



THE GLOBAL STANDARD  
FOR LIVESTOCK DATA

# Section 19 - Guidelines for Recording Feed Intake for Genetic Evaluation

Section 19 – Feed Intake

Version 1.02 June 2020

Ref: /Users/bww/Bitrix24/ICAR Guidelines/Section 19/02\_Approval/19 Feed Intake v20.03.docx

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## Summary of Changes

| <b>Date of Change</b> | <b>Nature of Change</b>   |
|-----------------------|---|
| March 2020            | Draft from Feed & Gas WG put into standard template for ICAR Guidelines.  |
| April 2020            | Edits and acknowledgements added by Feed & Gas WG.  |
| April 2020            | File paginated according the agreed template.   |
| May 2020              | Approved by ICAR Board on 26 <sup>th</sup> May subject to addition of disclaimer.<br><br>Disclaimer added as new chapter 2 - the fact specific device manufacturers are mentioned in these guidelines is in no way an endorsement of the devices or their accuracy by ICAR. |

## 1 Introduction

The widespread use of genomic information in dairy cattle breeding programs has presented the opportunity to select for feed intake and feed efficiency. This is because animals from research herds can be used as a reference population to calibrate a genomic prediction equation, which is then used to predict the breeding values for selection candidates based on their own genotype. Phenotypes for feed intake, however, are still an important limiting factor for obtaining high accuracy breeding values and performing genetic analysis for feed intake. Based on the experiences gained through several initiatives, we provide guidelines on the recording and handling of feed intake records for genomic and genetic evaluations.

## 2 Disclaimer

The fact that specific device manufacturers are mentioned in these guidelines is in no way an endorsement of the devices or their accuracy by ICAR.

## 3 Definitions and Terminology

Table 1 contains a list of important definitions for terms and abbreviations used in these guidelines.

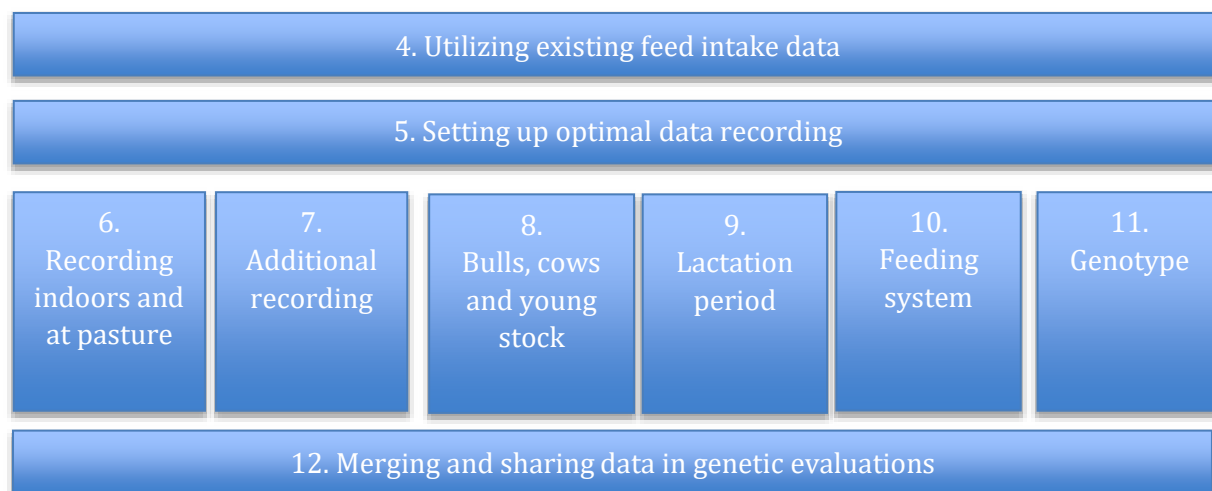
*Table 1. Definitions of Terms used in these guidelines.*

| Term | Definition                       |
|------|----------------------------------|
| DM   | Dry matter                       |
| DMI  | Dry matter intake                |
| EID  | Electronic identification device |
| PMR  | Partly mixed ration              |
| REML | Restricted maximum likelihood    |
| RFI  | Residual feed intake             |
| RFID | Radio-frequency identification   |
| RIC  | Roughage intake control system   |

## 4 Scope

Figure 1 illustrates the main elements of this guideline. The numbers in this figure refer to the chapter numbers of this guideline. The scope is to give guidelines of recording feed intake for genetic and genomic evaluations.

Figure 1. Scope of Guideline.



## 5 Utilizing existing feed intake data

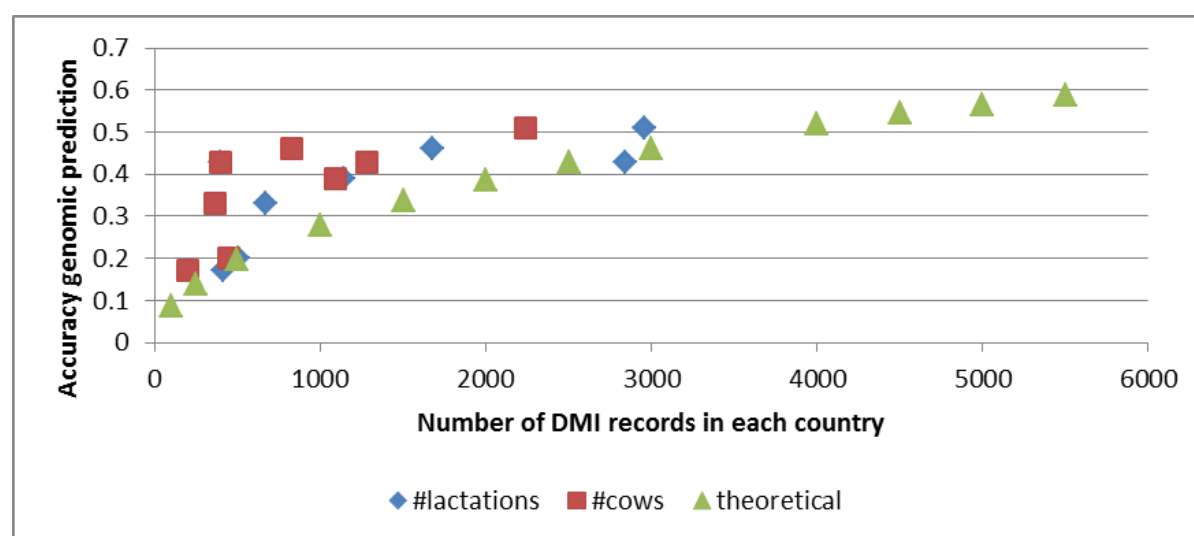
Worldwide, there are relatively few designed experiments specifically suited for genetic analysis of feed intake (and related traits). Examples are, the long term experiment at the Scottish Agricultural College (now SRUC) Dairy Research Centre based at Langhill herd, Edinburgh (Pryce et al., 1999, Veerkamp, 1996), the experiment at the Dutch farm ‘t Gen (Lelystad, the Netherlands) (Veerkamp et al., 2000), the data collection at the dairy research farm Karkendamm of the Christian-Albrechts-University Kiel in northern Germany (Buttchereit et al., 2011), or more recently data collected on young heifers in Australia (Williams et al., 2011) and New Zealand (Waghorn et al., 2012). The common denominator across these studies is that approximately 1000 animals were recorded, that were fed a total mixed ration (TMR) diet ad libitum, and the dairy cows were recorded from the start of lactation up to a fixed point in lactation (10, 26 or 38 weeks).

