INCLUDING FEED INTAKE AND GREENHOUSE GAS EMISSIONS INTENSITY INTO EXISTING SELECTION INDEXES – THEORY AND PRACTICE

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SUMMARY
Theoretical approaches used to calculate economic weights for feed intake and greenhouse gas emissions intensity that can be used to augment existing selection indexes are outlined. The approaches are discussed. Evaluation of these traits and their index weightings in a way that makes them independent of other traits already in the breeding objective is highly desirable to industry practitioners wishing to minimise disruption to current systems. However, this requires both biological and statistical concerns associated with definition of residual traits to be overcome.

INTRODUCTION
While collecting records, and undertaking genetic/genomic evaluations of merit for feed intake and greenhouse gas (GHG) emissions traits is costly, estimated breeding values for these traits are of growing interest for inclusion in national selection indexes, because of their current and potential high relative economic importance (Archer et al. 1997; Wall et al. 2010).

Substantial investment has been dedicated towards recording of phenotypes, but the specific options for explicitly defining the estimated breeding value traits and applying weighting to them remains contentious. The complexity of the issues is exacerbated by the fact that existing selection criteria and estimated breeding values are already linked to both the amount of feed consumed and the amount of GHG emissions by animals in a commercial farm system. This means that double counting must be avoided, either through the choice of novel estimated breeding value trait definitions, or through adjustments to the weightings applied to existing traits in the index.

This paper introduces the options for implementation of selection criteria for novel traits addressing GHG emissions and feed efficiency into selection indexes and discusses their strengths and weaknesses.

EXISTING SELECTION CRITERIA
Existing selection indexes for farmed ruminant livestock commonly affect GHG emissions intensity, defined as the amount of GHG emitted from the farm system per unit of product generated. Methods have recently been developed to show how output-increasing traits dilute the "fixed" GHG emissions that do not increase in proportion to the extra output. For example higher output per animal without any increase in animal rearing and maintenance feed requirements improves the biological efficiency of the farm system (Wall et al. 2010). This concept has been formalised recently into a methodological framework that can be applied across multiple livestock species (Amer et al. 2017). It can be expected that the relative importance of existing traits in selection indexes based on farm profitability will be different to their relative importance based on GHG emissions intensity. Thus, there is an opportunity to divert the selection direction slightly away from selection solely for farm profitability, so as to achieve greater than current gains in GHG emissions intensity (Quinton et al, 2017). For example, increasing breeding female survival improves GHG emissions intensity through a reduction in feed and associated emissions for rearing of replacements. In contrast, the trait maternal milk production in meat production systems, while desired by farmers, typically does not increase market output, and is less feed efficient than converting feed into meat

directly by the growing meat animal. Thus, weightings on emissions intensity traits do not fully align with farm profitability weightings. Because traits that improve GHG emissions intensity tend in most cases to also increase farm profitability, trade-offs from profitability weighting to emissions intensity weighting will in most cases be very efficient, in that significant improvements in emissions intensity gains may be achieved with only small reductions in profitability gains. These gains can be achieved with confidence because of the strong association between production efficiency (through both genetic and non-genetic means) and GHG emission intensity.

Existing selection indexes also typically account for correlated increases in feed intake associated with genetic changes in traits which are not direct measures of feed intake. Examples include the reductions in the economic values for milk component yields and young animal carcase output to account for well-known associations of these traits with feed intake. Mature breeding female weight is also often used as a proxy to predict the higher maintenance feed intake, and higher rearing feed costs associated with larger mature size individuals. While these proxy associations only account for a proportion of genetic variation in feed intake and production system efficiency, the proportion that they do account for is achieved with considerable prediction accuracy, because live weight and dairy system milk traits are typically evaluated with considerable accuracy, in a very large proportion of selection candidates and at modest recording expense.

DEFINITION OF NEW SELECTION CRITERIA

New measurement technologies may soon make it possible to record the feed intake and greenhouse gas emissions of animals on a sufficient scale for either conventional or genomic prediction of estimated breeding values, such that these traits can be included in selection indexes. It is important to consider though that many selection candidates are likely to be evaluated with only very modest accuracy. Even with genomic selection approaches, the accuracy of prediction of these novel selection criteria will at best be modest. This is due to the small size of training populations, and the risk of selection candidates having insufficient numbers of phenotyped close relatives in the training population.

Classical selection criteria typically predict fractional components of feed efficiency and GHG emissions intensity with high accuracy. Examples include milk yield and growth rate. It is well known that animals that produce more milk, or which grow faster, will on average require more feed than their contemporaries. The accuracy of novel selection criteria to predict the whole genetic variation is typically much lower (see Figure 1).
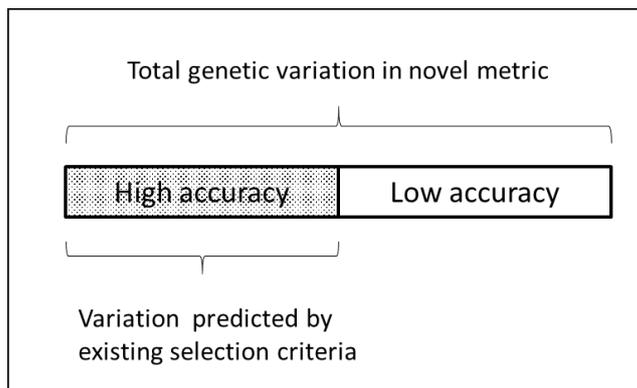
Figure 1. Partitioning of variation in a novel metric into the component predicted at high accuracy by existing selection criteria, and the component predicted at lower accuracy by phenotypes for the

novel metric.

