TOWARDS GENETIC IMPROVEMENT OF FEED EFFICIENCY IN DAIRY CATTLE
LYPSYLEHMIEN REHUHYÖTYSUHDE PAREMMAKSI ELÄINJALOSTUKSELLA

FINNISH FEED EFFICIENCY PROJECT
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A research project funded by Finnish public and private sources
making major contributions to the Nordic joint scientific research project

Feed Utilization in Nordic Cattle

to underpin the development of a future genetic evaluation for feed efficiency
in Finnish and Nordic dairy cattle

FINAL REPORT

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Contents

Abbreviations

AIA	Acid-insoluble ash
BCS	Body condition score
BW	Body weight
DIM	Days in milk
DM	Dry matter
DMD	Dry matter digestibility
DMI	Dry matter intake
EB	Energy balance
EBV	Estimated breeding value
ECE	Energy conversion efficiency
ECM	Energy-corrected milk
ECR	Energy conversion ratio
ES	Energy status
FA	Fatty acid
FDM	Faecal dry matter
FP	Fat-protein ratio
iNDF	Insoluble neutral detergent fibre
LCFA	Long-chain fatty acid
MBW	Metabolic body weight, $BW^{0.75}$
MCFA	Medium-chain fatty acid
MEE	Metabolizable energy efficiency
MEI	Metabolizable energy intake
MIRS	Mid-infrared reflectance spectroscopy
NEFA	Non-esterified fatty acids
NIRS	Near-infrared reflectance spectroscopy
OMD	Organic matter digestibility
PEG	Polyethylene glycol
REI	Residual energy intake
RFI	Residual feed intake

1. AIM OF THE PROJECT

Margin over cost of milk production is central to the financial sustainability of the Finnish dairy sector and agriculture as a whole. Milk production contributes to almost 50% of the annual turnover of the agriculture in Finland. Even though the productivity of Finnish dairy farms has increased, profitable milk production still relies on subsidies and profitability of milk production will be more reliant on better use of natural resources in the future. Because feeds account for more than one third of total milk production costs, improving the use of feed resources for milk production is an obvious target. Achieving improvements in the conversion of feeds into milk through genetic improvement of animal resources represents the most sustainable means to realise higher margins over feed costs. For this reason, incorporation of feed efficiency traits into genetic improvement programs for dairy cattle represents the most sustainable means to realise these benefits.

However, it has not been possible to include feed efficiency traits in breeding programs due to the technical challenges and costs of measuring the intake and nutrient digestibility of large numbers of individual dairy cows. What is required is the development of low-cost methods for making such measurements on commercial farms that can be incorporated into breeding programs that focus on improving the efficiency of dietary gross energy for milk production. Developing genetic evaluations for improving feed efficiency in dairy cattle will require identifying best suitable traits to cover the different characteristics of feed efficiency of which the most important ones are the general efficiency to digest and utilize feed, the efficiency to transfer dietary gross energy into milk production, and the ability to avoid severe negative energy status at the onset of lactation.

The overall aim of this project was to carry out scientific research that underpins future development of a genetic evaluation for feed efficiency in Finnish and Nordic dairy cattle and to carry out this research within a large joint Nordic research initiative (*Feed Utilization for Nordic Cattle - FUNC*) of universities and research institutes from Denmark, Finland, Norway and Sweden. The research project, in coordination with the FUNC initiative, had the following specific main objectives:

1) *Establish a large and comprehensive research database on feed efficiency and its component traits*
2) *Develop feed efficiency traits for genetic improvement that ensure high economic response*
3) *Develop simple and practical methods for on-farm measurement of new and complex traits*

To meet the objectives of the project our research was organized in three work packages (WP) and 15 specific work tasks. The aim of *WP1 - Phenotypic measuring of feed efficiency and metabolic functions* was to investigate the potential of establishing cow-specific digestibility traits, to collected comprehensive feed efficiency data, to address the role of methane exhalations with respect to feed efficiency, to improve modelling of bodyweight changes, and to establish an indicator trait for negative energy status. The aim of *WP2 - Modelling of feed efficiency and its economic and environmental value* was to assess the economic and environmental value of feed efficiency, to evaluate feed efficiency traits, to assess the predicted economical genetic response of feed efficiency, to assess genetic variation in energy pathways of the cow, and to model the genetics of feed efficiency traits. The aim of *WP3 - Development of a method for recording dry matter intake on-farm* was to assess the achievable accuracy of marker-based on-farm feed intake measurement methods, to identify external markers suitable for NIRS (near infrared reflectance spectroscopy) analyses, to assess how external markers need to be administrated to cows, and to validate a marker-based on-farm feed intake measuring method.

2. PROJECT PARTNERS AND COLLABORATION

Participating researchers and main role in the project

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Genetic Research

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Enyew Negussie, Ph.D., Senior Scientist, Nordic database, genetic analyses and simulation studies
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Anna-Elisa Liinamo, Ph.D., Doc., Research Assistant, data collection, analyses of samples, genetic analyses
Timo Pitkänen, M.Sc., Research Scientist, faecal sampling protocol, body weight analyses

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Egil Prestløkken, Ph.D., Doc., feed efficiency data collection, cows-specific digestibility

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Funding partners

MMM
Valio Ltd
Faba co-op
VikingGenetics
Finnish Cattle Breeding Foundation
RAISIOagro Ltd

Data acquisition partners

Mtech Digital Solutions Ltd
Nordic Cattle Genetic Evaluation NAV

Project steering group and reporting

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Intermediate reports: Intermediate and end report were delivered to funding partners in the course of the Makera project or directly to **VikingGenetics**, **Naudanjalostussäätiö**, **Valio Ltd**, and **Faba coop**.

3. PROJECT RESULTS

3.1 Material and Methods

WP1. Phenotypic measuring of feed efficiency and metabolic functions

Task 1.1 Measurement protocol for cow-specific digestibility

Marketta Rinne, Terhi Mehtiö, Päivi Mäntysaari, Auvo Sairanen, Laura Nyholm, Timo Pitkänen, Esa Mäntysaari, Martin Lidauer

Motivation

The possibility to improve organic matter digestibility of cows by means of animal breeding is under discussion in the scientific community. Using the NIRS approach as under research in this task is one possible approach to get a better understanding of the genetic variation in organic matter digestibility. Therefore we stress here the importance of this task to give answers to the scientific community and to the industry. NIRS can be used to determine diet digestibility of cows from faecal samples (Nyholm et al. 2009). This provides an opportunity to obtain digestibility determinations from on-farm samples, but faecal sampling needs to be minimized to make the method practically feasible. In this task, a faecal sampling protocol is determined. There are two issues to be resolved:

- A protocol for collecting faecal spot samples that allows sufficiently accurate digestibility measurements
- Which is the most appropriate time over lactation to take the digestibility measurements

Animal trial for collection of digestibility data

A trial with 44 cows was conducted at Luke Maaninka research farm during 2012-2013. The trial was designed to access cow-specific diet digestibility at different stages of lactation by samples taken during calendar weeks where a cow was approximately 50, 150 and 250 days in milk (DIM). Faecal samples were collected for five consecutive days every morning and every evening (10 samples in total per week). Composite samples were made for all 44 cows using 100 g of faeces per each sampling time over the whole 5-day period. For a subset of 20 cows, from each of the 10 individual collections also a 400 g faeces sample was retained (individual samples).

