Review of potential investment into recording feed efficiency in beef cattle

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Summary

1. Feed efficiency is considered in this review as net or residual feed intake, i.e., the feed intake occurring over and above that required for live weight and gain. While for most purposes the terms ‘net feed intake’ and ‘residual feed intake’ are synonymous, for convenience we use ‘net feed intake’ to refer to seedstock traits that are recorded post-weaning (NFI-P) or in the feedlot (NFI-F), and ‘residual feed intake’ (RFI) when referring to traits of the breeding objective.
2. Literature estimates of the heritability of NFI-P and NFI_F are consistently moderate in the range 0.2 to 0.4. However the number of records available in Australia for genetic parameter estimation is extremely low compared to other traits with less than 5000 records for NFI-P or NFI-F available when pooled across all breeds. Estimates of the genetic correlations between measures of NFI and fatness are generally positive but the sizes of the correlations differ depending on the measurement ages of the fatness and NFI traits.
3. Currently in BREEDPLAN there are trial EBVs for NFI-P and NFI-F in some breeds but little ongoing industry recording upon which to base the EBVs. $Indexes in use account for the feed that is needed for live weight and gain but do not account for residual feed intake. Inadequate data for estimating genetic relationships between residual feed traits and other recorded traits has so far prevented residual feed intake traits being included in breeding objectives.
4. Predictions of selection response are needed for a number of the review’s terms of reference. All available information on trait variances and relationships was assembled to enable those predictions. The available information is quite limited and was sometimes ‘best bet’; there is little information, for example, for residual feed intake as a trait of the cow. Knowledge was not considered sufficient to be able to model breed-specific relationships.
5. Selection on fatness records alone (i.e., scan rib and rump fat depths of bulls and heifers) is predicted would reduce NFI-P and NFI-F by 0.36 and 0.28 kg/d respectively over 10 years. This is respectively 44 % and 24 % of the reduction that would be possible from selection on an own NFI-P or NFI-F record. Any correlated effects on residual feed intake of the cow are uncertain. From the point of view of NFI-P and NFI-F, if an own NFI-P or NFI-F record were available there would be little additional benefit from having scan fat records available.
6. The overall impact of being able to include feed efficiency in selection is best gauged from the predicted increase in $ response (i.e., response in the whole breeding objective) that is possible when residual feed intake traits can be included in the breeding objective and when an own NFI-P or NFI-F record is also able to be available on selection candidates. This increase, over that currently occurring, is 45% to 60% for a long fed production system and 34% for a self-replacing grass fed system. The increase is less (9%) for a terminal grass fed system.
7. The current predictions suggest 50% or more of the increased $ response to selection is likely to come from being able to include residual feed intake traits in the breeding objective. Some of this would come from reversing unfavourable correlated changes that are occurring in RFI-P and RFI-F, for example in long fed production. It suggests there would be major benefits from investing in new NFI data to derive the needed genetic parameters, including relationships with other

traits. These benefits would be expected even without the ready availability of an industry feed efficiency measure. Investing in new data could both yield these benefits and simultaneously provide the basis for developing and testing an industry measure.

8. Cost of measuring individual feed intake is the main reason for the present lack of recording. It also follows that there is presently no sufficiently effective and suitably inexpensive indirect measure of feed efficiency that can be recorded across the industry.
9. Some commercial signals for improving feed efficiency exist at a number of levels. Despite there being not enough information available on seedstock for there to be a price incentive for producing more feed efficient seedstock, some breeders (Angus and Hereford breeders particularly) have shown a preparedness to pay for measurement at least to the price previously charged for IGF-I. The importance of feed efficiency is generally recognised in the feedlot sector. Also, the strong association of store price with feed availability is an indicator of the value placed on feed right across the industry.
10. The size of the associated standard error is a usual basis for deciding the number of animals and records needed to have confidence in an estimated genetic correlation. For calibrating a DNA test, it indicates about 1500 effective animal records (from 100 sires) are required if the genetic correlation of feed efficiency with the test is about 0.30. If it is 0.20, about 5000 records (from 330 sires) would be required. Having records available for calibration will be important for future industry uses of DNA markers.
11. The biggest current constraint to the development of DNA marker assisted selection for improving NFI is the lack of phenotypes available for marker discovery, particularly at the individual breed level. There are very few sires, anywhere in the world, that are accurately evaluated for NFI. The discovery of informative SNP and the development of suitable prediction equations will require the collection of large numbers of additional phenotypes.
12. Early research has indicated that selection to reduce NFI would favourably reduce methane production. Although the bulk of the improvement is likely to be associated with reduced feed intake rather than with a strong relationship between efficiency and methane production, selection to reduce NFI does offer the future beef industry an indirect means of reducing carbon emissions.
13. The options where infrastructure support might be provided to assist recording of feed efficiency include the research feedlot at Tullimba, commercial feedlots, and pasture intake recording by breeders. There are feasibility issues with both commercial feedlot and pasture intake recording by breeders. The research feedlot at Tullimba requires upgrading if it is to be used either for needed research or for industry testing.

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Terms of reference for proposed review

The review is intended to provide clarity about the options facing industry (including MLA) and to determine the economic value, to bull buyers, to individual breeders and to the industry, of further investment in R&D or extension to stimulate use of feed efficiency EBVs in their selection decisions.
The review will summarise:

- the feed efficiency traits that have been defined in research and in BREEDPLAN
- numbers of records by breed for feed efficiency
- genetic parameters for feed efficiency traits, and genetic correlations with other traits, including those for body composition and reproduction
- knowledge on the relationship of NFI feed lot and cow-calf efficiency on pasture
- potential for genetic improvement of feed efficiency (both itself, and of $Indexes of which it is a component) under the following scenarios:
    - all candidates have a record for the appropriate feed efficiency trait
    - animals in a nucleus have a record for the appropriate feed efficiency trait, but no other animals in the remainder of the population
    - as above, but with recording of body composition traits
- likely correlated responses in feed efficiency to current selection regimes for self-replacing British breeds, terminal sire breeds, and tropical breeds (which essentially establishes the baseline for the cost to industry of doing nothing, and a basis for estimating industry return on investment to date)
- reasons why recording of feed efficiency has not reached higher levels, despite predicted economically favourable impacts
- economic importance of feed efficiency in breed $Indexes – currently, and if appropriate, as would be recommended to industry by AGBU
- evidence for any commercial signals for feed efficiency either from the feedlot sector or anywhere
- numbers of animals/records required to calibrate hormonal and/or DNA marker tests to a specified level of accuracy
- the options for providing recording infrastructure for feed efficiency
    - a) by upgrading Tullimba
    - b) utilising commercial feedlots, including estimated cost in each case or
    - c) by developing on-farm systems for recording feed intake at pasture and weight change

1. Definition of feed efficiency in BREEDPLAN and number of records

Feed efficiency in BREEDPLAN is currently addressed at different ages of the animal not un-similar to weight. It is calculated as ‘net feed intake’ (NFI), also termed residual feed intake (RFI) by equating feed intake against metabolic mid weight and weight gain during a 70 day feed intake test. In broad terms NFI is the difference in feed intake from that which would be required for the animal’s weight and gain.

NFI is measured either post weaning, in young bulls and heifers, fed at around 300 days of age a 10MJ/kg DM ration (NFI-P), or in steers, fed at around 560 days of age a 12 MJ/kg DM ration (NFI-F).

The Australian data that is currently available is summarised in Table 1.

Table 1. Number of records by breed for feed efficiency traits NFI-P (kg/d), NFI-F (kg/d) and IGF-I recorded in BREEDPLAN and CRC databases

			Trait		Age (d)	
Breed	Trait	No. Records	Mean	SD	Mean	SD
BREEDPLAN						
Angus	NFI-P	2871	0.20	1.08	300.3	51.8
	NFI-F	1312	-0.98	2.31	535.5	88.0
	IGF-I	15188	37.38	19.80	206.1	26.8
Hereford	NFI-P	407	0.19	0.99	302.6	57.7
	NFI-F	282	-0.34	1.54	545.7	82.1
	IGF-I	4595	28.70	15.79	204.6	27.4
Shorthorn	NFI-P	67	0.84	1.13		
	NFI-F	554	-0.81	1.41	465.1	92.8
	IGF-I	346	29.09	12.96	220.3	20.5
CRC 1						
Crossbreds	NFI-F	528	0.00	1.20	593.30	48.0
Temperate breeds	NFI-F	785	0.01	1.19		
Tropical breeds	NFI-F	687	0.00	1.01		
CRC 2						
Brahman	NFI-F	680	-0.18	1.06	732.8	119.6
	IGF-I	953	51.03	18.34	662.2	124.2
Composite	NFI-F	783	0.15	1.17	736.8	125.2
	IGF-I	1105	50.45	17.47	662.5	129.3

Note: Some data from CRC 1 is counted in the BREEDPLAN data for Angus, Hereford and Shorthorn; these records have been transferred to the relevant BREEDPLAN database.

Residual feed intake traits are currently not included in breeding objectives derived for $Indexes. However the feed needed for the weight and gain of animals is included, as it is costed against the improvement of other traits. One of these other traits, for example, is the mature weight of cows. Commonly the economic weight for mature cow weight is negative, reflecting the increased feed requirement for maintenance of heavier cows.

Although ‘net feed intake’ and ‘residual feed intake’ are synonymous terms, in this review for convenience in making the distinction we use the former (NFI-P and NFI-F) when referring to records about seedstock, and the latter (RFI) when referring to the associated commercial herd traits that are a needed part of the breeding objective.

2. Genetic parameters for NFI and associations with other traits

Estimates of genetic parameters for NFI are accumulated in tables A1-A12 in Appendix 1. Some key results have been extracted and are discussed below. Heritability estimates for NFI-P and NFI-F are presented in Table 2.

Table 2: Heritability estimates for NFI-P and NFI-F. Standard errors in parentheses.

Breed	Trait	σ_a^2	h^2
Angus BREEDPLAN	NFI-P	0.23	0.41 (0.05)
Angus BREEDPLAN	**NFI-F**	0.53	0.35 (0.09)
Shorthorn BREEDPLAN	**NFI-F**	0.24	0.34 (0.14)
Angus Trangie	NFI-P	0.15	0.39 (0.03)
Mixed breeds CRC-1	**NFI-F**	0.14	0.18 (0.06)
Brahman CRC-2	**NFI-F**	0.19	0.24 (0.11)
Tropical Composite CRC-2	**NFI-F**	0.41	0.38 (0.12)
Bonsmara South Africa	NFI-P		0.31
Japanese Black	NFI-P	0.23	0.25
Hybrids (Canada)	**NFI-F**	0.40	0.21 (0.12)

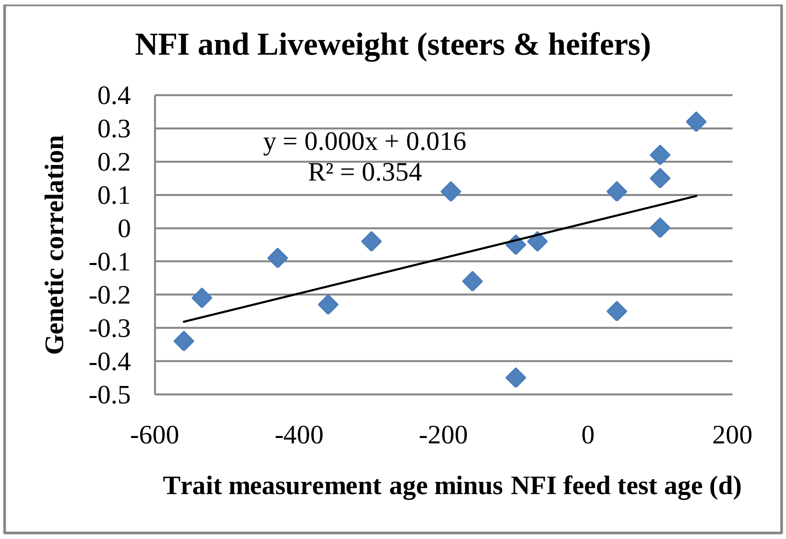
Heritability measured either in growing or finishing animals is consistently moderate with values between 0.2 and 0.5. Similar to body weight the additive genetic variance (σ_a^2) for heavier finishing cattle tends to be larger than that post weaning. The variance for NFI in mature cows might be expected to be larger again. We have only one estimate of the genetic correlation between NFI-P and NFI-F which is 0.67 (0.14) (Jeyaruban et al. 2009). It suggests different EBVs are required for NFI-P and NFI-F, and it is likely that a different EBV would also be required for the trait in cows.

