GENETIC ASSOCIATION OF NET FEED INTAKE MEASURED AT TWO STAGES WITH INSULIN-LIKE GROWTH FACTOR –I, GROWTH AND ULTRASOUND SCANNED TRAITS IN ANGUS CATTLE.

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SUMMARY

Net feed intake (NFI) is a measure of feed efficiency in beef cattle, calculated as the amount of feed eaten by an animal after adjusting for its growth rate and body weight. NFI was measured in weaned bulls and heifers of less than one year of age (NFI-P) and also in feedlot finishing steers mainly 18 months and older (NFI-F). Genetic parameters and their genetic relationship with insulin–like growth factor-I (IGF-I) around weaning age, growth traits and scanned traits were estimated for NFI-P and NFI-F. Estimated heritabilities for NFI-P and NFI-F were 0.41±0.05 and 0.34±0.09, respectively and the genetic correlation between the two was 0.65±0.14. Genetic correlations between NFI-P and IGF-I, ultrasound scanned subcutaneous fat depth at the rump (P8) in males and females and intramuscular fat percentage (IMF) in male and females were 0.18±0.11, 0.50±0.14, 0.49±0.10, 0.48±0.18 and 0.27±0.13, respectively. Genetic correlations between NFI-F and IGF-I, P8 in males and females and IMF in males and females were -0.14±0.18, 0.43±0.17, -0.13±0.14, 0.36±0.23 and -0.22±0.18 respectively. Both NFI-P and NFI-F had negative genetic correlation with weights at birth, 200, 400 and 600 days of age. This study showed that although the NFI measured at an early age and in the feedlot were moderately heritable, they were two different traits with varying genetic associations with growth and ultrasound scanned traits. Selecting for lower NFI at either stage will genetically decrease the ultrasound scanned fat traits in males. Selection for lower NFI-P can decrease fatness in heifers but this association was not evident with NFI-F. IGF-I, as recorded in this study, would have limited use as a genetic indicator trait for NFI in beef cattle due to genetic correlation differing in direction and of low magnitude with NFI-P and NFI-F.

INTRODUCTION

Feed cost constitutes the single largest expense in most beef cattle production systems. Any reduction in feed cost is expected to improve beef production profitability. The existence of variation for feed intake among animals of the same breed, sex and age class indicates that improvement for higher feed efficiency could be achieved through selection (Johnston *et al*. 2001). This individual variation in feed intake is being utilized in the form of net feed intake (NFI) to improve feed efficiency in beef cattle (Robinson and Oddy 2004). NFI is the difference between actual feed intake and the expected feed requirement for the growth rate and maintenance of body weight (Koch *et al*. 1963).

In Australia, NFI has been measured at two different stages of growth: in young post weaning bulls and heifers at around 300 days of age (NFI-P) and in feedlot finishing steers at around 18 months of age (NFI-F). As NFI-P and NFI-F are measured at two different stages of growth and maturity, they may not be genetically the same trait and could have different genetic associations with insulin–like growth factor I (IGF-I) and other production traits. Selection for lower NFI-P or NFI-F may therefore, produce different correlated responses in production traits. This study aimed to quantify the genetic associations of NFI-P and NFI-F with IGF-I, growth traits and ultrasound scanned fat traits.

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MATERIALS AND METHODS

Data used for this study were submitted to the Angus Society of Australia database until June 2006 for BREEDPLAN evaluation of NFI in Angus cattle. Feed efficiency test records for young bulls and heifers, fed at around 300 days of age with a ration containing an energy level of 10MJ/kg provided data for NFI-P. Steers fed at around 560 days of age, with a ration containing an energy level of 12MJ/kg provided data for NFI-F. Individual feed intakes for both groups of animals were measured over a 70 day feeding period, after an initial acclimatisation period. NFI-P and NFI-F were derived by adjusting the feed intake for the growth rate and metabolic mid test weight of individuals estimated for the two traits separately. Metabolic mid weight was calculated as the mid weight to the power of 0.73.