NIRS analyses

The composite samples from lactation stages 50, 150 and 250 DIM as well as the individual samples from the 20-cow subset were analysed by NIRS, from which three digestibility traits were obtained: Organic matter digestibility (OMD) predicted directly by NIRS, iNDF concentration in faeces ($\text{iNDF}_{\text{faeces}}$) predicted directly by NIRS and dry matter digestibility (DMD) obtained by predicting iNDF concentration in feed and faeces by NIRS. Additionally, a reference method (acid-insoluble ash (AIA)) was applied for all composite samples to obtain reference observations for OMD and DMD. The NIRS analyses were performed at Valio Ltd. laboratory. For the iNDF and organic matter digestibility calibration, 240 and 234 samples collected from previous Luke trials were used, respectively.

Statistical analyses for development of a sampling protocol

Linear models and linear mixed models were fitted to assess correlation between digestibility observations across different lactation stages, repeatability of digestibility observations, the phenotypic variation as well as the correlations of digestibility observations measured by different methods. To study the optimization of sampling protocol and differences between individual samples the NIRS scan data from the 20-cow subset with daily individual morning and evening measurements (10 measures in total per week) were used.

Task 1.2 Measurements to analyse feed efficiency

Päivi Mäntysaari, Anna-Elisa Liinamo, Sari Kajava, Annu Palmio, Auvo Sairanen, Tuomo Kokkonen

Motivation

In this task significant effort was made to collect more phenotypes to be included in a database of previous projects to build a rare and unique data that contain not only production traits but also feed intake and body measurements. The collected data were used to define efficiency traits; residual energy intake (REI, ME MJ/d), energy conversion efficiency (ECE, kg ECM/ME MJ) and energy balance (EB, ME MJ/d). The collected data were also used for the genetic analyses of feed efficiency traits and studying the partitioning of energy towards milk, body tissues and faeces during lactation.

Recording of data from research farms

The measurements to analyse feed efficiency of primiparous Nordic Red cows were collected at the experimental farms of Luke Jokioinen, Luke Maaninka and Helsinki University Viikki. During the first four years of the project (1.3.2013 – 31.12.2016) the number of new cows with measurements were 136 in Minkiö, 36 in Maaninka and 34 in Viikki. Daily measurements included individual dry matter intake (DMI), body weight (BW) and milk yield from lactation days 2 to 280. To correct the daily variation in BW, the daily weights were smoothened using the model developed in Task 1.4. (Mäntysaari & Mäntysaari, 2015). The milk samples for milk composition analyses (fat, protein, lactose, somatic cell and MIR spectra) were taken twice on lactation week 2 and 3 and once on lactation week 20 and also on routine milk recoding test days. The daily composition of milk was calculated with an assumption of linear change between measurements. The energy-corrected milk (ECM) was calculated according to Sjaunja et al. (1990). All feeds were sampled and analysed to get metabolizable energy and nutritional values for the feeds (Luke, 2017). Based on intake and feed values the daily energy and nutrient intake of the cows were calculated. The body condition scores (BCS) of the cows were assessed on a scale of 1-5 (1=skinny to 5=very fat) with intervals of 0.25 (Edmonson et al., 1989) monthly. Faecal grab samples and feed samples for digestibility estimation were collected bi-monthly based on the protocol developed in Task 1.1.

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Sjaunja, L. O., Baevre L., Junkkarinen L., Pedersen J., Setälä J. 1990. A Nordic proposal for an energy corrected milk (ECM) formula. In: Proc. of the 27th session of Intern. Committee of Recording and Productivity of Milk Animal, Paris. France, pp. 156– 157.

Task 1.3 Prediction of energy loss through methane exhalation

Enyew Negussie, Anna-Elisa Liinamo

Motivation

In modelling the genetics of feed efficiency in dairy cows (Task 2.4), inventory of energy intake and expenditures particularly, at different stages of lactation is essential. In this task the main focus was to estimate for individual cows the amount of relative energy lost through CH_4 exhalation. For this, the methane output of cows was monitored continuously using F10 multi-gas analyzer (GASERA Ltd. Turku, Finland) that is based on Photoacoustic Infrared Spectroscopy technique.

Measurement of methane

For the measurement of CH_4 and other gasses the multi-point F10 gas analyser was fitted to two feeding kiosks (two sampling points) for continuous measurement of CH_4, CO_2 and acetone outputs from individual cows at the Minkiö research dairy farm at the Natural Resources Institute Finland (Luke). Whenever a cow visited the feeding kiosk, her breath was sampled and analysed for the contents of the different gases. Measurements were made alternatively between the two sampling points and every other minute a gas was sampled and analysed from each sampling point. Sampling of the gas and its analysis required approximately 30 seconds each and a single CH_4 concentration measurement from one of the sampling points took about a minute. One of the main reasons for setting up sampling points in the feeding kiosks was that feeding kiosks are visited by cows several times during the day and this allows the collection of several measurements per animal. During each individual measurement, the cow ID, date, time and the concentration of the various gases measured were recorded automatically. A continuous 24/7 measurement system was employed for first lactation cows. In addition, each of the cow's visits to the kiosk as well as the corresponding concentrations of the gasses were recorded and stored in the internal memory of the F10 equipment. Each year between 35 to 38 new Nordic Red cattle cows were entering the recording, and by this securing the continuation of the of CH_4 recording on research dairy cows, which has been started during the GreenDairy project.

Repeatability of CH_4 measurements and size of CH_4 energy pathway as percent of gross energy intake

Task 1.3 was carried out in collaboration with the GreenDairy project. A study was conducted on an extracted part of the methane data generated. The main objective of the study with respect to Task 1.3 was to estimate the magnitude of between-animal variations in CH_4 output traits. Data was from 115 Nordic Red cattle cows of the Minkiö research dairy farm. Records on continuous daily measurements of CH_4, milk yield, feed intake and body weight measurements over two years period were compiled for data analysis. The daily methane output was calculated using carbon dioxide as a tracer method. Estimates from the non-invasive PAS-F10 technique were then tested against open-circuit indirect respiration calorimetric chamber measurements and against estimates from other widely used prediction models. Concordance analysis, based on measurements from 21 cows, was used to establish agreement between the chamber and PAS-F10 methods. A linear mixed model was used for the analysis of the large continuously collected CH_4 data from the 115 cows.

Task 1.4 Prediction of energy retained in or mobilized from body tissue

Päivi Mäntysaari, Esa Mäntysaari

Motivation

Trends in changes of body weight and body condition reflect the energy that is either released from or stored in body tissues. Therefore it is possible to develop a prediction model, based on BW, which describe the true energy balance of the cow. However, the change in BW reflects the true EB only if the BW is measured accurately. Also, unbiased BW and BW change estimates are required for the calculation of energy efficiency measurements like residual energy intake.