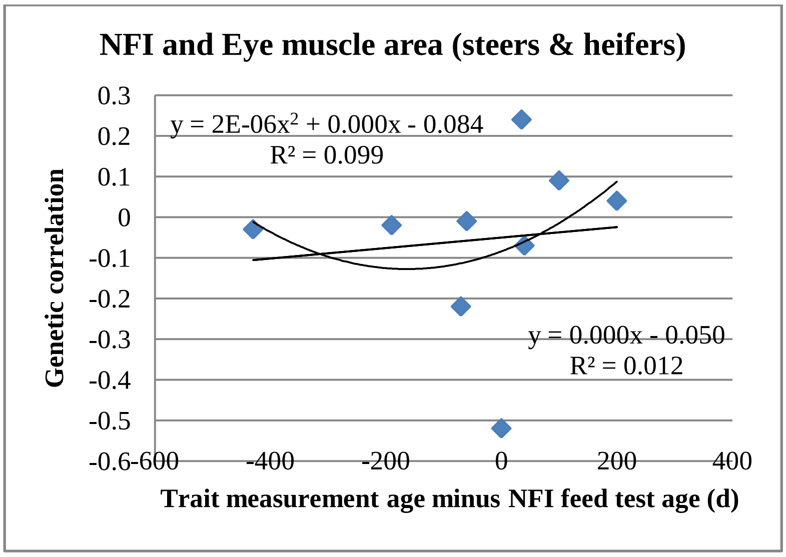
Genetic correlation between NFI and scan fat traits.

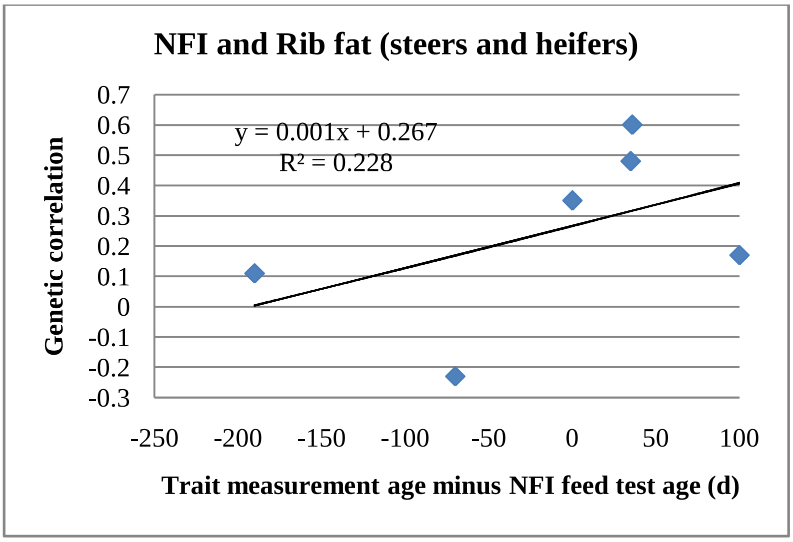
NFI as calculated does not adjust for body composition. As lean growth requires less energy than “fat growth”, reduced fat deposition is expected to contribute to lowering NFI. Tables A10 and A11 present genetic correlations between NFI-P and NFI-F, respectively, and other traits. While the correlations between NFI-P and fat traits are generally lowly positive, as expected, the direction of the correlations is much less clear for NFI-F. All estimates, however, have large standard errors.

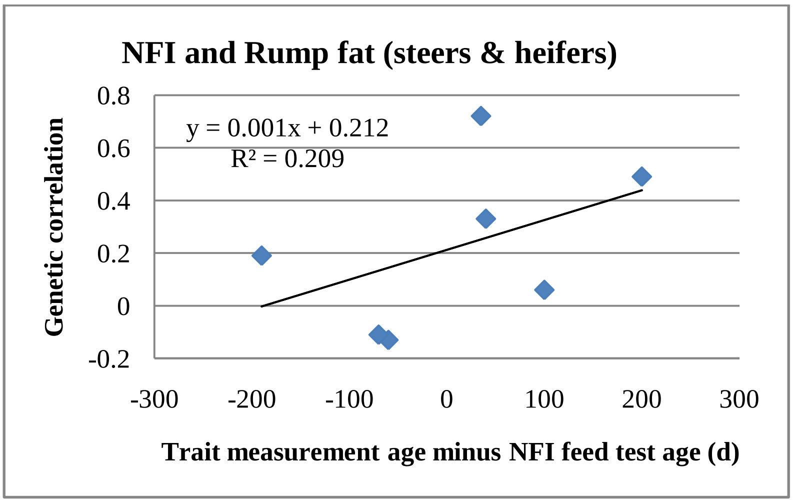
The analyses of CRC-1 data by Robinson and Oddy (2004) highlighted the potential of fatness to be an indirect measure for NFI. A strong positive genetic correlation with NFI-F was observed in that study for fatness measured at feedlot exit. Such strong genetic correlations however have not always been observed, especially when the fatness measurement is at an earlier age.

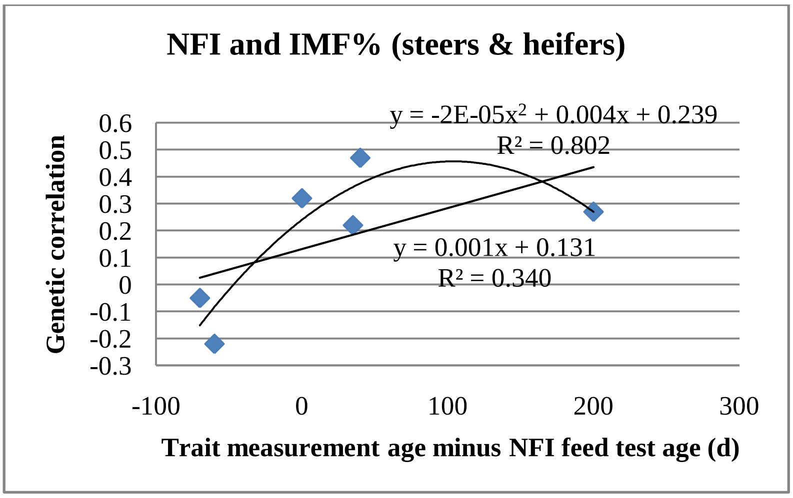
A recent analysis looked at the association, across studies, between the genetic correlation between fatness and NFI and when the fat measurement was taken. When the measurement was taken was assessed in relation to the NFI feed test. This was also done for liveweight and eye muscle area. Plots of these associations are shown below. Each dot shown represents a genetic correlation estimate. The plots include studies across both NFI-P and NFI-F.






NFI and Rib fat (steers and heifers)
y = 0.001x + 0.267
R² = 0.228
Genetic correlation
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
-0.2
-0.3
-250
-200
-150
-100
-50
0
50
100
Trait measurement age minus NFI feed test age (d)


NFI and Rump fat (steers & heifers)
y = 0.001x + 0.212
R² = 0.209
Genetic correlation
0.8
0.6
0.4
0.2
0
-0.2
-300
-200
-100
0
100
200
300
Trait measurement age minus NFI feed test age (d)


NFI and IMF% (steers & heifers)
y = -2E-05x² + 0.004x + 0.239
R² = 0.802
y = 0.001x + 0.131
R² = 0.340
Genetic correlation
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
-0.2
-0.3
-100
0
100
200
300
Trait measurement age minus NFI feed test age (d)

There was evidence of an association, usually small, for liveweight and fat measures, but no association for eye muscle area. Measures taken after the NFI feed test tended to be genetically more positively correlated with NFI than measures taken before the test. If the measures themselves reflect energy store levels, the genetic capacity to have a greater energy store appears to be favourably (negative genetic correlation) associated with subsequently-assessed NFI, but unfavourably (positive genetic correlation) associated with previously-assessed NFI.

3. Knowledge on the relationship between NFI and cow-calf efficiency on pasture

The difficulty of accurately measuring feed intake in beef cattle managed under pasture conditions has meant very little research has been conducted on feed efficiency at pasture. Studies exploiting the relationship between feed intake and alkane faecal concentration in treated animals at pasture have been limited by the inaccuracy of the method (Olivan et al. 2007) and not carried out on a large scale. Herd et al. (2004) applied this method to examine the relationship between Angus steer pasture intake and the NFI EBVs of their sires. While acknowledging the inaccuracies of the method, the study concluded that selecting for reduced NFI would produce steer progeny which grow more quickly under pasture conditions, and which would be more feed efficient.

Archer et al. (2002) conducted an experiment which measured NFI in female cattle as weaners, and again as cows after weaning their second calf. The study concluded that there was a strong genetic relationship between intake and efficiency traits in weaners and mature cows, and that selection to improve efficiency based on NFI tests conducted in weaners would have a positive effect on lifetime feed efficiency. The ration used for the NFI tests in the study was the same for animals at both stages of maturity, so the results may only be an indication of that expected for mature cows in a pasture environment.

Meyer et al. (2008) contrasted the feed efficiency of 54 Hereford female cattle that were NFI tested prior to joining or in early pregnancy, as well as at pasture in late pregnancy and with calves at foot. Low numbers for the experiment and inherent inaccuracies associated with the pasture feed intake estimation technique used meant no results were significant. There was a trend for females that were more efficient under initial NFI test conditions to also eat less when tested at pasture, and to grow less quickly.

Arthur et al. (2005) contrasted the maternal productivity of Angus females of high and low NFI after 1.5 generations of divergent selection for NFI. There were no significant differences in maternal productivity traits between the NFI lines. The closest to a significant result reported from the experiment was days to calving, with low NFI animals calving 5 days later than those in the high NFI line ($P = 0.07$).

Basarab et al. (2007) showed cow NFI was phenotypically related to the NFI of their progeny, though assessment of cow NFI was with the same ration and under the same conditions (~ feedlot) as for progeny measurements. Consistent with the trend observed by Arthur et al. (2005) there was a tendency for more efficient cows to show signs of being less fertile, producing fewer twins and calving later than the dams of less efficient progeny.

The results from these studies suggest selection to improve NFI based on a feed test early in life is likely to improve efficiency later in life under pasture conditions. This may come at the cost of lower feed intake at pasture, and a corresponding reduction in growth rate. More efficient females may tend to be less fertile, producing fewer twins and calving later.

There is work also underway in a Beef CRC study in South Australia and W.A. to compare high and low NFI cows at pasture. Early results show there are differences in fatness but at this stage no difference in conception rates, though numbers are small.

