

# Additive Genetic Parameters for Postweaning Growth, Feed Intake, and Ultrasound Traits in Angus-Brahman Multibreed Cattle

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Moderate to high estimates of heritability for postweaning feed intake, growth, and ultrasound traits indicated that selection for these traits would be effective in Angus-Brahman multibreed populations. Estimates of genetic correlations were too inaccurate to draw firm conclusions. Thus, additional postweaning feed intake, growth, and ultrasound data needs to be collected at the Feed Efficiency Facility to obtain reliable correlations for use in multiple-trait genetic evaluation and selection of purebred and crossbred animals under subtropical conditions.

## Summary

*Automated feed efficiency facilities permit the measurement of individual feed intake in large numbers of cattle of similar age and maintained under the same feeding regimen and management conditions. These facilities allow the construction of large contemporary groups that have the potential to become an integral component of national genetic evaluation programs. Feed consumption, growth, and ultrasound data collected in these facilities will provide essential information for the estimation of variance and covariance components needed for genetic evaluation of animals for all these traits and for residual feed intake (RFI). Thus, the objective of this research was the estimation of heritabilities for and genetic correlations between RFI, daily feed intake (DFI), feed conversion ratio (FCR), postweaning growth (PWG), ultrasound fat thickness (UFT), ultrasound percent of intramuscular fat (UIF), and ultrasound ribeye area (UREA) using data from a multibreed Angus-Brahman cattle population collected in an automated feeding facility located in Marianna, Florida. Heritabilities were low to moderate for all traits ( $0.14 \pm 0.06$  to  $0.34 \pm 0.09$ ), except for the high estimate for UIF ( $0.78 \pm 0.09$ ). Genetic correlations between RFI, DFI, FCR, and PWG, and UFT, UIF, and UREA tended to be low and to have large standard errors. This indicates that additional data from the automated feeding facility would be needed to obtain informative correlations for multiple-trait selection.*

## Introduction

Automated feed efficiency facilities permit the measurement of individual feed intake in large numbers of cattle of similar age and maintained under the same feeding regimen and management conditions. These facilities allow the construction of large contemporary groups that have the potential to become an integral component of national genetic evaluation programs. Feed consumption, growth, and ultrasound data collected in these facilities will provide essential information for the estimation of variance and covariance components needed for genetic evaluation of animals for all these traits and for residual feed intake. Postweaning feed intake, growth, and ultrasound data were collected on a large number of Angus, Brahman, and Angus x Brahman cattle at the GrowSafe 4000 Feed Efficiency Facility (FEF) of the University of Florida from 2006 to 2009. The objective of this research was the estimation of heritabilities for residual feed intake (RFI), daily feed intake (DFI), feed conversion ratio (FCR), postweaning growth (PWG), ultrasound fat thickness (UFT), ultrasound percent of intramuscular fat (UIF), and ultrasound ribeye area (UREA) as well as genetic correlations among these traits in a multibreed population composed of Angus (A), Brahman (B), and crossbred cattle of various A and B fractions under subtropical conditions.

## Materials and Methods

### *Animals, housing, feeding and management.*

Animals were from three Florida farms

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(n = 1,129), one located in Gainesville (n = 751) and two located in Marianna (n = 93 and n = 285). Calves were born in 2006 (n = 278), 2007 (n = 203), 2008 (n = 348), and 2009 (n = 300). Approved research protocols for animal care from the University of Florida Institutional Animal Care and Use Committee were followed (IACUC number D477). The dataset contained feed intake, growth, and ultrasound information from 208 bulls, 530 heifers, and 391 steers from six breed groups: A,  $\frac{3}{4}$  A  $\frac{1}{4}$  B, Brangus ( $\frac{5}{8}$  A  $\frac{3}{8}$  B),  $\frac{1}{2}$  A  $\frac{1}{2}$  B,  $\frac{1}{4}$  A  $\frac{3}{4}$  B, and B. These calves were the offspring of 74 bulls and 451 dams from these same six breed groups. Numbers of sires, dams, and calves per breed group are shown in Table 1. Calves from the three herds were transported to the FEF postweaning and assigned to 24 pens (1,162 square feet each; 2 GrowSafe nodes per pen) by sire group (A,  $\frac{3}{4}$  A  $\frac{1}{4}$  B, Brangus,  $\frac{1}{2}$  A  $\frac{1}{2}$  B,  $\frac{1}{4}$  A  $\frac{3}{4}$  B, and B) and sex (bull, heifer, and steer) combination. Calves were identified with half-duplex passive transponder ear tags (Allflex USA Inc., Dallas-Fort Worth, TX). The mean stocking density was 12.6 animals per pen and 6.3 animals per GrowSafe node. Animals were offered a concentrate diet composed of various percentages of corn, corn gluten feed, dried distilled grains plus solubles, soybean hulls, cottonseed hulls, chopped grass hay, and a vitamin-mineral-protein supplement (FRM, Bainbridge, GA) ad libitum. Dry matter (DM), crude protein, net energy for maintenance, and net energy for gain of the diet provided to calves each year is presented in Table 2. Calves were allowed to adjust to the diet and the FEF for 14 to 21 d prior to the 70-d trial period. GrowSafe software recorded feed intake information in real-time. Weights (lb) and exit velocity (feet per second) were measured every 2 wk.