The designed studies are too small for a reference population using genomic prediction, and therefore in many countries’ additional sources of feed intake records have been added. For example, from nutritional experiments (Tempelman et al., 2015, Veerkamp et al., 2014), consortia have been formed that combined data across countries (Banos et al., 2012, Berry et al., 2014, de Haas et al., 2012, Pryce et al., 2012, Tempelman et al., 2015), or utilising genomic information from beef breeds for dairy cattle (Khansefid et al., 2014). Combining all these types of data is an attractive and cost-effective way of increasing the reference population, but at the same time the data becomes more heterogeneous in many aspects. For example, the recording period during lactation might be different, repeated records within and across lactation might be available or not, and feeding systems might be different, especially across nutritional experiments. This heterogeneous data collection directed attention to a statistical “use what we have”-approach rather than attention to design of the most optimal recording of feed intake. This is further described in chapter 15 Genotyping and imputation.

## 6 Setting up optimal data recording

When starting to collect feed intake records, an important question is how to optimize the “number of gate-days per year” by “number of cows x recording period per cow”? The number of cows can be established by the theoretical prediction from Daetwyler et al. (2008). The actual accuracy obtained with cross validation when records were used within country follows this pattern closely (Figure 2). In this example, empirical accuracies were slightly higher than theoretical, likely because validation and training animals were closely related. Overall it is clear that thousands of cows need to be recorded to obtain accurate prediction equations.

*Figure 2. Accuracy of genomic prediction based on theoretical prediction (Daetwyler et al., 2008), and obtained by the gDMI analysis (De Haas et al., 2015), using information in each country individually, using either #lactations or #cows available in each count.*



## 7 Recording intake indoors and at pasture

The minimal requirement for recording individual feed intake is the amount of fresh feed offered and refused per cow per day, with the associated dry matter percentage. Direct measurement of stalled cows is straightforward, but contamination of refused feed by drinking water must be prevented, and stalled cows may not behave in the same way as cows in freestalls. Also, measurement of concentrates is relatively easy, since concentrate are often dispersed in limited and fixed amounts by the farmer or an automated system. Measuring the ad libitum intake of roughage or total mixed rations (TMR) is more complicated. Automated systems have been developed by Calan Broadbent (American Calan Inc. Northwood, NH, USA), Gallagher Animal Management Systems (Hamilton, New Zealand), GrowSafe 4000 System (GrowSafe Systems, Ltd., Airdrie, AB, Canada), the RIC-system (Insentec B.V., Marknesse, The Netherlands), the CRFI (BioControl, Technology for biology), SmartFeed (Clock Inc., Rapid City, SD, USA). Each system has unique features along with general features like opening a gate and weighing feed in a bin.

With the Calan Broadbent Feeding Gate, animals access food via ‘electronic Calan gates’, with each gate allowing access to a feed box mounted on a weigh scale and linked to an automatic cow identification system (Griffith Elder; Bury St Edmunds, UK). Opening of the Calan gates is controlled via a transponder mounted on a neck collar (Ferris et al., 2006).

With the Gallagher Animal Management Systems, feed intake units are hard-wired to data loggers, which poll each electronic identification reader and weight read out indicator every second to determine if an animal was present, its identification, and the weight of the feed bin at that particular time point (Williams et al., 2011).

In the Growsafe 4000 System, each bunk is equipped with an antenna to detect animal presence at the feed bunk, load cells to measure the eaten feed, a stanchion equipped with neck bars to allow only one animal to enter the feed bunk at a time, and data acquisition software (GrowSafe DAQ; v. 9.25). This records all the feeding behavior and intake data. The GrowSafe system was designed to monitor feeding behavior by continuously recording the presence of an animal at the feed bunk once an EID crosses the neck bars of the feed bunk stanchion. Concurrently, the electronic system measures individual feed intake by continuously weighing feed during each bunk visit. These data (EID number, bunk number, time stamp of each transponder recording, and scale weight) are continuously recorded via wireless transfer to the data-acquisition computer (Mendes et al., 2011).

The RIC system consists of intelligent feeding in combination with so-called RIC feed-weigh troughs, where feed is accurately weighed continuously. This version enables restricted and unrestricted (ad-lib) feeding. If an animal approaches one of the feeding troughs, it is identified. Then the animal number and starting time of the visit are recorded. After the visit, the end time and amount of feed intake is recorded. The amount of roughage intake is electronically measured by the RIC weighing trough and stored in the RIC database (Hokofarm Group, n.d.).

