

## **GENETIC ASSOCIATIONS OF EARLY GROWTH AND ULTRASOUND SCANNED TRAITS IN SEVERAL BEEF BREEDS**

**M. G. Jeyaruban and D. J. Johnston**

Animal Genetics and Breeding Unit<sup>1</sup>, University of New England, Armidale, NSW 2351

### **SUMMARY**

Genetic association of early growth traits with ultrasound scanned traits in heifers and bulls of Angus, Charolais, Hereford, Simmental and Santa Gertrudis were examined. Early growth traits such as birth weight (BW), 200 day weight (200D) and 400 day weight (400D) along with ultrasound scanned rump (P8), intramuscular fat (IMF) and eye muscle area (EMA) in heifers and bulls, were considered in this analysis. Estimated genetic correlations between BW and scanned fat traits were negative and ranged from -0.48 to -0.04. The 200D and 400D had positive genetic correlations with the scanned fat of heifers of all breeds, and also for the scanned fat of Angus and Herefords bulls. Breed influence on the genetic correlation of early growth traits with scanned traits was evident for all traits. The magnitude of the estimated genetic correlations of early growth traits with scanned fat traits may not be adequate to cause significant correlated changes in these traits. Therefore, selection objectives, combining early growth and ultrasound scanned traits, is required if it is necessary to change these traits in the five breeds studied.

### **INTRODUCTION**

BREEDPLAN, the national Australian genetic evaluation, has been used for nearly 30 years to improve the genetic potential of Australian seedstock herds (Graser *et al.* 2005). Estimated breeding values are calculated for more than twenty five economically important traits in various beef breeds by using a multi-trait genetic evaluation system (Johnston 2007). Genetic correlations between traits are breed specific. Therefore, knowledge of the genetic relationships between traits are important in the multi-trait genetic evaluation system for the accurate prediction of correlated responses in genetically correlated traits and the identification of early indicator traits for traits expressed later in life or which are difficult to measure. Currently growth traits are easy and cheap to record and are widely recorded in most of the beef breeds in Australia. Therefore, it is very important that their relationships with body composition traits (fat and eye muscle area) are well estimated for all breeds. The objective of this paper was to study the genetic association of early growth and scanned traits in commonly used beef breeds in Australia to understand the biological relationship of lean to fat content in these beef breeds.

### **MATERIALS AND METHODS**

Data used for this study were submitted by breeders to their breed societies for use in BREEDPLAN. The breeds included Angus (ANG), Charolais (CHA), Hereford (HER), Simmental (SIM) and Santa Gertrudis (SAN). Early growth traits considered were birth weight (BW), 200-day weight (200D) and 400-day weight (400D) with age at recording ranging from 80 to 300 days for 200D and 301 to 500 days for 400D. Real-time ultrasound scan measurements included fat depth at the P8 (rump) site for bulls (BP8) and heifers (HP8), intramuscular fat in bulls (BIMF) and heifers (HIMF) and longissimus muscle area in bulls (BEMA) and heifers (HEMA), with age at recording for all traits ranging from 300 to 800 days. For ANG and HER, data from animals born after 2004 were used to reduce computational requirements. Genetic parameters for growth and scanned traits were estimated using a univariate linear animal model as given below,

<sup>1</sup> AGBU is a joint venture of NSW Department of Primary Industries and University of New England

## Meat

$$Y_{ijkl} = cg_i + \beta_1 \text{age}_j(\text{season}_i) + \beta_2 \text{age}_j^2(\text{season}_i) + \beta_3 \text{hf}_j(\text{season}_i) + \beta_4 \text{age}_k(\text{sex}_k) + a_k + e_{ijkl}$$
 where  $Y_{ijkl}$  is the trait measured in animal  $k$  in a fixed contemporary group  $i$  ( $cg_i$ ),  $\text{age}_j$  is the age of dam  $j$  at calving deviated from five years of age nested within season (Autumn and Spring),  $\text{hf}_j$  (heifer factor) is the additional dam age function fitted to improve the fit for offspring of dams less than 2.5 years old,  $\text{age}_k$  is the age of animal  $k$  nested within sex of animal  $k$ ,  $\beta_1$ ,  $\beta_2$  and  $\beta_3$  are the regression coefficients for linear, quadratic and heifer factor effects of dam age,  $\beta_4$  is the regression coefficient for age of animal,  $a_k$  is the random genetic effect of animal  $k$  and  $e_{ijkl}$  is the random error associated with each observation. For 200D, 400D and scanned traits, the age was deviated from 200, 400 and 500 days, respectively, as currently implemented in BREEDPLAN. Additional random maternal genetic and random permanent maternal environment effects of dam  $j$  are fitted to BW, 200D and 400D to account for the maternal influence on these traits. Contemporary groups were as defined by Graser *et al.* (2005). Bivariate animal models were used to estimate genetic correlations of BW, 200D and 400D with scanned traits for each breed separately. Complete pedigree information going back three generations was used. Estimates of (co)variance components in the univariate and bivariate analyses were obtained using WOMBAT (Meyer 2007).

