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POSSIBILITIES OF SHORTENING THE NUMBER DAYS ON FEED FOR CALCULATING NFI IN CATTLE

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SUMMARY

Feed efficiency is an important trait in many beef cattle breeding programs. The current measure of feed efficiency used in beef cattle is net feed intake (NFI). Current measurement protocols stipulate a 70 day test period to obtain a reliable NFI phenotype, incurring a significant economic cost. This study examined the phenotypic and genetic implications of shortening the number of days on feed in the calculation of NFI phenotypes. Phenotypic and genetic parameters were estimated for 5 trial lengths (14, 28, 42, 56 and 70 days) for NFI and its component traits; average daily gain (ADG), metabolic mid weight (MMWT) and daily feed intake (DFI). For NFI, 56 days on feed was highly genetically correlated with 70 day estimates. For shorter periods correlations reduced and variance components changed substantially. In contrast, daily feed intake could be measured well in short periods of time with genetic correlations of > 0.95 for lengths greater than 14 days. To substantially reduce the time on feed it is suggested that breeders consider collecting DFI information rather than NFI. If this was seen to be desirable an alternative way of balancing feed intake and weight gain would need to be explored.

INTRODUCTION

The cost associated with feeding animals is one of the major expenses to all livestock production systems. How efficiently this feed is converted into animal products is often termed feed efficiency (Archer 1999). Feed efficiency (FE) is an important breeding objective trait in many beef cattle breeding programs as breeders attempt to find an optimum balance between increased production levels and costs of production. Many authors have suggested different ways of measuring feed efficiency which range from ratio traits like feed conversion ratio (FCR) to traits corrected for production like net (or residual) feed intake (Arthur *et al.* 2001). The current measure of feed efficiency used in beef cattle is NFI, which describes the difference between actual feed intake and the expected feed intake required for maintenance and growth (Arthur *et al.* 2001). This process makes NFI phenotypically independent of growth and maintenance; however, genetic correlations between each of the traits often remain (Archer 1999).

Current industry protocols require that daily feed intake (DFI) and live weight be recorded for 70 days so that an accurate NFI phenotype can be estimated (Archer *et al.,* 1999). Given the large economic cost associated with this, most recording has been limited to small groups of animals recorded at central testing sites (i.e. Tullimba feedlot). This study aimed to examine the phenotypic and genetic implications of shortening the number of days required to obtain a reliable phenotypes associated with feed efficiency.

MATERIALS AND METHODS

The phenotypic data examined in this study included live weights, and DFI measures from 1725 Angus Steers collected from 2012 to 2016 at Tullimba Feedlot. On entry to the feedlot, the animals in this study ranged from 470-700 days of age and weighed 400-520 kg. Initially animals were conditioned for 21 days and fed for an additional 70 days over which time all data was collected (NFI test period). All animals were weighed 6 times over the 70-day test period (fortnightly). Average daily gain was calculated as the regression of weight on time (days) while MMWT was obtained as the mid-point weight to the 0.73 power (Arthur *et al*., 2001; Berry and Crowley, 2013).

Net feed intake was estimated as the residuals from the following regression; $FI = b_1(ADG) + b_2(MMWT) + NFI$ (Arthur and Herd, 2008; Berry and Crowley, 2013). The regression coeffecients (b) were estimated across cohorts of steers. NFI, ADG, MMWT and DFI were calculated each for 5 trial lengths (14, 28, 42, 56 and 70 days), hence we considered 20 traits in total. Each reduced trial length was compared to the current 70 day period using a series of pairwise bivariate animal models using ASReml (Gilmour *et al*., 2009). Fixed effects of mean, cohort, Pen (within cohort), Age and Dam age where fitted for each comparison.

