GENOTYPE BY BIRTH OR REARING TYPE INTERACTION IN MERINO SHEEP

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SUMMARY

This study explores if there is an interaction between the genetic potential for growth in Merino lambs and their birth (BT) or rearing (RT) type. Data consisted of 3,920 singles and 4,492 twins which were the progeny of 285 sires and 5,279 dams. We found a significant sire by BT interaction with the effect accounting for 1.59% and 2.49% of the phenotypic variation for birth weight (BWT) and weaning weight (WWT), respectively. The effect was not significant for post weaning weight (PWWT), scanned fat (SF) and eye muscle depth (EMD) with sire by BT effects accounting for less than 1% of the variation in these traits. Sire by RT interaction effects were much smaller and not significant for WWT, PWWT and SF, but accounted for 1.83% of the variation in EMD, which was significant. A bivariate analysis treating phenotypes when expressed in singles and twins as two different traits resulted in genetic correlation estimates significantly lower than one, with BT having a larger effect on genotype expression than RT.

INTRODUCTION

Birth type (BT) and rearing type (RT) constitute environments that influence the early life of sheep. Animals born as singles have higher birth weight and grow faster than animals born as twins or triplets (Yilmaz *et al.* 2007). Furthermore lambs reared as singles are heavier than those reared as twins (Safari *et al.* 2007; David *et al.* 2011). Animals born as a single are more likely to have access to better nutrition in *utero* and animals reared as a single will also have access to more milk prior to weaning compared to those reared as twins.

What has not often been looked at is whether the expression of genetic merit depends on or interacts with the BT or the RT of lambs. If such an interaction exists, there could be implications for genetic evaluation as well as for breeding programs in general. It is not feasible to design breeding programs for expression of genotypes solely as single or twins. But it may be possible to predict that the expression of breeding value is more frequent in one of these classes, and this information can be used to predict progeny differences more accurately. In genetic evaluation, it may be important to account for such genotype by BT or RT interactions if they are found to be significant.

The objectives of this study were to investigate genotype by BT or RT interactions for a number of growth related traits in Merino sheep. In a linear mixed model we investigated the presence of sire by BT or RT interaction and we estimated the genetic correlations between expressions of these traits in lambs born or raised as singles or as twins and the genetic correlation among the traits. We also investigated whether the genetic correlations between growth traits differ when expressed in singles or in twins.

MATERIALS AND METHODS

Data of Merino sheep for this study was obtained from the Information Nucleus (IN) program of the CRC for Sheep Industry Innovation in Australia. Details on this program and its design are described by van der Werf *et al.* (2010). Data consisted of birth weight (BWT), weaning weight (WWT), post weaning weight (PWWT), scanned fat (SF), and eye muscle depth (EMD). WWT was measured at approximately 100 days and PWWT, SF and EMD were measured at approximately

250 days of age. Birth weight records were available from 8,412 lambs generated from 285 sires and 5,279 dams of Merino sheep.

Mixed model analysis was used in this study using the ASREML software (Gilmour *et al.* 2009). The fixed effects in the models were birth year (6 classes, 2007-2012 with 969-1,678 lambs per year), flock (8 classes, 521-2,483 lambs per flock), and management group within flock (GRP: up to 4 classes per flock) as one contemporary group effect, as well as a BT (2 classes) x RT (2 classes) effect. The other fixed effects included were age of dam (9 classes), sex (2 classes), and age at measurement as covariate. Live weight and age at scanning were included as fixed effects for SF and EMD.

Genetic group, animal, dam, and interaction between sire and BT or RT (SxBT/RT) were fitted as random effects in a univariate animal model. The number of genetic groups was 135 and determined by strain and flock of origin. The phenotypic variance was calculated as the sum of variance components for additive genetic effect of the animal, the dam effect, the SxBT/RT effect and the residual. A pedigree file consisting of 20,010 animals from 11 generations was used to determine additive genetic relationships among animals and account for them in the analysis. It was assumed that dams were unrelated, and in the SxBT/RT interaction terms, sires were assumed unrelated as well. We used the log likelihood ratio test (LRT) to compare the full model including SxBT/RT with a reduced model to test the significance of the SxBT/RT interaction effect.

In bivariate analyses, we considered the expression of a particular trait expressed in either singles or twins as two different traits with a genetic correlation between them (Falconer, 1952). The magnitude of the genotype by environment interaction (GEI) was evaluated based on the value of the estimated genetic correlation. Sire models were used in bivariate analyses with genetic group and sire as random effect and it was again assumed that sires were unrelated. Because of limited data in other subclasses, only traits expressed in the BT/RT combinations 11, 21, and 22 were used in the bivariate analyses to investigate GEI in an attempt to disentangle the effects of BT and of RT.

RESULTS AND DISCUSSION

Univariate analysis. Estimates of heritability (Table 1) in a model considering SxBT were lower than those without inclusion of SxBT for BWT and WWT. Heritability estimates for PWWT, SF and EMD were similar with and without inclusion of SxBT. When including SxRT in the model the heritability estimate changed only for EMD. Heritability estimates in this study are in the same ballpark as previous report (Safari and Fogarty, 2003; Safari *et al.* 2005; Mortimer *et al.* 2010).