## RESULTS AND DISCUSSION

The number of records used for each trait by breed is presented in Table 1. The ANG had the highest number of records for all the traits, while CHA had the least number of records, except for BW and BIMF. The number of animals recorded for growth traits were higher than the number of animals recorded for the scanned traits. Table 2 gives the estimated heritability ( $h^2$ ) for age adjusted growth and ultrasound scanned traits. The BW was moderately heritable in all breeds with the estimated  $h^2$  ranged from 0.24 to 0.40. Low and low to moderate  $h^2$  were estimated for 200D and 400D, respectively. The estimated  $h^2$  ranged from 0.12 to 0.17 for 200D and 0.19 to 0.26 for 400D. Ultrasound scanned traits on heifers were moderately heritable and were generally higher than the estimates for bulls, except for HIMF of SIM. Breed variations in  $h^2$  of HP8 (0.35 to 0.49), HIMF (0.23 to 0.49), HEMA (0.24 to 0.42), BP8 (0.21 to 0.28), BIMF (0.17 to 0.40) and BEMA (0.22 to 0.34) were observed. The estimated  $h^2$  of the scanned traits of ANG and HER were very similar. Estimated  $h^2$  for growth and ultrasound scanned traits were within the range published in the literature (Koots *et al.* 2005).

**Table 1. Number of growth and ultrasound scanned traits records used from Angus (ANG), Charolais (CHA), Hereford (HER), Simmental (SIM) and Santa Gertrudis (SAN)**

Breed		BW	200D	400D	HP8	HIMF	HEMA	BP8	BIMF	BEMA
ANG	N <sup>A</sup>	308938	273546	186377	73865	70752	74338	76265	73044	77243
HER	N <sup>A</sup>	155733	177749	114847	30105	27144	30339	39064	32256	39299
SIM	N	136541	121287	77103	6926	2254	6980	11425	2782	11566
CHA	N	48100	58554	33746	2740	1518	2767	4115	3163	9646
SAN	N	3832	111982	60910	11618	3966	11780	19820	6318	20023

<sup>A</sup> Using data from animals born after 2004 to reduce computational requirements

**Table 2. Estimated heritabilities (direct) for early growth and ultrasound scanned traits (standard error in parenthesis) using univariate animal model evaluation**

Breed	BW	200D	400D	HP8	HIMF	HEMA	BP8	BIMF	BEMA
ANG	0.32 (0.01)	0.12 (0.01)	0.22 (0.01)	0.43 (0.01)	0.28 (0.01)	0.26 (0.01)	0.28 (0.01)	0.17 (0.01)	0.24 (0.01)
HER	0.32 (0.02)	0.12 (0.01)	0.19 (0.01)	0.36 (0.02)	0.28 (0.02)	0.24 (0.02)	0.26 (0.02)	0.21 (0.02)	0.22 (0.01)
SIM	0.26 (0.02)	0.14 (0.01)	0.26 (0.01)	0.40 (0.03)	0.23 (0.03)	0.42 (0.06)	0.21 (0.03)	0.29 (0.03)	0.26 (0.06)
CHA	0.24 (0.03)	0.17 (0.01)	0.26 (0.02)	0.49 (0.06)	0.39 (0.09)	0.35 (0.06)	0.27 (0.03)	0.27 (0.06)	0.34 (0.03)
SAN	0.40 (0.07)	0.17 (0.01)	0.22 (0.02)	0.35 (0.03)	0.49 (0.06)	0.30 (0.03)	0.27 (0.02)	0.40 (0.05)	0.27 (0.02)

**Table 3. Estimated genetic correlations between early growth and ultrasound scanned traits (standard error in parenthesis)**