CRFI gives individual cows access to specific mangers. The mangers are placed on weighing cells that measure the weight of the manger before and after cow access. This weight difference is transferred to the central computer for analysis. Cows can be identified by ear tags or neck transponders. The cows will be let in, after identification by a gate that goes down. After a specific time set for feeding, the access gate rises and pushes the cow away from the manger. There are versions available without the access gate, a cow weighscale can be added, and a lid for the manger is available. The manger is easy to clean because it can tilt (BioControl, n.d.). Please note that these features are available for RIC feeders as well.

SmartFeed is a portable, self-contained system designed to measure total daily feed intake from individual large animals. The SmartFeed system includes an RFID reader, weigh scales, and feed bin which continuously logs data to determine the feed intake per visit per animal. The system calculates the feed intake in real-time within each SmartFeed system. They are different versions, one is for pasture

Bloch et al. (2017) argued that present measurement methods do not allow to determine individual animal feed efficiency, and that the existing nutrition models could only be used for group-wise feed intake prediction. They developed model systems for individual animal feed efficiency using measurements of behavior and production sensors combined with a mathematical model with accuracies up to  $R^2=0.93$ . The method is described in a patent (PCT/L2014/051071).

In each case, consideration must be given to minimize the amount of feed wasted or stolen. Sorting of feeds should also be minimized, especially in systems that use multiple cows per feeding station. All animals must have adequate space and time to eat an intake that is truly ad libitum and does not cause alterations in feeding behaviour.

Measurement of dry matter intake (DMI) at pasture can be difficult. As animals graze in a herd or group it can be particularly challenging to obtain individual estimates of DMI. It is

somewhat easier to obtain group dry matter intakes, although these can be crude and prone to error. Genetic analyses rely on comparison of animals within the same group, so therefore group estimates are not particularly useful. The n-alkane technique is one method by which individual cow DM intake can be estimated. The technique requires animals to be dosed twice daily with a synthetic even-chain length n-alkane, at a known amount per day, adjacent in chain length to a naturally occurring odd-chain length n-alkane present in the herbage consumed (Dove and Mayes, 1991). The best estimates of intake have been typically achieved with the n-alkane pair C33 and C32, as a result of similar faecal n-alkane recovery rates (Dillon, 1993; Wright et al. submitted). Wright et al. (submitted) recently validated the accuracy of the n-alkane technique compared to measurement of the quantity of grass offered compared to that refused on a daily basis and found the n-alkane technique was a good estimate of dry matter intake. There are a number of factors however which are critical for this technique. They are:

- homogenous perennial ryegrass swards,
- good herbage sampling technique (i.e. representative of what the cow actually ate paying particular attention to post-grazing height),
- no contamination of faecal samples (i.e. no urine, grass, soil, faeces from another cow)
- representative bulking of samples collected over a six-day measurement period
- extreme attention to detail in the lab when extracting the alkanes

## 8 Calibration

Calibration of a scale is essential to keep measurements accurate. Scales have to be calibrated regularly to make sure that problems in the scales will not have influence on your measurements. How often to calibrate is dependent on multiple factors: manufacturers recommendation, how often the scale is used, the environment the scale is in, and how detailed your observation has to be (Precision Solution Inc., 2018). When calibrating scales for feed it is important to measure both for bias of the scale (too high or too low weight measurement) and also for the slope (bias at different weights). To calibrate for bias, one known weight is used to check if the scale shows the correct weight. To calibrate for slope, multiple known weights are used to correct the scale for response errors. The calibration used by ICAR partners from the Feed and Gas working group can be seen in



Table 2. Calibration is often done weekly or monthly.

Partners calibrate differently and at different intervals because the situation is different on each farm. It is difficult to come up with a general recommendation since various factors (manufacturer's recommendation, usage, environment and the need for detail) differ per partner.

*Table 2. ICAR partners of the Feed and Gas working group, the automatic feeding system used and calibration information. Information is gathered from PowerPoints of an ICAR feed and gas meeting in 2017.*

| <b>Partner</b>   | <b>Automatic feeding system used</b>                                      | <b>Calibration</b>  |
|--|---|---|
| Wageningen University (Netherlands)  | RIC   | Weekly calibration of boxes with 20kg weight.   |
| Denmark  | RIC   | Monthly calibration 20kg weight +/- 200g.   |
| Dpto. Técnico de CONAFE (Spain)  | 'home made system'<br>DeLaval<br>'home made system'<br>Moofeeder Tecnozoo | Weekly  |
| Institut für Tierzucht und Tierhaltung der Christian-Albrechts-Universität zu Kiel (Germany) | Unknown   | Unknown   |
| Elora, University of Guelph (Canada)   | RIC   | Quarterly   |
| Dairy Research and Technology Centre, University of Alberta (Canada)                         | Calan   | Unknown   |
| ILVO (Belgium)   | RIC   | Before and after a trial (10 kg weight)   |
| Irish Cattle Breeding Federation (Ireland)   | RIC and Calan   | Before each performance test and every 3 weeks during the test. Also independently calibrated annually. |
| University of Piacenza (Italy)   | Estimated with alkane technique   | Unknown   |
| University of Milan (Italy)  | RIC   | Before each trial and every month if the trial last more then a month. (10 kg weight)                   |
| ANAFI  | RIC   | Before each trial (10 kg weight).   |
| SRUC Langhill (Scotland)   | RIC   | There is a 50kg weight that is weighed in every bin every week  |
| Trinottières (France)  | Unknown   | Once a month  |

| Partner             | Automatic feeding system used | Calibration   |
|---------------------|-------------------------------|---|
| Méjusseume (France) | Unknown                       | Roulimètre, weighing : every day with 10 kg, every week with a set of weights (10+20+2+10 kg) |
| (Switzerland)       | RIC                           | Unknown   |

## 9 Chemical analyses

In these guidelines only the determination of dry matter content is discussed. Determination of DM is a relatively simple and quick process that can be done easily. The most common way that moisture is determined is through evaporation of water from the feed, leaving only the dry contents behind. However, there are also electronic methods that have been used to determine moisture content of feeds. Dry matter can be determined using: Forced Air Oven, Koster Tester, Microwave, Vortex Dryer, Food Dehydrator and Electronic Methods (Nennich et al., 2007).

