

REMODELLING THE GENETIC EVALUATION OF NFI IN BEEF CATTLE – PART 2: SHORTENING THE LENGTH OF THE FEED INTAKE TEST

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SUMMARY

BREEDPLAN net feed intake (NFI) EBV is derived from a phenotypic regression based on a 70-day feed intake test. Genetic NFI (NFIg) EBVs have been proposed as an alternative EBV and this recent development may also allow for a shortened feed intake test period. This study used feed intake records of 3,088 Angus steers from the full 70-day test and compared them to daily feed intake (DFI) from shortened test periods. Results showed DFI from shortened test periods had similar means but increased phenotypic variation. Phenotypic correlation with DFI from the full test period decreased as the test period decreased in weekly intervals and ranged between 0.75 and 0.99. NFIg EBVs were predicted using DFI from different length tests. The mean of all NFIg EBVs was close to zero, but the EBV standard deviation increased as the test period decreased. Pearson correlations between NFIg EBVs from a full test period and reduced test periods ranged between 0.73 and 0.99, the regression slope of NFIg from reduced test periods on NFIg from the full test period ranged between 0.73 and 0.95, and the bias ranged between 0.00 and 0.02. These results indicate that as the test period decreases, the spread of EBVs increases, resulting in extreme animals having overestimated NFIg EBVs. A shortened DFI test period could be used to estimate NFIg EBVs.

INTRODUCTION

BREEDPLAN net feed intake (NFI) EBV is derived from a phenotypic regression based on a 70-day test with growth and maintenance measured from fortnightly body weight records during the test period (Koch *et al.* 1963, Arthur *et al.* 2001), which is a costly protocol. Reducing the test period would reduce recording costs per animal and allow more animals to be tested. The current NFI EBV requires average daily gain (ADG) to be recorded at regular intervals for a minimum of 56 days (Clark and van der Werf 2017; Archer *et al.* 1997; Culbertson *et al.* 2015). Kennedy *et al.* (1993) proposed calculating NFI EBVs using genetic regression (NFIg), and Vargovic *et al.* (2023) showed NFI EBVs could be predicted using genetic regression with a Pearson correlation of 0.99 between the current BREEDPLAN NFI EBV and NFIg. Vargovic *et al.* (2023) also explored alternative NFIg models where growth and maintenance traits were derived from BREEDPLAN live weight traits. The most promising alternative NFIg model considered DFI from the full test, ADG between 200 and 400-day live weight and maintenance requirements based on 600-day live weight. For this model, the Pearson correlation was 0.93, and the regression slope was 0.97 between the alternative NFIg EBV and the current NFI EBV. To reduce the test length an alternative model is required. This paper investigated the possibility of shortening the DFI test length using the alternative NFIg model proposed by Vargovic *et al.* (2023).

MATERIALS AND METHODS

Data preparation. Feed intake and BREEDPLAN live weight data were available for 3,088 Angus steers from 35 trial groups, and data preparation details are provided in Vargovic *et al.* (2023).

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A series of average DFI traits were constructed (DFIn), where n was the cumulative number of feed test weeks (i.e. DFI4 was the average DFI recorded over the first four weeks of the test period). DFI10 was the average DFI recorded over the full test period, and was used to compare results when the test period was shortened. Growth and maintenance traits were defined using BREEDPLAN live weight traits where ADG was calculated between 200 and 400 days of age ($ADG_{200-400} = (W400 - W200) / 200$) and metabolic weight was at 600 days (MWT_{600}) ($MWT_{600} = WT_{600}^{0.73}$).

Statistical analyses. Variance components were estimated for DFIn from univariate linear mixed animal models in ASReml (Gilmour *et al.* 2015), and bivariate models were used to estimate genetic and phenotypic correlations between DFI10 and DFIn traits. For all DFIn traits, the NFI CG defined by Vargovic *et al.* (2023) and test start age centred on the mean were fixed effects, and the animal was fitted as a random effect. Vargovic *et al.* (2023) describe the method for genetically derived NFI EBVs (NFIg) using BREEDPLAN live weight traits to model growth and metabolic weight. From this paper, the NFIgF model from Vargovic *et al.* (2023) was considered; NFIg EBV = $EBV(DFIn) - \beta_1 \times EBV(ADG_{200-400}) - \beta_2 \times EBV(MWT_{600})$. NFIg EBV was calculated for each DFIn phenotype to test the impact of reducing the test period, and the regression coefficients (β_1 and β_2) were calculated for each NFIg model. For each set of NFIg EBVs (DFIn, n=1 to 9), the Pearson correlation @ regression slope (b) and bias of means with NFIg EBVs (DFIn, n=10) were calculated.