Plasma IGF-I levels were measured from blood samples obtained prior to weaning in a large number of seedstock herds. Testing age ranged from 150 to 250 days. Plasma IGF-I concentration was determined by using a commercially available Enzyme Linked Immunosorbent assay (ELISA). Growth traits analysed were birth weight (BWT), 200-day weight (200D), 400-day weight (400D) and 600-day weight (600D) with age at recording ranging from 80 to 300 days, 301 to 500 days and 501 to 700 days for 200D, 400D and 600D, respectively. For animals with multiple records for 200D, 400D and 600D, only their first record was used. Real time ultrasound scanned fat measurements included fat depth at the P8 (rump) site for bulls (BP8) and heifers (HP8), intramuscular fat percent at the $12/13^{th}$ rib for bulls (BIMF) and heifers (HIMF) and longissimus muscle area at the $12/13^{th}$ rib of bulls (BEMA) and heifers (HEMA) with age at recording for all traits ranging from 300 to 800 days. A relatively small number of real time ultrasound scanned carcass measurements of steers were grouped with heifer measurements.

For each trait, sires with recorded progeny for NFI-P, NFI-F and IGF-I were identified as common sires, and all data and pedigree from those herds containing progeny of common sires were extracted to build genetically linked data for each bivariate analysis. There were 242, 180 and 479 sires with progeny recorded for NFI-P, NFI-F and IGF-I respectively and 42 common sires with progeny recorded for NFI-P and NFI-F. The number of common sires between NFI-P, NFI-F and ultrasound scanned traits ranged from 130 to 159 and for growth traits ranged from 159 to 184. Number of records and descriptive statistics for all traits are given in Table 1.

Genetic variances, genetic correlations and variance ratios were estimated by restricted maximum likelihood (REML) using a series of bivariate animal model evaluations, with three generations of pedigree in ASReml (Gilmour *et al.* 2006). Records for growth and ultrasound scanned traits were pre adjusted for animal age and dam age using standard BREEDPLAN procedures (Graser *et al*. 2005). Models with fixed effect of contemporary group, and random additive genetic effect of animal were used for all traits. Contemporary group definitions for each growth and ultrasound scanned traits were as defined in BREEDPLAN (Graser *et al*. 2005) and those for NFI-P, NFI-F and IGF-I were defined by Moore *et al*. (2005). Additional random effects for BWT, 200D and 400D weights were maternal genetic and permanent environmental effects.

RESULTS AND DISCUSSION

Estimated heritabilities were moderate for all traits (Table 1). Heritability estimates of 0.41 and 0.34 for NFI-P and NFI-F were consistent with the value of 0.38 reported by Arthur *et al.* (2001) for NFI in Angus cattle. The moderate heritability estimates for NFI-P and NFI-F suggest that selecting for lower NFI at either stage will improve the feed efficiency in beef cattle.

The genetic correlation between NFI-P and NFI-F was high, but different from unity, indicating that these two feed efficiency measures are genetically different. This is further supported by the differences in genetic correlations of these traits with IGF-I, growth and ultrasound scanned traits. NFI-P had a low positive genetic correlation with IGF-I, while NFI-F

had a low negative genetic correlation with IGF-I. The positive genetic correlation between NFI-P and IGF-I is in agreement with other literature estimates, however, it is lower than the correlation of 0.42 reported by Moore *et al*. (2005) for Angus cattle in Australia. IGF-I samples used in this study included those of Moore *et al.* (2005) with additional samples collected by seedstock producers between 150 to 250 days of age, where actual weaning date was not known. Furthermore, NFI used in Moore *et al.* (2005) study was derived by pooling the NFI-P and NFI-F records.

Table 1. Number of records, the descriptive statistics of data , heritability (h^2) and the genetic correlation (using bivariate analysis) for postweaning net feed intake (NFI-P), feedlot net feed intake (NFI-F), insulin like growth factor-I (IGF-I) growth and ultrasound scanned traits (approximate standard errors in parenthesis).