#### ***Postweaning feed intake, growth, and ultrasound traits.***

Traits were RFI (lb DM/d), DFI (lb DM/d), FCR (DFI/lb weight gain per day), PWG (lb), UFT (in), UIF (%), and UREA (in<sup>2</sup>). Intake traits were defined on a DM basis. Feed intake, growth, and ultrasound traits were measured at the University of Florida FEF in Marianna, Florida. Phenotypic RFI was obtained as the difference between expected and actual average

DFI during the 70-d postweaning feeding trial (Koch et al., 1963; Arthur et al., 2001a; Archer et al., 1997) within a batch of calves. A batch of calves was defined as a group of calves from a particular herd placed in the FEF at the same time. Expected feed intake was estimated using a linear regression of average DFI on average daily gain (ADG) and metabolic mid-weight within a batch of calves, and across breed groups and sexes of calves. This model explained 59% of the variation for average DFI. Ultrasound fat thickness and UIF within a batch of calves (Schenkel et al., 2004; Lancaster et al., 2009) were found to be non-significant and excluded from the final model. Average daily gain was estimated using a regression of calf weight on test day. Metabolic mid-weight was computed as the sum of the regression estimate for initial weight plus the regression estimate for ADG times 35 (midpoint day of trial) raised to the power of 0.75. Feed conversion ratio was obtained as the ratio of DFI to ADG. Postweaning gain was the difference between the weight of a calf at the beginning and at the end of the 70-d trial. Ultrasound images were taken and analyzed by certified technicians (Tallgrass Beef Co., Sedan, KS, Perryman Livestock Ultrasound Service, Micanopy, FL, and Walter and Associates, Ames, IA).

#### ***Heritabilities, genetic correlations, and phenotypic correlations.***

Restricted maximum likelihood estimates of genetic and phenotypic variances and heritabilities for RFI, DFI, FCR, PWG, UFT, UIF, and UREA as well as genetic and phenotypic covariances and correlations among these traits were computed using ASREML (Gilmour et al., 2006). Variances and heritabilities were computed using single-trait analyses. Covariances and correlations were computed using 2-trait analyses. The same model was used for all traits. Fixed effects were contemporary group (herd-year-pen subclass), sex of calf (bull, heifer, steer), age of calf, Brahman fraction of calf nested within sex of calf, heterozygosity of calf nested within sex of calf, and mean exit velocity (average of 6 records). Random effects were calf and residual. Calf effects were assumed to have mean zero and variance equal to the relationship matrix

times the genetic variance for a given trait (single-trait analyses), or a  $2 \times 2$  genetic variance-covariance matrix (2-trait analyses). Residual effects were assumed to have mean zero, common variance (single-trait analyses) or  $2 \times 2$  variance-covariance matrix (2-trait analyses) and uncorrelated.

### Results

Estimates of heritability in this Angus-Brahman multibreed population were low to moderate for postweaning feed intake and growth traits ( $0.14 \pm 0.06$  to  $0.33 \pm 0.09$ ; Table 3) and for ultrasound traits, except for the high heritability estimate for UIF ( $0.26 \pm 0.08$  to  $0.78 \pm 0.09$ ; Table 4). Heritability estimates for RFI, DFI, and FCR were lower than estimates in Canada ( $0.37$  to  $0.44$ ; Schenkel et al., 2004), Australia ( $0.32 \pm 0.05$  to  $0.38 \pm 0.06$ ; Arthur et al., 2001a), and France ( $0.32 \pm 0.02$  to  $0.44 \pm 0.02$ ; Arthur et al., 2001b). No comparable estimates for PWG were found in the literature. However, heritability estimates for ADG were similar ( $0.35$ ; Schenkel et al., 2004;  $0.31 \pm 0.05$ ; Arthur et al., 2001b) to the PWG heritability estimate here. The UFT heritability was lower than and the UREA heritability was similar to estimates from crossbred cattle (UFT:  $0.59 \pm 0.14$ ; UREA:  $0.39 \pm 0.13$ ; Nkrumah et al., 2007) and purebred bulls of several breeds (UFT:  $0.36$ ; UREA:  $0.30$ ; Schenkel et al., 2004). The UIF heritability was similar ( $0.75 \pm 0.16$ ) to that reported by Nkrumah et al. (2007) and higher than that estimated ( $0.14$ ) by Schenkel et al. (2004).

Most genetic and phenotypic correlations had large standard errors. The most accurate estimates of genetic and phenotypic correlations (Table 3) were the positive ones between RFI and DFI (less efficient animals had larger feed intakes) and between DFI and PWG (calves that ate more gained more weight) and the negative one between FCR and PWG (less efficient animals ate more and gained less than more efficient ones). Genetic and phenotypic correlations (Table 4) were positive between UFT and UIF, and near zero between UIF and UREA. Estimates of genetic (Table 5) and phenotypic (Table 6) correlations between RFI, DFI, FCR, and PWG, and UFT, UIF, and UREA had large standard errors and they were mostly smaller than those reported by Schenkel et al. (2004) and Nkrumah et al. (2007).

