each other at all times of the year with genetic correlations ranging from 0.34 to 0.65 and the phenotypic correlations ranging from 0.13 to 0.40 (Table 5). In contrast to the correlations within traits, the correlations between traits were significantly lower when estimated using records taken without any knowledge of physiological state. This may be due to the fact that records could have been taken at very different times of the year.

Table 5. Genetic correlations (r_g) and phenotypic correlations (r_n) between adult body weight and condition score from different physiological stages (using data from all ages, n=124.986).

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	Records	r _g	r _p
Dry ^{&}	6,791	0.61 (0.04)	0.32 (0.01)
Join	12,380	0.65 (0.03)	0.32 (0.01)
Preg	10,056	0.54 (0.03)	0.34 (0.01)
Lamb	6,112	0.63 (0.05)	0.40 (0.02)
Wean	4,604	0.54 (0.05)	0.45 (0.01)
Unk	84,874	0.34 (0.02)	0.13 (0.01)

* see Table 4.

Further research is required to investigate the genetic relationships between CS at different time points throughout the year with production traits to identify the value of this trait in a sheep breeding program and the best time to record CS in ewes.

Conclusion

Adult body weight was highly correlated phenotypically and genetically among ages suggesting that one assessment of adult weight is sufficient for selection purposes. As the genetic correlations were also very high between times within years this assessment could be made at any time. Condition score on the other hand while highly correlated between ages but not as highly correlated between times with the year. More research is required to identify the optimum time of measurement for condition score. Adult body weight and condition score were also moderately correlated with each other suggesting that they are different traits genetically and further research is required to determine the importance of condition score in sheep breeding programs.

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