

# Modelling live weight and feed intake during a feedlot test period in Australian Angus Cattle

*J.A. Torres-Vazquez<sup>1</sup>, J.H.J. van der Werf<sup>1</sup> & S.A. Clark<sup>1</sup>*

*School of Environmental and Rural Science, University of New England, Armidale, Australia, 2351*

[jtorresv@myune.edu.au](mailto:jtorresv@myune.edu.au) (Corresponding Author)

## Summary

Feed efficiency related traits modelled as repeated measurements may allow an increased precision of genetic parameters estimates, accuracy of selection and a subsequent increase in genetic gain. The objective of the present work was to compare different models for live weight (LW) and daily feed intake (DFI) during a 78-day feedlot test period using 1763 Angus Steers from the Australian Beef Information Nucleus (BIN). Genetic parameters were estimated using repeatability and random regression models for single and multiple traits. Using the bivariate random regression model, the heritabilities for LW and DFI were in the range of 0.46 to 0.56, and from 0.48 to 0.43, respectively; with repeatabilities ranging from 0.92 to 0.95, and from 0.69 to 0.72, respectively. And the corresponding genetic correlation increased from 0.50 in day 1 up to 0.85 at day 78. Based on the Akaike's information criterion and Bayesian-Schwarz information criterion values, random regression models presented smaller values indicating the best fit in comparison to the repeatability models. In practice, random regression analysis should be adopted for predicting more precisely the genetic merit in feed efficiency related traits. A positive and unfavourable genetic correlation was estimated for the studied traits, suggesting that it would be necessary to build a selection index to optimally select for both traits.

*Keywords: model comparison, feed efficiency, live weight, feed intake, Angus, cattle*

## Introduction

Feed intake represents a major cost to animal production systems, thus increasing the efficiency in which animals turn this feed into product is a major goal in breeding programs. In beef cattle, measurement of traits related to feed efficiency is expensive (Hill, 2012). Archer *et al.*, (1997) have recommended using a 70-day test with biweekly weight measurements and with daily intake measurements to obtain accurate estimates of average weight gain and daily feed intake. Traditionally, these averages of a group of phenotypes have been used to estimate genetic parameters for feed efficiency related traits (for example Residual Feed Intake), however, studies analysing these traits measured along a trajectory over time are scarce. Nonetheless, only few estimates of repeatability have been published for daily feed intake (DFI) or dry matter intake in feedlot testing periods, with low to moderate values ranging from 0.33 to 0.63 for DFI (Kelly *et al.*, 2010; Durunna *et al.*, 2012).

Feed efficiency traits modelled as repeated measurements of the same trait would allow accurate selection based on a few repeated measurements of such traits. However, for these traits measured along a trajectory of the animal's life, the mean and covariance between such

measurements can change over time, and random regression models (RRM) or covariance functions might be more appropriate for modelling multiple measurements of traits that may gradually change over time (Mrode, 2014).

The objective of this study was to compare RRM with repeatability models for estimating genetic parameters for live weight (LW) and daily feed intake (DFI), from records on Angus Steers from the Australian Beef Information Nucleus (BIN).

## **Material and methods**

The phenotypic data examined in this study included LW, and DFI measures from 1823 Angus Steers collected from 2013 to 2016 at Tullimba Feedlot (Armidale, NSW). On entry to the feedlot, the animals in this study ranged from 500-600 days of age and weighed 579 kg on average. Initially animals were conditioned for 21 days and they were subsequently fed for an additional 78-day test period, and fortnightly measures of body weight and daily measures of feed intake were available for all animals over the 78-day test period.

Daily feed intake was modelled such that average DFI obtained for fortnightly periods aligned with the measurements of weight. DFI averages with less than 7 records (out of 14) per day were eliminated. This resulted in 5 records for average DFI and 6 weights measured at the same time for each animal. The pedigree file included ancestors over 23 generations with 21,439 animals with 3,908 sires and 11,610 dams.

For all analyses, contemporary groups (which included trial, property management group and feedlot pen) were fitted as fixed effects, and days in feed at each measurement were used as covariate in the repeatability models. Additive genetic effects and permanent environmental effects of the animals were included as random effects for the repeatability model. In the random regression models, additive genetic and permanent environmental effects were regressed on days in test using a Legendre polynomial (Meyer, 1998). The most suitable order of fit for each of these polynomials were assessed based on the log likelihood (LogL), Akaike's information criterion (AIC), and the Bayesian information criterion (BIC).

The univariate random regression results were used as starting values in the bivariate random regression model (RRM). Genetic correlations between live weight and feed intake were estimated from the bivariate repeatability model and as well as the change of correlation over the entire test period from the bivariate random regression model. These results were compared with estimates from a bivariate animal model based on single measurements for each trait within each of 6 bi-weekly periods. All models were analysed using the ASReml software (Gilmour *et al.*, 2009).

## **Results and discussion**

Final descriptive statistics after the edition are presented in Table 1, and model comparison, together with the heritabilities and repeatabilities for LW and DFI are presented in Table 2.

Table 1. Descriptive statistics for live weight (kg), and Daily Feed Intake (kg/day).

Trait	Number	Mean	Min	Max	SD
Live weight (kg)	1703	579.5	468	720	55.7
Feed Intake (kg/day)	1723	14.97	8.19	20.76	1.98

Using repeatability models in univariate and bivariate analysis, heritabilities for LW and DFI were 0.48 and 0.41, respectively (Table 3). Using the single-trait RRM, the heritability for LW was lowest at day 1 (0.49) and increased gradually until the end of the 78-day test period (0.53). The heritability for DFI decreased with the RRM from day 1 (0.50) up to the end of the test period (0.39). Heritabilities estimated in a bivariate RRM were similar to those from a univariate RRM (Figure 1); ranging from 0.46 to 0.56, and from 0.48 to 0.43 for LW and DFI, respectively (Table 2).