Modelling body weight changes

One way to handle and minimize the effects of systematic error and day-to-day random noise in BW measurements is to fit a parametric or time series model into the BW measurements and thereafter use the predicted BWs in calculations. In this task we examined the accuracy of different models in predicting BW of cows based on daily BW measurements and investigated the benefits of modelling for increasing the value of BW measurements as management and breeding tools. The data included twice a day BW measurements and monthly body condition scores from 177 primiparous and 53 multiparous Nordic Red cows collected from research farms during earlier and ongoing research projects. Totally the data included 50594 daily records. Average BW of the cows in the data was 606 kg, with a range from 449 to 837 kg. The average body condition score was 3.02, varying from 2.36 to 3.85. In the data, the morning BW was an average 7.3 kg less than the evening BW. In the modelling the average daily BW was used.

Five different smoothing models were tested. The base model was fixed regression (FIX-model) by cow with Wilmink function (Wilmink, 1987) and second order polynomial terms of days in milk as covariables. In Wilmink function term, the exponential decay in the beginning of lactation depends on parameter c in exp(-c*dim). The second model (MIX-model) fitted was a random regression with a fixed and random animal lactation stage functions. The third model (PER-model) was the MIX-model with period of weighting added (k=1,…,13). Fourth approach was a cubic smoothing spline with 8 knots evenly distributed in the time span (SPk8-model) and the fifth model was a cubic smoothing spline but with a smoothing penalty of equivalent to 5 degrees of freedom (SPdf5-model). The models were evaluated with model fit statistics and by calculating the correlations between predicted weekly average BW change and EB indicators of the cow. Weekly average change in BCS, calculated EB and milk fat-protein ratio (FP) were used as EB indicators. The goodness of fit of the different BW models was also evaluated by the accuracy of models for predicting REI.

References

Wilmink, J. B. M. 1987. Adjustment of test-day milk, fat and protein yield for age, season and stage of lactation. Livest. Prod. Sci. 16:335–348.

Task 1.5 New indicator traits for tissue energy mobilization based on MIR spectral data

Tuomo Kokkonen, Päivi Mäntysaari, Sari Kajava, Annu Palmio, Terhi Mehtiö, Clément Grelet, Laura Nyholm, Esa Mäntysaari, Martin Lidauer

Motivation

An increase in plasma NEFA (non-esterified fatty acids) is an established but expensive indicator of tissue mobilization in cows. It is now possible to estimate milk fat composition at low cost by mid infrared reflectance spectroscopy (MIR). This offers an opportunity to develop an innovative non-invasive technique for monitoring tissue energy mobilization without additional costs. In this task, the aim was to develop indicator traits based on single fatty acids, groups of fatty acids or ratios, which are highly correlated to tissue energy mobilization.

Three main activities were carried out: establishing fatty acid recording for Finnish dairy farms, collecting reference data for development of prediction equations, and developing prediction equations.

Establishing milk fatty acid recording for Finnish dairy farms

For the development of prediction equations for fatty acids contents, based on MIR readings from routine milk samples, in a first step, a semi-automatic system was built at the Valio Ltd milk laboratory that allowed obtaining MIR spectral readings for the research purposes and collection of the reference data. For updating the EU RobustMilk OptiMIR database with Finnish reference samples, in total 500 milk samples were collected from different Finnish herds and breeds. Samples were sent to Valio Ltd milk laboratory for MIR analyses and parallel samples were frozen for later analyses by gas chromatography.

During indoor-feeding period, 250 milk samples from herds of Luke (Jokioinen and Maaninka), Viikki, Ahlman and Mustiala were collected and analysed by MIR. The MIR spectral readings of these samples were sent to Walloon Agricultural Research Centre (CRA-W), Gembloux, Belgium, where they selected 50 most variable samples of the data set. For these 50 samples, parallel frozen samples were sent to Belgium in March 2014, where they were analysed by gas chromatography. In the same manner, another 250 milk samples were collected during pasture season 2014 and the same process was carried out as explained for the indoor-feeding samples. In total 104 Finnish milk samples from Nordic Red Cattle, Finncattle and Holstein cows have been included in the OptiMIR reference database.

Fatty acid prediction equations were updated based on the included Finnish samples by the Belgium group. The prediction equation coefficients, as well as spectra standardization coefficients, were received from Belgium and a prediction module was programmed to obtain fatty acid profiles from MIR spectral readings. In the first validation step, fatty acid profiles (31 different compounds) have been predicted for 7411 milk samples for making first basic validations. Mean contents of the milk compounds of these samples are given in Figure 1. The coefficients of variation are between 0.2 and 0.3 (Figure 2) indicating considerable variation in the contents across samples. Based on the literature, contents of fatty acids C16, C18 and C18:1 cis-9 increase in case of negative energy status. Validation reliability was high for C16 and C18:1 cis-9 (R^2=0.95) but still moderate (R^2=0.85) for C18.

Meanwhile collection of MIR spectral readings has been automatized at Valio Ltd laboratory and a MIR database has been established at Mtech Digital Solutions Ltd, which is in connection with the Finnish milk recoding database. Since 2015, MIR spectral readings are automatically transferred to Mtech Digital Solutions Ltd. for all routine milk samples of the Finnish milk recording system that are analysed at Valio laboratory in Seinäjoki.