Therefore, care must be taken to maximise the efficiency of prediction of the full breeding objective, while maintaining clarity and transparency of the index to users in industry. There are three options. Firstly, it is possible to adjust the phenotype for the novel metric so that the estimated breeding value predicts only variation that is not already predicted by existing selection criteria. The second and third options involve a more substantial rebuild of the existing selection index. These options are discussed further below.

OPTION 1. RESIDUAL TRAIT DEFINITION

Residual feed intake is a classic example of implementation of option one. From a breeding objective perspective, this approach is very elegant, as no adjustment is required to existing selection criteria and the weightings that are applied to them in the existing breeding objective. The economic value for feed intake also does not require any major rework. The cost of an extra unit of feed is the same, irrespective of whether it is an extra unit of total feed intake, or an extra unit of feed required after accounting for the feed intake expected to be associated with maintenance, growth and/or milk production (i.e. other traits in the index). Furthermore, it is likely that feed intake is a different genetic trait (i.e. correlations less than one) across different life stages of the animal, but the selection criterion breeding value is likely to be based on phenotypes measured at only one life stage (e.g. feed intake measured in young males for a small test window, used to predict feed intake in both growing and mature females, with the mature females split into both dry and lactating states). It is reasonable to hypothesise that the residual feed intake trait will be more highly genetically correlated across different life stages than total feed intake, but this will be hard to prove definitively in practice. Never-the-less, some estimation of these correlations is required for appropriate selection index construction, irrespective of the option taken.

It is important to note that many quantitative geneticists and biologists have reservations about the definition and use of residual traits, particularly for feed intake. The arguments put forward are beyond the scope of this paper, but relate to both statistical properties of the resulting traits, and potential detrimental biological consequences for fitness traits resulting from selection for a narrow definition of the trait.

OPTION 2. GROSS TRAIT DEFINITION – USE OF CORRELATED PREDICTORS

An alternative to option one is to accommodate the novel metric in the breeding objective without any adjustments. For example, a gross methane estimated breeding value might be included with a negative economic value associated with methane output. Similarly, a breeding value for total feed intake could be included in the breeding objective, either with or without the gross methane trait. Because output traits such as growth rate, body size and milk production are highly genetically correlated with both feed intake and GHG emissions associated with methane output, then these output traits should in principle be included as correlated predictor traits in the genetic evaluation of the methane or total feed intake breeding values.

The only advantage of this approach is that the need to define an estimated breeding value for a residual or adjusted trait is circumvented. There are many disadvantages. Any accounting for feed costs or associated emissions in the existing trait economic values must be removed. This will result cosmetically in much larger economic weightings for output-increasing genetic traits. The extent to which existing selection criteria are useful as correlated predictors of feed intake and gross methane emissions will differ substantially for animals in different life stages. For example, milk yield potential will be an important predictor of total feed intake in lactating cows, but much less so in young growing animals. The reverse would be expected for body weight traits recorded in young animals. This makes the process of estimating breeding values quite arduous, whereby complex multi-trait predictions are required with many parameters. Many of these parameters will not be well

estimated. While the same parameters are likely required in option one, in that case they are more likely to be applied in the definition of the breeding objective, than in the computation of the estimated breeding values. Finally, for GHG traits, finding the balance of weighting on gross methane, gross feed intake and conventional traits that achieves a quantified and understood improvement in emissions intensity will be highly complex. For example, milk yield would be penalised heavily in an index including gross methane because of the strong association between milk production and GHG emissions in a lactating dairy cow, and it is well known that gain in milk production per cow is a substantial contributor to gains in GHG emissions intensity on dairy farms.

OPTION 3. GROSS TRAIT DEFINITION – IGNORING CORRELATED PREDICTORS

Option two is potentially complex to deploy, and so it might be tempting to completely ignore the fact that existing selection criteria are useful predictors of a component of the genetic variation in a target trait of interest. This would circumvent the problem stated above in terms of the implied complexity for the genetic evaluation system. For the situation of total feed intake as a trait with an economic value in the selection index, some weighting penalty should be left on existing selection criteria to account for their association with feed intake. Otherwise, it is likely that animals with low accuracy estimated breeding values for feed intake would have excessive weighting placed on output- and feed intake-increasing traits. However, the optimal amount of weighting would depend on the information sources available for both production traits and feed intake for each animal. Thus, such an implementation would likely be inefficient for many animals.

DISCUSSION AND CONCLUSION

Many quantitative geneticists are currently considering how novel selection criteria for feed intake and GHG emissions could be included in selection indexes. Two groupings exist. Firstly, there are researchers focused on development of the new traits, who view the options in terms of their biological interpretation. Secondly, there are practitioners who see the novel traits as a complex extension of systems and processes already in place and accepted by industry users. This paper has presented some options for deployment, and discussed their advantages and disadvantages. In general, option one, whereby the novel phenotypes are evaluated in a way that makes them independent of other traits already in the breeding objective is highly desirable to industry practitioners wishing to minimise disruption to current systems. However, this requires both biological and statistical concerns associated with definition of residual traits to be overcome. Failure to do so is likely to delay industry deployment, and so the challenge to overcome the objections will need to be addressed by those advocating for inclusion of the new information in industry selection indexes.

REFERENCES

Amer, P, Quinton, C, Hely, F. and Cromie, A. (2017) *Animal* In submission

Archer, J.A., Arthur, P.F., Herd, R.M., Parnell, P.F. and Pitchford, W.S. (1997) *J Anim Sci*, **75**:2024-2032

Quinton, C.D., Hely, F.S., Amer, P.R., Byrne, T. and Cromie, A.R. (2017) *Animal* In submission

Wall, E., Simm, G. and Moran, D. (2010) *Animal*, **4**(3):366–376.