4. The relationship between feedlot tested NFI and methane production

The examination of the relationship between methane production and feed efficiency in beef cattle is still at an early stage. Work has been primarily motivated by pressure on the beef industry to reduce greenhouse gas emissions. Arthur et al. (2009) reviewed various ways to reduce emissions, one of these being through improvement of NFI. They cite theoretical work which predicts a 15-21% difference in direct methane emission between high and low NFI animals, with a 15% difference in methane from manure and a 17% reduction in nitrous oxide. It was not clear how large the NFI differences needed to be for these reductions to occur.

Hegarty et al. (2007) reported that NFI EBVs and daily feed intake (DFI) were significantly associated with methane production in Angus steers from lines divergently selected for feed efficiency. The steer NFI EBVs were estimated as mid parent values. It was found that genetically more efficient animals (P = 0.002) and animals which ate less (P = 0.01) were both expected to produce less methane. The study concluded that selection to reduce NFI would decrease methane production without compromising productivity, though it was observed that this is largely driven by high efficiency animals having a lower feed intake.

Nkrumah et al. (2006) examined methane production in 27 British breed x European cross steers which were selected from 306 animals to represent extremes of NFI. Results showed low NFI animals produced less methane (P = 0.04), which was proposed as being a result of digesting feed more thoroughly. The study concluded that differences in methane production and digestibility of feed were related to NFI.

Alford *et al.* (2006) modelled the effect of selection for improved NFI on methane production from the Australian beef herd over a 25 year period, with 2002 levels set as the base. Results indicated a herd that conformed to the initial assumptions would decrease methane production by 15.9% over the 25 year period. With less than total adoption a methane reduction of 3.1% was predicted for the entire Australian beef herd.

In summary, the few papers published to date suggest selection to reduce NFI would favourably reduce methane production, though the bulk of the improvement is likely to be associated with reduced feed intake rather than with a strong relationship between efficiency and methane production.

5. Potential for genetic improvement of feed efficiency under differing availabilities of NFI and body composition records

For simplicity, predictions of selection response in this and subsequent sections assume a generation interval of 5 years, a standardised selection intensity of 1.40 (20% selected), and no change in genetic variance with selection. Predictions were made with the assistance of the MTIndex spreadsheet; we are grateful to Julius van der Werf for making that spreadsheet software available.

i) NFI records available on candidates or relatives

The potential for genetic change in NFI-P and NFI-F from selection on records for either trait is shown in Table 3. A likely range is also shown for the associated correlated change based on varying the level of genetic correlation assumed between NFI-P and NFI-F. A very substantial reduction in feed intake, for the same weight and gain of the animal, is possible in both traits where selection can be based on an own record on all candidates. In 10 years reductions of more than 0.8 kg feed/day are possible in NFI-P from selection on NFI-P, with a similar correlated gain expected in NFI-F.

Direct selection on NFI-F would change NFI-F more than NFI-P but an own record for NFI-F would not usually be available in seedstock. Records on NFI-F for 6 progeny would allow selection of equivalent accuracy to that for an own record, but at some cost in increased generation interval.

The expected gains in each trait are halved when a record on only the sire is available.

Table 3. Predicted 10 year direct and correlated response[1] (and likely range) in post-weaning net feed intake (NFI-P) and feedlot net feed intake (NFI-F) from single trait selection on an own record[2] or a sire record[3] for either NFI trait

	Selection on NFI-P		Selection on NFI-F	
Records available	Response in NFI-P (kg/d)	Response in NFI-F (kg/d)	Response in NFI-P (kg/d)	Response in NFI-F (kg/d)
Own record	-0.81	-0.81	-0.50	-1.18
		(-0.73 to -1.09)	(-0.45 to -0.67)	
Sire record	-0.39	-0.39	-0.25	-0.59
		(-0.36 to -0.53)	(-0.22 to -0.34)	

[1] Genetic correlation of 0.65 (range 0.58 to 0.88) assumed between NFI-P and NFI-F

[2] Accuracy of selection 0.62 for NFI-P, 0.59 for NFI-F

[3] Accuracy of selection 0.31 for NFI-P, 0.30 for NFI-F

ii) Scanned rib and rump fat depth records available on candidates

The genetic change in NFI-P and NFI-F that would be expected under indirect selection to reduce fatness is shown in Table 4. These predictions assume an own record available for each of P8 and rib fat depths in both bulls and heifers. These records on seedstock are those that can be taken with ultrasound scanning. A likely range is also shown for each result based on differing levels of assumed genetic correlation between fat depth measurements and NFI-P and NFI-F.

While the ranges of genetic correlation considered are those that are thought likely, it should be noted that estimates of the genetic correlation of fat depth with NFI are usually within two standard errors of zero, meaning there is also a chance that indirect selection on fat depth records would not reduce NFI-P and NFI-F at all.

From the estimates in Tables 3 and 4, selection on an Index of fat depth records to reduce NFI-P might be expected to be about 44% as effective as selection on an own NFI-P record. The predicted correlated change in NFI-F was 34% of that for selection on an own NFI-P record. Selection on an Index of fat depth records to reduce NFI-F is predicted to be 24% as effective as selection on an own NFI-F record. The correlated change in NFI-P would be 72% of that for selection on an own NFI-F record.

Table 4. Predicted 10 year response[1] (and likely range) in post-weaning net feed intake (NFI-P) and feedlot net feed intake (NFI-F) from single trait selection for either NFI-P or NFI-F based on an Index of scanned rib and rump fat depth records[2]

Records available	Selection objective NFI-P		Selection objective NFI-F	
	Response in NFI-P (kg/d)	Response in NFI-F (kg/d)	Response in NFI-P (kg/d)	Response in NFI-F (kg/d)
Scanned rib & rump fat depths on both bulls & heifers (own records)	-0.36	-0.28	-0.36	-0.28
	(-0.17 to -0.53)	(-0.14 to -0.42)	(-0.17 to -0.53)	(-0.14 to -0.42)

[1] Genetic correlations assumed for fat depths: 0.40 (range 0.20 to 0.60) with NFI-P, 0.20 (range 0.10 to 0.30) with NFI-F

[2] Accuracy of selection: 0.28 (range 0.14 to 0.42) for NFI-P, 0.14 (range 0.07 to 0.21) for NFI-F

iii) NFI and scanned fat depth records jointly available

The genetic change in NFI-P and NFI-F expected for selection using both NFI and scanned fat depth records is shown in Table 5. Comparison of the results for direct selection from Tables 3 and 5 suggests having fat depth records available would add little to the effectiveness of selection to reduce NFI-P when an own NFI-P record is available. It would improve the effectiveness of selection when it is only an NFI-P record on the sire that is available.

In selection to reduce NFI-F there would be a small advantage to having fat depth records over and above an NFI-F record, whether this is an own record or a record only on the sire.

6. Potential for genetic improvement of overall $ merit under differing availabilities of NFI records

Despite the benefits from reducing production system feed costs, there is uncertainty in the literature as to whether, on balance, residual feed intake should be decreased or increased. Some of this comes from residual feed intake being seen as just one trait, which is clearly not the case, and some of it comes from intensive livestock species where there is a perceived need for feed intake to increase to sustain very high production levels. There is also the general concern, evident in reports by Rauw and others, that reducing residual feed intake could deleteriously affect the capacity of animals to cope with fluctuating environments.

Table 5. Predicted 10 year response[1] (and likely range) in post-weaning net feed intake (NFI-P) and feedlot net feed intake (NFI-F) from selection for either NFI-P or NFI-F based on an Index of NFI-P[2] or NFI-F[3] records jointly with fat depth records

	Selection objective NFI-P		Selection objective NFI-F	
Records available	Response in NFI-P (kg/d)	Response in NFI-F (kg/d)	Response in NFI-P (kg/d)	Response in NFI-F (kg/d)
Scanned fat depths: + own NFI-P	-0.84	-0.81	-0.81	-0.81
	(-0.81 to -0.90)	(-0.81 to -0.84)	(-0.81 to -0.87)	(-0.81 to -0.84)
+ sire NFI-P	-0.53	-0.48	-0.50	-0.48
	(-0.45 to -0.64)	(-0.42 to -0.53)	(-0.45 to -0.64)	(-0.42 to -0.53)
Scanned fat depths: + own NFI-F	-0.67	-1.24	-0.64	-1.32
	(-0.59 to -0.81)	(-1.24 to -1.26)	(-0.56 to -0.73)	(-1.29 to -1.37)
+ sire NFI-F	-0.42	-0.54	-0.36	-0.64
	(-0.31 to -0.59)	(-0.54 to -0.59)	(-0.28 to -0.50)	(-0.59 to -0.70)

[1] Genetic correlations assumed for fat depths: 0.40 (range 0.20 to 0.60) with NFI-P, 0.20 (range 0.10 to 0.30) with NFI-F

[2] Accuracy of selection: with own records 0.64 (range 0.63 to 0.68) for NFI-P, 0.41 (range 0.41 to 0.42) for NFI-F; with sire records 0.40 (range 0.34 to 0.49) for NFI-P, 0.24 (range 0.21 to 0.27) for NFI-F

[3] Accuracy of selection: with own records 0.52 (range 0.45 to 0.62) for NFI-P, 0.67 (range 0.65 to 0.69) for NFI-F; with sire records 0.33 (range 0.24 to 0.45) for NFI-P, 0.32 (range 0.30 to 0.35) for NFI-F

It should be clear from the above that the net benefit or otherwise of reducing residual feed intake can only really be assessed for the whole breeding objective, i.e., in the context of overall $ merit. The completely-defined breeding objective should account for all of the genetic variation existing for feed intake, as feed is a principal cost component in all production systems. Complete account of feed cost in breeding objectives is rare or non-existent, certainly in grazed animal species, anywhere in the world. In BreedObject, the feed required for the weight and gain of animals (and for gestation and lactation in cows) is costed against the value of improvement in other traits. The remaining (residual) feed intake variation is presently not included. The residual feed intake traits that need to be included in the breeding objective are those applying post-weaning to young animals at pasture (RFI-P), in the feedlot (RFI-F), and in cows (RFI-C).

Two levels of incorporation of residual feed traits in selection were modelled here. The first involved the incorporation of residual feed traits RFI-P, RFI-F, and RFI-C in the breeding objective. The interest was in the effect adding the residual feed traits to the breeding objective has on the predicted response to selection when the Index being considered was derived for the breeding objective without residual feed traits (ie., as currently occurs for industry). The records assumed available to the Index were those which are commonly available to BREEDPLAN.

The second level of incorporation of residual feed traits involved modelling the predicted response to selection for an $Index constructed with or without NFI-P and NFI-F records being available in addition to the commonly available records. The $Index in each case here was derived for breeding objectives with residual feed traits included.

Genetic relationships

Information on the required genetic and phenotypic relationships was assembled to enable the effects of incorporation of residual feed intake in selection to be considered. This built on earlier efforts made for other AGBU-influenced modelling (Kahi et al. 2003; Archer et al. 2004). The present estimates utilised information on Angus, supplemented with literature estimates from a range of studies across other British, European and tropical breeds. The information available was in some cases quite limited and necessitated the use of ‘best bet’ estimates. There is little information available, for example, for RFI-C. Because of this shortage of information for genetic parameter estimates it was considered not sensible to attempt to develop more than one version of the assumed genetic parameters. Matrices of parameters specific to Brahmans, and to tropical composites, may be able to be developed on completion of the Beef CRC study of these genotypes. Note that it should be considered likely that some breeds will differ in their use of feed and in the genetic relationships that underlie that. This might be expected from the evolution of breeds in differing environments and, in some cases, from their being initially bred for different purposes.

