Measuring feed efficiency in beef cattle - minimizing inputs across the whole production chain

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Introduction

The profitability of any enterprise is determined by the difference between the input costs and the revenues from sales. In growing beef cattle the major input cost is that of feed, that may be as much as 70% of the total fixed costs (Herd et al. 2003). Clearly, a reduction in the cost of feed or the amount of feed required to produce a marketable animal is a key determinant of profitability both in the cow-calf sector and in the feedlot. Therefore, there has been a growing interest in feed efficiency particularly in the feedlot sector, made more important by the increasing cost of feed due to a number of factors including the growing biofuels sector.

Traditional measures of feed efficiency have been a simple comparison of the amount of feed consumed compared to the growth achieved by animals, expressed as gain to feed ratio (**G:F**) or the inverse feed conversion ratio (FCR). These measures are relatively easy to measure on individual animals or pens of animals but suffer from a number of issues. The trait is highly correlated with growth and confounded with the maturity patterns of animals (Kennedy et al., 1993; Archer et al., 1999). As a selection tool, G:F has the potential to increase growth rate in young animals. It could also result in substantial increases in mature cow size as well as in the feed intake of the cow herd thereby resulting in negative impacts on the overall production system efficiency (Dickerson, 1978).

An alternative to G:F was proposed by Koch et al. (1963). Residual feed intake (RFI) is the difference between an animal's actual intake and its expected intake based on its body weight and growth rate over a particular period. It has been shown to have great potential as an index of feed efficiency for beef cattle (Archer et al., 1999; Arthur et al., 2001a). The trait is moderately heritable with estimates ranging from 0.16-0.58 (Herd and Bishop, 2000; Crews et al. 2003) and considerable variation within groups of cattle tested has been observed (Herd and Bishop, 2000; Basarab et al. 2003). A great deal of focus has been given to RFI over the last 15 years to evaluate its utility as a breeding or management tool in the beef industry.

Residual Feed Intake and Correlated Traits

Residual feed intake is generally calculated as the difference between the actual Dry Matter Intake (DMI) of each animal and its predicted feed intake, which can be calculated either using a phenotypic regression (RFIp) or genetic regression (RFIg) of on DMI on weight (metabolic body weight) and Average Daily Gain (ADG) (Arthur et al. 2001a,b; Crews 2005). Thus, individual animal feed intake and frequent weight measurements have to be collected in order to estimate RFI, which has made it difficult to estimate RFI on large numbers of animals. Recent technology has improved on this, for example the Growsafe equipment widely used in North America, however the cost of phenotypic measurement remains a hurdle to widespread adoption.

A number of studies have looked at correlated traits, particularly carcass and meat quality, resulting in the finding of a small effect on general fatness (Basarab et al. 2003; Nkrumah, 2007). More recently, difficult-to-measure traits such as bull and cow fertility have been investigated (Basarab personal communication), however to date the investigations are not complete as the

number of animals tested remains low.

Factors Confounding RFI Measurement

More recently, a number of factors including diet, season of testing and animal maturity have been shown to influence RFI estimates in growing beef cattle. Mujibi et al. (2010) reported seasonality effects on feed intake and efficiency. Although correlations were found between feed intake and temperature, wind speed and humidity, the nature and the magnitude of the correlations differed between fall-winter and winter-spring feeding periods. More detailed work is required to better understand these effects.

Durunna et al. (2011) examined the effect of grower versus finisher diet on the ranking of steers when measured for RFI. More than half the steers tested changed their RFI estimate by more than 0.5 Standard Deviations (SD) or 0.20 kg DM d^{-1} when measured on grower and finisher diets sequentially (Figure 1). The rank correlation between the first and the second period in these steers was 0.33 but smaller re-ranking (rank correlation = 0.42-0.44) was seen in the control animals maintained on grower or finisher diets in the two periods and measured for RFI in each period. This suggests other environmental or developmental effects such as animal maturity are in play. Interestingly, much better correlations were seen between RFI measured over the combined testing periods and RFI measured in the second period (Durunna et al., 2011). This might suggest that the accepted testing period of 63-90 days for estimating RFI might be too short, or that testing young animals may not reflect the overall RFI particularly in circumstances where large seasonal effects or different diets come into play.

