Heritabilities And Genetic Correlations Between Postweaning Feed Intake, Growth, And Ultrasound Traits In A Multibreed Angus-Brahman Cattle Population In The Subtropics

M.A. Elzo[*], D.D. Johnson[*], G.C. Lamb[†], T.D. Maddock[†], R.O. Myer[†], D.G. Riley[‡], G.R. Hansen[§], J.G. Wasdin[*], and J.D. Driver[*]

Introduction

The development of feed efficiency facilities has made the measurement of individual feed intake feasible in large numbers of cattle of similar age maintained under the same feeding regimen and management conditions. These facilities have allowed the creation 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 would provide essential information for the estimation of variance and covariance components needed for genetic evaluation of animals for these traits and for residual feed intake. Postweaning feed intake, growth, and ultrasound data were collected on a sizable number of Angus, Brahman, and Angus x Brahman cattle at the GrowSafe 4000 (GrowSafe Systems, Ltd., Airdrie, Alberta, Canada) 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 area of the longissimus muscle (ULM) 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.

Material and methods

Animals, housing, feeding and management. Animals were from three Florida farms (n = 1129), 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 (n = 420), ¾ A ¼ B (n = 142), Brangus

---

[*] Department of Animal Sciences, University of Florida, Gainesville, FL 32611-0910, USA.

[†] University of Florida, North Florida Research and Education Center, Marianna, FL 32446-7906, USA.

[‡] Department of Animal Science, Texas A&M University, College Station, TX 77843-2471, USA.

[§] North Carolina State University, Tidewater Research Station, Plymouth, NC 27962-7526, USA.

(5/8A 3/8 B; n = 184), ½ A ½ B (n = 183), ¼ A ¾ B (n = 79), and B (n = 121). These calves were the progeny of 74 bulls (12 A, nine ¾ A ¼ B, 28 Brangus, eight ½ A ½ B, six ¼ A ¾ B, and 11 B) and 451 dams (97 A, sixty eight ¾ A ¼ B, 99 Brangus, ninety seven ½ A ½ B, forty two ¼ A ¾ B, and 48 B). Calves from the three herds were transported postweaning to the GrowSafe FEF and assigned to 24 pens (108 m^2/pen; 2 GrowSafe nodes per pen) by sire group (A, ¾ A ¼ B, Brangus, ½ A ½ B, ¼ A ¾ B, and B) and by sex (bull, heifer, and steer) subclass. Calves were identified with half-duplex passive transponder ear tags (Allflex USA Inc., Dallas-Fort Worth, TX). The mean stocking rate 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, crude protein, net energy for maintenance, and net energy for gain were 91.2%, 17.3%, 1.7 mcal/kg DM, and1.2 mcal/kg DM in 2006, 90.0%, 14.1%, 1.5 mcal/kg DM, and 0.9 mcal/kg DM in 2007, 84.5%, 11.1%, 1.6 mcal/kg DM, and 1.0 mcal/kg DM in 2008, and 93.0%, 12.3%, 1.4 mcal/kg DM, and 0.9 mcal/kg DM in 2009. Calves were adapted to diets and facility for 14 to 21 days prior to the 70-day trial period. GrowSafe software recorded feed intake information in real-time. Weights (kg) and exit velocity (m/s) data were collected every 2 weeks.

Postweaning feed intake, growth, and ultrasound traits. Traits were RFI (kg DM*day^{-1}), DFI (kg DM*day^{-1}), FCR (kg DM*day^{-1}/kg DM*day^{-1}), PWG (kg), UFT (cm), UIF (%), and ULM (cm^2). Intake traits were defined on a dry matter basis. Feed intake, growth, and ultrasound traits were measured at the University of Florida FEF in Marianna, Florida. Phenotypic residual feed intake was obtained as the difference between expected and actual average DFI during the 70-day 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 daily feed intake 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 non-significant, thus excluded from the 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-day 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 ULM as well as genetic and phenotypic covariances and correlations among these traits were computed using ASREML (Gilmour et al. (2006)). Single-trait analyses were used to compute variances and heritabilities, and 2-trait analyses were used to compute covariances and correlations. The same model was used for all seven 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 x 2 genetic variance-covariance matrix (2-trait analyses). Residual effects were assumed to have mean zero, common variance (single-trait analyses) or 2 x 2 variance-covariance matrix (2-trait analyses) and uncorrelated.