Breeding objective cases

The modelling undertaken aimed to provide an appreciation of what might be expected for residual feed intake in a range of situations. Three breeding objectives were considered, covering self-replacing and terminal production and grass or long fed feedlot finishing. With respect to the residual feed intake traits, the terminal system breeding objective implicated RFI-P; the self-replacing grass finished system implicated both RFI-P and RFI-C; and the self-replacing long fed system implicated all of RFI-P, RFI-F, and RFI-C.

Results

Table 6 shows the responses predicted for selection on Indexes derived for breeding objectives that did not include residual feed traits (the current situation in industry). The responses are shown first for the breeding objective for which the Indexes were derived; and associated with this, what correlated responses in NFI-P and NFI-F would be expected for selection on those Indexes. Responses are then also shown for the corresponding breeding objective with residual feed traits included. In the long fed case, unfavourable changes are currently occurring in the residual feed traits, especially where measured post-weaning, when the residual feed traits are not in the breeding objective.

The performance of Indexes for the grass fed breeding objectives is much less affected by whether or not the residual feed traits are part of the breeding objective (Table 6). In both the terminal and self-replacing cases, the Index constructed for the objective without residual traits still leads to some favourable correlated responses in NFI-P and NFI-F. Note that since there is no feedlot phase in these cases, there is no value associated with a correlated change in feedlot residual feed intake.

Including residual feed traits in the breeding objective resulted in an increased variance of the breeding objective for all of the cases in Table 6.

Table 6. Predicted 10 year response in 3 example breeding objectives, defined without and with residual feed traits, for selection on an Index of commonly available records[1] *that was derived for the breeding objective without residual traits*. Correlated responses in post-weaning net feed intake (NFI-P) and feedlot net feed intake (NFI-F) are also shown.

Characteristic	Breeding objective		
	Terminal Grass fed	Self-replacing Grass fed	Long fed Export (Self-repl)
Response in the breeding objective defined without residual feed traits ($/cow)	38.11	32.31	40.52
Index accuracy	0.48	0.38	0.40
correlated responses:			
NFIp (kg/d)	-0.08	-0.03	+0.22
NFIf (kg/d)	-0.25	-0.03	+0.01
Response in the breeding objective defined with residual feed traits ($/cow)	39.90	32.31	34.38
Index accuracy	0.46	0.32	0.28

[1] Commonly available records: an own record, sire and dam record (where relevant), and 25 half-sib records for 17 measures commonly recorded in BREEDPLAN

Table 7 shows the predicted response to selection for Indexes constructed with and without the availability of NFI-P or NFI-F records, assuming here that the residual feed intake traits (RFI-P, RFI-F, and RFI-C) are included in the breeding objective. Compared with selection using commonly available measures, response in the long fed case is increased by up to 19% (with an own record for NFI-P) when an NFI record is available. The increase in response is less (up to 12%, with an own NFI-P record) for the grass-fed self-replacing case, and is least (up to 5%) for the terminal case.

Of most importance is the predicted total effect on response that occurs from being able to incorporate residual feed intake in selection. The current industry position on predicted response, for breeding objectives with the residual feed traits included, is shown in the bottom section of Table 6. Comparing this with that applying when an own NFI-P record is available (Table 7) shows the total increase in predicted response is 9%, 34%, and 60% for the terminal, self-replacing grass-fed, and long-fed cases respectively. The corresponding increases when an own NFI-F record (or equivalent) is available are 13%, 27%, and 45%. These effects are clearly large. They are largest for the long fed feedlot case, where RFI-P, RFI-F, and RFI-C are all implicated in the breeding objective, and least for the terminal case, where RFI-P is the only RFI trait in the breeding objective.

These results also show that a sizeable amount (perhaps 50% or more) of the total increase in the predicted selection response occurs through being able to include the

Table 7. Predicted 10 year response ($/cow) in 3 example breeding objectives for selection on an Index of commonly available records[1] or those records jointly with NFI-P or NFI-F records. Indexes in each case are for the breeding objective with residual feed traits included.

Records available	Breeding objective		
	Terminal Grass fed	Self-replacing Grass fed	Long fed Export (Self-repl.)
Commonly available records	42.73	38.64	45.95
Index accuracy	0.49	0.38	0.38
Commonly available records: + own NFI-P	43.34	43.18	54.85
Index accuracy	0.49	0.43	0.45
+ sire NFI-P	42.81	39.37	47.10
Index accuracy	0.49	0.39	0.38
Commonly available records: + own NFI-F	45.08	41.10	49.84
Index accuracy	0.51	0.41	0.41
+ sire NFI-F	42.95	38.98	46.90
Index accuracy	0.49	0.39	0.38

[1] Commonly available records: an own record, sire and dam record (where relevant), and 25 half-sib records for 17 measures commonly recorded in BREEDPLAN

residual feed traits in the breeding objective. The increases from this alone were 7%, 19%, and 33% for the terminal, self-replacing grass-fed, and long-fed cases respectively (Tables 6 and 7).

While it will almost always be best to have a direct measure of important traits, it is significant that being able to include residual feed intake traits in the breeding objective itself would capture large benefits. This result of course depends on the genetic parameter estimates that were utilised here, and as stated earlier this information (e.g. for RFI-C) was not strong. It emphasises the need for this information to be available, where feasible, for the major breeds.

The other significant aspect to the above result is that the benefits from investment into recording feed efficiency do not completely depend on there being a cost-effective industry measure of residual feed intake. In contrast, if investment were to be undertaken to obtain the needed data, 50% or more of the total benefit could be being realised while the data are simultaneously being used (e.g. perhaps for more enlightened DNA marker studies) to derive a cost-effective industry measure.

7. Predicted correlated responses in feed efficiency from selection for overall $ merit under differing availabilities of NFI records

Table 8 shows the predicted correlated responses in NFI-P and NFI-F for selection on Indexes with differing availability of NFI records. Much greater reductions in NFI-P (increases of 35% to 112%) and NFI-F (26% to 86%) were possible when NFI-P or NFI-F records were available in addition to commonly recorded measures. It is worth remembering that the changes in NFI-P and NFI-F shown are those that are expected to occur whilst selection is simultaneously also making improvement in all other major traits.

Overall effects on the correlated change in NFI-P and NFI-F are again best gauged relative to the current industry position. The current industry position on the correlated change occurring under selection is that illustrated in Table 6. A comparison of this with that applying when an own NFI-P record is available (Table 8) shows the total increase in the predicted response in NFI-P is from -0.08 to -0.42 kg/d and from -0.03 to -0.59 kg/d for the terminal and self-replacing grass-fed cases respectively. The increase is much greater for the long fed case, involving as it does the turnaround from +0.22 kg/d to -0.53 kg/d. When an own record (or equivalent) for NFI-F is available, there is also a large expected increase in correlated response in NFI-F in the long fed case, the increase being from +0.01kg/d to -0.87 kg/d (Tables 6 and 8).

Again, a very sizeable amount of the increased response in NFI-P and NFI-F comes from being able to include the residual feed traits in the breeding objective.

8. Reasons for lack of recording

Cost of recording is the main reason for a lack of recording. On farm recording has been tested by some breeders, but for most breeders it means at least 3 months without a weekend break away from the farm as the feeders need to be attended every day. Recording at a central location (Tullimba) avoids these constraints, but adds transport costs and a biosecurity risk which we haven't tried to quantify if the testing is done on young bulls. Further, young bulls can only be tested during a post weaning phase as the ration in the finishing phase normally used for steers is not designed to enhance the health and length of working live of young bulls destined for natural service.

In one noteworthy case in industry, recording and selection on feed efficiency has been going on for about 18 years. At 'Coota Park' in central NSW an on-farm testing facility consisting of 48 pens was developed, and feed intake recording started, in 1992. Since then the operation has conducted over 27 tests (2 per year) and to-date almost 900 bulls have been tested. The testing is for an Angus x Shorthorn – based composite breeding program of a line of cattle called "BLUE-E".

Table 8. Predicted 10 year correlated response in post-weaning net feed intake (NFI-P) and feedlot net feed intake (NFI-F) from selection on an Index of either commonly available records[1], or these records jointly with NFI-P or NFI-F records. Indexes in each case are for the breeding objective with residual feed traits included.

Records available	Breeding objective		
	Terminal Grass fed	Self-replacing Grass fed	Long fed Export (Self-repl.)
Commonly available records:			
Response in NFI-P	-0.31	-0.36	-0.25
Response in NFI-F	-0.42	-0.36	-0.53
Commonly available records + NFI-P (own record):			
Response in NFI-P	-0.42	-0.59	-0.53
Response in NFI-F	-0.53	-0.62	-0.81
Commonly available records + NFI-F (own record) :			
Response in NFI-P	-0.45	-0.50	-0.42
Response in NFI-F	-0.73	-0.67	-0.87

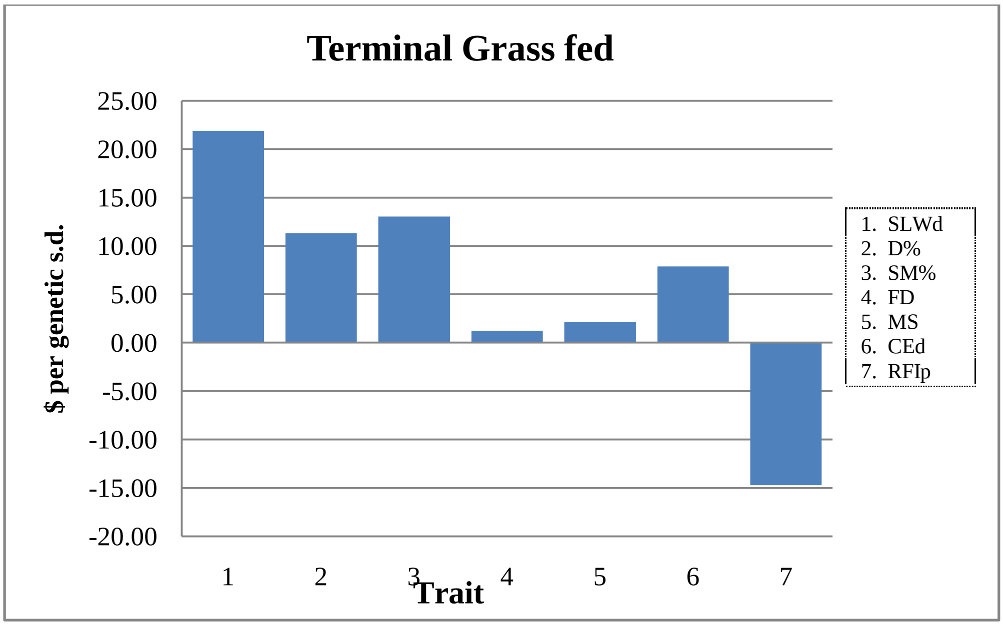
[1] Commonly available records: an own record, sire and dam record (where relevant), and 25 half-sib records for 17 measures commonly recorded in BREEDPLAN