### 9.1 Forced Air Oven

The most common means used to dry feedstuffs in a laboratory is with a forced-air oven. However, forced air ovens are usually quite expensive compared to other drying equipment, and have longer drying times compared to the methods discussed below. Drying time for silage samples is 24 to 48 hours.

### 9.2 Koster Tester

A Koster tester is an electrical appliance that blows heated air through a screen on which the feedstuff is placed. A Koster tester provides a relatively quick and inexpensive means of drying feedstuffs. Some sample loss can occur, which increases the likelihood of errors. It takes about 25 to 50 minutes to dry a sample using this tester.

### 9.3 Microwave

Microwaves provide a relative quick means of drying feedstuffs. The greatest challenge with the use of a microwave is the possibility of burning. Due to the likelihood of burning, samples dried in a microwave should not be submitted to a laboratory for nutrient analyses. The use of a microwave requires constant monitoring. Drying time is about 5 to 10 minutes for silage samples.

### 9.4 Vortex Dryer

A vortex dryer is an easy and inexpensive method to dry feedstuffs. Since the sample remains in the enclosed container, there is less chance for losses, which will reduce error. Drying times are similar to the Koster tester (25 to 50 minutes).

### 9.5 Food Dehydrator

A research trial at the US Dairy Forage Research Center evaluated the use of a food dehydrator with 9 shelves to dry forage samples (Mertens et al., 2004). This method requires minimal operator attention and takes about 2 to 8 hours to determine the DM of silages.

## 9.6 Electronic Methods

Electronic methods are a rapid way to determine DM of feeds. Most of these are designed for use with hay or grain samples. However, at least one tester based on this principle can be used with silage samples. A paper comparing this tester to other DM determination methods has been published (Oetzel et al., 1993). These testers provide a DM reading in under 5 minutes.

## 9.7 Near infrared spectroscopy

Near infrared spectroscopy (NIRS) is widely used in (commercial) laboratories for analysis of forages and concentrate ingredients. Because water is opaque to NIR light, DM is very accurate. NIRS is ideal for large-scale determinations because scanning each sample takes less than one minute and no samples weighing is needed. An advantage of NIRS is that it also provides values for all other nutrients that have calibration equation. It goes from advance devices to handhelds.

## 9.8 Device Choice

The device used depends on the priorities for the dry matter determination. The microwave is the cheapest and quickest option but has to be monitored due to burning risk. Also, the samples dried in a microwave should not be submitted for nutrient analysis. If there is enough time available, the forced air oven is a reliable way to determine dry matter content. The machine is expensive to buy, but the forced air oven is often used because of reliability. The vortex dryer is a safe option when drying should be done quickly because the chance of losses is small. The food dehydrator and electronic methods are often not used because of a lack of knowledge and research. NIRS gives fast results and is often used, certainly in commercial laboratories.

To accurately determine the DM of a feed, the sample collected must be representative of the feed (Nennich, 2007). Ideally dry matter determination should be done constantly, to have an accurate observation of the feed eaten by the individual cow. This is not done in practice. In Table 3 is shown how, and how often, the dry matter content is determined by the different ICAR partners from the Feed and Gas working group.

*Table 3. ICAR partners from the Feed and Gas working group and dry matter determination information. Information is gathered from PowerPoints of an ICAR feed and gas meeting in 2017.*

| Partner    | How DM determined  | How often measured   |
|------------|--|--|
| NL         | PMR-samples taken of each load for nutritional analyses.<br><br>Residues are taken out daily but no analyses done on residues. |  |
| Denmark    |  |  |
| Nottingham | See appendix A   |  |
| Spain      |  | Farm 1: weekly<br>Farm 2: 3 times/week<br>Farm 3: daily<br>Farm 4: daily |

| Partner      | How DM determined   | How often measured   |
|--------------|---|--|
| Kiel         |   | Daily  |
| Canada       | DM is determined by drying feed samples in a forced air oven at 105°C overnight                 | Dry matter is determined when the ration changes, DM of leftover feed is not determined<br>Three samples are collected on 3 different days per week and pooled to get a weekly DM percentage. DM also reported in a monthly feed sample analysis.  |
| ILVO BE      | Chemical methods  | Biweekly, grass and grass silage weekly. If the ration and the individual components are the same during the trial, the samples are pooled for data processing to convert fresh matter back to dry matter intake.  |
| ICBF Ireland |   | RIC: animals feed intake is recorded in real-time on a fresh-weight basis and then brought back to a dry matter basis.<br>Calan: weekly weigh backs to remove left overs.<br>DM of leftover is not determined.<br>Dairy: grass samples for each day for the 6-day intake run are analysed. |
| Italy        | Piacenza: see appendix B<br><br>Milan: according to EU reg. 152/2009                            | Once during the last 12 days of emission measurements. Refusals are oven-dried to measure DM content, DM is determined for leftovers.<br>Every batch of dry TMR. No leftovers are mentioned.   |
| Langhill     | DM of the whole diet is determined by drying a thoroughly mixed sample in a drying oven for 24h | A grab sample is taken from every bin every delivery and stored until the end of the week. Samples of refusals are taken from each bin, assimilated then dried.  |
| France       | Tinottières: oven 105°C – 24h<br><br>M'jusseume: oven 80°C – 48h                                | Every day, Monday to Friday. Leftovers DM of a global sample, not individual.<br>Forage, every day Monday to Friday. Concentrate, once a week. No leftover determination.  |
| Switzerland  | Standard methods for DM determination and prox. analyses (AOAC, VDLUFA)                         | Determination of DM of feeds and refusals – frequency depends on feed components.  |

## 10 Number of animals per bin

The behaviour of the animal has influence on how they should be held. Cows are diurnal animals; they prefer to synchronise their behaviour. This has influence on how much space they need while eating. Enough space needs to be available so that natural cow behaviour is not affected.

The number of animals per bin is also influenced by the amount of feed that is given to the animals. Cows can be fed a set amount of feed, which is often done on farms, or ad libitum, which is often done in research. Feed composition also has an influence, because different components have different energy values.

The method of milking affects feeding behaviour of cows. If all animals are milked at the same time, they will all go eat afterwards. So, most cows will want to eat at the same time. If there is an automated milking system, feeding time will differ between individual animals in the herd.

