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SELECTING FOR EFFICIENCY IN LONG-FED CATTLE IS IMPORTANT

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SUMMARY

Genetic parameters for 17 traits were obtained from a leading Wagyu nucleus program. Genetic variation (SD) in daily feed intake was 0.58 kg/d, residual feed intake 0.46 kg/d and after adjustment for carcass traits (weight, muscle, subcutaneous and intramuscular fat) was still 0.37 kg/d. Assuming this variation remains through feedlot finishing, this represents large variation in the cost of production so steers from top 1% bulls joined to average cows could cost $146 less to feed than using average bulls. It is most likely this is associated with variation in visceral fat depots.

INTRODUCTION

The largest cost in livestock production systems is feed. Thus, it makes sense that feed intake is an important trait to be measured if aiming to make genetic gain in profitability. In the 1990's there was a large Australian research effort placed on understanding biological mechanisms of growth through intense measurement of Merino lambs from High vs Low growth selection lines (Herd *et al.* 1993; Oddy *et al.* 1995). They found very few differences in partial efficiencies and concluded that differences in growth were driven by differences in appetite.

Koch (1963) introduced the concept of residual feed intake (RFI) representing variation in intake which is net of that associated with animal size and growth rate during the intake test. Robinson and Oddy (2004) and Barwick *et al.* (2009) demonstrated strong relationships between RFI and fatness in separate datasets. Cows from the beef High and Low-RFI selection and High and Low-Fat EBV lines were run on two properties with two stocking rate treatments to evaluate the impact of RFI selection on maternal productivity. Efficiency results were reported by Hebart *et al.* (2018) and variation in fat by Accioly *et al.* (2018). It was clear differences in RFI were associated with fat. Lines *et al.* (2018) quantified protein metabolism on the beef RFI lines and also concluded that differences in RFI were primarily associated with differences in fatness rather than efficiency.

Pitchford *et al.* (2018) published a summary of results from multiple projects that demonstrated more generally that variation in RFI is associated with variation in appetite rather than maintenance efficiency. They concluded that when appetite is not satisfied, then there is unlikely to be variation in RFI and, therefore, efficiency. They questioned the value of selection for low-RFI in many production systems. The obvious exception is for animals on expensive long-fed regimes. The aim of this analysis is to estimate the amount of genetic variation in residual feed intake that is independent of (conditional on) multiple growth and composition measures in long-fed cattle.

MATERIALS AND METHODS

Genetic parameters were supplied from a leading Wagyu nucleus program's within-herd analysis. The 17 traits were birth weight (BWT, kg), weaning weight (WWT, kg), yearling weight (WT400, kg), ultrasound scanned eye muscle area (UEMA, cm^2), rump fat depth (UP8, mm), rib fat depth (URib, mm), intramuscular fat (UIMF, %), post-weaning feed test daily feed intake (DFI, kg/d), growth rate (FTADG, kg/d), metabolic mid weight (MMWT, $kg^{0.75}$), residual feed intake (RFI, kg/d), 600 day weight (WT600, kg), carcass weight (HSCW, kg), AUSMEAT rump fat depth (AP8), marbling score (AMarb) and two traits measured with the Meat Industry Japan camera being digital marbling percentage (DMP, %) and digital muscle area at the 5th rib (DMA5, cm^2). The genetic standard deviations and correlations after bending to ensure positive definite (using nearPD in R, https://github.com/joehl, following Higham 2002) are presented (Table 1).

The method of calculating conditional genetic covariances was:

$$C_{X,Y} = \begin{bmatrix} \Sigma_{11} & \Sigma_{12} \\ \Sigma_{21} & \Sigma_{22} \end{bmatrix}$$

$$C_{Y|X} = \Sigma_{22} - \Sigma_{21}\Sigma_{11}^{-1}\Sigma_{12}$$

where Σ_{11} is the genetic covariance matrix for Y variables, Σ_{22} is the genetic covariance for the X variables, and Σ_{12} is the genetic covariances between growth, composition and intake traits. Matrix calculations to estimate variation in post-weaning residual feed intake being conditional on other traits was conducted three times: 1) pre-weaning growth (BWT, WWT); 2) yearling (WT400, UEMA, UP8, URib, UIMF); and 3) carcass traits (WT600, HSCW, AP8, AMarb, DMP, DMA5). Each time was cumulative so when conditional on carcass traits, genetic variation was evaluated conditional on both 2) yearling and 1) early growth.

Table 1. Genetic variation (SD) and genetic correlations (x100, trait abbreviations in text)

	BWT	WWT	WT400	UEMA	UP8	URib	UIMF	DFI	FTADG	MMWT	RFI	WT600	HSCW	AP8	AMarb	DMP	DMA5
GenSD	2.2	10.4	19.1	2.1	1.2	0.7	0.4	0.6	0.1	4.3	0.5	23	33	2.9	1.0	5.2	4.6
BWT																	
WWT	84																
WT400	84	94															
UEMA	53	73	70														
UP8	-29	-10	-11	14													
URib	-26	-9	-5	17	83												
UIMF	-10	-1	-10	7	43	36											
DFI	38	48	61	50	4	17	1										
FTADG	59	59	65	70	10	19	13	74									
MMWT	79	96	86	67	-10	-8	5	47	61								
RFI	-15	-18	-14	-4	13	13	11	29	6	-21							
WT600	85	94	99	70	-12	-7	-9	60	65	84	-10						
HSCW	67	67	79	49	-10	0	-7	71	73	62	7	82					
AP8	-10	1	8	13	70	50	10	11	6	-3	16	9	26				
AMarb	-21	-7	1	-3	6	13	32	20	3	0	10	-1	9	-5			
DMP	-22	-10	-11	-9	9	11	43	2	3	-2	4	-12	-1	-13	90		
DMA5	18	23	25	44	-11	-15	6	29	33	24	8	27	32	-2	32	21	