Results and discussion

Estimates of heritability in this Angus-Brahman multibreed population were low to moderate for postweaning feed intake and growth traits (Table 1) and for ultrasound traits (Table 2), except for UIF which was high. 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 ± 0.05 to 0.38 ± 0.06; Arthur et al. (2001a)), and France (0.32 ± 0.02 to 0.44 ± 0.02; Arthur et al. (2001b)). No comparable estimates for PWG existed in feed efficiency studies, but heritability estimates for ADG were similar (0.35; Schenkel et al. (2004); 0.31 ± 0.05; Arthur et al. (2001b)) to the PWG heritability estimate here. The UFT heritability was lower than and the ULM heritability was similar to estimates from crossbred cattle (UFT: 0.59 ± 0.14; ULM: 0.39 ± 0.13; Nkrumah et al. (2007)) and purebred bulls of several breeds (UFT: 0.36; ULM: 0.30; Schenkel et al. (2004)). The UIF heritability was similar (0.75 ± 0.16) to that reported by Nkrumah et al. (2007) and higher than that estimated (0.14) by Schenkel et al. (2004).

Table 1: 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	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

Table 2: Estimates of heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for ultrasound traits in an Angus-Brahman multibreed population

Trait	UFT	UIF	ULM
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
ULM	0.32 ± 0.09	0.00 ± 0.10	0.34 ± 0.08

Most genetic and correlation estimates had large standard errors. The most accurate estimates of genetic and phenotypic correlations (Table 1) 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 2) were positive between UFT and UIF, and near zero between UIF and ULM. Estimates of genetic (Table 3) and phenotypic (Table 4) correlations between RFI, DFI, FCR, and PWG, and UFT, UIF, and ULM were mostly smaller than those reported by Schenkel et al. (2004) and Nkrumah et al. (2007) and had large standard errors.

Table 3: Estimates of genetic correlations between postweaning feed intake and growth traits and ultrasound traits in an Angus-Brahman multibreed population

Trait	UFT	UIF	ULM
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

Table 4: Estimates of phenotypic correlations between postweaning feed intake and growth traits and ultrasound traits in an Angus-Brahman multibreed population

Trait	UFT	UIF	ULM
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

Conclusion

Estimates of heritabilities for postweaning feed intake, growth, and ultrasound traits suggested that there exists substantial genetic variability in the Angus-Brahman multibreed population for selection to be effective for all these traits. On the other hand, estimates of genetic correlations, particularly between postweaning feed intake and growth, and ultrasound traits were too inaccurate to draw firm conclusions. Thus, additional postweaning feed intake, growth, and ultrasound data need to be collected at the feed efficiency facility to obtain useful correlations for multiple-trait selection under subtropical conditions.

References

Archer, J.A., Arthur, P.F., Herd, R.M. *et al.* (1997). *J. Anim. Sci.*, 75:2024-2032.

Arthur, P.F., Archer, J.A., Johnston, D. J. *et al.* (2001a). *J. Anim. Sci.*, 79:2805-2811.

Arthur, P.F., Archer, J.A., and Krauss, D. (2001b). *Livest. Prod. Sci.*, 68:131-139.

Gilmour, A.R., Gogel, B.J., Cullis, B.R. and Thompson, R. (2006) « ASReml User Guide Release 2.0 ». VSN International Ltd., Hemel Hempstead, HP1 1ES, UK.

Koch, R.M., Swiger, L.A., Chambers, D. *et al.* (1963). *J. Anim. Sci.*, 22:486-494.

Lancaster, P.A., Carstens, G.E., Ribeiro, F. R. *et al.* (2009). *J. Anim. Sci.*, 87:1528-1539.

Nkrumah, J.D., Basarab, J.A., Wang, Z. *et al.* (2007). *J. Anim. Sci.*, 85:2711-2720.

Schenkel, F.S., Miller, S.P., and Wilton, J.W. (2004). *Can. J. Anim. Sci.*, 84:177-185.