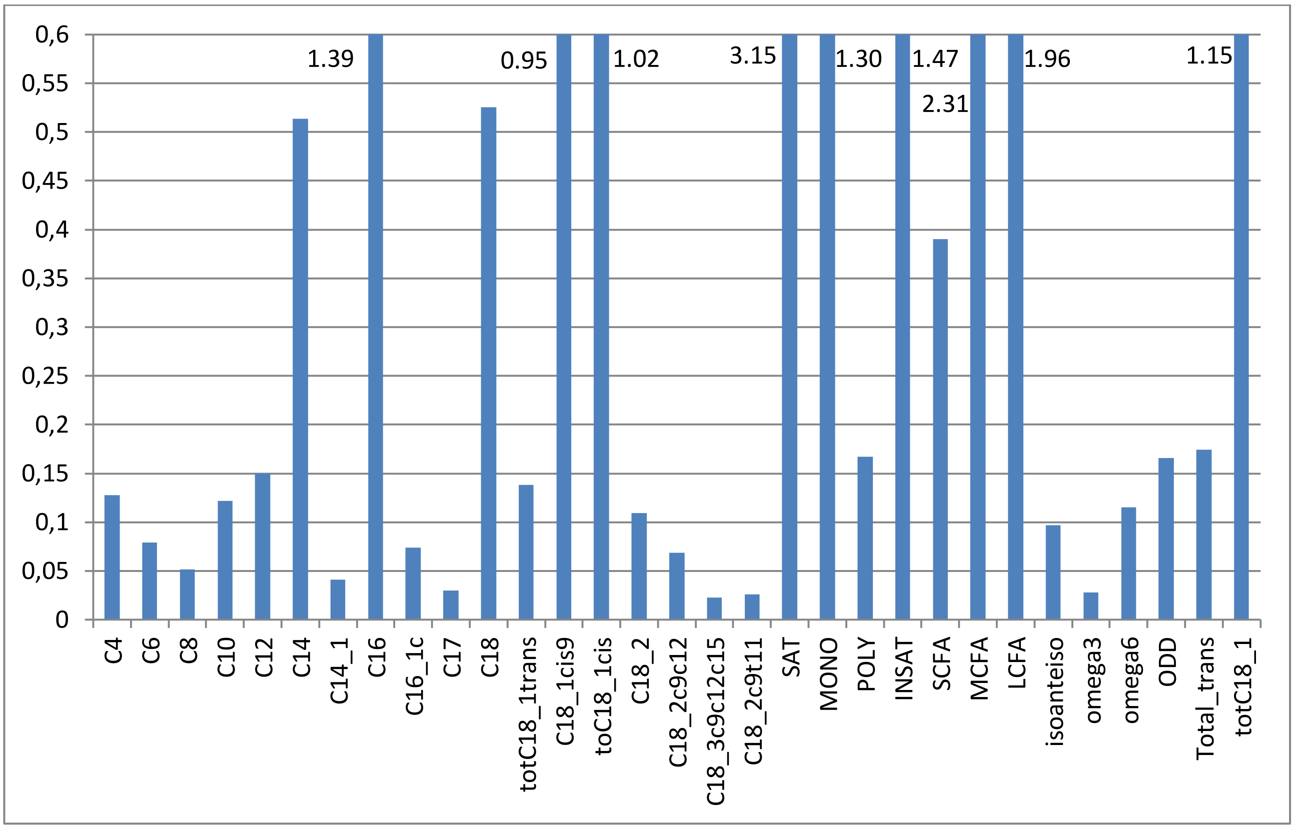

Figure 1: Mean content of milk components (g/100ml) of 7411 milk samples from Finnish dairy cows.

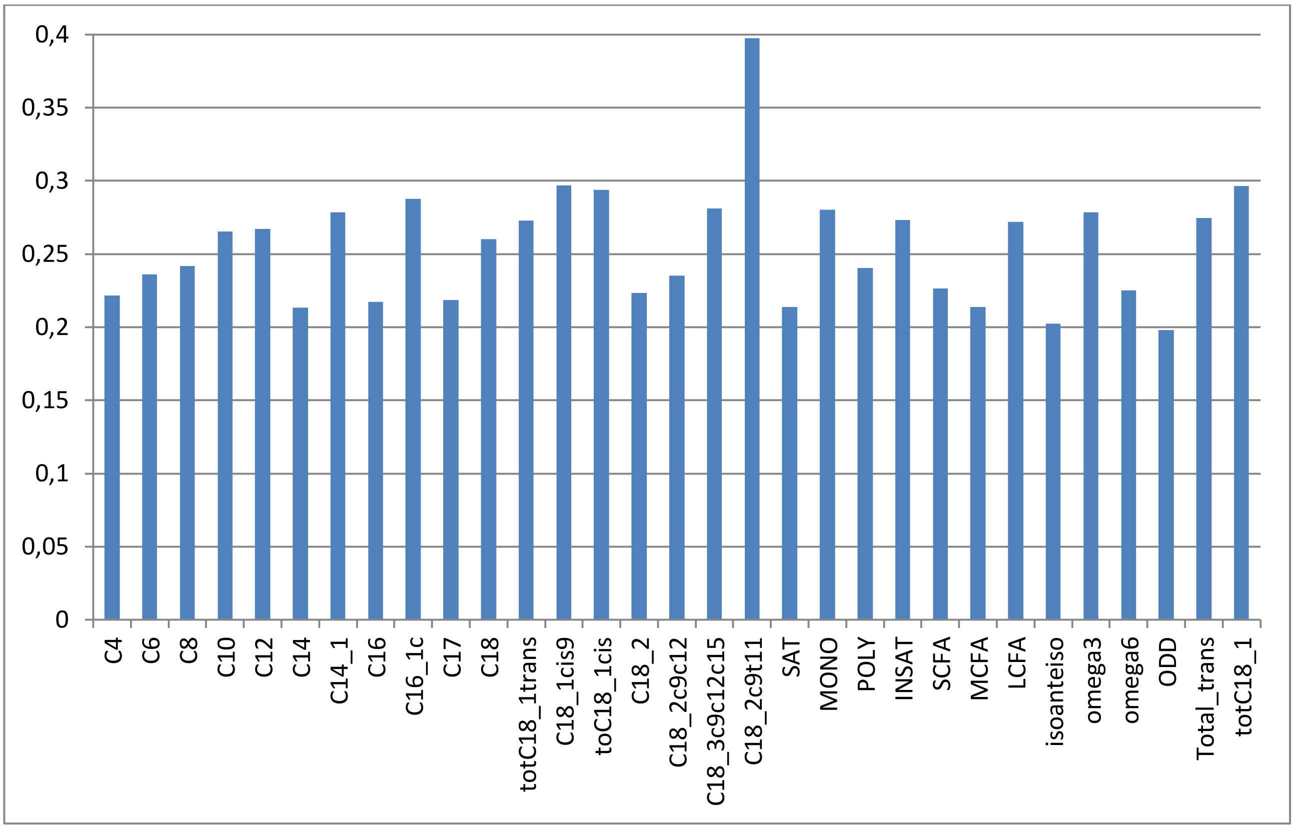

Figure 2: Coefficient of variation in milk components of 7411 milk samples from Finnish dairy cows.

Collecting reference data for development of prediction equations

A reference data with simultaneous measurements of blood NEFA concentrations and MIR spectral readings was built by collecting blood and milk samples over a period of two years. Data collection from primiparious cows started on September 2013 at Jokioinen, Maaninka and Viikki research farms. From September 2014 onwards also data from second lactations were collected.

Milk and blood samples were taken on lactation weeks 2 and 3 and lactation week 20. In weeks 2 and 3, two samples were taken (Monday + Thursday or Tuesday + Friday). Milk samples were taken from morning and evening milking whereas blood samples were taken after morning milking. Plasma was separated by centrifugation and sent to University of Helsinki for analysis of NEFA concentration.

Obtained NEFA observations and predicted fatty acid profiles for morning and evening milk samples, together with the original MIR spectral readings were merged with the milk production and feed efficiency data to form the reference data for developing prediction equations. The final reference data includes 809 NEFA observations from 143 cows of which 49 cows have observations also from the second lactation (Minkiö 103, Viikki 24 and Maaninka 16). For 778 NEFA observations also evening fatty acid profiles and MIR spectral readings are available.