In Table 4 is shown how many animals per bin are used for different feed recording systems. In the research from Corkum et al. (1994) is shown that a mildly competitive group feeding situation encourages intake by social facilitation, this has an influence on the ideal number of animals per bin.

*Table 4. Different ways of use of an automatic feeding system in research and the animal used in that research.*

| <b>Automated system</b>             | <b>Source</b>          | <b>Number of animals per bin</b> | <b>Animal used</b>                         |
|-------------------------------------|------------------------|----------------------------------|--|
| Calan Broadbent                     | Krawczel et al., 2012  | 1 individual per bin             | Lactating Holstein dairy cows              |
|                                     | Corkum et al., 1994    | 1 individual per bin             | Hereford steers                            |
|                                     |                        | 12 individuals per 3 bins        | Hereford steers                            |
|                                     |                        | 12 individuals per 4 bins        | Hereford steers                            |
|                                     | ICBF <sup>1</sup>      | 1 individual per bin             | Beef breeds                                |
| Gallagher Animal Management Systems | Macdonald et al., 2014 | 9 or 10 individuals per 7 bins   | Holstein Friesian heifer calves            |
|                                     |                        | 54 individuals per 30 bins       | Holstein Friesian heifer calves            |
|                                     |                        | 1 individual per bin             | Holstein Friesian heifer calves            |
|                                     | Williams et al., 2011  | 15 to 20 individuals per 2 bins  | Holstein Friesian heifer calves            |
|                                     | Waghorn et al., 2012   | 8 Individuals per bin            | Holstein Friesian heifers                  |
| Growsafe 4000 System                | Mendes et al., 2011    | 32 individuals per 4 bins        | Heifers (Angus, Braford, Brangus, Simbrah) |

| Automated system | Source                | Number of animals per bin  | Animal used                                      |
|------------------|-----------------------|--|--|
| RIC-system       | Dairy campus, n.d.    | 2 individuals per bin  |  |
|                  | Chapinal et al., 2007 | 42 individuals per 24 bins   | Holstein cows                                    |
|                  | Nottingham            | 50 individuals per 32 bins   | Holstein cows                                    |
|                  | Canada <sup>1</sup>   | 2 individuals per bin  | Pregnant heifers and first parity cows           |
|                  | ICBF <sup>1</sup>     | 3 individuals per bin  | Beef breeds                                      |
|                  | Langhill <sup>1</sup> | 2 individuals per bin  |  |
|                  | University of Milan   | Max 2 individuals per bin  | Holstein cows                                    |
|                  | ANAFI                 | Max 7 individual per 2 bins  | Growing Holstein Bulls                           |
|                  | ILVO                  | 40 individuals per 20 bins<br>or 13 individuals per 6 bins<br>20 individuals per 10 bins | Lactating Holstein cows<br><br>Dry Holstein cows |

## 11 Additional recording

In addition to recording feed intake, it seems obvious that cow identification and pedigree must be recorded for genetic analysis. However, nutritional experiments often use their own anonymous local identification number for cows, which makes it hard to trace the cow back to a national pedigree register. Ideally a DNA, or a hair or blood sample, should be collected from each cow to allow subsequent genotyping.

Other traits that should be considered for weekly recording are milk yield and composition, liveweight, and body condition score. These energy sink traits can be especially useful for feed intake records that are of short duration and might be related to temporary production records that are not representative of the whole lactation. The utilisation of feed intake records determines which traits to record. For example, for national breeding values for AI bulls, there is little extra information in recording milk yield on this limited number of cows. On growing bulls and heifers in Italy also weekly height and chest width is measured. However, to establish the genetic correlation between yield and feed intake, it might be very useful to collect these extra records, or when a genomic prediction is to be developed for residual feed intake (RFI). For RFI, recording the energy sink traits is essential. Health and fertility traits should also be considered for examining relationships with both intake and production. Ration composition might be useful for understanding Genotype x Diet interactions or calculating energy or protein efficiency. As mentioned, the choice depends on the purpose of recording. However, sometimes extra records are recorded as insurance: records might be important in the future and, compared with recording feed intake, the costs are relatively small.

## 12 Bulls, cows and young stock

Recording on milking cows might be difficult, and practically it might be easier to record feed intake on young stock or bulls. Genetic correlations of these non-lactating animals with lactating animals were above 0.74 (Nieuwhof et al., 1992) indicating that more than 50% of the genetic variation among lactating animals can be observed in the non-lactating animals. In Australia and New Zealand, RFI was calculated for growing heifers. The extremes (top and bottom 10%) were retained for a lactating cow experiment, where it was shown that divergence for RFI was maintained ( $P < 0.01$ ) (Macdonald et al. 2014).

When feed intake records are available on bulls and cows, these can be combined in one reference population (Calus et al., 2013). Hence, there is potential in recording the number of records combining cow and bull reference populations. There is still little information on the optimal design for recording feed intake, and genetic parameters are likely not yet accurate enough, to do precise index calculations.

## 13 Lactation period

Ideally feed intake should be measured across the lifetime of an animal. This is not realistic and often only short periods of recording are available. In lactating animals, it might be of particular importance to consider the period that feed intake is measured. Cows might compensate a more negative energy balance in early lactation by a higher intake during late lactation. Hence, biological feed intake might be a different trait during different parts of the lactation, which is supported by the relatively low genetic correlation between DMI during early and late lactation (Berry et al., 2007, Buttchereit et al., 2011, Coffey et al., 2001, Koenen and Veerkamp, 1998, Li et al., 2014, Manzanilla Pech et al., 2014b, Spurlock et al., 2012, Veerkamp and Thompson, 1999). One way to overcome this bias due to tissue mobilisation might be to use RFI, which is adjusted for energy sinks. Hence, in terms of improving feed efficiency across the whole lactation, it seems necessary to have feed intake records available during all stages of lactation, rather than focus collection on the first part of the lactation alone, as most designed experiment have done.

