GENETIC AND NON-GENETIC EFFECTS ON PLASMA INSULIN-LIKE GROWTH FACTOR-I (IGF-I) CONCENTRATION AND PRODUCTION TRAITS IN ANGUS CATTLE

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SUMMARY
Plasma insulin-like growth factor-1 concentration (IGF-I) was measured at weaning on 1756 Angus beef cattle from herds in the New England and surrounding regions of NSW to estimate the heritability of IGF-I and phenotypic and genetic correlations with other production traits. Average IGF-I was 253.9 ng/mL measured at the mean age of 237 days. IGF-I had a moderate heritability of 0.36. Phenotypic correlations were essentially zero between IGF-I and birth weight, 200-day weight and pre-weaning average daily gain. IGF-I concentration was not genetically correlated with birth weight and scanned eye muscle area, but was correlated with both 200-day weight and average daily gain with genetic correlations of –0.40 and –0.52, respectively. Daily feed intake and IGF-I concentration were estimated to have a negative genetic correlation of –0.33. Scanned rump and rib fat depth, intramuscular fat content and residual feed intake were all estimated to have positive genetic correlations between 0.31 and 0.33 with IGF-I concentration. These estimates indicate that plasma IGF-I concentration measured in seedstock herds at weaning will be a suitable trait to indirectly select for fat and feed efficiency traits.
Key words: IGF-I, beef cattle, selection, heritability, genetic correlation

INTRODUCTION
Plasma insulin-like growth factor-1 concentration (IGF-I) has been shown to be heritable in beef cattle as well as having phenotypic and genetic correlations with economically important beef cattle production traits (Herd *et al*. 1995; Johnston *et al.* 2002). IGF-I concentration is likely to be cheaper to measure, can be measured earlier in life, and potentially on more animals, than both fat and feed intake traits. Previous estimates for the heritability of IGF-I concentration and correlations with production traits have been based on cattle in research herds. The purpose of this study was to measure the plasma IGF-I concentration from seedstock herds to verify the heritability and phenotypic and genetic correlations between IGF-I concentration with economical beef cattle production traits (growth, scanned fat and feed intake traits) in commercial cattle production systems.

METHODS
Angus beef cattle (N=1756) from 7 seedstock herds in the New England and surrounding regions of NSW were sampled at weaning for IGF-I. Blood was taken by venipuncture from the vein under the tail and

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allowed to flow onto, and saturate, an absorbent paper card. The card was allowed to dry before being sent to Primegro Limited, Adelaide, SA. An Enzyme-linked Immunosorbent Assay (ELISA) patented and licensed to Primegro was used to determine the concentration of IGF-I present in the blood. Each sample was assigned an assay code based on when the assay was performed and the sample location within the assay. All animals measured were from herds with a history of performance recording and were to be scanned for fat depth and/or have residual feed intake (RFI) measured at a later time. Scanned subcutaneous fat depths at the P8 rump site (P8) and between the 12/13th ribs (RIB), area of the eye-muscle (EMA), and intramuscular fat (IMF) are measured using ultrasound at approximately 400 days of age. Daily feed intake (DFI) and RFI (a measure of feed efficiency calculated to be independent of liveweight and growth rate) are measured over standardised tests either between weaning and yearling age or during feedlot finishing of older cattle. Additional performance information and pedigrees was obtained from the Angus breed society. For the traits where the animals measured for IGF-I did not yet have performance data (scanned fat and feed intake traits) additional information was obtained from related animals and the relationship matrix was used to estimate the genetic correlation between these traits and IGF-I.

Fixed effects for IGF-I and production traits were determined using the PROC GLM procedure of SAS (SAS Institute Inc. 1989). For IGF-I the herd, sex, IGF-I sampling age, group nested within herd, assay code nested in herd*group, and the first order interaction herd*sex were found to be significant accounting for 49.1% of IGF-I variation. Group was defined by the variables IGF-I sample date, user defined birth and 200-day management groups, and the 200-day weight date. For genetic analysis these effects were combined to form a single fixed contemporary group (CG) and included herd, user defined birth and 200-day weight management groups, IGF-I sample date, 200-day weight date, sex and IGF-I assay code. The CG for birth weight (BWT) was defined as herd, sex, birth month and user defined birth management group. CGs for 200-day weight (200WT) and pre-weaning average daily gain (ADG) were defined as herd, sex, user defined weaning management group, birth month and the date weaning weight was measured. For the scanned traits the CG was defined as the owner identification, birth month, sex, user defined scan management group and the date the scans were taken. For the feed intake traits the CG was defined as the test station, test identification number, sex, user define management group, weight date, previous weight management group, present owner and the breeder.

Variance components were estimated using residual maximum likelihood (REML) in either univariate or bivariate animal models using ASREML (Gilmour *et al*. 1999). IGF-I was analysed in a series of bivariate models along with BWT, 200WT, ADG, EMA, P8, RIB, IMF, DFI and RFI. In all models the maternal components were not partitioned, animal was included as a random effect, IGF-I and the appropriate trait CG were fixed effects and IGF-I sample age was included as a covariate. For all growth traits age of dam was included as a linear covariate, for 200WT and ADG the quadratic effect of age of dam was also included. Genetic and phenotypic correlations were estimated from these variance components, however phenotypic correlations were unable to be estimated between IGF-I and the scanned fat and feed intake traits due to none of the animals having their own records.

