EVIDENCE OF IGF-I AS A GENETIC PREDICTOR OF FEED EFFICIENCY TRAITS IN BEEF CATTLE

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INTRODUCTION

There is increasing evidence for the suitability of circulating plasma insulin-like growth factor-I concentrations (IGF-I) as genetic predictors of some economically important traits in beef cattle (Herd *et al.* 1995, Davis and Simmen 2000, Johnston *et al.* 2001). This has lead to the suggestion that IGF-I might also be used as an indirect selection criterion for improving feed efficiency in cattle, particularly given the results from pigs (Bunter *et al.* 2002). Measures of feed efficiency, such as residual feed intake or feed conversion ratio, are heritable in beef cattle (Arthur *et al.* 2001), but expensive to measure making widespread industry recording of the trait unlikely. Therefore to improve feed efficiency across a breed or industry we need correlated trait(s) that can be easily measured on large numbers of cattle prior to the time when the major selection decisions are made. Records on IGF-I could be supplemented in a genetic evaluation with actual feed intake records collected on a subset of elite young animals or their progeny. Therefore the objective of this study was to estimate the genetic correlations between IGF-I and feed intake and efficiency traits.

MATERIALS AND METHODS

Data analysed were from two large genetics experiments in Australia, The Cooperative Research Centre for Cattle and Beef Quality (CRC) and NSW Agriculture, Agricultural Research Centre, Trangie (TRN).

CRC data. The Cooperative Research Centre for Cattle and Beef Quality was an integrated research program that investigated production and processing factors affecting meat quality. A large scale straightbreeding breeding program provided almost 8000 pedigree recorded animals for both quantitative and molecular genetics work. A subset of the data from the straightbreeding project was used in this study. The complete design and management are described by Upton *et al.* (2001). Animals used in this study were from four temperate breeds (Angus, Hereford, Shorthorn and Murray Grey) and three tropically adapted breeds (Brahman, Santa Gertrudis and Belmont Red). Within a year and season (autumn and spring), animals purchased from co-operating breeders were trucked soon after weaning to the CRC managed properties, for grow-out prior to finishing. At arrival all animals were assigned to different finishing regimes (pasture or feedlot) to either the Domestic (220kg carcase), Korean (280 kg carcase) or Japanese market (320 kg carcase) weight specifications. For the temperate breeds, animals were bled for IGF-I measurements when all animals had arrived from the cooperating herds in a year and season (approximately 9 months of age). Tropically adapted breeds were

bled for IGF-I just prior to feedlot entry (ie. at the end of grow out at about 19 months of age). Individual daily feed intakes was measured on a number of the feedlot finished groups. Feed intakes were measured using computerised automatic feeders in pens of approximately 12 animals for an average of 60 days.

Trangie data. Data originated from a large feed efficiency experiment conducted at Agricultural Research Centre, Trangie, NSW, Australia, using Angus cattle. For a description of the animals and design see Arthur *et al.* (2001). In brief, 1369 animals were measured at around 9 months of age for individual feed intake over a 70 day period. Blood was taken at the end of the feed intake testing period on a subset of the test groups. Also available was data from steers (N=198) generated from the divergent feed efficiency selection lines at Trangie over two years. These steers were the progeny of the postweaning tested animals but were managed as commercial feedlot steers. They were bled for IGF-I at feedlot entry, at approximately 22 months of age.

IGF-I measurement. Blood samples were obtained by venipuncture from the tail into vacutainers® with EDTA as anticoagulant. They were stored briefly at 4°C, then centrifuged and the plasma stored frozen until subsequent analysis. Prior to radioimmunoassay an ultrafiltration step was used to remove interference by binding proteins, as described by Hall *et al.* (1992). The radioimmunoassay was performed using recombinant human IGF-I standard and anti-human IGF-I polyclonal antisera from rabbits (Gro-pep, Australia). In the final year of sample collection the commercial ELISA test provided by PrimeGRO Pty Ltd, Adelaide, SA was used.

Feed intake records. Feed intake records at both TRN and CRC included individual records on the daily amount of food eaten and the start and end time of feeding session. Feed intake records were pooled to give daily feed intake values which were then averaged over the test period to give average daily feed intake (FI), and were adjusted to a 10 MJ ME/kg dry matter basis. Average daily weight gain over the test period (TADG) was computed using a linear regression of all weights over the test period for TRN and over the entire feedlot period for CRC. Mid-test weight (TWT) was the weight of the animal half way through the testing period. Residual feed intake (RFI) was computed as described by Arthur et al. (2001) where FI was adjusted for TADG and TWT raised to the power 0.73 (ie. metabolic weight) using linear regressions. Feed conversion ratio (FCR) was the computed as FI divided by TADG.

