GENETIC AND PHENOTYPIC PARAMETERS FOR FEED EFFICIENCY TRAITS IN AUSTRALIAN ANGUS BEEF CATTLE

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SUMMARY

Feed intake represents a major cost to all animal production systems. Increasing the efficiency in which animals turn this feed into product can be a major goal in many animal breeding programs. Consequently, Australian beef producers have been measuring many traits associated with feed efficiency in an attempt to increase the accuracy of selection, precision of genetic parameters estimates and ultimately increase the amount of genetic gain achieved. The objective of this study was to estimate genetic and phenotypic parameters for traits associated with feed efficiency from records on 1614 Angus Steers from the Australian Beef Information Nucleus (BIN). Traits analysed included Average Daily Weight Gain (ADG), Metabolic Mid-Weight (MMWT), Daily Feed Intake (FI), Feed Conversion Ratio (FCR) and Residual (or Net) Feed Intake (RFI). Parameters were estimated using bivariate animal models in ASReml. Heritability estimates ranged from 0.12 ± 0.06 for FCR to 0.49 ± 0.09 for FI. High genetic correlations were estimated between FI and RFI (0.83 ± 0.05) and FI and ADG (0.81 ± 0.08). Significant genetic correlation also existed between ADG and MMWT (0.65 ± 0.12) and between MMWT and FI (0.68 ± 0.08). Heritability estimates show that there would be a favourable response to selection for the efficiency traits in this population. The positive and unfavourable genetic correlation between ADG and RFI, suggest that improving RFI would result in lower ADG. Given this, further studies are required to investigate genetic associations between efficiency traits and other economically important traits, in addition to examine new ways of utilizing feed efficiency information in breeding programs.

INTRODUCTION

Feed intake represents a major input cost in almost all animal production systems (Archer 1999). The efficiency of converting this feed into useable animal products, commonly referred to as feed efficiency, is becoming a common breeding objective. In order to include feed efficiency traits in the breeding goal, genetic parameters are needed for accurate and unbiased prediction of breeding values, as well as to develop selection indices, and to predict selection responses (Hofer, 1998). Several authors have documented significant genetic variation for feed efficiency traits, however, genetic parameters can vary can vary depending on each population.

The objective of the present study was to estimate genetic and phenotypic parameters for Average Daily Weight Gain (ADG), Metabolic Mid-Weight (MMWT), Daily Feed Intake (FI), Feed Conversion Ratio (FCR) and Residual Feed Intake (RFI) from data collected in the Australian Angus Beef Information Nucleus (BIN) (also known as the Angus Sire Benchmarking Program).

MATERIALS AND METHODS

The phenotypic data examined in this study included live weights, and FI measures from 1823 Angus Steers collected from 2013 to 2016 at Tullimba Feedlot. On entry to the feedlot, the animals in this study ranged from 500-600 days of age and weighed approximately 450-500 kg. Initially animals were conditioned for 21 days and fed for an additional 70 days over which time all data was collected. All animals were weighed 6 times over the 70-day test period (fortnightly). ADG was calculated as the regression of weight on time (days), while MMWT was obtained as the mid-point raised to the 0.73 power (Arthur *et al*., 2001; Berry and Crowley, 2013).

The original information was edited to guarantee the quality of the data to be analysed. Duplicated records and incomplete information were eliminated. FCR was obtained as feed intake divided by the ADG, while RFI was estimated by regressing FI on ADG and MMWT (Arthur and Herd, 2008; Berry and Crowley, 2013).

Fixed effects of mean and Contemporary group (CG) (obtained from BREEDPLAN, which included trial, property management group and feedlot pen) were fitted for all analyses. CG of less of 10 animals were removed from the analysis. In the present study, estimates of both maternal genetic and maternal permanent environmental components for RFI were 0 therefore not included in the model (data do not show).

The final data file consisted of 1614 Angus steers with complete information for ADG, MMWT, FI, RFC and RFI. The pedigree file included an historical file with 21,439 animals with 3,908 sires and 11,610 dams.

Data were analysed using AIREML methodology implemented in the software ASReml (Gilmour *et al*., 2009). Starting values for bivariate analysis were estimated using single trait animal models, and bivariate animal models were used to estimate genetic and phenotypic correlations.

For each trait, the following bivariate animal model was used:

[1] $y = Xb + Zu + e$

where **y** is the vector of the phenotypes for the traits; **X** is a matrix relating animals to fixed effects; **b** is vector of fixed effects for the traits analysed; **Z** is a matrix relating animal effects to the data; **u** is a vector which contains animal random effects; and **e** is a vector of residual effects for the analysed traits. Furthermore, expectations and variance matrices of random vectors are described as:

$$E = \begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \end{bmatrix}; \quad V = \begin{bmatrix} u \\ e \end{bmatrix} = \begin{bmatrix} A \otimes G_0 & 0 \\ 0 & I \otimes R_0 \end{bmatrix}$$

where G_0, and R_0 denote 2x2 matrices containing additive genetic and residual covariance components, respectively; **A** is the numerator relationship matrix; **I** is the identity matrix; and $\otimes$ is the Kronecker product.

RESULTS AND DISCUSSION

Descriptive statistics for the studied traits are presented in Table 1. Heritability estimates, together with genetic and phenotypic correlations using bivariate animal models are presented in Table 2.