The question on when to record feed intake can also be approached from the quantitative genetics perspective using selection index methodology. Genetic parameters can be used to estimate the accuracy of DMI breeding values across the whole lactation, when only part of the lactation is recorded (Manzanilla Pech et al., 2014a). These authors concluded that recording DMI for 15 weeks gave an accuracy of 0.58, which was on average 0.25 more accurate than recording DMI for 5 weeks, and 0.11 more accurate than recording DMI for 10 weeks. Also, starting to record DMI in mid or late lactation gave more accurate estimates for predicting lactation DMI than starting recording in early lactation (Manzanilla Pech et al., 2014a). Still, more reliable estimates for genetic correlations between feed intake measurements across lactation are required to define more precisely when to record DMI.

If feed intake is measured as part of a comprehensive analysis of feed efficiency examining all energy sinks and calculating RFI, then the time and duration to record feed intake can be shortened and conducted earlier in lactation. Connor et al. (2013) found that correlations for weekly RFI across weeks, even as early as 4 wk, were high ( $r = 0.8$ ) and that the heritability of RFI was similar ( $h^2 = 0.45$ ) whether only the first 50 DIM or the first 100 DIM were considered; heritability for earlier assessments of RFI were lower.



## 14 Feeding system

The diet fed to the cows should be balanced to meet requirements for energy, protein, minerals, and vitamins, and feeding a well-mixed TMR using silages or other wet feeds is likely to minimize sorting. If the feed is dry, such as a dry cubed feed, it can be important to measure the %DM in the refused feed separately.

Common practice is that the diet is fed *ad libitum*, but there is little known about the effects of not doing so. The diet should be comparable to that fed to commercial herds, representative of the average for a country. This is not always easy for a diverse country like the USA, where diets may differ markedly by region. RFI might then be useful, as this can be calculated within contemporary group (Tempelman et al., 2015) which makes the composition of the diet less important. A high correlation of RFI was obtained when a cow was fed a high starch or low starch diet (Burczynski et al., 2013). However, it is clear that feeding a diet formulated according to level of production leads to bias; this would unfairly result in feeding a more digestible diet to the high producers and also might increase the correlation between DMI and milk yield. In some countries, in nutrition trials cows get a partly mixed ration (PMR) instead of TMR and are individually supplemented with concentrates according to their needs (and milk production). Perhaps the most important criterion is that diet must be the same for all cows that are in the same contemporary group, and contemporary groups should be sufficiently large (> 5 animals) and genetically connected through common (grand-)sires.

## 15 Genotyping and imputation

One of the issues with combining data from research herds for genomic analysis is that different SNP chips may be used for each experiment. Fortunately, most of the commercially available SNP chips have many SNP in common, so a set of common SNPs can generally be identified. Another option is to impute genotypes from a low density to a higher one (e.g. from 50K to 777K (HD)), which may be advantageous for some (Bayesian) approaches for genomic prediction. This strategy relies on a reference dataset of bulls or cows that are genotyped at high density and that have some genetic ties (i.e. haplotypes in common) with the animals in the dataset that is to be imputed. Pryce et al. (2014) showed that it was possible to impute the genotypes of research herd animals from 50K to HD using two independent reference datasets with high concordance. For animals with historical feed intake records, but no DNA information, imputation of the genotypes might be considered (Bouwman et al., 2014, Pimentel et al., 2013), when offspring are genotyped.

## 16 Merging and sharing data in genetic evaluations

To increase the accuracy, it is important that feed intake records are collected on animals as closely related to the selection candidates as possible. A large genetic distance between historical data and current selection candidates is therefore a disadvantage. Also, the genetic connectedness between contemporary groups, through common sires, is important to separate the permanent environmental and genetic effects in the data. With many small, disconnected nutritional experiments, this could be a problem.

One aspect when considering suitable statistical approaches is dealing with the different recording periods within and across parity. Nutritional experiments are often done on second or later parity animals, and data collection might focus on the transition period (early lactation) or mid to late lactation. Experiments might be short (a month) or several months.

Hence, a solution is required to standardize the data. One solution may be to standardise the records to one DMI record for each cow, and to use that one record in subsequent genetic analysis. The one trait could be standardised based on a random regression model prediction for a cow, based on the (repeated) records collected during different parties and the covariance structure found in the population (Banos et al., 2012, Berry et al., 2014), or the one trait could be based on the phenotypic records available for a cow in a standardised time, e.g. first 28-d period between 50 and 205 days (Tempelman et al., 2015). An alternative to standardising to one trait is to utilise all available feed intake records in the genetic analyses accounting for no genetic permanent cow effects by using a fixed regressions test-day model (Veerkamp et al., 2014).

A second important aspect when considering statistical approaches is to account for differences in the mean and variance of DMI. The most common method to account for mean differences in genetic analysis is to perform the analysis within contemporary group: comparing daughters of different sires within a group of herd mates that receive the same treatment. Well established REML techniques are common practice for this. Traditionally, contemporary groups are based on treatment and season of calving, however, feeding treatments within studies change over time, and rations might also change over time (i.e., all cows on a given day get silage out of the same silage pit, independent of calving date). Therefore it is often wise to adjust for time-dependent contemporary groups. Also, differences between animals might be larger due to experimental treatment, herd, diet or lactation stage of recording. For this reason, often heterogeneous residual variances across treatments, or herds are fitted. Tempelman et al. (2015) demonstrated that care should be taken to allow for different relationships between DMI and for example, yield or live weight across environments.

A third important aspect when considering statistical approaches is to assume that trait definitions vary across countries, and therefore fitting a multitrait model allowing for non-unity genetic correlations between countries. Although this might appear obvious, this is only possible when each country has enough data to estimate the genetic correlation with reasonable precision. Ideally this requires common sires between the environments, but using genomic relationships assists in establishing genetic links between the countries (Pryce et al., 2014).

Altogether, a reasonable amount of statistics is required to merge DMI data and perform subsequent genetic analysis; however, the common experience is generally positive. Genetic correlations between countries are relatively large and genomic predictions across countries have higher reliabilities than using a smaller within country dataset (de Haas et al., 2012, de Haas et al., 2015, Tempelman et al., 2015).