The SxBT effect explained 1.59% and 2.49% of the phenotypic variance of BWT and WWT, respectively, which was significant and 0.76%, 0.80% and 0.06% for PWWT, SF and EMD, which was not significant. Brown *et al.* (2009) reported a similar pattern with inclusion of sire by flock-year interaction in a model, which explained 2%, 3% and 4% of variation of WWT, PWWT and yearling body weight of lambs, respectively, reducing heritability estimates by up to 50%. Maniatis and Pollott (2002) reported a similar pattern when including sire by flock-year interaction in a model, explaining only 2 to 3% of the phenotypic variation in 8 week weight and scanning weight of lambs. This result of sire x contemporary group effect explaining 2.4% of variation in body weight is similar to that reported by Pollott and Greeff (2004). The interaction term in their study explained 2% and 2% to 4% of EMD and SF variation, respectively, and heritability estimates deflated by up to 50% after accounting for GEI.

In our analysis, maternal effect contributed significantly to BWT and WWT variation (31 and 23%), but it was smaller (10%) for PWWT and these figures were very similar with and without including the SxBT effect in the model. The contribution of dam effect was also similar when including SxRT in the model. Overall these results indicate that it may be important to include SxBT effects in the genetic evaluation of Merino sheep, particularly for BWT and WWT.

Table 1. Estimates of variance additive genetic, maternal and sire by BT(RT) effects and direct and maternal heritabilities of Merino sheep growth traits based on univariate analysis

Traits	*Variance components without SxBT or SxBT in the model**						
	σ_a^2	σ_m^2	$\sigma^2_{SxBT(RT)}$	σ_e^2	h^2	m^2	LRT
BWT	0.141	0.182		0.268	0.24 ± 0.04	0.31 ± 0.02	
WWT	1.909	2.839		7.358	0.16 ± 0.03	0.23 ± 0.02	
PWWT	7.673	2.850		16.702	0.28 ± 0.04	0.10 ± 0.02	
SF	0.087			0.283	0.23 ± 0.04		
EMD	1.590			4.074	0.28 ± 0.04		
	Variance components with SxBT in the model						
BWT	0.125	0.185	0.009	0.272	0.21 ± 0.04	0.31 ± 0.02	7.16
WWT	1.389	2.942	0.302	7.491	0.11 ± 0.03	0.24 ± 0.02	16.20
PWWT	7.207	2.673	0.205	16.856	0.27 ± 0.05	0.10 ± 0.02	1.62
SF	0.080		0.003	0.287	0.22 ± 0.04		0.67
EMD	1.582		0.005	4.078	0.28 ± 0.05		0.00
	Variance components with SxRT in the model						
WWT	1.898	2.842	0.004	7.362	0.16 ± 0.03	0.23 ± 0.02	0.00
PWWT	7.564	2.600	0.038	16.745	0.28 ± 0.05	0.10 ± 0.02	0.06
SF	0.084		0.001	0.284	0.23 ± 0.04		0.13
EMD	1.395		0.103	4.164	0.25 ± 0.05		3.90

Note: *σ_a^2 = additive genetic variance, σ_m^2 = maternal variance, σ^2_{SxBT} = sire by birth type interaction variance, σ^2_{SxRT} = sire by rearing type interaction variance, and σ_e^2 = residual variance; and h^2 = direct genetic heritability, and m^2 = maternal heritability

Bivariate analysis. Results of this study (Table 2) show that the genetic correlation between traits expressed in singles versus twins differed significantly from one for most traits, with BT having a slightly larger effect on genotype expression than RT. This suggests that both pre- and postnatal environments significantly affect the genotype expression of weight traits in lambs. This finding agrees with Carrick and van der Werf (2005) who found that the genetic correlation between traits expressed in extreme environments (as defined by the mean performance of a cohort) was lower for earlier growth traits of sheep. In this study the expression of PWWT (at around 250 days of age) and EMD in single BT and RT might reflect the same trait and differs only in scale from twin BT and RT with genetic correlations of 0.88 ± 0.04 and 0.89 ± 0.04, respectively. Similarly, SF with the same RT but different BT (11x21) had a genetic correlation of 0.95 ± 0.02. The expression of WWT and SF in twin BT but with different RT might be the same as in twin BT and RT with genetic correlations of 0.96 ± 0.02 and 0.92 ± 0.05, respectively. Overall, these results indicate that differences in BT and RT will influence the expression of breeding values of growth traits in Merino sheep.

Table 2. Genetic correlation between traits expressed in singles or twins (born or reared) based on sire model bivariate analysis

Type of correlation*	Traits				
	BWT	WWT	PWWT	SF	EMD
11x22	0.73 ± 0.07	0.83 ± 0.06	0.88 ± 0.04	0.82 ± 0.05	0.89 ± 0.04
11x21		0.77 ± 0.05	0.70 ± 0.09	0.95 ± 0.02	0.71 ± 0.14
21x22		0.96 ± 0.02	0.80 ± 0.07	0.92 ± 0.05	0.71 ± 0.13

Note: *11x22 = correlation between lambs born-reared as single and lambs born-reared as twins, 11x21 = correlation between lambs born-reared as single and lambs born as twins but reared as single, and 21x22 = correlation between lambs born as twins but reared as single and lambs born-reared as twins

CONCLUSION AND IMPLICATIONS

The contribution of sire by birth type interaction to the expression of birth weight and weaning weight was significant, while the contribution of sire by rearing type was only significant for eye muscle depth. In general there was genotype by environment interaction indicating that birth and rearing type influenced the expression of traits of lambs. This study suggests that BT and RT are biologically important environments that influence the genetic potential for growth of lambs. This was the case particularly for BWT and WWT which were influenced by BT and EMD that was influenced by RT. The relatively stronger interaction for BT suggests that the prenatal environment has a larger influence on the genetic expression for growth after birth compared to the postnatal environment. These results also suggest that sires could re-rank when evaluated based on single versus twin birth or rearing type. Therefore, sire by birth or rearing type interactions should be included in models used for genetic evaluation.

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