9. Economic importance of feed efficiency in Indexes of overall $ merit

Importance to the breeding objective

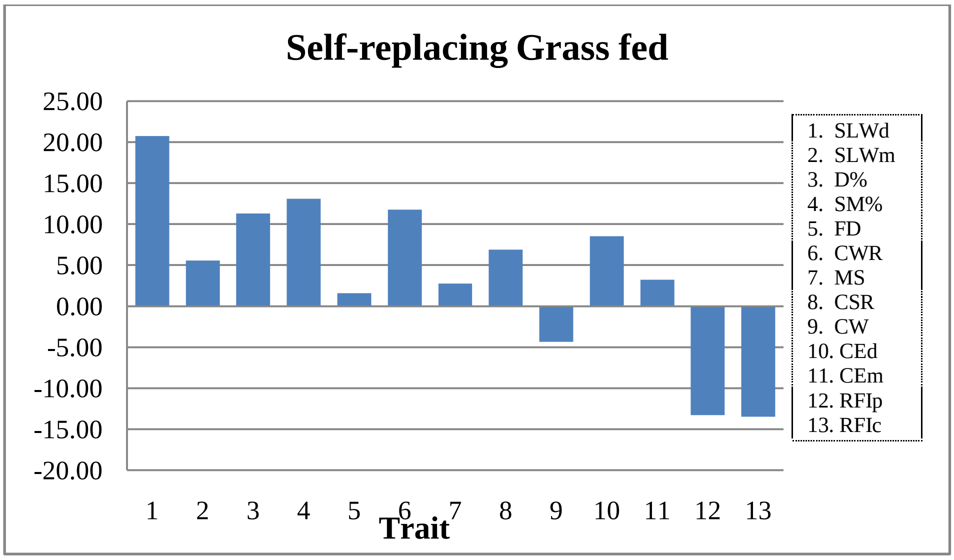
One measure of the economic importance of feed efficiency is the importance of the residual feed traits to each of the breeding objectives examined. This relative importance is assessed from the $ value of one genetic standard deviation of change in each of the traits. It is illustrated below for all traits, including the residual feed intake traits, for each breeding objective case. Trait abbreviations used are: SLWd – sale liveweight (direct), SLWm – sale liveweight (maternal), D% - dressing %, SM% - saleable meat %, FD – fat depth (rump), CWR – cow weaning rate, MS – marbling score, CSR – cow survival rate, CW – cow liveweight, CEd – calving ease (direct), CEm – calving ease (maternal), RFIp – post-weaning residual feed intake (pasture), RFIf – post-weaning residual feed intake (feedlot), RFIc- cow residual feed intake.

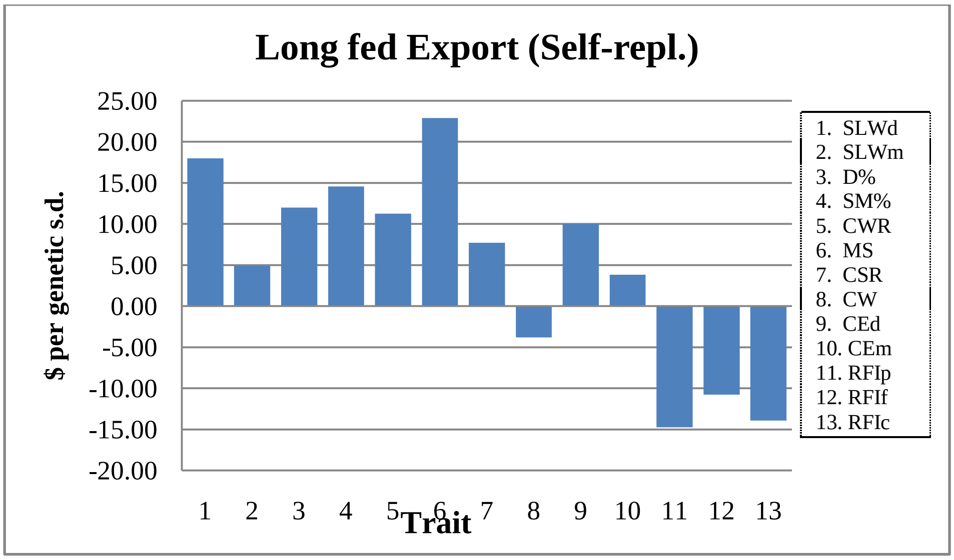
In the terminal case RFI-P is the only residual feed intake trait implicated. The size of the bar for RFI-P shows it to be second only to sale liveweight (direct) in importance. The negative sign of the $ value shows it is desirable for RFI-P to be reduced.



In the self-replacing grass-fed case, both RFI-P and RFI-C are implicated (although little is really known about RFI-C, as indicated elsewhere). The size of the bars for RFI-P and RFI-C show that each is among the second-most important of all of the traits for improvement.

In the long fed case, RFI-P, RFI-F, and RFI-C are all implicated. Considered in total, they are more important than any single trait. The size of the individual bars shows RFI-F to be a little less important for improvement than RFI-P. This is a consequence of only steers being feedlot finished in the production system modelled. In addition to steers being pasture-grown to feedlot entry and heifers pasture-grown to breeding age, heifers that are not needed for replacement in this system are also assumed to be pasture-finished.





10. Evidence for any commercial signals for feed efficiency

We are currently unaware of any higher prices necessarily being paid for progeny from more feed efficient lines to encourage performance recording for this trait. However this is not unexpected given the lack of data on feed efficiency for different lines of seedstock cattle.

In the Coota Park composite breeding program referred to above, the NFI data derived has been pivotal in the breeding program. Young bulls are feed intake recorded post-weaning using the standard 70-day test and results used to select new bulls for yearling mating. Selection is for a multiple-trait breeding objective with NFI the primary selection criterion. New AI sires are regularly introduced but commonly these sires have no information on NFI. In more recent years the herd has been recorded through the Angus Australia multi-breed register, providing access to a full range of EBVs including NFI.

According to Coota Park principal Jon Wright, cattle in the program are improving for feed efficiency each generation and he believes he is clearly seeing benefits in the cow herd. Although the recording is time consuming he is fully convinced it is worthwhile, and is slowly building a client base for about 50 bulls offered through an annual on-farm bull sale. Jon believes his operation could be improved through research into better feeding systems utilising advances in electronics. In his opinion the Australian industry cannot afford to ignore the genetic differences that exist for feed efficiency and he considers the seedstock sector has a responsibility to the commercial cattle producer to provide this information.

The economic value of feed efficiency is clearly understood by the feedlot sector. However reliable data for the trait is required before higher prices for efficient animals can be achieved. In the grazing sector, producers perhaps don’t recognise the full value of the feed they produce. There is a strong association between store cattle price and feed availability, and that is a clear everyday sign of the value that is placed on feed by the industry.

Other broad commercial signals about feed efficiency include the widely recognised need for beef production costs to be contained, and that feed costs are a big component of this;

and the evidence that greater feed intake means greater methane production, at a time of mounting concern about climate change.

11. Numbers of animals and records required to calibrate a DNA test

To include SNP predictions (e.g. MBV or MVP) in genetic evaluation will require an independent estimate of the genetic correlation (r_g) between the SNP prediction and the traits in the evaluation, particularly the target trait. One approach to quantifying the possible number of NFI phenotypes and genotypes that are required is to compute the number needed for the genetic correlation estimate to be significantly different from zero (i.e., $r_g > 2$ * standard error). The approximate standard error of the genetic correlation can be computed for different total numbers of animals with (effective) records, see Robertson (1959).

If the heritability of NFI is assumed to be 30% and the MBV has an assumed very high heritability (i.e. 95%) then the expected standard error on the genetic correlation can be predicted for different numbers of animals with records. Figure 1 plots the expected standard errors for a range of genetic correlation between NFI and the SNP prediction of 0.20, 0.30, 0.50, 0.70, corresponding to a percentage of NFI additive genetic variance explained of 4, 9, 25 and 49 %. It was assumed there are 15 progeny per sire, which is likely if NFI phenotypes are collected from a progeny test design.

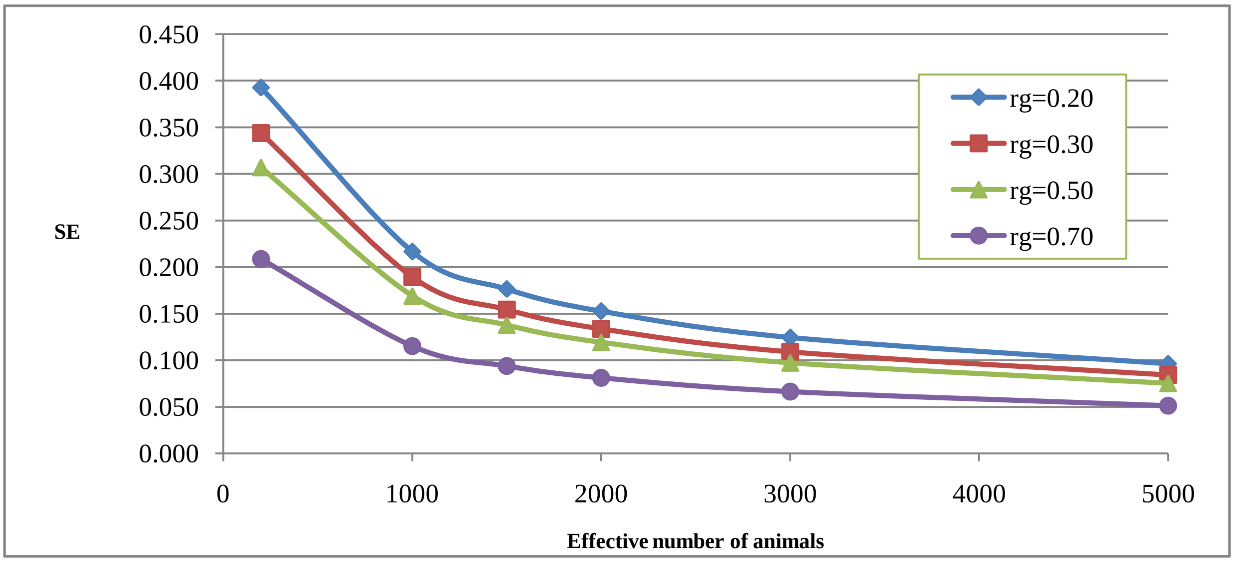


Figure 1. Expected standard errors for different numbers of recorded animals and different genetic correlations

The results show that if the genetic correlation is 0.2 then approximately 5000 animals from more than 330 sires would be required to be confident the correlation is different from zero. For a genetic correlation of 0.10 (not shown) the expected number of animals required would be approximately 20,000. For a genetic correlation of 0.3 and 0.5 the expected numbers required would be more than 1,500 (from 100 sires) and 500 (from 33 sires), respectively. If the correlation was as high as 0.7, then theoretically about 200 animals would be required. Alternatively, to achieve a standard error of 0.1 on the genetic correlations of 0.2, 0.3, 0.5 and 0.7 would require approximately 1300, 2800, 4000 and 5000 records, respectively.

Note: The predicted numbers will increase with unequal numbers of progeny per sire, with a reduction in the effectiveness of records in smaller contemporary groups, and if there is a more limited number of sires. This could add about 20% more to records required, depending on the design (e.g. field data versus design progeny test), to achieve the predicted standard errors.

The approach described above is based on the estimation of the genetic correlation (and its standard error) from traditional structured pedigree and performance data and animal model variance component estimation. However an alternative approach to estimating a genetic correlation is to estimate the phenotypic correlation between the SNP breeding value and the phenotypic trait. A genetic correlation can be derived by then dividing by the square root of the heritability of the phenotypic trait. Ideally this heritability should also be estimated from the data but it has been proposed a literature estimate could be used. If so this would allow more timely calibration of DNA SNP panels by avoiding the need to generate structured pedigree data (but would limit the use of the phenotypes generated i.e. not suitable for the computation of EBVs). However it is not clear what the approximate standard error would be on the imputed genetic correlation or the degree to which the number of records required could be reduced.