Heritability estimates obtained in this work using repeatability and random regression animal models were close to estimates, based on average DFI and body weight over the full test period, published by Berry and Crowley (2013). They found in a meta-analysis of up to 39 scientific publications, a pooled heritability for body weight and DFI of  $0.39 \pm 0.010$  and  $0.40 \pm 0.012$ , respectively.

For both traits, RRM had significantly higher log likelihood values, and smaller values for the Akaike's information criterion, and Schwarz Bayesian information criterion, showing the best fit for these models (Table 2).

Table 2. Number of parameters (N), log likelihood function (Log L), Akaike's information criterion (AIC), Schwarz Bayesian information criterion, heritability ( $h^2$ ) and repeatability (rep) for the implemented models.

Trait	Model <sup>1</sup>	N	Log L	AIC	BIC	$h^2$	rep
Live Weight	REP	3	-3685.1	47376.2	47396.7	$0.48 \pm 0.08$	$0.91 \pm 0.01$
	RRM	7	-2994.3	46002.6	46050.4	0.49 - 0.53	0.93 - 0.94
	TT-REP	9	-7558.1	55134.2	55201.5	$0.48 \pm 0.08$	$0.91 \pm 0.01$
	TT-RRM	23	3455.8	53134.3	53306.0	0.46 - 0.56	0.92 - 0.95
Feed Intake	REP	3	-4462.3	8930.7	8950.8	$0.41 \pm 0.07$	$0.64 \pm 0.01$
	RRM	7	-4170.7	8355.5	8402.4	0.50 - 0.39	0.69 - 0.72
	TT-REP	9	-7558.1	55134.2	55201.5	$0.41 \pm 0.07$	$0.63 \pm 0.01$
	TT-RRM	23	3455.8	53134.3	53306.0	0.48 - 0.43	0.69 - 0.72

<sup>1</sup> REP = Repeatability animal model; RRM = Random regression animal model; TT-REP = Two-trait repeatability animal model; and TT-RRM = Two-trait random regression animal model.

Using the bivariate repeatability animal model, the genetic correlation was  $0.69 \pm 0.08$ , and using the bivariate RRM, the genetic correlation increased from 0.50 on day 1 to 0.85 on day 78 (Figure 1). After dividing the period into 6 parts to use the two-trait animal models, the genetic correlations followed the same pattern as the bivariate RRM from day 1 until day

64 (first 5 parts), and from day 65 to 78 (last part), the correlation decreased to  $0.53 \pm 0.19$ ; while this estimate, with the two-trait RRM, rose from 0.82 to 0.85 (Figure 1). This low genetic correlation together with the high standard errors, estimated with the two-trait animal model at the end of the period, could be the result of small number of records used to estimate this genetic parameter. In general, these estimates agreed with the average genetic correlation ( $0.75 \pm 0.02$ ) published by Berry and Crowley (2013) using a meta-analysis with 9 scientific publications.

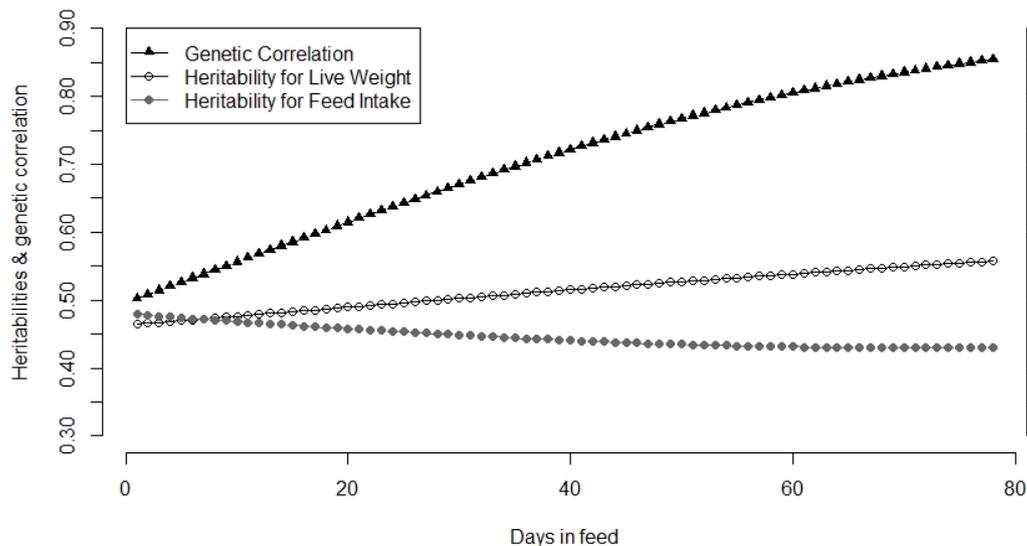


Figure 1. Genetic correlation and heritabilities using a two-trait random regression model.

In conclusion, extending the repeatability model by adding Legendre polynomials of first order significantly improved the model for predicting genetic parameters, showing that the genetic parameters had a tendency to change over time. Heritability estimates, obtained with random regression models, were moderate to high with a positive and unfavourable genetic correlation increasing from 0.50 in day 1 to 0.85 at day 78. Estimated genetic parameters in this study were consistent with the international literature using animal models without repeated records. In case that was not desirable to increase the DFI, it would be necessary to build a selection indices that avoid increase of this trait as correlated response to the improvement of LW. Results implies that genetic merit should be predicted more precisely with random regression analysis for feed efficiency related traits. Further studies are necessary to investigate genetic associations between efficiency related traits and other economically important traits for this population.

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