Statistical analyses. Variance components were estimated by restricted maximum likelihood using ASREML (Gilmour *et al.* 1999). Data were analysed separately for the two projects in a series of bivariate analyses. IGF-I was included as trait 1 along with FI, FCR, RFI, TADG and TWT. The model for IGF-I included a single fixed contemporary group effect. For CRC data contemporary group was defined as herd of origin, year, season, sex, market and measurement date subclass. Herd of origin accounted also for breed differences. For TRN data the contemporary group included herd, sex, test group, and management group subclass. For all feed intake measures the model included a fixed effect of test group which comprised herd, year, season, sex, management group (and market for CRC animals). Age was included as a linear covariate for all traits. For all analyses, additive genetic effects and residuals were modelled as random effects. A relationship matrix using up to three generations of pedigree was included. A total of 121 and 63 sires had progeny recorded for both IGF-I and RFI in the CRC data and TRN datasets, respectively.

RESULTS AND DISCUSSION

Means for the traits analysed are presented in Table 1. Mean IGF-I concentrations were 164 and 253 ng/mL for the CRC and TRN data, respectively. This difference in mean IGF-I concentration between CRC and TRN may be due to differences in mean age at measurement and also differences in the nutritional history ie. pasture grow-out versus end of postweaning feed test measure of IGF-I. The large range in values and trait standard deviations reflect in part the cattle being managed differently. These different effects were taken into account by including appropriate fixed effects in the model of analysis for variance component estimation. The CRC animals were heavier, with higher FI compared to the majority of the TRN data. This difference is mainly due to the type of animal being measured. The CRC animals were steers and heifers being finished on a feedlot diet, versus TRN where the majority of the feed intake records were on young bulls and heifers measured postweaning (198 out of the 1567 TRN records were from feedlot finished steers).

Table 1. Raw means, standard deviation and ranges for IGF-I and feed intake traits.

Dataset	Variable	No. of records	Mean	SD	Range	
CRC	RFI (kg/d)	1462	0.0	0.9	-4.5	4.4
	DFI (kg/d)	1462	12.4	2.0	6.5	18.7
	FCR (kg/kg)	1462	9.5	2.2	5.0	21.5
	TADG (kg/d)	1462	1.4	0.4	0.5	2.7
	TWT (kg)	1462	503.0	81.7	254.7	753.9
	IGF-I (ng/mL)	1432	164.2	81.8	18	517
TRN	RFI (kg/d)	1567	-1.6	1.1	-5.9	2.3
	DFI (kg/d)	1567	10.1	1.7	4.0	16.5
	FCR (kg/kg)	1567	7.7	1.5	3.7	22.8
	TADG (kg/d)	1567	1.3	0.3	0.54	2.43
	TWT (kg)	1567	364.7	107.5	172.9	812.7
	IGF-I (ng/mL)	646	253.4	108.8	37	632

Heritability estimates for IGF-I concentration were 0.34 and 0.43 for CRC and TRN, respectively (Table 2) and were similar to other published estimates (Johnston *et al.* 2001, Herd *et al.* 1995, Davis and Simmen 2000). All genetic correlations between IGF-I concentration and other traits had large standard errors but when considered across the two datasets they indicate possible associations. In both datasets, IGF-I was genetically positively associated with both RFI and FCR. The positive relationships estimated are consistent in direction with estimates of a positive relationship (0.38) between IGF-I and fatness (Johnston *et al.* 2001), and a positive relationship (0.42) between RFI and P8 fat in the CRC data (unpublished). These estimates suggest that selection for reduced IGF-I will result in a correlated reduction in fatness, RFI and FCR. Bunter *et al.* (2002) report a pooled genetic correlation estimate of 0.65 between IGF-I and FCR in *ad lib* fed pigs. The genetic correlations between IGF-I and TADG suggests a slight negative relationship. The correlations with FI and TWT are inconsistent across datasets with no clear indication of the likely direction of the relationship, but were small.

Table 2. Heritability (h^2) of IGF-I and genetic correlations (r_g) (SE in brackets) between IGF-I and feed intake and efficiency traits

	h^2	r_g				
	IGF-I[a]	RFI	FCR	FI	TADG	TWT
CRC	**0.34** (0.09)	**0.56** (0.35)	**0.37** (0.42)	**0.01** (0.30)	**-0.23** (0.32)	**-0.25** (0.25)
TRN	**0.43** (0.12)	**0.39** (0.13)	**0.55** (0.16)	**0.27** (0.14)	**-0.20** (0.17)	**0.03** (0.14)

[a] estimates pooled over bivariate analyses

CONCLUSIONS

IGF-I concentration is inexpensive to measure when compared to carcase and feed intake traits and opportunities exist to use this early life measure as a selection criterion for the genetic improvement of feed efficiency and carcase traits. It is important to collect additional data to allow the genetic correlations to be estimated with greater accuracy. In addition, to be useful as an industry measure it will be important to investigate the optimal time to measure IGF-I. This research will need to consider the magnitude of the correlation with RFI and also the timing of major selection decisions and culling and management of animals in seedstock herds.

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