

## REMODELLING THE GENETIC EVALUATION OF NFI IN BEEF CATTLE – PART 1: DEVELOPING AN EQUIVALENT GENETIC MODEL

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### SUMMARY

Net feed intake (NFI) is the residual portion of daily feed intake (DFI) not explained by growth or maintenance requirements. The NFI phenotype (NFIP) is based on a 70-day test period where DFI and fortnightly weights (to calculate average daily gain (ADG) and maintenance as metabolic mid-weight (MMWT)) are measured. Recording NFIP is costly, and shortening the test length would be advantageous. However, research has shown that ADG cannot be accurately measured from a shortened test. Genetic NFI EBVs (NFIG) were calculated using DFI EBV adjusted for ADG and MMWT EBV and were shown to have a Pearson correlation of 0.99 with the NFIP EBV from 3,088 Angus steers. The regression slope between NFIG and NFIP EBVs was 1.14. Alternative NFIG models where growth and maintenance requirements were obtained from BREEDPLAN live weight traits instead of live weights recorded in the test period, demonstrated high Pearson correlations ( $r=0.87$  to  $0.93$ ) and regression slopes between 0.63 and 0.97 with NFIP EBVs. Results suggest that genetic NFI EBVs can be obtained, with growth and maintenance requirements being determined from BREEDPLAN live weight traits. This provides the opportunity to determine if the length of the test to measure DFI can be shortened, reducing the cost of recording NFI per animal.

### INTRODUCTION

Net feed intake (NFI) measures feed efficiency and is the residual portion of daily feed intake (DFI) adjusted for growth and maintenance (Koch *et al.* 1963). Over a 70-day feed efficiency test, individual DFI and fortnightly live weight have been recorded in beef cattle in Australia (Arthur *et al.* 2001). Recording NFI is costly due to the test length. Previous studies (Culbertson *et al.* 2015; Clark and van der Werf 2017) demonstrated that DFI could be measured from a shorter test, but to measure average daily gain (ADG), a minimum of 56 test days was required (Archer *et al.* 1997; Culbertson *et al.* 2015), and this represents a limiting factor to reducing the test length. Estimating genetic NFI EBVs (NFIG) has been proposed as an alternative to EBVs based on NFI phenotype (NFIP) (Kennedy *et al.* 1993; MacNeil *et al.* 2011). The method utilises genetic (co)variances and EBVs from tri-variate (DFI, ADG and metabolic mid-weight (MMWT)) analysis to construct a genetic NFI EBV. This study aimed to develop NFIG EBVs to compare against NFIP EBVs and assess if NFIG models may be a suitable alternative for genetic evaluation of feed efficiency when NFIG EBVs were developed using growth and maintenance recorded from a 70-day test or derived from BREEDPLAN live weight traits.

### MATERIALS AND METHODS

**Data preparation.** Feed intake data and the NFI contemporary group (NFI CG; defined as the birth herd, birth year, sex, trial cohort, and previously recorded BREEDPLAN trait CG (i.e. 200-day live weight)) were extracted from the Angus Australia BREEDPLAN database for 3,215 steers. The data was recorded at Tullimba Research Feedlot (Torryburn, NSW) between 2012 and 2021. Individual DFI was measured using the VYTELLE-SENSE system, formerly known as GrowSafe

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Feeders, and the Ruddweight system ([www.vytelle.com/vytelle-sense](http://www.vytelle.com/vytelle-sense)). Animals were fed a standard feedlot diet (energy level of 12 MJ/kg). DFI was recorded over 70 – 77 days, after an initial 21-day acclimatisation period. Weight was recorded fortnightly, up to six times, during the test period. The average DFI, ADG and MMWT were computed across the full test period. ADG during the feed intake test was computed as the linear regression across all trial weights, and MMWT =  $(\frac{ADG * test\ length}{2} + start\ weight)^{0.73}$ . Animals with fewer than 56 days of feed intake data over the 70-day test duration, or with fewer than four live weights recorded during the test were removed (n=31). Animals in an NFI CG with fewer than three animals (n=96) were also removed. The final dataset included 3,088 steers from 35 trial groups with DFI, ADG and MMWT records. Steer age at the start of the test (SAGE) was on average  $513 \pm 73$  days (range: 373 – 767 days). These were the progeny of 327 sires and 2,523 dams, and an up to five-generation pedigree containing 9,497 animals built.

To develop NFIg EBVs when ADG and MMWT are not available from the test period (i.e. from a proposed shortened test), BREEDPLAN live weight traits (W200, W400 and W600) and their respective CG at 200, 400 and 600 days of age were extracted from the Angus Australia BREEDPLAN database for all animals in the final NFI dataset. Where there were multiple weights per trait, the weight closest to the target age (i.e. 200 days) was used. These live weight traits were pre-adjusted for heifer factor, animal age and dam age using standard BREEDPLAN procedures (Graser *et al.* 2005). Using BREEDPLAN live weight phenotypes, three ADG terms were constructed to represent gain between 200 and 600 days of age, 200 and 400 days of age and 400 and 600 days of age, i.e.  $ADG_{200-600} = (W600 - W200) / 400$ . At 200, 400 and 600 days of age, metabolic weights (MWT) were constructed based on BREEDPLAN live weight phenotypes, i.e.  $MWT_{200} = WT_{200}^{0.73}$ . Descriptive statistics for the traits used in this study are shown in Table 1.