Breed	Trait	HP8	HIMF	HEMA	BP8	BIMF	BEMA
ANG	BW	-0.26(0.02)	-0.22(0.02)	0.25(0.02)	-0.29(0.03)	-0.16(0.03)	0.13(0.03)
	200D	0.21(0.03)	0.34(0.03)	0.79(0.02)	0.01(0.04)	0.26(0.04)	0.67(0.03)
	400D	0.21(0.05)	0.19(0.03)	0.60(0.02)	0.08(0.03)	0.19(0.04)	0.57(0.02)
HER	BW	-0.40(0.03)	-0.26(0.04)	0.22(0.04)	-0.34(0.04)	-0.15(0.05)	0.24(0.04)
	200D	0.05(0.06)	0.16(0.06)	0.74(0.04)	0.08(0.06)	0.05(0.07)	0.72(0.04)
	400D	0.01(0.04)	0.07(0.05)	0.66(0.03)	0.11(0.05)	0.12(0.05)	0.65(0.03)
SIM	BW	-0.19(0.06)	-0.38(0.10)	0.31(0.07)	-0.21(0.07)	-0.02(0.15)	0.36(0.07)
	200D	0.05(0.08)	0.01(0.14)	0.63(0.07)	-0.24(0.08)	0.04(0.18)	0.47(0.07)
	400D	0.20(0.06)	0.01(0.12)	0.60(0.06)	-0.11(0.07)	0.04(0.17)	0.45(0.06)
CHA	BW	-0.24(0.08)	-0.48(0.14)	0.25(0.10)	-0.23(0.10)	-0.28(0.13)	0.13(0.07)
	200D	0.03(0.10)	0.25(0.14)	0.52(0.09)	0.20(0.10)	-0.07(0.12)	0.48(0.06)
	400D	0.07(0.10)	0.31(0.15)	0.45(0.09)	-0.01(0.11)	-0.01(0.13)	0.53(0.06)
SAN	BW	-0.33(0.10)	-0.13(0.09)	0.17(0.11)	-0.17(0.13)	-0.04(0.11)	0.16(0.14)
	200D	0.15(0.05)	0.08(0.08)	0.52(0.04)	-0.01(0.04)	-0.01(0.07)	0.47(0.04)
	400D	0.21(0.05)	0.16(0.09)	0.59(0.04)	0.04(0.05)	0.18(0.07)	0.49(0.04)

Table 3 presents the estimated genetic correlations between age adjusted early growth and ultrasound scanned traits. Ultrasound scanned fat traits (P8 and IMF) on heifers and bulls had low to moderate negative correlation with BW. The genetic correlations of BW with scanned fat traits in heifers ranged from -0.40 (HER) to -0.19 (SIM) for HP8 and -0.48 (CHA) to -0.13 (SAN) for HIMF. The genetic correlations of BW with scanned fat traits in bulls ranged from -0.34 (HER) to -0.17 (SAN) for BP8 and -0.28 (CHA) to -0.02 (SIM) for BIMF. However, BW had low to moderate positive correlations with HEMA and BEMA. The breed influence was evident on the genetic correlations of BW with HEMA (0.17 to 0.31) and BEMA (0.13 to 0.36).

The 200D had low to moderate positive genetic correlations with scanned fat traits of heifers. The genetic correlations of 200D with the scanned fat traits of bulls were also generally positive, with the exception of BP8 in SIM, BIMF in CHA and BP8 and BIMF in SAN. The 400D had low

## *Meat*

to moderate positive correlations with scanned fat traits of heifers. The genetic correlation observed between 400D and scanned fat traits in bulls were low and ranged from -0.11 to 0.11 for BP8 and -0.01 to 0.19 for BIMF. The 200D and 400D were moderately to highly correlated with HEMA and BEMA in all breeds and the correlations ranged from 0.52 to 0.79 for HEMA and 0.47 to 0.72 for BEMA.

Low to moderate correlations of BW and scanned fat traits in heifers and bulls indicated that selection for lower BW would result in slightly higher fat depths in all breeds. Selecting for higher 200D and 400D is expected to increase the fat in heifers of all breeds, and also for the scanned fat of Angus and Herefords bulls. However, the magnitude of the estimated correlations of age adjusted early growth traits with age-adjusted scanned fat traits indicated that the expected changes in the fat content of heifers and bulls would not alter the body composition significantly in any of the five breeds studied.

### **CONCLUSIONS**

There was variation for the estimated heritabilities of early growth and ultrasound scanned traits of the five breeds. For all breeds, correlations indicate that genetically high BW is associated with reduced fatness and increased EMA when considered on an age-constant basis. Similarly, genetically heavier animals at 200D and 400D have larger EMA. However, there is some variation in the magnitude of estimates between breeds and genders. In contrast, there appears no consistent genetic relationship between 200D and 400D weight traits with fatness when considered on an age constant basis corrected to 500 days of age. All of these relationships might change if scan traits are corrected based on weight-constant basis. Further research is required to validate this claim. Results demonstrated the importance of combining early growth and scanned traits in selection objectives to alter the body composition to fulfil different market requirements.

### **ACKNOWLEDGEMENT**

The authors would like to thank Meat and Livestock Australia for their financial support through B.BFG.0050 and the Angus, Charolais, Hereford, Simmental and Santa Gertrudis Breeders Associations for providing data for this study. The authors also would like to acknowledge the contribution of Kim Bunter for her comments on the manuscript.

### **REFERENCES**

- Graser H-U., Tier B., Johnston D.J. and Barwick S.A. (2005) *Aust. J. Exp. Agric.* **45**:913.  
Johnston D.J. (2007) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **17**:8  
Koots K.R., Gibson J.P., Smith C. and Wilton J.W. (1994). *Anim. Breed. Abst.* **62**:309  
Meyer K (2007) *J. Zhej. Uni. Sci.* **8**:815.