Developing prediction equations for energy status

The relationships between milk composition and plasma NEFA concentration described by calculation of Pearson's correlation coefficients. Regression model to predict NEFA was developed using MIXED procedure of SAS. Parameters describing milk long-chain fatty acid (LCFA) composition were strongly correlated with each other and due to multicollinearity they were tested as individual predictors in linear multiple random regression models with fixed effects of parity, lactation day (DIM) and fat-protein ratio as additional predictors, random intercept and slope (LCFA) and cow nested within parity and herd specified as a subject.

Combining of body and milk traits to develop an energy status indicator was studied by testing various prediction models In the prediction models the changes of body weight (ΔBW) and body condition score (ΔBCS), milk fat-protein ratio (FP) and milk fatty acid (FA) composition were used as energy status (ES) indicators. The NEFA concentration was used as a biomarker for ES, and the associations between NEFA concentration and ES indicators were addressed. Multiple linear regression models to predict NEFA were developed without (model 1) or with (model 2) fatty acids (MIXED-procedure; SAS).

A further approach was to predict NEFA directly from the MIR spectral readings. For this, 212 most informative spectra points from the whole spectral reading (1060 points) were selected as a first set of covariables used for the partial least squares (PLS) analyses of the reference data. A first derivate transformation of the original absorption values was carried out prior to the analyses.

WP2. Modelling of feed efficiency and its economic and environmental value

Task 2.1 Economic and environmental value of total feed efficiency

Timo Sipiläinen, Päivi Akkanen

Motivation

The economic value of improving feed efficiency (FE) should be addressed more thoroughly. In this task the economic value of better input-output relation and lower environmental impacts were assessed using a bio-economic model of farm profit. The profit was derived on the basis of biological production relationships. We took into account the effect of improved feed efficiency on crop production. Increasing feed efficiency may adversely influence on some important traits like fertility and mastitis, which reduces the economic value of improved feed efficiency.

Developing an economic model for feed efficiency

There are only few analyses about the economic consequences of changing feed efficiency in milk production although there are quite a number of studies about efficiency of farming. Our approach is based on farm level modelling, which allows us to simulate effects of factors like feed efficiency on productivity and profitability of milk production. This model could also approximate the economics of the FE improvement process, although we are not constructing a dynamic model.

Production functions of milk with respect to silage and barley- rapeseed cake (80:20) concentrate are derived on the basis of isoquants presented in Ryhänen et al. (1996). Using the substitution rate estimates on different concentrate-silage ratios and assuming that they are independent on the production levels of the isoquants, it is possible to derive the level curves for the milk production function. We simulated the data for different production levels and estimated the production function on the basis of them. The second order polynomial function is the following (Table 1, vr refers to concentrate and sr to grass silage).

Table 1. Coefficients of the milk production function.

	Coefficients	*Standard Error*	*t Stat*	*P-value*
Intercept	-10,948	0,748	-14,634	0,000
vr	2,324	0,060	38,888	0,000
sr	1,991	0,092	21,685	0,000
vr2	-0,075	0,001	-58,723	0,000
sr2	0,004	0,003	1,412	0,160
vrsr	0,007	0,004	1,868	0,063

The derivative of the function (at each level of silage intake) provides the marginal physical product of milk with respect to the concentrate. We assumed the milk price of 0.35 €/kg ECM and the concentrate 0.24 €/kg dry matter (DM). This gave an optimal intensity for the concentrate of 11.5 kg DM when silage intake was 12 kg DM. The optimal level of concentrate was almost independent on the silage (D-value 680 g/kg DM) intake (a small cross effect) and thus the shape of the production functions remain almost the same at different intensity levels of e.g. silage, too. There is practically only a shift in levels of milk output. If we raise the value of ECM to 0.42 €/kg the optimal concentrate level increases approximately to 12 kg DM.

The starting point in our analysis is that the ratio includes 11.5 kg DM concentrates and 12 kg DM grass silage. This provides a milk yield of 31.3 kg ECM and comparable annual (305 days) milk yield is 9 546 kg ECM. This is close to the average milk yield of Holstein cows in the milk recording system in recording year 2014-15 (ProAgria 2015).

Simulated scenarios

For all scenarios we assumed that the farms could improve their feed efficiency in milk production by 5 percent. We assumed that there are no other changes in returns or costs. In principle there are three possible options for a farmer, which were addressed by the simulation study: 1) the farmer may increase the milk production per cow but keep the total amount produced at the earlier level; 2) keep the current yield level and use less concentrates in feeding; and 3) to increase milk production by 5 percent when keeping the feed input and the number of cows constant.

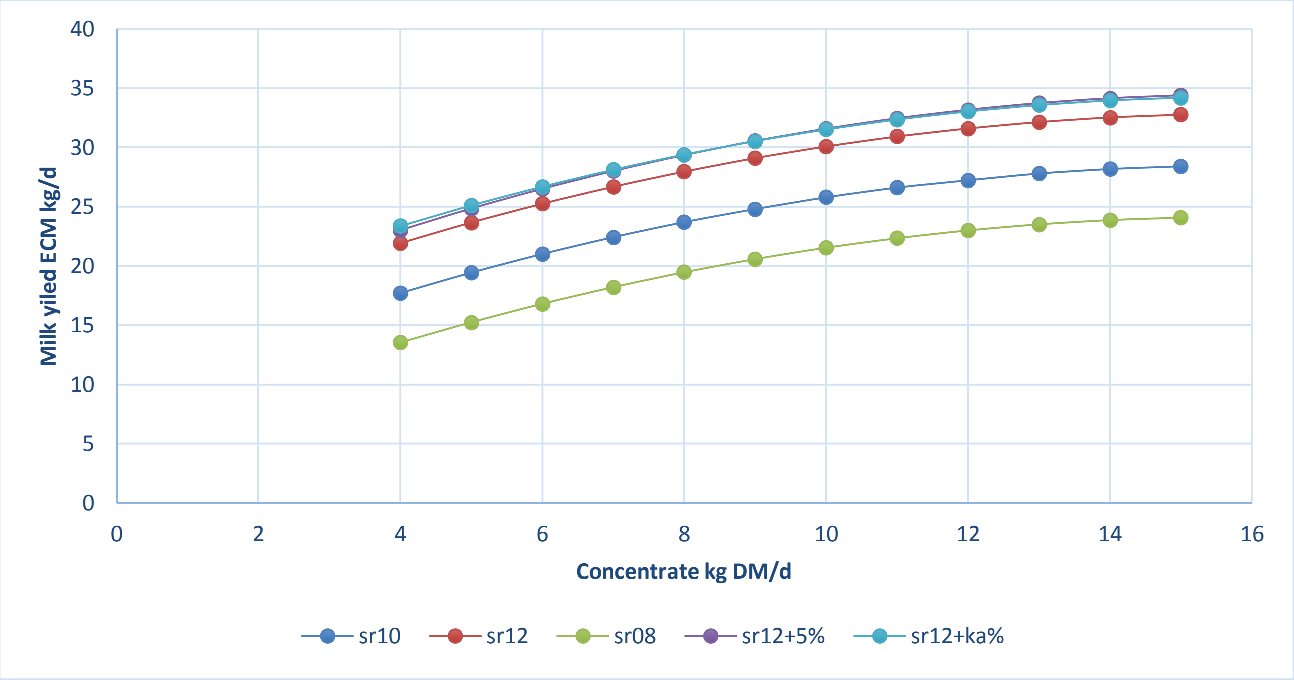

Figure 3. The daily milk production as a function of concentrates at different levels of grass silage intake.