**Statistical analyses.** The NFI phenotype (NFIp) was calculated by adjusting DFI for growth and maintenance, as per Koch *et al.* (1963.).  $NFIp = DFI - \mu - (\beta_{adg} \times ADG) - (\beta_{mmwt} \times MMWT)$ , where  $\mu$ ,  $\beta_{adg}$  and  $\beta_{mmwt}$  were regression coefficients obtained from the model  $DFI = \mu + NFI\ CG + (\beta_{adg} \times ADG) + (\beta_{mmwt} \times MMWT) + SAGE$ . Linear mixed animal models were fit in ASReml (Gilmour *et al.* 2015) to estimate variance components and animal solutions (EBVs). The model to predict NFIp EBVs fitted SAGE and NFI CG as fixed effects in the model.

Genetic NFI (NFIg) EBVs were derived following the procedure of Kennedy *et al.* (1993) using the EBVs of DFI, ADG and MMWT from a tri-variate model.  $NFIg\ EBV = DFI\ EBV - (\beta_{adg} \times ADG\ EBV) - (\beta_{mmwt} \times MMWT\ EBV)$ . The genetic regression coefficients  $\begin{bmatrix} \beta_{adg} \\ \beta_{mmwt} \end{bmatrix} = G^{-1}c$ , where G was the genetic covariance matrix of ADG and MMWT from the tri-variate model and c was the vector of the genetic covariance of DFI with ADG and MMWT.

Six alternative NFIg EBVs (denoted A through to F) were derived from replacing feed test ADG and MMWT with alternative measures derived from BREEDPLAN weight records. The same procedure described for NFIg EBVs was used for these alternative genetic NFI EBVs, and Table 2 describes these models. To avoid autocorrelation issues for the alternative NFIg EBVs, BREEDPLAN-derived MWT recorded at the end of the specified ADG period was not considered. The alternative NFIg models were evaluated using Pearson correlation coefficients (r), regression slope of NFIg EBV on NFIp EBV (b) and difference of means ( $u^- - u^{\bar{}}$ ) between NFIp EBV and NFIg EBVs, and these were reported in Table 2.

## RESULTS AND DISCUSSION

A Pearson correlation of 0.99 was calculated between NFIp and NFIg EBVs, and EBV means was similar with a difference of means of 0.01 (Table 2). This indicates that NFIg EBVs were unbiased, but the standard deviation was smaller than NFIp EBVs. The regression slope was 1.14,

suggesting that the spread of NFIg EBV is narrower and animals at the edge of the distribution may be overestimated. These results demonstrate that NFIg was an equivalent model to NFIp when the same ADG and MMWT terms were modelled. These results agreed with Hoque and Oikawa (2004), who estimated a correlation of 0.97 for a similar comparison in Wagyu cattle.

**Table 1. Descriptive statistics for average daily feed intake (DFI), average daily gain (ADG) and metabolic mid-weight (MMWT) measured from a 70-day feed intake test and ADG representing different periods between 200 and 600 days of age (ADG200-600, ADG200-400 and ADG400-600) and metabolic weight at 200 (MWT200), 400 (MWT400) and 600 (MWT600) days of age from BREEDPLAN records for Angus steers**

Trait	Unit	N	Mean	SD	Range
1) Feed test records					
DFI	kg/d	3,088	14.8	1.99	6.89 – 22.6
ADG	kg/d	3,088	1.61	0.34	0.52 – 2.90
MMWT	kg <sup>0.73</sup>	3,088	104	6.83	81.8 - 135
2) BREEDPLAN data					
ADG <sub>200-600</sub>	kg/d	2,915	1.02	0.16	0.58 – 1.65
ADG <sub>200-400</sub>	kg/d	2,360	0.82	0.29	0.07 – 1.90
ADG <sub>400-600</sub>	kg/d	2,198	1.30	0.21	0.72 – 2.25
MWT <sub>200</sub>	kg <sup>0.73</sup>	3,078	55.8	6.01	31.9 – 74.0
MWT <sub>400</sub>	kg <sup>0.73</sup>	2,367	80.5	8.59	58.0 – 109.5
MWT <sub>600</sub>	kg <sup>0.73</sup>	2,919	114.0	8.16	86.4 – 141.5

**Table 2. Models for genetic NFI (NFIg) EBVs when growth and maintenance were derived from feedlot weights or BREEDPLAN live weights, EBV summary statistics (mean and SD), the Pearson correlation (r), regression slope (b) and difference of means ( $\bar{u} - \bar{\tilde{u}}$ ) between NFIp EBV and genetic NFI EBVs**