12. Options for providing recording infrastructure for feed intake/efficiency

Research Feedlot Tullimba

The Tullimba beef cattle research facility, 60 km west of Armidale, is the principal research facility available in Australia which has feed intake recording equipment for beef cattle. Each pen has one feeder which allows feeding of up to 12 animals. However the current feeders are more than 15 years old, are no longer reliable, and need to be decommissioned. No more animals should be bred with the expectation that they be tested in the existing feeders.

The Beef CRC has made enquiries about replacing those feeders and the best solution seems to be the Canadian ‘GrowSafe’ system. Depending on the number of animals to be tested a new system will cost around A$1,620 per animal feed space. (See attached quote which is now at least 15% higher in US$). Exact costs will depend on final on-site work yet to be quoted (estimated to be at least A$100,000 as the feeders need to be protected from rain) and on the exchange rate. A new quote from GrowSafe will also need to be requested.

Advantages of the GrowSafe feeders are:

- animals can be fed in larger groups (around 40)
- adjustment period to the feeder can be shortened as they are similar to bunks (4.5 runs rather than 3.4 runs per year possible)
- the feed mix can be more flexible (a higher roughage diet could be fed compared to the current Tullimba feeders). This would allow lower density feeds for maintenance tests and perhaps feeds that better approximate pasture energy density.

Commercial feedlots

Although serious negotiations with commercial feedlots have not taken place, it can be anticipated that installation costs will not be cheaper as the hardware from Canada is the same and on-site costs will most likely be greater as the pen sizes in commercial feedlots are larger and would need to be reduced.

Equipment-independent costs (feed and labour) could be lower in a commercial feedlot if we assume feed and labour could be provided there more cheaply ($20/tonne = $30 per tested animal). However we don't know if the feed mix in commercial feedlots can be as standard as in the smaller research feedlot as the throughput of feed through feed mixers will be much greater. Repeated feed sampling for DM, energy and protein determination might be required.

There is a risk with commercial feedlots that they might become temporarily uneconomic, so that the plant is mothballed. The Tullimba feedlot has always been kept open regardless of the costs.

So far all initial interest shown by commercial feedlots in the technology has come to nothing, given the cost. However this might change if the installation of the hardware was supported.

Pasture intake recording

The best known system to allow recording individual feed intake at pasture involves Alkane capsules with expensive repeated sampling of individual faeces and subsequent analysis to measure trace element dilution in animals. The start-up cost for hardware (electronic feeders) is not required and any project can be easily scaled up or down with costs changing on a per animal basis. For this technology to work paddocks that are as even as possible in pasture quality are required so animals are given equal opportunity, which is something that would be difficult to control on commercial farms.

Texas A&M has initiated a project "Measuring residual feed intake traits on pasture". However we know little more than the objectives (http://agriliferesearch.tamu.edu/library/files/corporate_relations_beef/):

- Develop methods for delivering internal markers to large numbers of grazing animals
- Determine the optimal frequency of dosing and faecal sampling
- Determine the effect of forage type, quality and availability on estimation of intake

We are in contact with this group. No further information was available at the time of writing.

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14. Appendix 1: Tables of genetic parameters for net feed intake traits and correlated performance data.

Table A1. Estimated additive genetic variance (σ_a^2), heritability (h^2) and genetic correlations for NFI-P and BREEDPLAN traits (with approximate sampling errors). *Source: Jeyaruban, GJ., Johnston, DJ, Graser, H-U (2009) Proc. Assoc. Advmt. Anim. Breed Genet.* ***18****.*

DTC, days to calving; HIMF, intra muscular fat heifers, steers; BIMF, intra muscular fat bulls; HEMA, eye muscle area in heifer, steers; BEMA, eye muscle area in bulls; HP8, rump fat in heifer, steers; BP8, rump fat in bulls; BWT, birth weight; 200D, 200 day weight; 400D,400 day weight; 600D, 600 day weight

NFI-P			**BREEDPLAN traits**				**Genetic Correlation**
No of records	σ_a^2	h^2	**Trait**	**No of records**	σ_a^2	h^2	
2030	0.25	0.47 ± 0.05	**DTC***	30276	9.74	0.02 ± 0.01	-0.04 ± 0.25
2030	0.25	0.47 ± 0.05	**HIMF**	22578	0.62	0.30 ± 0.02	0.27 ± 0.13
2030	0.25	0.47 ± 0.05	**BIMF**	15550	0.28	0.21 ± 0.02	0.48 ± 0.18
2030	0.25	0.47 ± 0.05	**HEMA**	28542	8.81	0.29 ± 0.01	0.04 ± 0.12
2030	0.25	0.47 ± 0.05	**BEMA**	20761	11.86	0.26 ± 0.02	-0.16 ± 0.17
2030	0.25	0.47 ± 0.05	**HP8**	28773	1.86	0.44 ± 0.02	0.49 ± 0.10
2030	0.25	0.47 ± 0.05	**BP8**	20679	0.70	0.42 ± 0.02	0.50 ± 0.14
2030	0.26	0.48 ± 0.05	**BWT**	74261	7.21	0.37 ± 0.01	-0.04 ± 0.08
2030	0.25	0.47 ± 0.05	**200D**	89958	119.02	0.22 ± 0.01	-0.05 ± 0.09
2030	0.26	0.47 ± 0.05	**400D**	64748	329.78	0.39 ± 0.01	0.001 ± 0.08
2030	0.25	0.47 ± 0.05	**600D**	41106	476.52	0.40 ± 0.01	-0.02 ± 0.10
			IGF-I	9216	41.86	0.36 ± 0.04	0.18 ± 0.11

Table A2. Estimated additive genetic variance (σ_a^2), heritability (h^2) and genetic correlations for NFI-F and BREEDPLAN traits

NFI-F			**BREEDPLAN traits**				**Genetic Correlation**
No of records	σ_a^2	h^2	**Trait**	**No of records**	σ_a^2	h^2	
1220	0.54	0.35 ± 0.09	**DTC***	30276	9.37	0.02 ± 0.01	-0.64 ± 0.33
1220	0.57	0.37 ± 0.09	**HIMF**	22578	0.62	0.31 ± 0.02	-0.22 ± 0.18
1220	0.53	0.35 ± 0.09	**BIMF**	15550	0.27	0.20 ± 0.02	0.36 ± 0.23
1220	0.54	0.35 ± 0.09	**HEMA**	28542	8.86	0.29 ± 0.01	-0.01 ± 0.15
1220	0.55	0.36 ± 0.09	**BEMA**	20761	11.90	0.27 ± 0.02	-0.01 ± 0.21
1220	0.57	0.37 ± 0.09	**HP8**	28773	1.89	0.44 ± 0.01	-0.13 ± 0.14
1220	0.47	0.31 ± 0.09	**BP8**	20679	0.89	0.48 ± 0.02	0.43 ± 0.17
1220	0.55	0.36 ± 0.09	**BWT**	74261	7.21	0.37 ± 0.01	-0.34 ± 0.13
1220	0.55	0.36 ± 0.09	**200D**	89958	118.84	0.22 ± 0.01	-0.23 ± 0.13
1220	0.57	0.37 ± 0.09	**400D**	64748	329.46	0.39 ± 0.01	-0.16 ± 0.12
1220	0.55	0.36 ± 0.09	**600D**	41106	476.52	0.40 ± 0.01	-0.25 ± 0.14
			IGF-I	9216	41.86	0.36 ± 0.04	-0.14 ± 0.18

*** Not included in the referenced paper**

Table A3. Additive genetic variance (σ_a^2), heritability (h^2) and genetic correlations for RFI and other production traits (with standard errors) based on Arthur *et al* (2001). *Source: Arthur, P.F., Archer, J.A., Johnston, D.J., Herd, R.M., Richardson, E.C. and Parnell, P.F. (2001) J.Anim. Sci. 79:2805.*

SS, scrotal circumference; RIB, 12/13th rib fat depth; P8, rump fat depth; EMA, eye muscle area; 200D-D, direct genetic effect of 200 day weight; 200D-M, maternal genetic effect of 200 day weight; 400D-D, direct genetic effect of 400 day weight; 400D-M, maternal genetic effect of 400 day weight; FCR, feed conversion ration; DFI, daily feed intake

RFI (= NFI-P)			production traits				Genetic Correlation
No of records	σ_a^2	h^2	Trait	No of records	σ_a^2	h^2	
1177	0.15	0.39 ± 0.03	**SS**	7,260	2.00	0.43 ± 0.06	-0.03 ± 0.11
1177	0.15	0.39 ± 0.03	**RIB**	26,892	0.47	0.35 ± 0.04	0.17 ± 0.05
1177	0.15	0.39 ± 0.03	**P8**	27,010	1.04	0.38 ± 0.03	0.06 ± 0.06
1177	0.15	0.39 ± 0.03	**EMA**	26,791	8.61	0.27 ± 0.04	0.09 ± 0.09
1177	0.15	0.39 ± 0.03	**200D-D**	26,030	70.90	0.17 ± 0.03	-0.45 ± 0.17
1177	0.15	0.39 ± 0.03	**200D-M**	26,030	54.90	0.13 ± 0.02	-0.26 ± 0.13
1177	0.15	0.39 ± 0.03	**400D-D**	27,229	211.50	0.27 ± 0.03	0.22 ± 0.20
1177	0.15	0.39 ± 0.03	**400D-M**	27,229	30.80	0.04 ± 0.01	0.14 ± 0.25
1177	0.15	0.39 ± 0.03	**FCR**	1,180	0.27	0.29 ± 0.04	0.66 ± 0.05
1177	0.15	0.39 ± 0.03	**MWT**	1,180	5.11	0.40 ± 0.02	-0.06 ± 0.06
1177	0.15	0.39 ± 0.03	**ADG**	1,180	0.01	0.28 ± 0.04	-0.04 ± 0.08
1177	0.15	0.39 ± 0.03	**DFI**	1,180	0.28	0.39 ± 0.03	0.69 ± 0.03

RFI in males and females using a diet containing 10 MJ ME/kg dry matter, which is equal to the NFI-P of Jeyaruban, Johnston and Graser (2009).

Table A4. Additive genetic variance (σ_a^2), heritability (h^2) and genetic correlations for RFI and other production traits measured on the CRC I cattle (with standard errors) based on Robinson and Oddy (2004). *Source: Robinson, D.L. and Oddy, V.H. (2004) Livest. Prod. Sci.* ***90****:255.*

RIB, 12/13th rib fat depth; P8, rump fat depth; EMA, eye muscle area; IMF, intra muscular fat; ADG, average daily gain; MWT, metabolic weight; FEDT,feeding time; ER, eating rate; FCR, feed conversion ration; DFI, daily feed intake

RFI (=NFI-F)			production traits				Genetic Correlation
No of records	σ_a^2	h^2	Trait	No of records	σ_a^2	h^2	
1472	0.14	0.18 ± 0.06	**RIB**	1472	3.61	0.45 ± 0.06	0.48 ± 0.12
1472	0.14	0.18 ± 0.06	**P8**	1472	5.30	0.43 ± 0.06	0.72 ± 0.17
1472	0.14	0.18 ± 0.06	**EMA**	1472	5.33	0.13 ± 0.05	0.24 ± 0.26
1472	0.14	0.18 ± 0.06	**IMF**	1472	0.63	0.33 ± 0.06	0.22 ± 0.17
1472	0.14	0.18 ± 0.06	**ADG**	1472	0.01	0.23 ± 0.06	0.09 ± 0.20
1472	0.14	0.18 ± 0.06	**MWT**	1472	13.40	0.41 ± 0.07	-0.20 ± 0.16
1472	0.14	0.18 ± 0.06	**FEDT**	1472	120.00	0.36 ± 0.05	0.35 ± 0.17
1472	0.14	0.18 ± 0.06	**ER**	1472	531.00	0.51 ± 0.06	-0.07 ± 0.17
1472	0.14	0.18 ± 0.06	**FCR**	1472	0.13	0.06 ± 0.04	0.41 ± 0.32
1472	0.14	0.18 ± 0.06	**DFI**	1472	0.64	0.27 ± 0.06	0.43 ± 0.15

RFI in steers and heifers at the age of 450 days or more by using a diet containing 12.1 MJ ME/kg dry matter, which is equal to the NFI-F of Jeyaruban, Johnston and Graser (2009).