RESULTS AND DISCUSSION

Plasma IGF-I concentration had an additive variance of 1701 ng^2/ml^2 and heritability of 0.36 ± 0.09 (Table 1). This estimated heritability for IGF-I concentration is similar to those reported in previous literature with Herd *et al*. (1995) and Johnston *et al.* (2001) of 0.31 ± 0.18 and 0.32 ± 0.06 respectively. Heritabilities for production traits ranged between 0.27 ± 0.05 and 0.66 ± 0.05 for IMF and DFI, respectively (Table 2). These heritabilities were generally higher than expected because maternal effects were not considered and only the direct genetic effects were modeled.

Table 1. Summary of the production traits recorded in Angus beef cattle

	number	mean	standard	range
IGF-1 (ng/mL)	1756	253.9	83.8	57 - 297
IGF-1 age (days)	1756	236.8	36.5	103 - 345
Birth weight (kg)	1722	36.5	4.9	18 - 53
200-day weight (kg)	1659	233.2	41.1	111 - 382
200-day weight age (days)	1659	187.5	36.1	100 - 290
Average daily gain (kg/day)	1627	1.1	0.2	0.54 - 1.75
Scanned EMA (cm^2)	13548	63.2	13.4	28 - 129
Scanned P8 fat (mm)	13878	4.7	2.7	1 - 26
Scanned rib fat (mm)	14418	3.5	1.9	1 - 18
Scanned IMF (%)	6847	3.8	1.8	0.1 - 14.3
Daily feed intake (kg/day)	2129	11.3	2.9	4 - 22.2
Residual feed intake (kg/day)	2129	-1.7	1.7	-6.55 - 5.83

Table 2. The heritabilities (h^2) of production traits, phenotypic (r_p) and genetic correlations (r_g) between the production traits and plasma IGF-I concentration (standard errors in brackets)

	h^2	r_p	r_g
Birth weight (kg)	0.54 (0.1)	-0.07 (0.03)	**-0.08 (0.18)**
200-day weight (kg)	0.53 (0.1)	0.08 (0.03)	**-0.40 (0.17)**
Average daily gain (kg/day)	0.53 (0.1)	0.08 (0.03)	**-0.52 (0.16)**
Scanned EMA (cm^2)	0.34 (0.02)	-	**-0.08 (0.15)**
Scanned P8 fat (mm)	0.51 (0.02)	-	**0.32 (0.11)**
Scanned rib fat (mm)	0.46 (0.02)	-	**0.31 (0.11)**
Scanned IMF (%)	0.27 (0.03)	-	**0.33 (0.14)**
Daily feed intake (kg/day)	0.66 (0.05)	-	**-0.33 (0.32)**
Residual feed intake (kg/day)	0.50 (0.06)	-	**0.31 (0.36)**

Phenotypic correlations were estimated to be close to zero for plasma IGF-I concentration with BWT, 200WT and ADG. Genetic correlations close to zero were also estimated for BWT and EMA. Davis and Simmen (1997) estimated from 730 animals a genetic correlation of –0.75 between mean IGF-I concentration over a post-weaning feedlot test period and BWT, however no standard errors were included with this estimate. 200WT and ADG were estimated to have negative genetic correlations with IGF-I concentration. Unlike BWT, the genetic correlation estimated between 200WT and IGF-I concentration was similar to the estimate of Davis and Simmen (1997).

Positive genetic correlations were estimated between plasma IGF-I and scanned fat traits. These correlations were slightly smaller than those estimated by Johnston *et al*. (2001), who also estimated positive genetic correlations between IGF-I and fat depth. The estimated genetic correlations differed in direction from those estimated by Davis and Simmen (2000) who estimated negative genetic correlations. The reason for the difference in the direction of the correlations is unknown.

Fewer studies have reported genetic correlation estimates between plasma IGF-I concentration and feed intake traits. DFI and IGF-I were negatively genetically correlated whereas RFI and IGF-I had a positive genetic correlation. The correlation with DFI is in the opposite direction than the estimate by Johnston *et al*. (2002) but the estimate of RFI and IGF-I was similar. Fat traits and feed intake traits have been estimated to have a positive genetic correlation (Robinson *et al*. 1999; Arthur *et al*. 2001). It is therefore plausible that fat and feed intake traits are both positively correlated with IGF-I.

CONCLUSIONS

Plasma IGF-I concentration is heritable and will respond to selection. It is likely to be less expensive to measure IGF-I concentration compared with measuring fat and feed intake traits. IGF-I concentration is genetically correlated with fat and feed intake traits and has the potential to be used to indirectly select for these traits. Indirect selection of fat and feed intake traits based on IGF-I concentration could not only reduce the costs associated with selection but IGF-I concentration can also be measured earlier before any selection or culling has occurred, thus increasing the selection intensity and thus the selection response achieved.

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