### Literature Cited

- Archer. et al. 1997. *J. Anim. Sci.* 75:2024.  
Arthur. et al. 2001a. *J. Anim. Sci.* 79:2805.  
Arthur. et al. 2001b. *Livest. Prod. Sci.* 68:131.  
Gilmour. et al. 2006. VSN International Ltd., Hemel Hempstead, HP1 1ES, UK.  
Koch. et al. 1963. *J. Anim. Sci.* 22:486.  
Lancaster. et al. 2009. *J. Anim. Sci.* 87:1528.  
Nkrumah. et al. 2007). *J. Anim. Sci.* 85:2711.  
Schenkel. et al. 2004. *Can. J. Anim. Sci.* 84:177.

**Table 1.** Numbers of sires, dams, and calves per breed group

	Angus	$\frac{3}{4}$ A $\frac{1}{4}$ B	Brangus	$\frac{1}{2}$ A $\frac{1}{2}$ B	$\frac{1}{4}$ A $\frac{3}{4}$ B	Brahman
Sires	12	9	28	8	6	11
Dams	97	68	99	97	42	48
Calves	420	142	184	183	79	121

**Table 2.** Nutritional analysis of the diet at the Feed Efficiency Facility by year

	2006	2007	2008	2009
Dry Matter, %	91.2	90.0	84.5	93.0
Crude Protein, %	17.3	14.1	11.1	12.3
Net Energy for Maintenance, mcal/lb DM	0.8	0.8	0.7	0.6
Net Energy for Gain, mcal/lb DM	0.6	0.5	0.5	0.4

**Table 3.** Estimates of heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for postweaning feed intake and growth traits in an Angus-Brahman multibreed population

Trait <sup>1</sup>	RFI	DFI	FCR	PWG
RFI	0.14 ± 0.06	0.77 ± 0.10	0.24 ± 0.27	0.14 ± 0.25
DFI	0.88 ± 0.03	0.21 ± 0.07	-0.07 ± 0.25	0.55 ± 0.16
FCR	0.34 ± 0.10	0.11 ± 0.10	0.18 ± 0.07	-0.82 ± 0.11
PWG	0.07 ± 0.11	0.43 ± 0.08	-0.66 ± 0.06	0.33 ± 0.09

<sup>1</sup>RFI = residual feed intake; DFI = daily feed intake; FCR = feed conversion ratio; PWG = postweaning gain.

**Table 4.** Estimates of heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for ultrasound traits in an Angus-Brahman multibreed population

Trait <sup>1</sup>	UFT	UIF	UREA
UFT	0.26 ± 0.08	0.68 ± 0.11	0.28 ± 0.18
UIF	0.50 ± 0.07	0.78 ± 0.09	-0.02 ± 0.15
UREA	0.32 ± 0.09	0.00 ± 0.10	0.34 ± 0.08

<sup>1</sup>UFT = ultrasound fat thickness; UIF = ultrasound percent of intramuscular fat; UREA = ultrasound ribeye area.

**Table 5.** Estimates of genetic correlations between postweaning feed intake and growth traits and ultrasound traits in an Angus-Brahman multibreed population

Trait <sup>1</sup>	UFT	UIF	UREA
RFI	-0.09 ± 0.27	0.01 ± 0.21	0.01 ± 0.25
DFI	-0.11 ± 0.24	0.16 ± 0.17	0.34 ± 0.19
FCR	0.38 ± 0.24	0.17 ± 0.19	0.21 ± 0.22
PWG	-0.54 ± 0.21	-0.08 ± 0.16	-0.09 ± 0.18

<sup>1</sup>UFT = ultrasound fat thickness; UIF = ultrasound percent of intramuscular fat; UREA = ultrasound ribeye area; RFI = residual feed intake; DFI = daily feed intake; FCR = feed conversion ratio; PWG = postweaning gain.

**Table 6.** Estimates of phenotypic correlations between postweaning feed intake and growth traits and ultrasound traits in an Angus-Brahman multibreed population

Trait <sup>1</sup>	UFT	UIF	UREA
RFI	-0.03 ± 0.10	0.03 ± 0.10	0.03 ± 0.10
DFI	0.02 ± 0.10	0.12 ± 0.10	0.29 ± 0.09
FCR	0.18 ± 0.10	0.14 ± 0.11	0.09 ± 0.11
PWG	-0.23 ± 0.10	-0.05 ± 0.10	0.06 ± 0.10

<sup>1</sup>UFT = ultrasound fat thickness; UIF = ultrasound percent of intramuscular fat; UREA = ultrasound ribeye area; RFI = residual feed intake; DFI = daily feed intake; FCR = feed conversion ratio; PWG = postweaning gain.