Table A5. Additive genetic variance (σ_a^2), heritability (h^2) and genetic correlations for RFI and other production traits measured on Brahman (BRAH) and Composite (COMP) breeds (CRC II cattle) (with standard errors) based on Barwick *et al* (2009).

RFI (=NFI-F)	Other traits	Genetic	Source

RFI was measured in steers at the age of 732 days by using a diet containing 12.2 MJ ME/kg dry matter, which

No of records		BRAH		COMP		Trait	No of records		Correlation	
BRAH	COMP	**σ_a^2**	**h^2**	**σ_a^2**	**h^2**		BRAH	COMP		
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**WWT**	1007	1210	-0.21 ± 0.19	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**LWT**	1000	1192	-0.09 ± 0.19	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**SEMA-P**	591	850	-0.03 ± 0.22	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**HH-P**	715	774	-0.19 ± 0.19	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**FT-P**	695	722	0.15 ± 0.24	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**IGF-I-P**	612	735	-0.38 ± 0.21	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**LWT-EN**	987	1194	-0.04 ± 0.18	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**ADG-EN**	981		-0.68 ± 0.30	BRAH
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**ADG-EN**		1190	0.17 ± 0.24	COMP
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**SP8-EN**	986	1192	-0.11 ± 0.18	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**SRIB-EN**	988	1193	-0.23 ±0.18	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**SEMA-EN**	987	1191	-0.22 ± 0.17	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**SIMF-EN**	981	1190	-0.05 ± 0.18	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**HH-EN**	735		-0.56 ± 0.26	BRAH
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**HH-EN**		895	0.05 ± 0.24	COMP
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**IGF-I-EN**	953	1105	-0.28 ± 0.20	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**DFI**	700	787	0.59 ± 0.12	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**MWT**	700	787	0.15 ± 0.18	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**TADG**	681	783	0.18 ± 0.21	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**LWT-EX**	979	1192	0.11 ± 0.17	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**ADG-EX**	974	1191	0.20 ± 0.17	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**SP8-EX**	922	1191	0.33 ± 0.16	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**SRIB-EX**	922		0.16 ± 0.25	BRAH
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**SRIB-EX**		1190	0.60 ± 0.18	COMP
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**SEMA-EX**	921	1190	-0.07 ± 0.20	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**SIMF-EX**	809	1104	0.47 ± 0.17	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**CS**	568	960	0.37 ± 0.20	Pooled
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**HH-EX**	831		-0.61 ± 0.23	BRAH
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**HH-EX**		1142	-0.12 ± 0.25	COMP
680	783	0.19	0.24±0.11	0.41	0.38±0.12	**IGF-I-EX**	738	1129	-0.56 ± 0.18	Pooled

Source: Barwick, SA, Wolcott, ML, Johnston, DJ, Burrow, HM, Sullivan, MT (2009) Animal Production Science. ***49****:351-366.*

WWT, weight at weaning; LWT weight at post weaning; SEMA-P, scan eye muscle area at post weaning; HH-P, hip height at post weaning; FT-P flight time at post weaning; IGF-I-P, Serum IGF-I at post weaning; LWT-EN, live weight at feedlot entry; ADG-EN, average daily gain at feedlot entry; SP8-EN, scan P8 fat depth at feedlot entry; SRIB-EN, scan rib fat depth at feedlot entry; SEMA-EN, scan eye muscle area at feedlot entry; SIMF-EN, scanned intramuscular fat at feedlot entry; HH-EN, hip height at feedlot entry; IGF-I-EN, Serum IGF-I at feedlot entry; DFI, daily feed intake; MWT, metabolic mid-weight; LWT-EX, live weight at feedlot exit; ADG-EX, average daily gain at feedlot exit; SP8-EX, scan P8 fat depth at feedlot exit; SRIB-EX, scan rib fat depth at feedlot exit; SEMA-EX, scan eye muscle area at feedlot exit; SIMF-EX, scanned intramuscular fat at feedlot exit; HH-EX, hip height at feedlot exit; IGF-I-EX, Serum IGF-I at feedlot exit

Table A6. Additive genetic variance (σ_a^2), heritability (h^2) and genetic correlations for RFI measured on post weaning cattle (RFI-pw) and on mature cows (RFI-cow) with other cow traits measured. *Source: Archer et al. (2002) 7th World congress of Genetic applied to livestock production.*

DFI-cow, daily feed intake of mature cow; ADG- cow, average daily gain of mature cow; MWT-cow; metabolic weight of mature cow; FCR-cow, feed conversion rato of mature cow

RFI		**Trait**	**No of records**	**h^2**	**Genetic Correlation**
No of records	**h^2**				
RFI-cow					
751	0.23	**DFI-cow**	751	0.28	0.71
751	0.23	**ADG-cow**	751	0.33	0.02
751	0.23	**MWT-cow**	751	0.71	-0.21
751	0.23	**FCR-cow**	751	0.26	-0.21
RFI-pw					
1781		**RFI-cow**	751		0.98
1781		**DFI-cow**	751		0.64
1781		**ADG-cow**	751		0.22
1781		**MWT-cow**	751		-0.22
1781		**FCR-cow**	751		-0.06

RFI-pw was measured in bulls and heifers at 270 days of age by using a diet containing 10 MJ ME/kg dry matter, which is equal to the NFI-P of Jeyaruban, Johnston and Graser (2009).

Table A7. Genetic relationships of different measures of efficiency with growth rate, ultrasound traits and carcass traits in hybrid steers. *Source: Nkrumah et al (2007) J. Anim. Sci.* ***85:*** *2711-2720 (A) and Nkrumah et al (2007) J. Anim. Sci.* ***85:*** *2382-2390 (B)*

Feed efficiency		**production traits**			**Genetic Correlation**	**Source**
No of records	**h^2**	**Trait**	**No of records**	**h^2**		
Phenotypic residual feed intake (NFI-F)						
464	0.21 ± 0.12	**ADG**	464	0.59 ± 0.17	0.46 ± 0.45	A
464	0.21 ± 0.12	**MWT**	464	0.31 ± 0.14	0.27 ± 0.33	A
464	0.21 ± 0.12	**UBF**	464	0.59 ± 0.14	0.35 ± 0.30	A

RFI was measured in steers by using a diet containing 2.9 Mcal (12.1MJ) ME/kg dry matter, which is equal to the NFI-F of Jeyaruban, Johnston and Graser (2009).

464	0.21 ± 0.12	**UMAR**	464	0.75 ± 0.16	0.32 ± 0.29	A
464	0.21 ± 0.12	**ULMA**	464	0.39 ± 0.13	-0.52 ± 0.32	A
464	0.21 ± 0.12	**CWT**	381	0.33 ± 0.14	0.05 ± 0.38	A
464	0.21 ± 0.12	**CGF**	381	0.51 ± 0.15	0.33 ± 0.29	A
464	0.21 ± 0.12	**CLMA**	381	0.45 ± 0.15	-0.64 ± 0.26	A
464	0.21 ± 0.12	**LMY**	381	0.63 ± 0.17	-0.54 ± 0.29	A
464	0.21 ± 0.12	**CMAR**	381	0.49 ± 0.16	0.28 ± 0.38	A
464	0.21 ± 0.12	**CYG**	381	0.58 ± 0.18	0.03 ± 0.47	A
464	0.21 ± 0.12	**FD**	464	0.28 ± 0.12	0.57 ± 0.28	B
464	0.21 ± 0.12	**HD**	464	0.33 ± 0.12	0.33 ± 0.30	B
464	0.21 ± 0.12	**FF**	464	0.38 ± 0.13	-0.34 ± 0.30	B
464	0.21 ± 0.12	**FS**	302	0.49 ± 0.18	-0.59 ± 0.45	B

Genetic residual feed intake						
464	0.42 ± 0.15	**ADG**	464	0.59 ± 0.17	-0.04 ± 0.25	A
464	0.42 ± 0.15	**MWT**	464	0.31 ± 0.14	0.12 ± 0.30	A
464	0.42 ± 0.15	**UBF**	464	0.59 ± 0.14	-0.04 ± 0.22	A
464	0.42 ± 0.15	**UMAR**	464	0.75 ± 0.16	0.44 ± 0.19	A
464	0.42 ± 0.15	**ULMA**	464	0.39 ± 0.13	-0.65 ± 0.20	A
464	0.42 ± 0.15	**CWT**	381	0.33 ± 0.14	-0.03 ± 0.30	A
464	0.42 ± 0.15	**CGF**	381	0.51 ± 0.15	0.27 ± 0.24	A
464	0.42 ± 0.15	**CLMA**	381	0.45 ± 0.15	-0.69 ± 0.32	A
464	0.42 ± 0.15	**LMY**	381	0.63 ± 0.17	-0.43 ± 0.37	A
464	0.42 ± 0.15	**CMAR**	381	0.49 ± 0.16	0.18 ± 0.26	A
464	0.42 ± 0.15	**CYG**	381	0.58 ± 0.18	0.09 ± 0.32	A
464	0.42 ± 0.15	**FD**	464	0.28 ± 0.12	0.43 ± 0.24	B
464	0.42 ± 0.15	**HD**	464	0.33 ± 0.12	0.42 ± 0.40	B
464	0.42 ± 0.15	**FF**	464	0.38 ± 0.13	-0.77 ± 0.21	B
464	0.42 ± 0.15	**FS**	302	0.49 ± 0.18	-0.44 ± 0.23	B

ADG, average daily gain; MWT, Metabolic body weight; UBF, ultrasound backfat; UMAR, ultrasound marbling score; ULMA, ultrasound LM area; CWT, carcass weight; CGF, carcass grade fat; CLMA, carcass LM area; LMY, lean meat yield; CMAR, carcass marbling score; CYG, carcass yield grade; FD, daily feeding duration; HD, daily feeding head down time; FF, daily feeding frequency; FS, flight speed

Table A8. Genetic relationships of different measures of efficiency with growth rate in Japanese black bulls.

ADG, average daily gain; MWT, Metabolic body weight; BWF, body weight at finish; DFI, daily feed intake

RFI			production traits				Genetic Correlation
No of records	σ_a^2	h^2	Trait	No of records	σ_a^2	h^2	
Phenotypic residual feed intake (RFI-P)							
740	0.25	0.24 ± 0.11	**ADG**	740	0.014	0.20 ± 0.10	0.25 ± 0.16
740	0.25	0.24 ± 0.11	**MWT**	740	7.20	0.49 ± 0.09	0.16 ± 0.13
740	0.25	0.24 ± 0.11	**BWF**	740	374.14	0.47 ± 0.10	0.19 ± 0.15
740	0.25	0.24 ± 0.11	**DFI**	740	0.44	0.34 ± 0.11	0.78 ± 0.06
Genetic residual feed intake (RFI-G)							
740	0.23	0.25 ± 0.10	**ADG**	740	0.014	0.20 ± 0.10	0.18 ± 0.20
740	0.23	0.25 ± 0.10	**MWT**	740	7.20	0.49 ± 0.09	-0.07 ± 0.14
740	0.23	0.25 ± 0.10	**BWF**	740	374.14	0.47 ± 0.10	-0.04 ± 0.15
740	0.23	0.25 ± 0.10	**DFI**	740	0.44	0.34 ± 0.11	0.61 ± 0.10
740	0.23	0.25 ± 0.10	**RFI-P**	740	0.25	0.24 ± 0.11	0.97 ± 0.02

Source: Hoque, MA, Arthur, PF, Hiramoto, K, Oikawa, T (2006) Livestock Science. ***99****:111-118.*

RFI in bulls at 230 days of age with average body weight of 338 kg, which is equal to the NFI-P of Jeyaruban, Johnston and Graser (2009).