Table 1. Descriptive statistics for Average Daily Gain (kg d), Metabolic Mid-Weight (kg), Feed Intake (kg), Feed Conversion Ratio (kg), and Residual Feed Intake (kg d)

Trait	Number	Mean	Min	Max	SD
Average Daily Gain	1614	1.61	0.44	2.90	0.33
Metabolic Mid-Weight	1614	104.31	85.62	135.18	7.35
Feed Intake	1614	14.89	6.78	22.63	2.11
Feed Conversion Ratio	1614	9.55	4.09	32.55	2.09
Residual Feed Intake	1614	0.01	-7.09	5.18	1.70

Table 2. Heritabilities (on diagonal), genetic (above diagonal), and phenotypic correlations (below diagonal) for Average Daily Weight Gain (ADG), Metabolic Mid-Weight (MMWT), Feed Intake (FI), Feed Conversion Ratio (FCR) and Residual Feed Intake (RFI)

	ADG	MMWT	FI	FCR	RFI
ADG	0.31 ± 0.07	0.65 ± 0.12	0.81 ± 0.08	-0.61 ± 0.15	0.42 ± 0.17
MMWT	0.35 ± 0.02	0.46 ± 0.09	0.68 ± 0.08	-0.22 ± 0.23	0.21 ± 0.16
FI	0.46 ± 0.02	0.56 ± 0.02	0.49 ± 0.09	-0.13 ± 0.23	0.83 ± 0.05
FCR	-0.76 ± 0.01	0.00 ± 0.03	0.11 ± 0.03	0.12 ± 0.06	0.24 ± 0.23
RFI	-0.09 ± 0.03	0.09 ± 0.03	0.78 ± 0.01	0.52 ± 0.02	0.30 ± 0.09

Heritability estimates indicate, for ADG, MMWT, FI and RFI, that a moderate amount of additive genetic variation exists ranging from 0.30 to 0.49. The heritability estimates for ADG, FI and RFI were very close to the pooled heritably estimates published by Berry and Crowley (2013) using a meta-analysis on feed efficiency traits. In this meta-analysis up to 39 scientific publications were analysed, and they reported a polled heritably for ADG, FI and RFI as 0.31 ± 0.014, 0.40 ± 0.012, and 0.33 ± 0.013, respectively. The lowest heritability was for FCR and was associated with a high standard error (0.12 ± 0.06), and although this estimate was lower than the pooled heritability estimate of 0.23 ± 0.013, published by Berry and Crowley (2013), was within the range of the published values (0.09 to 0.46) for different beef cattle populations. In addition to this, FCR is a ratio trait and it has been documented several problems related to predict the genetic change in subsequent generations that can be avoided by using linear index traits such as RFI that increases selection responses (Gunsett, 1984; Arthur *et al*., 2001). The heritability estimate in this work for MMWT (of 0.46 ± 0.09) was slightly higher compared to the estimated provided by Arthur *et al*. (2001) of 0.40 ± 0.02 in Angus cattle of Australia.

The genetic correlations between ADG and FI, between ADG and FCR, between FI and RFI, and between FCR and RFI, were in agreement with the average genetic correlations of 0.76 ± 0.09, -0.57 ± 0.16, 0.82 ± 0.05, and 0.35 ± 0.22, respectively, using a meta-analysis of genetic parameters reported by several authors in beef cattle populations (Berry and Crowley, 2013). In a similar way, genetic correlations between MMWT and ADG, between MMWT and FI are in agreement with the estimated values, published by Arthur *et al*. (2001), of 0.53 ± 0.07 and 0.65 ± 0.03, respectively. Different to the genetic correlation, reported in this work, between FCR and FI (-0.13 ± 0.23), the genetic correlation between RFI and FI was positive (0.83 ± 0.05); in addition, only the genetic correlation of FCR was negative and favourable correlated with ADG, meaning that improving FCR was associated with greater ADG.

The phenotypic correlations between ADG and MMWT, ADG and FI, MMWT and FI, FI and FCR, FI and RFI, and between FCR and RFI were positive. These results are in agreement with the phenotypic correlations reported by Arthur *et al*. (2001) of 0.26, 0.41, 0.63, 0.23, 0.72 and 0.53, respectively. Arthur *et al*. (2001) also reported high negative phenotypic correlation between ADG and FCR of -0.77, similar to the estimate obtained in the present work. Since RFI was obtained by regression, it is expected to be phenotypically independent of the ADG, and MMWT (Arthur *et al*., 2001). However, in this study a non-zero phenotypic correlation between RFI and ADG and MMWT was observed. A possible explanation for this is that RFI was estimated from many different trials. Once RFI was fitted in a full mixed model some of this variability is corrected for by contemporary group estimates and a non-zero correlation remains. All the phenotypic correlation involving ADG, FI, FCR and RFI were within range estimated by different authors in beef cattle populations (Berry and Crowley, 2013).

In conclusion, all heritability estimates in the current work were within the range of estimates obtained in several beef cattle populations which in most cases involved small numbers of animals. A moderate heritability was found for FCR with high standard errors, suggesting that RFI will represent a better option for improving response to selection. The results from this study suggest that is some situations RFI is neither phenotypically or genetically independent of ADG or MMWT. Given this, additional research is required to investigate other ways to select for feed efficiency and, due to the lack of consistency across several studies and considering that the analysis of feed efficiency traits alone provides little information. Additional research is required to investigate genetic associations between efficiency traits and other economically important traits.

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