Guidelines to measure individual feed intake of dairy cows for genomic and genetic evaluations

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Abstract

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 value for selection candidates based on their own genotype. To implement genomic prediction and perform genetic analysis for feed intake, several partners have brought together their expertise and existing feed intake records. Based on this experience we aim to provide some guidelines on the recording and handling of feed intake records. The consortium used a mixture of standardised experimental data coming from larger genetic experiments or several smaller nutritional studies. The latter has provided some statistical challenges. Also, data was combined across countries, experimental herds and feeding systems. Despite the perceived roughness of such data, it has proven to be very successful for genomic prediction, with proper statistical modelling. Ideally the whole lifetime of all cows should be measured, but this is unrealistic. Often, animals are recorded for part of one (or more) lactation(s) only. Guidelines on the proper statistical modelling and usefulness of existing data are needed. Selection index theory can help to establish the optimal recording period across and within lactation. It is also critical to identify how many records are required and what are the most informative animals for measuring feed intake. Genetic relationships with the selection candidates are an important criterion. Finally, since (residual) feed intake is only part of the breeding goal, it is important to consider recording of other traits as well, and the genetic parameters are needed to define the breeding goals properly.

Keywords: Feed intake, genomic selection, DMI, genetic evaluation

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. In the Netherlands (Veerkamp *et al.*, 2014) and Australia (Gonzalez- Recio *et al.*, 2014) the first breeding values for (residual) feed intake have been made available to the industry, but still phenotypes for feed intake are an important limiting factor to obtain high accuracy breeding values and perform genetic analysis for feed intake. To overcome this limitation, several initiatives have been taken, and partners have brought together their expertise and existing feed intake records. Based on these experiences, we aim to provide some guidelines on the recording and handling of feed intake records for genomic and genetic evaluations.

Utilising existing feed intake data

Designed experiments for genetic studies

Worldwide, there are relatively few designed experiments specifically suited for investigating genetics 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 a 1000 animals were recorded, that were fed ad libitum a total mixed ratio (TMR) diet, and the dairy cows were recorded from the start of the lactation up to a fixed point in lactation (10, 26 or 38 weeks).

Merging and sharing data

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 attractive and a cost effective way of increasing the reference population, but at the same time the data becomes more heterogeneous in many aspects. For example 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 the 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.

One element of the statistical approaches is dealing with the different recording periods within and across parity. Nutritional experiments are often on second or later parity, 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 attempts to standardise the records to one DMI record for each cow, and that one record is utilised in sub sequential 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 element of the 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 practices for this. Traditionally, contemporary groups are based on treatment and season of calving, however, feeding treatments within studies change over time, and also rations might change over time (i.e., all cows on that 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 were fitted. Tempelman *et al.* (2015) demonstrated also that nevertheless, care should be taken to allow for different relationships between DMI and for example, yield or live weight across environments.

A third important element of the 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.*).

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).

Recommendations when setting up data collection

Merging and sharing datasets will be part of the future reference population, but also new data might be collected. Based on the experiences with setting up the experiments, but also with analysing the existing data, we make the following recommendations.

What and how to record?

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. Automated systems have been developed by Calan Broadbent (American Calan Inc. Northwood, NH), Gallagher Animal Management Systems (Hamilton, New Zealand), GrowSafe 4000 System (GrowSafe Systems, Ltd., Airdrie, AB, Canada), and the RIC-system (Insentec B.V., Marknesse, The Netherlands). Each system has unique challenges. 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. Measuring DMI for grazing cows is obviously even more difficult; however, there has been some success, notably in Ireland with the n-alkane technique (Dillon *et al.*, 1993, Mayes *et al.*, 1986).

In addition to recording feed intake, it seems obvious that the 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. 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 RFI. For RFI recording the energy sink traits are 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.

Bulls, cows or youngstock?

Recording on milking cows might be difficult, and practically it might be easier to record feed intake on young stock or bulls, and 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.*).

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 probably genetic parameters are not accurate enough yet, to do precise index calculations.

Which and how many cows?

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 Deatwyler *et al.* (2008). The actual accuracy obtained with cross validation when records were used within country follows this pattern closely (Figure 1). In this example, actual 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.

To increase the accuracy, it is important that feed intake records should be collected on animals as closely related to the selection candidates as possible. The large genetic distance between historical data and current selection candidates is therefore a disadvantage.

Also, is 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 nutritional experiments this could be a problem.

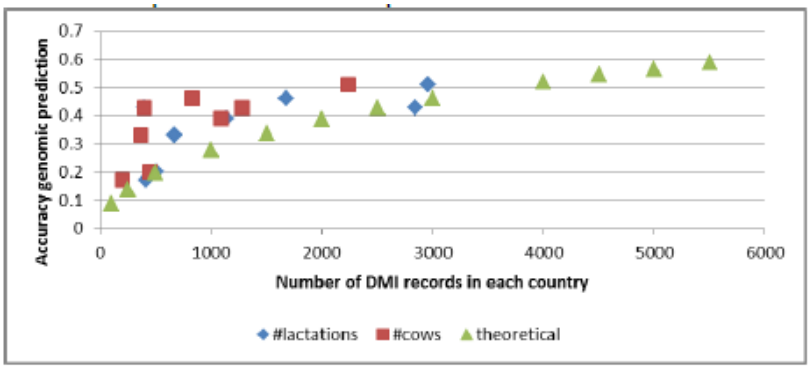

Figure 1 Accuracy of genomic prediction based on theoretical prediction (Daetwyler et al.*, 2008), and obtained by the gDMI analysis (De Haas et al., 2015), using information in each country alone. Using either #lactations or #cows available in each country as reference.*

When to record feed intake during lactation?

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 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 (h2=0.45) whether only the first 50 DIM or the first 100 DIM were considered; heritability for earlier assessments of RFI were lower.

What feeding system to apply?

The diet fed to the cows should be balanced to meet requirements for 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 practise 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.*, 2015, in press). 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. 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.

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 50K to high density (HD), which may be advantageous for some (Bayesian) approaches to genomic prediction. This 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 from low density to HD. 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 were genotyped.

Conclusion

To implement genomic prediction and perform genetic analysis for feed intake, the "use what we have"-approach will be important for the foreseeable future. Based on this experience we were able to provide some initial guidelines on the recording of feed intake records.

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