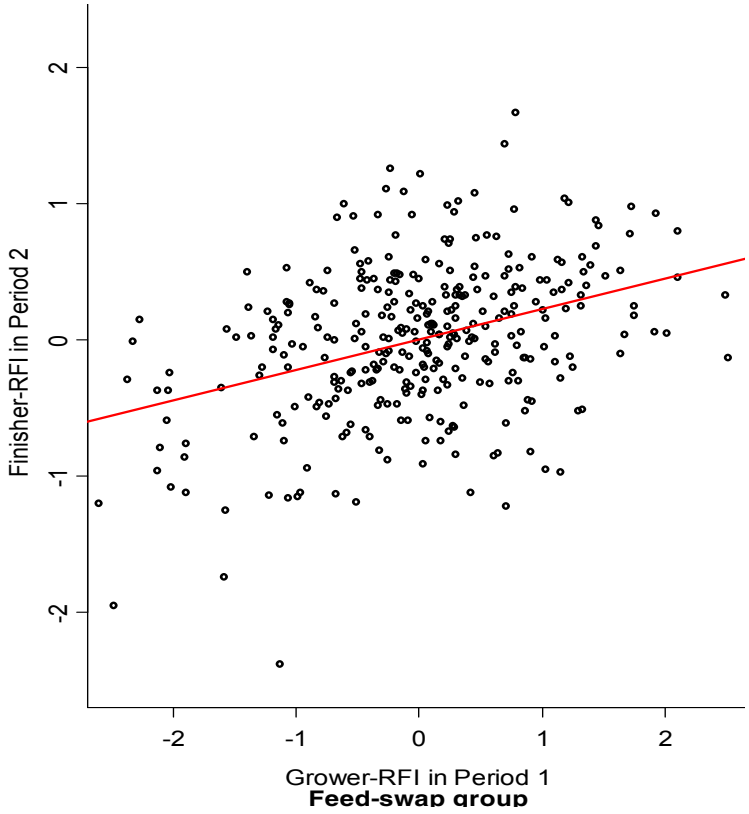

Figure 1. RFI values measured sequentially on grower diet (X-Axis), and finisher Diet (Y-Axis). (Durunna pers. Communication)

Molecular Markers for Feed Intake and Efficiency

The cost and difficulty in measuring RFI makes the trait a strong candidate for marker assisted selection. Clearly if the cost of a gene test is below that of the direct phenotypic measurement and the estimate can be made at an earlier age, selection of breeding animals that are superior for the trait could be greatly enhanced.

A number of studies have attempted to develop marker panels for feed efficiency in cattle (Barendse el al. 2007, Nkrumah et al. 2007a, Sherman et al. 2008, Moore et al. 2009). The common factor with all of these studies is that the markers have generally performed better in the population used in the discovery step than in subsequent populations used to validate the markers. That being said, some markers have been validated biologically across multiple populations and are being sold commercially to cattle producers.

The variability of the amount of the genetic variation explained by any one marker panel across different populations makes it difficult to assess the economic value of the markers in any one circumstance. Certainly, a better estimate of the biological and economic potential of any marker set can be achieved if the application is restricted to a single population or breed (Rolf et al. 2010), but this limits the applicability of the technology in an industry made up of multiple breeds or breed crosses.

The different breeds of cattle have been genetically separated for long enough that trait associated markers that lie somewhat distant along the chromosome to the causal mutation may not tag the advantageous causal allele in all the breeds. In other words when summing up the effect of a marker panel, although each marker may tag a positive effect in the discovery population, in a different population or breed, some markers may now tag a mixture of positive and negative alleles diminishing the overall predictive power of the marker panel overall. In addition, some causal mutations may be invariant in some breeds making a particular marker redundant.

The solution for this is simple, but until recently unachievable. Simply increasing the density of the markers will ensure that a marker close enough to the causal mutation can be found in most if not all breeds. The development of a marker panel with 50,000 Single Nucleotide Polymorphisms (SNPs), the Bov50SNP chip (Matukumalli et al. 2009), meant that at least within breeds it was possible to develop predictive equations for numerous traits (Cole et al. 2009). The Bov50SNP chip however still does not have sufficient density of markers to work across breeds, providing a marker approximately only at 100,000 base pair intervals on each chromosome. Estimates of conservation of chromosome segments known as Linkage Disequilibrium or LD Blocks, would suggest marker densities at least 10 fold higher than this will be required to develop technologies that work across breeds (Gibbs et al. 2009).

Now with the availability of 600,000 and 700,000 SNP panels it is now possible to test this proposition. The issues around equivalence of phenotype discussed above however remain to be resolved.

Conclusion

Selection for feed efficiency measured as RFI is becoming possible for some breeds of beef cattle. The major hurdles remain the cost of collecting the phenotype, ie. individual animal feed intake and weight gain, and the consistency of the phenotype measured considering environmental effects such as diet and season and possible confounding effects such as animal maturity.

Marker assisted techniques such as Whole Genome Selection using dense marker panels, or

derived smaller marker panels remains a maturing technology requiring some further validation in terms of the amount of genetic variation tagged in each population and hence the economic value of the marker panels to the producer. Recent advances in DNA marker technology in cattle give cause for optimism that useful marker panels that will have wider applicability across beef cattle breeds or populations are becoming available.

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