Table A9. Additive genetic variance (σ_a^2), heritability (h^2) and genetic correlations for RFI and other production traits measured on Bonsmara cattle in South Africa

WW, weaning weight; ADG, average daily gain; SC, scrotal circumference; SHD, shoulder height; FCR, feed conversion ratio

RFI (=NFI-P)		production traits			Genetic Correlation
No of records	h^2	Trait	No of records	h^2	
6738	0.31	**WW**	6738	0.32	-0.05
6738	0.31	**ADG**	6738	0.37	-0.09
6738	0.31	**SC**	6738	0.42	0.05
6738	0.31	**SHD**	6738	0.52	-0.02
6738	0.31	**FCR**	6738	0.34	0.75

Source: van der Westhuizen, RR, van der Westhuizen, J, Schoeman, SJ, (2004) South African Journal of Animal Science, ***34****:257-264.*

RFI in bulls at 358 days of age with average body weight of 234 kg, which is equal to the NFI-P of Jeyaruban, Johnston and Graser (2009).

Table A10. Summary for NFI-P

Feed efficiency trait	**Trait**	**Genetic correlation**								**Summary**
		Source								
		1[a]	**2**	**3**	**4**	**5**	**6**	**7**	**8**	
NFI-P	BWT	-0.04 ± 0.08								Negative

	200D-D	-0.05 ± 0.09	-0.45 ± 0.17						-0.05	Negative
	200D-M		-0.26 ± 0.13							Negative
	400D-D	0.00 ± 0.08	0.22 ±0.20							Positive
	400D-M		0.14± 0.25							Positive
	600D	-0.02 ± 0.10								Negative
	MWT	-0.03 ± 0.10	-0.06 ± 0.06			-0.22		0.16±0.13		Variable
	ADG	-0.08 ±0.10	-0.04± 0.08			0.22		0.25±0.16	-0.09	Variable
	FCR	0.86 ± 0.02	0.66 ± 0.05			-0.06			0.75	Variable
	SS		-0.03 ± 0.11						0.05	Variable
	DTC	-0.04±0.25								Negative
	IMF									
	HIMF	0.27±0.13								Positive
	BIMF	0.48±0.18								Positive
	EMA		0.09 ± 0.09							Positive
	HEMA	0.04±0.12								Positive
	BEMA	-0.16 ± 0.17								Negative
	P8		0.06 ± 0.06							Positive
	HP8	0.49±0.10								Positive
	BP8	0.50±0.14								Positive
	RIB		0.17 ± 0.05							Positive
	HRIB									
	BRIB									
	DFI	0.56± 0.12	0.69± 0.03			0.98		0.78±0.06		Positive
	FT									
	IGF-I	0.18 ± 0.11								Positive

[a] 1, *Jeyaruban, Johnston, and Graser (2009)* ; 2, *Arthur et al (2001);* 3, *Robinson. and Oddy (2004) ;* 4, *Barwick et al (2009);* 5, *Archer et al. (2002* ; 6, *Nkrumah et al (2007) J. Anim. Sci.* ***85:*** *2711-2720* (A) *and Nkrumah et al (2007)* ;7, *Hoque et al (2006)*; 8, *van der Westhuizen, van der Westhuizen and Schoeman (2004)*

Table A11. Summary for NFI-F

Feed efficiency trait	Trait	Genetic correlation								**Summary**
		Source								
		1	2	3	4	5	6	7	8	
NFI-F	BWT	-0.34 ±0.13								Negative
	200D-D	-0.23± 0.13			-0.21±0.19					Negative
	200D-M									

	400D-D	-0.16±0.12								Negative
	400D-M									
	600D	-0.25±0.14								Negative
	MWT	0.01± 0.20		-0.20±0.16	0.15 ± 0.18		0.27±0.33			Variable
	CWT						0.05 ± 0.38			
	ADG	0.22± 0.20		0.09±0.20	-0.68±0.30 0.17±0.24		0.46±0.45			Variable
	FCR	0.85± 0.05		0.41±0.32						Positive
	SS									
	DTC	-0.64±0.33								Negative
	IMF			0.22±0.17						Positive
	HIMF	-0.22±0.18			-0.05 ± 0.18					Negative
	BIMF	0.36±0.23								Positive
	EMA			0.24±0.26			-0.52±0.32			Variable
	HEMA	-0.01±0.15			-0.03±0.22 -0.22 ± 0.17					Negative
	BEMA	-0.01± 0.21								Negative
	Carcass EMA						-0.64±0.26			Negative
	P8			0.72±0.17						Positive
	HP8	-0.13±0.14			-0.11 ± 0.18					Negative
	BP8	0.43±0.17								Positive
	Carcass P8	0.30± 0.22								Positive
	RIB			0.48±0.12			0.35±0.30			Positive
	HRIB				-0.23 ±0.18					Negative
	BRIB									
	Carcass yield						-0.54±0.29			Negative
	FT						-0.59 ± 0.45			Negative
	DFI	0.85± 0.21		0.43±0.15	0.59±0.12					Positive
	IGF-I	-0.14±0.18			-0.38 ± 0.21					Negative

15. Appendix 2: GrowSafe quote:

GrowSafe Systems Ltd.
RR#1 Site #1 Box 19, Airdrie, Alberta, Canada, T4B 2A3
Toll Free North America 1 866 929 1879 Telephone 403-912-1879 Fax 403-398-1327
www.growsafe.com

GrowSafe Feed Intake System		**US $**	**US $**	**US $**	
# of Sires to be Measured		**320**	**640**	**960**	
# of Pens- 4 nodes to each pen - 32 bulls/pen		**10**	**20**	**30**	
Total # of nodes required		**40**	**80**	**120**	
# of panels shared between 2 pens		**5**	**10**	**15**	
Item Description	**Unit Cost**	**Extension**	**Extension**	**Extension**	
Feed Intake Node (Note 1)	$4,900	$196,000	$392,000	$588,000	
Main GrowSafe Panel	$12,000	$60,000	$120,000	$360,000	
Sub Total		**$256,000**	**$512,000**	**$948,000**	
Volume Discount % (Note 2)		5%	15%	20%	
Discount Calculated		-$12,800	-$76,800	-$189,600	
Sub Total after discount applied		**$243,200**	**$435,200**	**$758,400**	
Master Panel (Note 3)	$5,400	$5,400	$5,400	$5,400	
Data Acquisition Software (Note 4)	$16,000	$16,000	$16,000	$16,000	
Total Base System		**$264,600**	**$456,600**	**$779,800**	
Additional Software and Services:					
Enhanced Intake Software (Note 5)	$20,000	$20,000	$20,000	$20,000	
Delivery to Sydney (Note 6)	Estimated	$6,700	$13,400	$20,100	
Installation (Note 7)					
Economy Airfare	Estimated	$2,000	$2,000	$2,000	
Labor ($75.00/hr)	Estimated	$8,400	$12,600	$16,800	
Subsistence	Estimated	$3,500	$5,250	$7,000	
Total Additional Services	**US $**	**$40,600**	**$53,250**	**$65,900**	
Total Installed Price	**US $**	**$305,200**	**$509,850**	**$845,700**	
Est. conversion to Australian Dollars	**AUS $**	**$457,800**	**$764,775**	**$1,268,550**	**Less any applicable duties or taxes**
GrowSafe Beef (Beta System)					
# units required - 1 unit shared between 2 pens		**5**	**10**	**15**	
Est. price without water system	15,000	75,000	150,000	225,000	
Additional Installation (delivery included in above)		3,000	6,000	12,000	
Sub Total GrowSafe Beef	**US $**	**78,000**	**156,000**	**237,000**	
Est. conversion to Australian Dollars	**AUS $**	**$117,000**	**$234,000**	**$355,500**	
Total Feed Intake and GrowSafe Beef	**US $**	**$383,200**	**$665,850**	**$1,082,700**	
Est. conversion to Australian Dollars	**AUS $**	**$574,800**	**$998,775**	**$1,624,050**	**Less any applicable duties or taxes**

Notes:

(1) A feed intake node includes metalwork, 2 load cells cabled to junction box, spillage protectors and windscreens

(2) The volume discount is based and applied on the volume of feed intake nodes and panels required

(3) 1 Master Panel is required for each site installation

(4) Data Acquisition Site License is required for each installation. Includes daily feed intake calculations.

(5) Enhanced intake Software is available to researchers requiring advanced behavior and intake analysis capability

(6) Point of Manufacture is Lethbridge and Airdrie, Alberta, Canada, Least cost Delivery will be estimated, and charged at actual delivery cost

Delivery has been estimated from manufacturer to Sydney, local transport costs to Tullimba to be estimated and is the responsibility of the customer.

Standard Configuration:

The pricing quoted above is for standard configuration of nodes and panel placement within an 80' radius. Standard configuration is defined as follows:

a) Wiring must run from the master panel (mounted to the panel post we supply) to each node.

b) Up to 4 nodes can be placed on either side of the master panel mounting post.

c) The furthest away of the 4 nodes can be no more than a 50 foot cable distance from the panel.

GrowSafe will supply wiring and panel posts when the system meets standard configuration

Installation Note 7:

When GrowSafe field engineers install the system all cabling, antennas (when within line of sight specification) and installation hardware will be supplied.

Installation will be estimated on an hourly basis including travel and install time and charged at $75.00/hour

Installation will also include subsistence at $250 per day, economy airfare at cost and/or mileage as it applies

If labor to assist GrowSafe Field Engineer is provided by the client onsite - installation hours will may be reduced

Service Package:

Due to the distance from our primary repair facility GrowSafe will provide a "Service Package in trust" as specified above. All major components which might fail will be included in this package in sufficient quantity to enable swap in swap out repair on site.

During the warranty period (Year 1) there will be no charge for returned units or supplies - GrowSafe will pay for return freight.

After warranty concludes - GrowSafe will invoice at standard repair cost for return of item including freight.

Feed Intake Service Package	**Provided in trust - will only be billed when parts used after warranty period**			
Nodes complete		$9,800	$14,700	$19,600
Panels		$24,000	$48,000	$72,000
Trough and other connectors		$500	$1,000	$1,500
Load Cell Sets		$22,000	$33,000	$44,000
Feed Intake Service Package Estimated Value	**US$**	$56,300	$96,700	$137,100
GrowSafe Beef Service Package Estimated Value	**US$**	$17,000	$34,000	$68,000

Customer to Supply:

a) A dedicated data acquisition computer will be required and supply is the responsibility of the customer.

b) To obtain remote technical software support from GrowSafe you must provide a high speed Internet connection to the data acquisition computer.

c) All power to the system must be supplied by the customer; preferably on a dedicated circuit.

d) Site preparation is the responsibility of the customer and includes a concrete apron on which to install the feed intake nodes. Site preparation must be concluded before installation technicians arrive on site.