NFI EBV*	EBV		r	b	$\bar{u} - \bar{\tilde{u}}$
	Mean	SD			
NFIp	0.02	0.41			
NFIg = EBV(DFI) – $\beta_1$ x EBV(ADG) – $\beta_2$ x EBV(MMWT)	0.02	0.37	0.99	1.14	0.01
NFIgA = EBV(DFI) – $\beta_1$ x EBV(ADG <sub>200-600</sub> ) – $\beta_2$ x EBV(MWT <sub>200</sub> )	0.01	0.44	0.93	0.89	0.02
NFIgB = EBV(DFI) – $\beta_1$ x EBV(ADG <sub>200-600</sub> ) – $\beta_2$ x EBV(MWT <sub>400</sub> )	0.01	0.45	0.91	0.86	0.01
NFIgC = EBV(DFI) – $\beta_1$ x EBV(ADG <sub>400-600</sub> ) – $\beta_2$ x EBV(MWT <sub>400</sub> )	0.02	0.46	0.90	0.84	0.00
NFIgD = EBV(DFI) – $\beta_1$ x EBV(ADG <sub>400-600</sub> ) – $\beta_2$ x EBV(MWT <sub>200</sub> )	0.01	0.44	0.87	0.84	0.01
NFIgE = EBV(DFI) – $\beta_1$ x EBV(ADG <sub>200-400</sub> ) – $\beta_2$ x EBV(MWT <sub>200</sub> )	0.04	0.59	0.88	0.63	-0.01
NFIgF = EBV(DFI) – $\beta_1$ x EBV(ADG <sub>200-400</sub> ) – $\beta_2$ x EBV(MWT <sub>600</sub> )	0.01	0.40	0.93	0.97	0.01

\* see Table 1 for abbreviations;  $\beta_1$  and  $\beta_2$  were estimated for each model and varied across the models

Six alternative NFIg models were considered using ADG and MWT derived from BREEDPLAN live weight traits (Table 2). For all alternative models, the Pearson correlation coefficient with NFIp EBVs ranged from 0.87 (model D) to 0.93 (models A & F). The highest correlations were observed when ADG<sub>200-600</sub> and MWT<sub>200</sub> or ADG<sub>200-400</sub> and MWT<sub>600</sub> were modelled. Models A, B, C and D all showed similar regression slopes (b=0.84 to 0.89) and a slightly higher standard deviation than the NFIp EBV. This suggests that EBVs for animals at the edge of the distribution may be overestimated. For all NFIg EBVs the bias was small (-0.01 to 0.02). The mean and standard deviation of the alternative NFIg EBVs were generally similar, although the NFIgE EBV showed a higher mean and standard deviation. NFIgE fitted ADG<sub>200-400</sub> and MWT<sub>200</sub>. The regression slope was also much lower (0.63) than in other models. The reasons for these differences are not clear. ADG<sub>200-400</sub> had the smallest gain (0.82 kg/day) compared with ADG<sub>200-600</sub> (1.02 kg/day) and ADG<sub>400-600</sub> (1.30

kg/d) (Table 1). NFIgF also modelled ADG<sub>200-400</sub>, with MWT<sub>600</sub> fitted instead of MWT<sub>200</sub>. The standard deviation of NFIgF EBVs was similar to NFIP EBVs with a regression slope of 0.97; this suggests that it is important to include WT<sub>600</sub> in either the ADG or MWT term in the alternative NFIg model. Model F fitting ADG<sub>200-400</sub> and MWT<sub>600</sub> yielded the alternative NFIg EBV with the highest Pearson correlation with NFIP EBV, a regression slope close to 1 and EBVs with similar means and standard deviations compared with NFIP EBVs.

Genetic NFI EBVs where the test period ADG and MMWT was replaced with ADG and MWT derived from BREEDPLAN live weight traits have shown potential as an alternative approach to computing feed efficiency. The next step of this research is to explore if the length of the test period to record DFI can be shortened and genetic NFI EBVs computed using the proposed alternative genetic NFI models. If the test length is reduced, this could lead to more animals being recorded for DFI, reduced cost of recording per animal, and an overall increase in selection response due to a larger number of recorded animals. Further research will be needed to investigate the method in a larger dataset where BREEDPLAN live weights from the whole breed will influence the component EBVs used in this study. In this study, the majority of animals had BREEDPLAN live weights recorded. If genetic NFI EBVs use BREEDPLAN live weights to model growth and maintenance, and especially if the feed intake test length is reduced, animals will potentially no longer be weighed at the feedlot, and BREEDPLAN live weights may be unavailable. More testing is required to ensure that the proposed approach for selecting for feed efficiency is robust for potential scenarios that could occur in practice. The current data structure could not consider maternal effects; with a larger dataset, the potential maternal effects of MWT<sub>200</sub> and how best to model MWT<sub>200</sub> can be tested.

## CONCLUSIONS

When growth and maintenance terms in the NFIg model were the same as NFIP, phenotypic and genetically derived NFI EBVs were shown to be equivalent models. This study proves, in principle, that feed intake test ADG and MMWT could be replaced with growth and maintenance derived from BREEDPLAN live weights, and the next step is to test if the DFI test length can also be shortened. Before this research can be implemented into national genetic evaluations, further research will be needed using an expanded dataset and testing how robust the approach is in scenarios likely to occur in the industry if the feed intake test were shortened, i.e. missing weights.

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