For each pair of traits, the following bivariate animal model was used:

$$[1]\ y = Xb + Za + e$$

where **y** is the vector of the phenotypes for two traits; **X** is a matrix relating phenotypes to fixed effects; **b** is vector of fixed effects for the traits analysed; **Z** is a matrix relating animals to the data; **a** is a vector which contains random additive genetic effects of animals; and **e** is a vector with residuals for the analysed traits. Furthermore, variance structures of random effects are described as:

$$var = \begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} A \otimes G_0 & 0 \\ 0 & I \otimes R_0 \end{bmatrix}$$

where $\boldsymbol{G}_0$, and $\boldsymbol{R}_0$ denote 2x2 matrices containing additive genetic and residual covariance components, respectively; **A** is the numerator relationship matrix derived from pedigree information; **I** is the identity matrix; and $\otimes$ is the direct product of the matrix.

RESULTS AND DISCUSSION

Genetic correlations for all traits were high (>0.90) when comparing 70 day test period with 56 day test period (Table 1, 2 and 3). Genetic (σ^2_A) and phenotypic (σ^2_p) variance similar when comparing traits recorded at 56 days and 70 days, respectively. The lowest genetic correlation, between 56 and 70 days on feed, was NFI whilst the highest correlations were observed for DFI. Phenotypic correlations between each time period were lower than the genetic correlations for all traits.

Table 1. Variance component and heritability (h^2) estimates for NFI (kg/day) across all trial lengths and the phenotypic (r_p) and genetic (r_A) correlations of the reduced days with the full 70 days trial

Days on feed	σ^2_P	σ^2_A	h^2	*SE*	r_A	*SE*	r_p	*SE*
70	**0.25**	**0.05**	**0.20**	*0.06*				
56	**0.25**	**0.06**	**0.22**	*0.06*	**0.92**	*0.07*	**0.80**	*0.01*
42	**0.37**	**0.09**	**0.23**	*0.06*	**0.87**	*0.09*	**0.54**	*0.02*
28	**0.64**	**0.11**	**0.17**	*0.06*	**0.88**	*0.13*	**0.40**	*0.02*
14	**0.94**	**0.20**	**0.21**	*0.06*	**0.75**	*0.16*	**0.30**	*0.02*

Table 2. Variance components and heritability (h^2) estimates for ADG (kg/day) across all trial lengths and the phenotypic (r_p) and genetic (r_A) correlations of the reduced days with the full 70 days trial

Days on feed	σ^2_P	σ^2_A	h^2	*SE*	r_A	*SE*	r_p	*SE*
70	**0.09**	**0.02**	**0.27**	*0.07*				
56	**0.11**	**0.03**	**0.27**	*0.07*	**0.98**	*0.02*	**0.89**	*0.01*
42	**0.17**	**0.04**	**0.22**	*0.06*	**0.94**	*0.05*	**0.76**	*0.01*
28	**0.31**	**0.06**	**0.19**	*0.06*	**0.88**	*0.09*	**0.57**	*0.02*
14	**1.30**	**0.03**	**0.02**	*0.04*	**0.82**	*0.65*	**0.23**	*0.02*

Table 3. Variance components and heritability (h^2) estimates for DFI (kg/day) across all trial lengths and the phenotypic (r_p) and genetic (r_A) correlations of the reduced days with the full 70 days trial

Days on feed	σ^2_P	σ^2_A	h^2	*SE*	r_A	*SE*	r_p	*SE*
70	**1.48**	**0.71**	**0.48**	*0.08*				
56	**1.56**	**0.75**	**0.48**	*0.08*	**1.00**	*0.00*	**0.98**	*0.00*
42	**1.69**	**0.83**	**0.49**	*0.08*	**0.99**	*0.01*	**0.95**	*0.00*
28	**1.85**	**0.85**	**0.46**	*0.08*	**0.97**	*0.01*	**0.89**	*0.01*
14	**2.12**	**0.81**	**0.38**	*0.08*	**0.95**	*0.03*	**0.78**	*0.03*

For all traits, as the number of days was reduced the amount of genetic and phenotypic variance that was observed increased substantially. This was most evident for ADG where phenotypic variance increased such that for 28 days and 14 days on feed σ^2_P was 3 times or 15 times greater than 70 day estimates, respectively. In contrast, MMWT was very consistent across all NFI test periods, with r_A >0.97 and r_p>0.96 across all test lengths (results not shown). The inability to estimate ADG accurately was a major limitation to reducing the time in which NFI can be recorded. The impact of this declining accuracy with reduced NFI test length can be observed in Figure 1a which shows that, as NFI test period is reduced, the regression coefficient relating to the adjustment of DFI for ADG (b1), in the calculation of NFI, is greatly reduced. Furthermore, Figure 1b shows that NFI gradually becomes more like DFI with phenotypic and genetic correlation between NFI and DFI increasing as the number of days is reduced.