RESULTS AND DISCUSSION

Decreasing the length of the feed test period resulted in an increase in DFI phenotypic variance, but the raw mean remained similar (Table 1). Heritability estimates were generally similar for DFI measured between 4 and 10 weeks and were slightly lower for DFI measured between 1 and 3 weeks. The phenotypic and additive variances increased as the test length reduced. Genetic correlations between DFIn (n=1 to 9) and DFI10 were not significantly different from 1 indicating that all DFIn traits were genetically the same. Phenotypic correlation with DFI10 decreased as the test period decreased and ranged between 0.75 (DFI1) and 0.99 (DFI9).

Table 1. Phenotypic Mean and standard deviation (SD), additive genetic (V_A) and phenotypic (V_P) variance components, heritability and genetic (r_A) and phenotypic (r_P) correlations with daily feed intake at 10 weeks (DFI10) for DFIn (n=1 to 10 weeks)

Trait	Phenotype Mean (SD)	V_A (SE)	V_P (SE)	h^2 (SE)	r_A	r_P
DFI10	14.8 (1.99)	1.10 (0.15)	2.39 (0.07)	0.46 (0.06)		
DFI9	14.9 (1.99)	1.10 (0.16)	2.42 (0.07)	0.46 (0.06)	0.99	0.99
DFI8	15.0 (2.00)	1.14 (0.16)	2.47 (0.07)	0.46 (0.06)	0.99	0.99
DFI7	15.1 (2.02)	1.18 (0.17)	2.52 (0.07)	0.47 (0.06)	0.99	0.98
DFI6	15.1 (2.06)	1.20 (0.17)	2.59 (0.07)	0.46 (0.06)	0.99	0.97
DFI5	15.2 (2.12)	1.24 (0.18)	2.64 (0.07)	0.47 (0.06)	0.99	0.95
DFI4	15.2 (2.12)	1.21 (0.18)	2.71 (0.08)	0.45 (0.06)	0.99	0.93
DFI3	15.1 (2.15)	1.21 (0.18)	2.78 (0.08)	0.43 (0.06)	0.99	0.90
DFI2	15.1 (2.23)	1.22 (0.19)	2.89 (0.08)	0.42 (0.06)	0.99	0.85
DFI1	14.9 (2.29)	1.14 (0.20)	3.22 (0.09)	0.35 (0.06)	1.00*	0.75

*estimate at bounds

The mean of all NFIg EBVs was close to zero, with standard deviations ranging from 0.38 to 0.50 (Table 2). Generally, as the DFI test period reduced, NFIg EBVs showed more variation with standard deviations increasing. Pearson correlations between NFIg EBV (DFIn, n=10) and NFIg EBV (DFIn, n=1 to 9) ranged between 0.73 and 0.99, the regression slope ranged between 0.73 and 0.95, and the difference of means ranged between 0.00 and 0.02. As the test period reduced, the Pearson correlation and regression slopes decreased, and the NFIg EBV standard deviation and the

difference of means between NFIg EBV (DFIn, n=10) and NFIg EBV (DFIn, n=1 to 9) increased. These results indicate that the bias increased as the test period decreased, and NFIg EBVs for animals at either end of the distribution were over-estimated.

Table 2. Summary statistics for NFIg EBVs using daily feed intake (DFI) from reduced test lengths and BREEDPLAN live weight records to model growth and maintenance, the Pearson correlation (r), regression slope (b) and bias of means (bias) between NFIg EBVs when DFI was recorded over the full test period, and DFI recorded from a reduced test period

DFIn modelled	NFIg EBV				r	b	bias
	Mean	SD	Min	Max			
DFI10	0.01	0.41	-1.85	1.58			
DFI9	0.01	0.41	-1.85	1.56	0.99	0.95	0.00
DFI8	0.01	0.44	-1.90	1.66	0.99	0.89	0.00
DFI7	0.01	0.46	-1.92	1.74	0.98	0.85	0.00
DFI6	0.00	0.48	-1.99	1.79	0.97	0.80	0.01
DFI5	0.00	0.50	-2.13	1.79	0.95	0.76	0.01
DFI4	0.00	0.49	-2.69	1.67	0.92	0.75	0.01
DFI3	-0.01	0.48	-2.64	1.82	0.89	0.74	0.02
DFI2	-0.03	0.46	-2.33	1.93	0.84	0.73	0.03
DFI1	-0.01	0.38	-1.74	1.99	0.73	0.77	0.02

