Efficient Nutrient Utilization And Its Relationship With Carcass And Meat Quality Traits - Is There A Trade Off?

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Introduction

Interest in Residual Feed Intake (RFI) as a measurement of feed efficiency has increased substantially over recent years driven by the increased cost of feed, a result in part of the bio fuel industry, and a worldwide scrutiny of ruminants as a source of greenhouse gas, particularly methane (Ellis *et al*. 2009, Nkrumah *et al*. 2006). Measurement of RFI is a regression of individual animal feed intake against metabolic mid weight and ADG on test (Koch *et al*. 1963). As such RFI is difficult and expensive to measure, making it a prime target for Genetic Marker Selection strategies. Some success has been achieved at characterizing DNA markers that can be used for selection of efficient animals (Nkrumah *et al*. 2006, Sherman *et al*. 2009 and 2010), and commercial tests are currently available from Pfizer animal Health and Igenity (www.igenity.com). However the correlations between RFI and many other traits remains poorly understood. This is due mainly to the expense of measuring RFI coupled with the additional cost of collecting other important traits, particularly meat quality measurements. The result has been that few individual animals have phenotypic measurements on all the traits of interest. Further work will be required to define the phenotypic and genetic correlations between efficiency and other quality traits.

Phenotypic Correlations with RFI

RFI has been shown to be correlated to a number of performance traits such as feed intake, feed conversion ratio (FCR), Dry Matter Intake (DMI) and Metabolizable Energy Intake (MEI) (Nkrumah *et al*., 2004). Although not correlated to average daily gain, RFI does show a negative correlation to gain in backfat (Nkrumah *et al*. 2007a,b), which may indicate some association with patterns of maturity in feedlot steers.

Of interest low RFI (efficient) animals have been shown to produce less methane (Nkrumah et al. 2006), leading to the proposition that RFI can be used as a tool for greenhouse gas mitigation in cattle. Subsequent studies on the rumen microbial population (Guan et al, 2008) have shown that the microbial population profiles of efficient and inefficient animals differ, with a subsequent significant increase in both butarate to valerate levels in efficient animals.

A negative correlation between RFI and general fatness has been well documented (Basarab *et al.* 2003, Nkrumah *et al.* 2004, 2007a,b), however the effect is small (2-5%). There has been no report of a correlation with marbling.

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In a recent study no correlation was shown between RFI and bull fertility (Basarab, personal communication). Further although the progeny of low RFI bulls were themselves more efficient than those of high RFI bulls there was no correlation with progeny daily gain, backfat, marbling or any yield traits. There was a positive correlation between bull RFI and DMI in the offspring.

The prospect for selection for RFI without impacting important traits such as meat quality therefore looks bright. However there are still a number of issues that remaining that need to be resolved. These include female fertility, and meat quality traits such as tenderness and fatty acid profile.

Strategies for Selection of RFI and the Implications for Impact on Other Traits

Selection for RFI in beef cattle will, due to the high cost of phenotypic measurement, be a combination of direct phenotypic measurement and genetic marker based selection. The number of animals with direct phenotypic measurement will likely remain small, which may limit some whole genome selection approaches. This may cause some problems as many of the markers or QTL regions for RFI and other traits may overlap or be close enough to effect even non correlated traits. An example (Table 1 and 2) are the multiple mutations in FGF8 (Moore and Marquess, 2009) affecting feed intake traits as well as carcass backfat, carcass marbling and quality grade. Clearly with SNPs in such close proximity there is a likelihood that traits associated with any one marker will be affected by selection based on any other marker in FGF8.

Table 1. Summary of FGF8 SNP alleles, GenBank Accession number, and nucleotide position.

SNP 1.	C/A Exon Silent (Glycine to NW_930497.1 - 142892 Glycine)
SNP 2.	C/T Exon glutamic acid (E) to NW_930497.1 - 142864 lysine (L) change
SNP 3.	G/C Intron NW_930497.1 - 142606
SNP 4.	G/C Exon Glycine (G) to Arginine NW_930497.1 - 139686 (R) change

Most QTL studies, or marker association studies on RFI, (Nkrumah et al. 2007, Sherman et al. 2009) or carcass and meat quality traits (Barendse et al 2007, Gutierrez-Gil et al. 2008, Casas et al. 2000, 2003) published to date have wide confidence limits on regions identified with any traits. When examining potential for overlap nearly half the regions associated with RFI identified in these studies overlap with at least one association for meat or carcass quality, principally marbling (14 regions), fatness (9 regions), tenderness (5 regions) and flavour (1 region).

More encouraging results have been seen with higher marker density scans. Sherman et al, (2010), using a panel of 2,633 SNP across the entire genome, identified 27 SNP associated with RFI. Of these 33% were within or close (5cM) previously identified SNPs associated with RFI. Only one SNP was in a region closely associated with a meat quality trait. SNP rs17872022 on BTA29 at position 44,373,740 occurs very close to the CAPN1 gene (BTA20, 45,215,707-45,242,224) which has been associated with meat tenderness in beef cattle (Barendse et al. 2007)

Table 2. Effect of different FGF 8 markers on different traits in feedlot *cattle*

Trait	Marker	Estimate	Std Err	P-value
Days on Feed	1	0.215	0.135	0.1098
Days on Feed	2	0.157	0.107	0.1441
Carcass Value, $	2	0.355	0.205	0.0837
Carcass Backfat, in	3	-0.010	0.007	0.1168
Percent Choice (QG)	3	-0.039	0.022	0.0837
Average daily gain, lb	4	-0.104	0.044	0.0189
Carcass Backfat,	4	0.025	0.014	0.0832
Live Weight, lb	4	-19.199	9.813	0.0506
Yield Grade	4	0.108	0.068	0.1100
Percent choice (MBS)	4	0.148	0.058	0.0116
Dry matter intake, lb	4	-86.396	40.266	0.0321
Hot carcass weight, lb	4	-13.007	6.561	0.0476
Marbling	4	20.569	10.243	0.0449
Rib eye area, in sq	4	-0.310	0.159	0.0510

Conclusion

The impact of selection for feed efficiency (RFI) on meat quality traits remains ill defined. Both efficiency and meat quality traits are difficult or expensive to measure. Further to this the measurements often take place at different stages of the life cycle, or on different groups of animals, eg. bulls in early life for RFI versus commercial steers at or after slaughter for meat quality. The result has been that the populations of animals with both measurements have been limited and sometimes not commercially relevant, such as research herds rather than industry animals. The issue has been confounded due to the lack of precision of many of the historical QTL studies. This situation is however rapidly improving with the application of dense marker panels, more recently the Bov50SNP chip, across large numbers of beef herds.

The lack of any phenotypic correlation coupled with more closely defined genomic regions will increase confidence that marker selection for RFI can be implemented without having negative impacts on other traits. It would be expected that as the marker associations for all traits are better understood that further examples of markers associated with RFI and meat quality such as rs17872022 and CAPN1will be characterized, enabling appropriate strategies to be developed.

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