Task 2.2 Justification of feed efficiency traits and predicted economical genetic response

Martin Lidauer, Esa Mäntysaari, Terhi Mehtiö, Enyew Negussie, Anna-Elisa Liinamo, Paulina Kokko, Jarmo Juga

Motivation

Breeding for feed efficiency will require choosing traits, which closely describe the breeding goal. Considering the complexity of feed efficiency in dairy cattle, it is a reasonable assumption that several traits will be needed to describe the feed efficiency breeding goal. The genetic variation of the traits, their correlation among each other and with other traits, their measurability and their economic importance are key factors needed, to conclude about a breeding goal and which traits are suitable for it. The aim of this task was threefold: 1) evaluation of different feed efficiency traits for the development of a breeding goal; 2) screening of possible indicator traits for feed efficiency applicable for genetic evaluations and 3) assessing the economic value of most suitable feed efficiency measurement.

Task 2.2.1 Evaluation of different feed efficiency traits for development of a breeding goal

Terhi Mehtiö, Anna-Elisa Liinamo, Esa Mäntysaari, Enyew Negussie, Martin Lidauer

For this task we reviewed the literature and research results from the earlier project "*Lehmän rehunkäyttökyky*". The literature study focused on literature with respect to the "biology of feed efficiency in dairy cattle" and with respect to the "definition of feed efficiency in dairy cattle". Summaries were written from the review work, which address the definition of feed efficiency from a biological, genetic, economic, environmental and animal breeding point of view.

Results considered for the earlier “*Lehmän rehunkäyttökyky*” project were variance component analyses for REI, ECE and EB. In that earlier project a data set was analysed that included weekly feed efficiency records from 400 Nordic Red nucleus dairy cattle at Luke research farm. The traits were analysed by repeatability and random regression modes to access heritabilities across first lactation, and genetic correlations with ECM, DMI, BW and BCS. The applied repeatability model was

$$y_{ijklm} = CY_i + CA_j + \sum_{n=1}^{4} b_n x_{ijklmn}(w) + p_k + a_l + e_{ijklm},$$

where fixed effects were calving-year (CY), calving age (CA), fixed lactation curve according to Ali and Schaeffer (1987), and random effects were permanent environment (p), animal (a) and residual (e). The random regression model was otherwise similar to the repeatability model except that the permanent environmental effect and the additive genetic effects were modelled by second order Legendre polynomials.

Reference

Ali, T.E., and L.R. Schaeffer. 1987. Accounting for covariances among test day milk yields in dairy cows. Can. J. Anim. Sci. 67:637-644.

Task 2.2.2 Feed efficiency indicator traits measureable on-farm

Terhi Mehtiö, Enyew Negussie, Esa Mäntysaari, Martin Lidauer

Initiating genetic evaluations for feed efficiency requires feed efficiency indicator traits which are routinely measurable on a large number of cows. Feed intake measurements are needed for almost all feed efficiency traits. However, on-farm measurement methods for feed intake are not available yet. Therefore, here we investigated two feed efficiency indicator traits, which have the potential to be recorded on a larger number of animals in the absence of feed intake measurements.

Indicator traits for energy conversion efficiency or energy conversion ratio

Ratio traits like ECE and energy conversion ratio (ECR) describe the efficiency of a cow in transforming energy of the diet into milk energy and therefore are of interest. If desired, such ratio traits can be transferred into a linear index *via* Taylor series expansion. Aim of this study was to find traits which are closely correlated to ECE or ECR under the absence of feed intake measurements. Daily feed efficiency records, collected from 539 primiparous Nordic Red dairy cows at Luke’s experimental farm in Jokioinen, were used. Traits were whole-lactation observations for metabolizable energy intake (MEI), ECM, metabolic body weight ($BW^{0.75}$), ECE=ECM/MEI and ECR=MEI/ECM. Because so far MEI is not available for cows under conventional recording, we included also indicator traits into the analyses. Therefore, MEI was substituted either by its expectation or by the expectation of MEI for maintenance. Thus the studied indicator traits for energy conversion efficiency were EE=ECM/E[MEI] and EE_M=ECM/E[MEI_M], and for energy conversion ratio ER=E[MEI]/ECM, ER_M=E[MEI_M]/ECM. The indicate EE_M is an easily understandable efficiency trait of its own (ECM produced by kg metabolic body weight) and could be named maintenance efficiency (MAE). It’s reciprocal is EE_M and could be named maintenance requirement ratio (MRR). Relationship among the cows was considered by including 3055 informative animals from four generations into the REML analyses. Bivariate analyses were carried out with an animal model including a calving-year-season as a fixed effect to assess the genetic correlations of indicator traits with direct trait as well as with the component traits.

The effect of inclusion of MRR into the current Nordic yield index on genetic improvement of feed efficiency and on net merit was assessed by investigating different selection indices. Necessary economic values were derived from the results of Task 2.2.3. These were for milk yield €0.0013/kg, for protein yield €4.56/kg, for fat yield €1.23/kg, and metabolizable energy intake €–0.0164/MJ ME.

Indicator trait for cow-specific dry matter digestibility

Motivation

In Task 1.1 we found high reliability for iNDF concentrations in faeces ($\text{iNDF}_{\text{faeces}}$) predicted by NIRS (Mehtiö et al. 2015). The $\text{iNDF}_{\text{faeces}}$ can be used as indicator for DMD, given that cows of the same comparison group consume the same diet, which is usually the case on dairy farms. To assess the heritability of $\text{iNDF}_{\text{faeces}}$ and its correlation with DMD, collection of faecal samples from research farm cows was carried out in Task 1.2 applying the protocol developed in Task 1.1. Also it was of interest to study the relationship between feed efficiency and cow-specific digestibility. For this the feed efficiency data (661 RDC cows) was used to estimate residual energy intake breeding values for the cows with digestibility records (129 cows).

Data

The research data for studying diet digestibility were compiled from three research farms in Finland and one research farm in Norway. From Finland there were 153 RDC cows with 490 observations from Luke Jokioinen research farm, 34 RDC cows with 83 observations from University of Helsinki research farm in Viikki, 40 RDC and 45 HOL cows with 285 observations from Luke Maaninka research farm and from Norway 48 RDC cows with 96 observations.