Trait	No.	Mean	SD	Min	Max	h^2	Genetic correlation with NFI-P	Genetic correlation with NFI-F
NFI-P (kg/day)	2030	0.25	1.12	-3.9	3.6	0.41 (0.05)		0.65 (0.14)
NFI-F (kg/day)	1220	-1.09	2.21	-9.4	5.1	0.34 (0.09)	0.65 (0.14)	
IGF-I (ng/ml)	9216	393.56	190.52	27.0	1287.0	0.36 (0.04)	0.18 (0.11)	-0.14 (0.18)
Scanned traits								
HIMF (%)	22504	4.37	1.86	0.0	12.7	0.30 (0.02)	0.27 (0.13)	-0.22 (0.18)
BIMF (%)	14759	2.73	1.64	0.0	10.1	0.21 (0.02)	0.48 (0.18)	0.36 (0.23)
HEMA (cm^2)	28126	58.25	8.47	29.3	101.4	0.29 (0.01)	0.04 (0.12)	-0.01 (0.15)
BEMA (cm^2)	19579	75.91	10.11	33.0	113.8	0.26 (0.02)	-0.16 (0.17)	-0.01 (0.21)
HP8 (mm)	28424	6.20	2.93	0.0	41.9	0.44 (0.02)	0.49 (0.10)	-0.13 (0.14)
BP8 (mm)	19583	4.10	1.91	0.0	36.6	0.42 (0.02)	0.50 (0.14)	0.43 (0.17)
Growth traits								
BWT (kg)	74261	37.1	5.4	15.2	65.2	0.37 (0.01)	-0.04 (0.08)	-0.34 (0.13)
200D (kg)	89958	232.2	36.8	69.0	452.9	0.22 (0.01)	-0.05 (0.09)	-0.23 (0.13)
400D (kg)	64748	359.3	71.2	114.0	669.5	0.29 (0.01)	0.00 (0.08)	-0.16 (0.12)
600D (kg)	41106	496.9	94.4	217.6	886.4	0.40 (0.01)	-0.02 (0.10)	-0.25 (0.14)

Estimated genetic correlations of NFI-P and NFI-F with ultrasound scanned traits were variable in sign and magnitude. Ultrasound scanned fat traits had positive genetic correlations with NFI-P, with the estimates ranging from 0.27 for HIMF to 0.50 with BP8. Moderate to high genetic correlations between NFI-P and ultrasound scanned fat traits are in agreement with the correlations reported by Robinson and Oddy (2004). NFI-F had low negative genetic correlations with HIMF and HP8 in contrast to positive correlations with BIMF and BP8. The obvious differences between NFI-P and NFI-F were their correlation with P8 and IMF in females, where selection for lower NFI-P would decrease P8 but this association was not evident with NFI-F. Lower number of records in NFI-F increased the standard errors for the correlation of NFI-F with other traits. The HEMA and BEMA had low or no correlation with both NFIs. Both NFI-P and NFI-F had negative genetic correlations with growth traits, however the magnitudes of the correlations were different for the two feed efficiency measures. However, these estimates, combined with the non-unity correlation between NFI-P and NFI-F suggest that selection on the different net feed intake measures may lead to different correlated response on growth and ultrasound scanned traits.

CONCLUSIONS

Net feed intake measured in weaned young bulls and heifers and feedlot finished steers are moderately heritable. Genetic correlations less than unity and different genetic associations with growth and ultrasound scanned traits, however, indicate that these two feed efficiency measurements are genetically different. Improving feed efficiency at these two stages might yield different correlated responses in growth and ultrasound scanned traits. Selecting animals for lower NFI at either stage will genetically decrease ultrasound scanned fat traits in males, but selecting for lower NFI-F may increase P8 and IMF in females. Therefore, including both NFI-P and NFI-F in a genetic evaluation system is important to incorporate these changes. IGF-I, which had low and opposite different genetic correlations with NFI-P and NFI-F, is of limited use as a genetic indicator trait of NFI.

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