## 17 Proxies for feed intake

Regardless of international collaboration, recording of feed intake will always be a limiting factor for accurate breeding values (Veerkamp, 2013). Therefore, there is an interest in using predictors to improve the accuracy of the breeding values. DMI might be predicted by the yield traits with reasonable accuracy. However, this predicted DMI can never be used to identify genetic variation in feed efficiency as all variation between animals is due to difference in the milk yield traits. So DMI data are always required to select for improved feed utilisation.

Next to yield, an obvious group of predictor traits are the conformation traits; chest width, stature, body depth, and angularity which help to predict live weight (Coffey et al., 2003),

and therefore provide a good predictor for estimating feed required for maintenance. Other potential predictors are:

- Body condition score (BCS) to indicate levels of body fat and protein
- Activity data can be used to account for variation in maintenance,
- Thermal infra-red cameras can be used to collect heat measures (related to DMI)
- MIR analysis of milk samples performed regularly by milk recording agencies have been shown to be correlated to energy balance, which is mathematically related to RFI (McParland et al., 2011)
- Changes in eating pattern is informative to predict disease. Eating pattern might also be affected by social hierarchy.

## 18 Feed efficiency in the breeding goal

At first sight, the inclusion of feed intake or efficiency in the breeding goal may seem a relatively simple matter. The goal is more milk with less feed. Several factors, however, complicate the inclusion of feed intake or efficiency in a balanced breeding goal (Veerkamp et al., 2013).

Life-time feed efficiency, as well as including milk performance and feed intake, must also consider longevity, reproductive performance, days dry, and body weight when slaughtered (income from beef). This suggests that efficiency must be quantified at the production system level and so it might be more complex than feed efficiency at a single cow level. However, in the short term it was assumed for the discussion that a small change at the cow level will contribute to efficiency of the whole system.

More milk (i.e., output) per kg feed intake (i.e., input) suggests that feed efficiency should be presented as a ratio of input and output, i.e., gross feed efficiency or feed conversion ratio. Such traits appeal to producers since they appear easily interpretable, but ratio traits have several disadvantages in animal breeding (Veerkamp and Emmans, 1995). Gross feed efficiency favours animals with high output, because maintenance costs are diluted (Veerkamp and Emmans, 1995). Even worse, increasing gross efficiency does not necessarily favour more efficient feed conversion towards milk (Vandehaar, 2012). For these reasons the outcome of the discussion of gDMI was that the ratio traits, feed conversion or gross feed efficiency, could be presented as a stand-alone trait because of its appeal. However, its direct inclusion in the overall breeding goal could be complicated and may be best represented as a linearised expression of the ratio. Then there are two options, which in an ideal world should result in a similar outcome.

The first option is to calculate residual feed intake (RFI) for all animals that have feed intake records. RFI is the measured feed intake minus the expected feed intake for milk production, growth (including body tissue mobilisation) and maintenance (as well as other energy sinks if data are available) based on feed requirement equations. RFI is popular in growing cattle (Berry and Crowley, 2013) and is probably the closest approximation of net feed efficiency at a population level for genetic/genomic evaluations. However, RFI is made to be independent of milk production and maintenance costs. Hence, these feed costs for yield, growth and maintenance should ideally also be considered in the breeding goal as traits in themselves with their respective economic values. This complexity may result in a negative economic value on body size which may affect producer acceptance. Nonetheless a negative economic

value for body size is already adopted and accepted by producers in New Zealand, Ireland, and in the US (\$NM - by means of reduced Stature).

The second option for linearized inclusion of feed efficiency in the breeding goal is not to predict the breeding value for RFI, but to predict the breeding value for DMI itself; this would need to be undertaken in any case if RFI is to be defined at the genetic level. The breeding goal can then be defined as the milk returns, minus the cost of DMI. Since DMI automatically includes the feed consumed for growth, maintenance and production, there is no need to separately account for the cost of differently sized animals or differences in for example the fat:protein ratio in the milk. Subsequent inclusion of body size in the breeding goal can be left to the desired outcome of the index.

It can be a lengthy discussion choosing between these two approaches and both have their own advantages and disadvantages and many different definitions have been applied (Table 5). Both approaches however are a linear combination of the same traits, and therefore are expected to yield the same result (Kennedy, 1993). When selecting animals based on RFI it is certain that animals with a negative RFI eat less than expected based on their outputs (assuming the definition of RFI is correct). Feed efficient animals are more difficult to identify if DMI itself is used. Also, computation of RFI is more flexible (e.g., relationship between DMI and production or maintenance may be non-linear), but must be properly modelled (i.e., cognisance must be taken of the contribution of body tissue mobilisation to energy kinetics). However, RFI may be more difficult to understand as it is currently not clear what exactly RFI is and whether it is simply an accumulation of variance associated with an inaccurate statistical model. RFI might depend on lactation stage, and so within parity the correlations among, and the contributions of, the components to RFI may change. Therefore, if you use one set of parameters, RFI may not be calculated correctly. Also, RFI breeding values will be based on a small reference population, whereas alongside DMI, body size and yield can be used as predictor traits, as well as other potential predictors like milk Mid Infra-Red (MIR) (McParland et al., 2011). RFI, however, is essentially a sub-index and there is already a precedence of decomposing total merit indexes into sub-indexes. Using DMI makes the index more amenable to individual herd customisation of the index by altering the economic value on feed costs for that farm. Wulfhorst et al. (2010) concluded that RFI is a difficult concept and therefore including feed intake directly in breeding objectives may avoid confusion among the end-users.

One compromise that has currently been chosen in most countries is the feed saved definition (Australia and the Netherlands). This allows for the extra expected intake due to an increase in milk yield, but not for extra intake for maintenance or residual feed intake.