During the pilot study period (2012-2014) faecal samples were collected from cows during different stages of lactation. In Maaninka research farm the faecal sampling started in 2012 with a protocol of collecting samples for five consecutive days every morning and every evening, and combining the individual samples to one composite sample of the week (protocol C10). These data collected according to protocol C10 was used in Mehtiö et al. (2016) study. In April 2013 all three research farms Finland started collecting faecal samples for three consecutive days every morning (protocol C3). These three samples were combined to one composite sample. Until the end of 2014 faecal samples were collected at three different lactation stages (around 50, 150 and 250 DIM). After this the new sampling protocol, based on the results of the pilot study, was introduced and samples were collected for three consecutive days every morning from all cows in milk (between 29 and 294 DIM) every second month (according to Mehtiö et al., 2016). This was done to form large contemporary groups consuming the same feed. In Norway the samples were collected from all cows in milk for two times, in February and in March 2015.

Thus, the data set **A** (ALL data) consisted of all C10 and C3 samples collected in four different farms between 2012 and 2016, including in total 956 observations from 330 cows. This data set A also contained the data set **B** (Bi-monthly data), which consisted of 441 faeces samples from 144 cows that were collected according to the new protocol design between November 2014 and May 2016 in Jokioinen, Viikki and Maaninka research farms. The data set **B1** consisted of day one faecal and feed samples, the data set **B2** consisted of composite samples from day one and two and the data set **B3** consisted of composite samples from day one, two and three collected according to the new protocol. In total there were 441 observations from 144 cows from three Finnish research herds.

Modelling diet digestibility

A univariate repeated-measure animal model was fitted for the data set A. The model included fixed effects of breed, parity, lactation stage, feeding level and herd-year-month –interaction (HYM), $iNDF_{feed}$ as covariable and random effects of permanent environment, animal genetic effect and random residual. There were two breeds (RDC and HOL), two parity classes (primiparous or multiparous), three lactation stages (<100 DIM, 100-199 DIM and >199 DIM), three different feeding levels and 54 classes for HYM. The fixed effect of feeding level was included to model the difference between two concentrate levels in Maaninka C10 and two silage crude protein levels in Norway data sets. The HYM-variable was designed to describe the contemporary groups of animals consuming the same feed. However, only 47% of the data were collected using the new protocol (all the cows were sampled at the same time every second month) and forming large enough comparison groups was only possible for this data. Thus, there was still quite a large variation between iNDF content in feed within the same HYM-class of observations collected using the old protocol. To model the feeding more comprehensively $iNDF_{feed}$ was included in the model as covariate. Thus, the model for data set A was:

$y_{ijklmn} = breed_i + parity_j + lactation\ stage_k + feeding\ level_l + HYM_m + iNDF_{feedn} + g_n + pe_n + e_{ijklmn}$,

where y is a vector for $iNDF_{feces}$ or DMD_{iNDF} observations, breed, parity, lactation stage and HYM are the fixed effects, $iNDF_{feedn}$ is a regression coefficient and g_n is the random additive genetic effect for animal *n* [$g \sim N(0, \mathbf{A}\sigma^2_g)$, where **A** is the additive genetic relationship matrix among animals and σ^2_g is the additive genetic variance], pe_n is the random permanent environmental effect for animal *n* [$pe \sim N(0, \mathbf{I}\sigma^2_{pe})$, where **I** is an identity matrix and σ^2_{pe} is the permanent environmental variance] , and e_{ijklmn} random error term. Because the residual variances between three sampling protocols (C10, old and new C3) were varying, different residual variances were fitted for different protocols. Also, it was found that residual variance of Norway data was clearly different from other herds, and thus four different residual classes were fitted. Variance components were estimated by REML method applying expectation maximization (EM-REML) implemented in MiX99 software package.

For data set B the model was otherwise the same, but the fixed effect of feeding level and different residual variances were not needed as the data consisted only of samples collected according to the new protocol in Finland. Statistical analyses for repeatability estimates were performed using MIXED procedure in SAS®Studio software release 3.4 (SAS Institute Inc., Cary, NC, USA) and genetic parameters by REML method applying EM-REML implemented in the DMU software package.

Task 2.2.3 Prediction of economical genetic response

Pauliina Kokko, Jarmo Juga

Work on prediction of economical genetic response was carried out at Helsinki University. The main aim of this task was to investigate sustainable breeding strategies to increase the productivity and efficiency in dairy herds. Different breeding goals were constructed to evaluate the effect of including feed efficiency, growth and carcass traits in the breeding goal for RDC on the economic outcome of the breeding scheme. The expected genetic response in the new traits and current breeding objective traits were estimated for several different scenarios in the genomic selection scheme taking into account the investments needed for measuring residual feed intake (RFI) in AI test stations. The additional breeding goal traits analysed were growth traits (average daily gain of animals in the fattening and rearing periods), carcass traits (fat covering, fleshiness and dressing percentage), mature live weight (LW) of cows and RFI traits. For RFI, three breeding goal traits were applied (RFI in fattening animals, growing heifers and lactating cows) which were selected through two indicator traits (RFI measured in young bulls in a test station and an indicator trait for RFI in lactating cows). The breeding scheme was modelled under the current market situation in Finland using the deterministic simulation software ZPLAN+.

Task 2.3 Modelling of energy pathways in the cow

Terhi Mehtiö, Päivi Mäntysaari, Enyew Negussie, Esa Mäntysaari, Martin Lidauer

Motivation

The aim was to understand the genetic variation in partitioning the metabolizable energy to be used for the different biological pathways. For this, in a first attempt, metabolizable energy intake (MEI) was modelled by a mixed model with general fixed effects and cow-specific random effects. A model should be developed that describes the different pathways to which MEI is allocated by the cow: metabolic body weight ($BW^{0.75}$), body weight change (BWC) and ECM. Results should increase understanding about which pathways have the largest potential for improving feed efficiency.

Energy intake data

Data used for this study were from 495 cows from Rehtijärvi and Minkiö research farms collected between 1998 and 2014. Weekly averages of MEI were formed from daily feed intake records covering a period from 2nd to 40th week of lactation (n=12 350). Relationships between cows were modelled by a pedigree that included 2409 informative animals.

The studied traits included REI (ME MJ/d), MEI (MJ/d), ECM (kg/d), $BW^{0.75}$ (kg), body weight loss (BWL, kg/d) and body weight gain (BWG, kg/d). REI was estimated by modelling MEI by a multiple linear first-order regression including ECM output, $BW^{0.75}$, and piecewise regressions of BWL and BWG. Weekly cow-wise means of residuals were used as cow's REI measures. MEI was based on DMI of the feeds and their energy values. The energy values (ME MJ/kg DM) of the feeds were calculated according to Luke (2015). The daily MEI was corrected by the total DMI and concentration of ME and protein in the diet according to the correction equation given by Luke (2015).

Modelling of the data

Different kinds of least squares, repeatability and random regression models have been studied. Numerous publications have reported analyses of REI and RFI in dairy cows. Therefore, we used REI as a reference trait in this study and fitted a simple repeatability animal model:

$$\mathrm{REI}_{ijl} = \mathrm{rym}_i + \mathrm{lw}_j + \ \mathrm{a}_l + \mathrm{pe}_l + \epsilon_{ijl},$$

where REI is residual energy intake (ME MJ/d), rym is a fixed effect of recording year-month, lw is lactation week (2-40), a is a random animal genetic effect and pe is a random permanent environmental effect.