The time taken to precisely estimate ADG and therefore NFI has previously been reduced from 140 to 112 now to 70 days (McPeake, C. A., and D. S. Buchanan. 1986, Archer *et al.* 1997). Results from this current study suggest, given the high genetic correlation between 56 and 70 days, it may be possible to reduce the testing period further (to 56 days). The results in this study were similar to those presented by Archer *et al*. 1997. Differences between the results of the current study and that of Archer *et al*. (1997) may be a result of test animals in that study being in an earlier growth stage (250 days of age) compared to a finishing stage (~500 days of age) in the current study. This may explain why the genetic correlation for 56 days is higher in this present study than those presented by Archer *et al.* 1997.

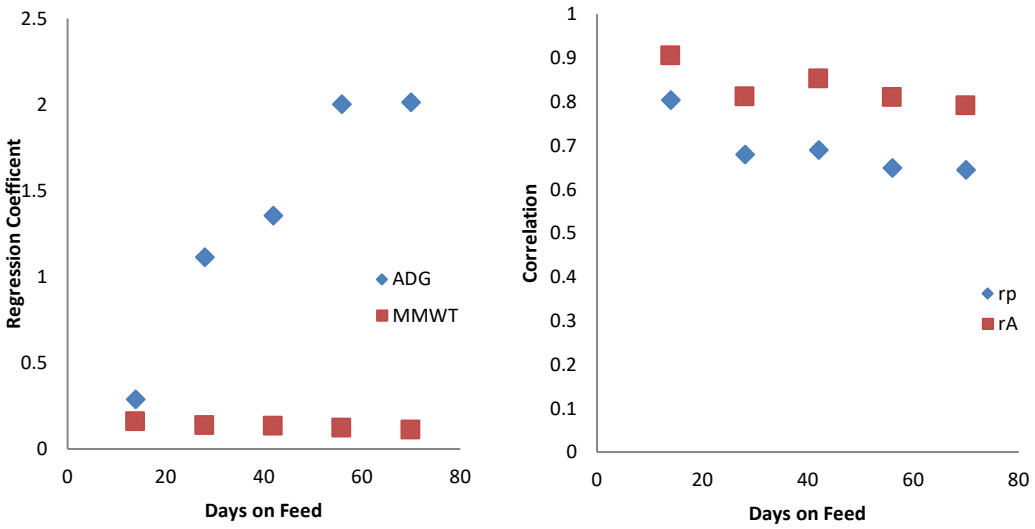

Figure 1. a) The regression coefficients (b) for ADG and MMWT used to calculate NFI, and b) the phenotypic and genetic correlations between NFI and DFI for reduced NFI test periods

In contrast to NFI and ADG, it appears that testing length for MMWT and DFI could be reduced as genetic and phenotypic correlations indicate that MMWT and DFI were very consistent over time. The time taken to record DFI could be reduced to 28 days and even short periods could be examined as larger amounts of data become available. Possible alternatives to collecting NFI routinely may be to collect a series of DFI measurements for a single animal or test more animals for shorter test periods. The later would reduce the costs associated with collecting feed intake information. It is likely that it would also increase overall response to selection as more animals could be recorded. This would only be possible if growth traits (like ADG) were measured at different stages (additional records) in the breeding program. Some consideration is needed, prior to the reduction of the number of days on feed, to understand the relationship between growth and feed intake to ensure breeders achieve what is desired in their given breeding program. A key question is: are we happy with the current definition of NFI, or would a different definition of feed efficiency better serve breeders, feeders and processors? It could be plausible that only recording feed intake or creating an disconnect between feed intake and growth, by measuring both traits at different times, may in fact completely change the weight placed on each trait when selecting for feed efficiency.

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