The results in Table 2 demonstrate that reducing the feed intake test period may be possible using genetic NFI EBVs obtained where growth and maintenance are modelled using BREEDPLAN live weight traits. Results from Table 1 agree with earlier studies by Clark and van der Werf (2017), who suggested that the DFI test length could be reduced to 4 weeks. However, Table 2 showed that NFIg EBVs had a regression slope of 0.75 when DFI was measured from a 4-week test and a larger spread of EBVs, especially for the more feed-efficient animals. Given the strong Pearson correlation, a degree of overestimation of extreme animals may be acceptable. Examination of the animal with the most negative NFIg EBV when DFI was recorded over 4 weeks showed that the animal had lower DFI in the earlier weeks of the feed intake test. DFI in weeks 1 to 4 ranged between 5.32 to 6.11 kg/d and increased to between 10.26 and 10.98 kg/d in weeks 8 to 10. This may be because the animal was ill or took longer than usual to become acclimatised to the feeders. The difference in DFI at 4 and 10 weeks was extreme, across the dataset the difference between DFI at 4 and 10-weeks averaged 0.32 kg/d with a standard deviation of 0.77. Other animals with extreme negative NFIg EBVs consistently had negative NFIg EBVs overall test length periods. Figure 1 plots the NFIg EBVs for sires when the feed intake test period was 4 or 10 weeks and illustrates that although the correlation between EBVs is strong, there are changes in EBV at the distribution edges.

Further research is needed to investigate the impact of reducing the test period in a larger dataset where BREEDPLAN live weights from the whole breed may contribute to the component EBVs used to estimate NFIg EBVs. 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 for ages occurring during the feed intake test. More testing is required to ensure that the proposal to shorten the DFI test period and estimate NFIg EBVs is robust for potential scenarios that could occur in practice. A challenge with NFIg EBVs is that variance components were unavailable, so the present study could not calculate correlated selection responses. Correlated selection response is expected to increase with increased selection intensity but will decrease as the genetic correlation between NFIg EBVs decreases. Reducing the test period potentially allows more animals to be tested. Allowing for a 21-day

acclimatisation period, reducing the DFI test to between 1 and 9 weeks potentially increases the number of animals recorded for DFI by 1.1 to 3.3 times, which may increase the selection intensity. However, as the test period is decreased, the genetic correlation between NFIg from full or reduced DFI tests also decreases, which may reduce the correlated selection response. Therefore, the increase in selection intensity and the decrease in genetic correlation will need to be balanced when determining the ideal test period, which will allow the financial savings of a reduced test but still allow effective NFIg EBVs to be estimated and genetic improvement for feed efficiency.

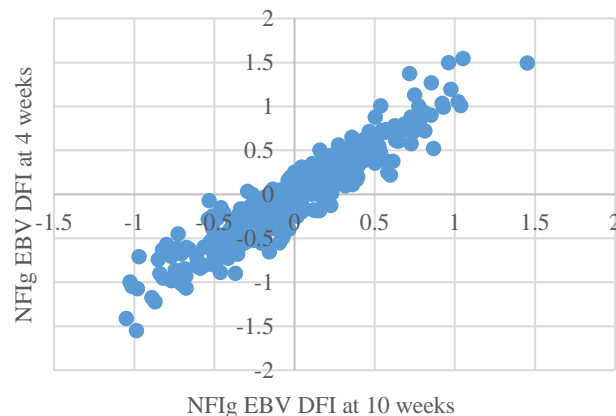


Figure 1. The relationship between NFIg EBVs for sires when daily feed intake (DFI) was recorded from 4 or 10 week feed intake test period

CONCLUSIONS

This study showed that reducing the DFI test period and estimating genetic NFI EBVs with growth and maintenance derived from BREEDPLAN live weights may be possible. Preliminary results are promising, but before implementation, more testing needs to be done and implementation strategies explored.

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REFERENCES

- Archer J.A., Arthur P.F., Herd R.M., Parnell P.F. and Pitchford W.S. (1997) *J.Anim.Sci.* **75**: 2024.
Arthur P.F., Archer A.A., Johnston D. J., Herd R.M., Richardson E.C. and Parnell P.F. (2001) *J. Anim. Sci.* **79**: 2805.
Clark S. and van der Werf J.H.J. (2017) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **22**: 175.
Culbertson M.M., Speidel S.E., Peel R.K., Cockrum R.R., Thomas M.G. and Enns R.M. (2015) *J. Anim. Sci.* **93**: 2482.
Gilmour A.R., Gogel B.J., Cullis B.R., Welham S.J. and Thompson R. (2015) VSN International Ltd, Hemel Hempstead, HP1 1ES, UK.
Kennedy B., Van der Werf J.H.J. and Meuwissen T. (1993) *J. Anim. Sci.* **71**: 3239.
Koch R.M., Swiger L.A., Chambers D. and Gregory K.E. (1963) *J. Anim. Sci.* **22**: 486.
Vargovic L., Moore K., Johnston D., Jeyaruban G., Girard C., Cook J., Torres-Vázquez A. and Miller S. (2023) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **25** These proceedings.