*Table 5. Definitions of feed efficiency in growing and lactating/mature animals; analogous definitions of feed efficiency in growing and mature animals are on the same row.*

| Growing animals  | Lactating/mature animals  |
|--|---|
| $FCE = \frac{ADG}{FI}$   | $FCE = \frac{ECM}{FI}; FCE_{Adj} = \frac{ECM + b_{1a}\Delta WT^+}{FI - b_{1b}\Delta WT^-}$  |
| $PEG = \frac{ADG}{FI - FI_{Maintenance}}$  | $PEMP = \frac{ECM}{FI - b_1 WT^{0.75}}$   |
| $RGR = \frac{100 \cdot (\log_e WT_{END} - \log_e WT_{START})}{\text{Days on test}}$                          |   |
| $KR = \frac{ADG}{WT^{0.75}}$   | $KR = \frac{ECM}{WT^{0.75}}; KR = \frac{ECM + b_{1a}\Delta WT^+}{WT^{0.75}}$  |
|  | $FtW = \frac{FI}{WT^{0.75}}$  |
| $RFI = FI - (b_1 WT^{0.75} + b_2 ADG + b_3(\Delta)FAT + b_4 WT^{0.75} \cdot FAT + b_5 ADG \cdot \Delta FAT)$ | $RFI = FI - (\text{Parity} \cdot \sum_{i=1}^n DIM^n + b_1 WT^{0.75} + b_2 ECM + b_3(\Delta)BCS + b_4 \Delta WT + b_5 WT^{0.75} \cdot BCS + b_6 \Delta WT \cdot \Delta BCS)$ |
| $RG = ADG - (b_1 WT^{0.75} + b_2 FI + b_3(\Delta)FAT + b_4 WT^{0.75} \cdot FAT)$                             | $RSP = ECM - (\text{Parity} \cdot \sum_{i=1}^n DIM^n + b_1 WT^{0.75} + b_2 FI + b_3(\Delta)BCS + b_4 \Delta WT + b_5 WT^{0.75} \cdot BCS + b_6 \Delta WT \cdot \Delta BCS)$ |
| $RIG = RG - RFI$   | $RISP = RSP - RFI$  |

FCE=feed conversion efficiency, ADG=average daily gain, ECM=energy corrected milk; FI=feed intake,  $[\Delta WT]^+ =$  live-weight gain;  $[\Delta WT]^- =$  live-weight loss; PEG= partial efficiency of gain, PEMP=partial efficiency of milk production; WT=live-weight; RGR=relative growth rate; KR=Kleiber ratio; RFI=residual feed intake; FAT=fat depth; BCS=body condition score; FtW=feed to weight ratio; RG=residual gain; RIG=residual intake and gain; ECM=energy corrected milk; PEMP=partial efficiency of milk production; DIM=days in milk; RSP=residual solids production, RISP=residual intake and solids production.

## 19 Acknowledgements

This document is the result of the ICAR Feed and Gas Working Group and its industry and research liaison group. The members of the ICAR Feed and Gas Working Group at the time of publication are, in alphabetical order:

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The work of Marinus te Pas and Lillie Zegeling (both Animal Breeding and Genomics, Wageningen Livestock Research) in compiling draft versions is highly acknowledged.

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## 21 Appendix A: Standard Operating Procedure Nottingham

### Dry Matter Determination of Feed and Faecal Samples.

#### 21.1 Equipment required:

1. Oven set at 80°C
2. Foil trays (ensure they are a suitable size for the sample you have)
3. Balance (PAT tested)
4. Lab coat and gloves
5. Heatproof safety gloves

#### 21.2 Method:

1. Zero balance.
2. Weigh empty foil tray and record the weight.
3. Add your sample to the foil tray DO NOT zero the balance before adding your sample.
4. Record the weight of sample + foil.
5. For faecal samples a single tray is used for each sample and feed samples are usually dried in triplicate. This is dependent on the amount of sample you have.
6. Dry at 80°C for 5-7 days until samples are completely dry.
7. To check the dryness of samples, foil and sample should be weighed twice over two consecutive days. If the weight drops again (>0.3g) then they should be weighed a third time.
8. To calculate dry matter work out the pre and post drying sample weights by subtracting the weight of the foil tray from the weight of sample + foil.
9. Then Dry Matter = post sample weight/pre sample weight.
10. Multiply this value by 100 to get DM% and by a 1000 to get DM g/kg.
11. An average DM value can be calculated for samples run in duplicate or triplicate. If replicate values differ by >5%, repeat the determination.

#### 21.3 Training:

Users should be supervised by a trained individual when first carrying out the procedure.

## 22 Appendix B Alkane Feed intake technique Piacenza, Italy

Estimation of individual feed intake is carried out utilising all cows in a group (maximum 50 cows). Cows are fed a Total Mixed Ration, fed ad libitum, with about 3-5 % refusals.

Feed intake is estimated adopting the alkane technique. A fixed amount of C32 Dotriacontane dispersed in 50 g of corn meal is included in a bolus and gun dosed to dairy cows at feeding time. The first day, a double dose of the marker is dosed. After 7 days of administration of the marker, faeces are collected in the morning at feeding time for 5 consecutive days (day 8 to day 12), continuing with marker dosing. Faeces are homogenized and a 200 g sample is oven dried.

Representative samples of TMR are collected from the day before the collecting period to the day before ending collection of faeces. Feed refusals are sampled daily in combination with collection of faeces.

Amounts of TMR offered and refused are weighed each day during the period of sampling (day 7 to 11 for TMR, day 8 to 12 for refusals).

At the end of the faeces collecting period, dried faecal samples are pooled by animal, milled and analyzed for alkanes by GC. TMR samples are similarly processed. Refusals are oven dried to measure dry matter content.

Individual intakes are preliminary predicted for each cow, assuming the same recovery values for the alkanes C31, C32 and C33, according to the equation (Dove and Mayes 1996 ):

$$y = (F_i/F_j * D_j) / [ H_i - (F_i/F_j) * H_j]$$

where: y is predicted dry matter intake (kg of DM/ d);  $F_i$  and  $H_i$  are the respective concentrations (mg/kg of DM) of natural odd-chain n-alkane in diet and faeces;  $F_j$  and  $H_j$  the respective concentrations (mg/kg of DM) of even chain n-alkane in diet and faeces;  $D_j$  is the dose rate of even chain n-alkane (mg/d).

Feed intake is calculated by correcting the preliminary data based on the ratio between average predicted intake of the whole group of cows and the dry matter intake calculated as difference between feed offered and refused.