RESULTS AND DISCUSSION

Standard practice in Australia for genetic evaluation of feed efficiency is to conduct a feed test post-weaning and this is becoming increasingly common on commercial properties. During the post-weaning test, the average dry matter intake (DFI) was 7.16 kg/d with a genetic SD of 0.58 kg/d (Table 2). Residual feed intake (RFI) is calculated by regressing feed intake on feed test growth rate (FTADG) and animal size as metabolic mid-weight (MMWT) which is average of start and end test weight raised to power of 0.75. Thus, by definition, there is less variation in RFI (SD 0.46 kg/d) than DFI.

Regressing feed efficiency test traits on birth and weaning weight accounted for 92% of the variation in MMWT but only 38% of the variation in FTADG (Table 2). As RFI is already adjusted for weight it was not surprising that only 3% of the variation was associated with pre-weaning growth. Regressing on yearling growth, muscling, fatness and marbling accounted for an additional 30% of variation in DFI but only 5% of variation in RFI. Regressing on WT600 and carcass traits accounted for 29% of the variation in RFI. Thus, there is both significant variation accounted for (37%) and variation remaining (63%).

Pitchford *et al.* (2018) proposed that measuring RFI in seedstock herds with clients producing grass-fed or short-fed steers was unlikely to be profitable because of the relationship between RFI and appetite leading to increased fatness. However, for long-fed steers where both the cost of feed and fat levels are high it is possibly worthwhile. Even after adjustment for two measures (live ultrasound and carcass) of muscle, sub-cutaneous fat and intramuscular fat, 63% of the variation in RFI remained.

The genetic SD of RFI conditional on growth and carcass traits was 0.37 kg/d (Table 2) for animals with a mean intake of 7.16 kg/d, representing a CV of 5.2% (0.37/7.16). High Content (Purebred & Fullblood) Wagyu are typically fed for 450 days at 12kg as fed (72% DM) costing $450/tonne which equates to $2,430 per head. If the genetic variation in RFI remains from post-weaning to throughout the long finishing period, then 5.2% would represent a genetic SD of $126. With this much variation, the top 1% of bulls would have breeding values $292 above average and steers from breed average cows sired by these bulls would have $146 lower feed costs with the same carcass value.

At 12 MJ ME/kg DM, the total energy intake during finishing would be 46,656 MJ (i.e. 450 days x 12 kg as fed x 72% DM x 12 MJ ME/kg DM) and the genetic SD would be 2,426 MJ (i.e. 5.2%). Oddy *et al.* (2024) reported that 70-80% of metabolisable energy intake above maintenance is lost as heat. Thus, of the 2,426 MJ, there may be just 25% or 606 MJ retained. The null hypothesis implied by Pitchford *et al.* (2018) was that the variation in RFI remaining after adjustment for growth and carcass fatness would primarily be associated with other fat depots.

Table 2. Genetic variation (SD and proportion of variance) in feed test traits conditional on other traits

Scenario	DFI	FTADG	MMWT	RFI
Base	0.58, 100%	0.12, 100%	4.3, 100%	0.46, 100%
1) Pre-weaning	0.51, 77%	0.10, 62%	1.2, 8%	0.45, 97%
2) Yearling	0.40, 47%	0.07, 34%	1.1, 6%	0.44, 92%
3) Carcass	0.27, 22%	0.02, 4%	0.3, 0.4%	0.37, 63%

Yamada *et al.* (2020) reported that the phenotypic SD in visceral fat in Wagyu steers was 8 kg. Given that fat contains 39.3 MJ/kg and has an efficiency of conversion of approximately 70%, 8kg would cost approximately 450 MJ (8 x 39.3 / 0.7) to deposit. This 450 MJ represents 74% of the 606

MJ retained based on the calculations herein. Thus, variation in fat deposition does account for the majority of the residual variation in RFI in Wagyu cattle.

The remaining 26% could be explained by four primary reasons: 1) variation in residual feed intake throughout feeding is greater than on feed test; 2) Yamada's (2020) cattle being fed for less time (not stated in paper) resulting in less variation in fat; 3) other biological mechanisms such as variation in visceral weight which is associated with intake, movement, digestibility and energy lost as methane; and 4) simply variation in the genetic covariances between traits which all have significant standard errors despite being diligently recorded on 2,459 animals.

CONCLUSION

This paper has affirmed the value of measuring RFI in Wagyu herds by demonstrating significant variation independent of carcass value. As expected, it is likely that the bulk of this variation is associated with variation in body fat. Given this is mostly visceral fat, it can be considered a waste which selection for low-RFI would minimise.

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