REI, which describes the efficiency of ME use, can be modelled alternatively by modelling MEI observations and including regressions on energy sinks ($BW^{0.75}$, ECM, BWG, BWL) into the model, which shall allow a better fit of the data.

$$\mathrm{MEI}_{ijls} = \mathrm{rym}_i + \mathrm{lw}_j + \mathrm{b}_{1_s}\mathrm{BW}_{jl}^{0.75} + \mathrm{b}_{2_s}\mathrm{ECM}_{jl} + \mathrm{b}_{3_s}\mathrm{BWG}_{jl} + \mathrm{b}_{4_s}\mathrm{BWL}_{jl} + \epsilon_{ijls},$$

where MEI is metabolizable energy intake (MJ/d), b_{cs} is a fixed regression coefficient b_c nested within lactation class s, where c = 1, 2, 3, 4 is a regression coefficient for maintenance, milk production, BWG, and BWL, respectively, and where lactation classes s are8 (classes: 2-5, 6-10, 11-15, 16-20, 21-25, 26-30, 31-35, 36-40 weeks of lactation), and ϵ is a random error term.
In contrary to the model for REI, the repeatability animal model for metabolizable energy efficiency (MEE) includes regressions on energy sinks as fixed effects:

$$\mathrm{MEI_{ijsl}} = \mathrm{rym_i} + \mathrm{lw_j} + \mathrm{b_{1_s}BW_{jl}^{0.75}} + \mathrm{b_{2_s}ECM_{jl}} + \mathrm{b_{3_s}BWG_{jl}} + \mathrm{b_{4_s}BWL_{jl}} + \mathrm{a_l} + \mathrm{pe_l} + \epsilon_{\mathrm{ijsl}}$$

For modelling partial metabolizable energy efficiency (pMEE) cow-specific partial regression coefficients are included for each energy pathway and by this resulting in a random regression model:

$$\begin{aligned}\mathrm{MEI_{ijsl}} = {} & \mathrm{rym_i} + \mathrm{lw_j} + \mathrm{b_{1_s}BW_{jl}^{0.75}} + \mathrm{b_{2_s}ECM_{jl}} + \mathrm{b_{3_s}BWG_{jl}} + \mathrm{b_{4_s}BWL_{jl}} + \mathrm{a_{0l}} + \mathrm{a_{1l}BW_{jl}^{0.75}} + \mathrm{a_{2l}ECM_{jl}} \\ & + \mathrm{a_{3l}BWG_{jl}} + \mathrm{a_{4l}BWL_{jl}} + \mathrm{pe_{0l}} + \mathrm{pe_{1l}BW_{jl}^{0.75}} + \mathrm{pe_{2l}ECM_{jl}} + \mathrm{pe_{3l}BWG_{jl}} + \mathrm{pe_{4l}BWL_{jl}} \\ & + \epsilon_{\mathrm{ijsl}}\end{aligned}$$

This model is similar to previous models, but also the random additive genetic and non-genetic effects are partitioned for intercept and random regression effects. As this model is very complex, three simpler random models were studied. The submodels differed in the number of random regression effects included into the permanent environmental and additive genetic effects. The alternative models included the following random regressions: on intercept and ECM (pMEE1); intercept, $BW^{0.75}$, ECM and BWG (pMEE2); and intercept, $BW^{0.75}$, BWG and BWL (pMEE3).

Task 2.4 Modelling of the genetics of feed efficiency and energy status

Enyew Negussie, Bingjie Li, Terhi Mehtiö, Päivi Mäntysaari, Peter Løvendahl, Britt Berglund, Martin Lidauer

Motivation

Modelling the genetics of feed efficiency requires comprehensive measurements from a large number of experimental cows. Therefore, in this task the cooperation among Nordic partners is important to create a sufficiently large research database. Research in this task focused on three main topics: 1) Building of a Nordic feed efficiency database and harmonization of feed efficiency recording across Nordic research farms, 2) investigating the suitability of using the Nordic feed efficiency database to develop genetic evaluations for feed efficiency, and 3) using the database to assess recording protocol for on-farm measuring of feed efficiency. The fourth topic planned was genetic analyses of field data for feed efficiency traits. However, first data became available in the second half of 2017 and therefore only first pilot analyses have been conducted.

Task 2.4.1 Combining of feed efficiency data across Nordic countries (required for the Nordic cooperation)

Enyew Negussie, Päivi Mäntysaari, Peter Løvendahl, Britt Berglund, Martin Lidauer

A contract, which defines ownership of data and conditions on use of data, has been signed by the participating research bodies from Denmark, Finland, Norway and Sweden (FUNC project). A protocol for combining of feed efficiency data from the Nordic countries has been developed and all countries except Norway have contributed basic feed efficiency data routinely to the Nordic feed efficiency database. Feed efficiency data with weekly measurements on dry matter intake, body weight, milk yield, protein %, fat %, lactose % and body condition score have been merged and a common pedigree was built. No agreement was found about including also energy intake data into the common database. To some extent, this was due to the different energy systems used in the Nordic countries. Thus, research on common Nordic feed efficiency data was restricted to dry matter intake. After extracting and validating all existing data, suitable data was included into the database. Furthermore, a common feed intake measurement protocol was agreed and implemented on the research farms for new recordings. Altogether, by the end of 2016, the Nordic feed efficiency database comprised of records from 2493 cows including Holstein, Nordic Red cattle, Jersey and Swedish local breeds (Table 2). Records were validated and a common pedigree was built. Therefore, Nordic dairy cattle pedigree information was used and extracted information was pruned to five generations.

Table 2. Breeds and number of dairy cows in the Nordic feed efficiency data by country (Total 2943)

Breeds	DNK	FIN	SWE	NOR	Total
HOL	789	---	207	---	996
RDC	228	525	179	---	932
JER	388	---	---	---	388
SKB	---	---	105	---	105
SKBxHOL	---	---	72	---	72

Task 2.4.2 Genetic analyses of dry matter intake in Nordic Red, Holstein and Jersey

Bingjie Li, Britt Berglund, Päivi Mäntysaari, Martin Lidauer, Peter Løvendahl

Motivation

The compiled Nordic feed efficiency data (see above) consists of many different feeding trials of which a large part was collected for different research questions. Furthermore, data was collected from different breeds, under different feeding and managing schemes and over a long time period. Dry matter intake was selected to be the most suitable trait for assessing the quality of the data, the genetic differences among breeds and whether obtained results are consistent with results reported in the literature from similar studies. Results should allow us to conclude about the value of the data for building a reference population for feed efficiency evaluation.

Nordic dry matter intake data

For the first study weekly avaerages of daily dry matter intake overvations from 1751 primiparous cows (771 HOL, 696 RDC, 284 JER) were included. The data was collected from 22 herds and 35 trials. Dry matter intake was on the same level for Holstein and Nordic Red cows but lower for Jersey (Figure 4).

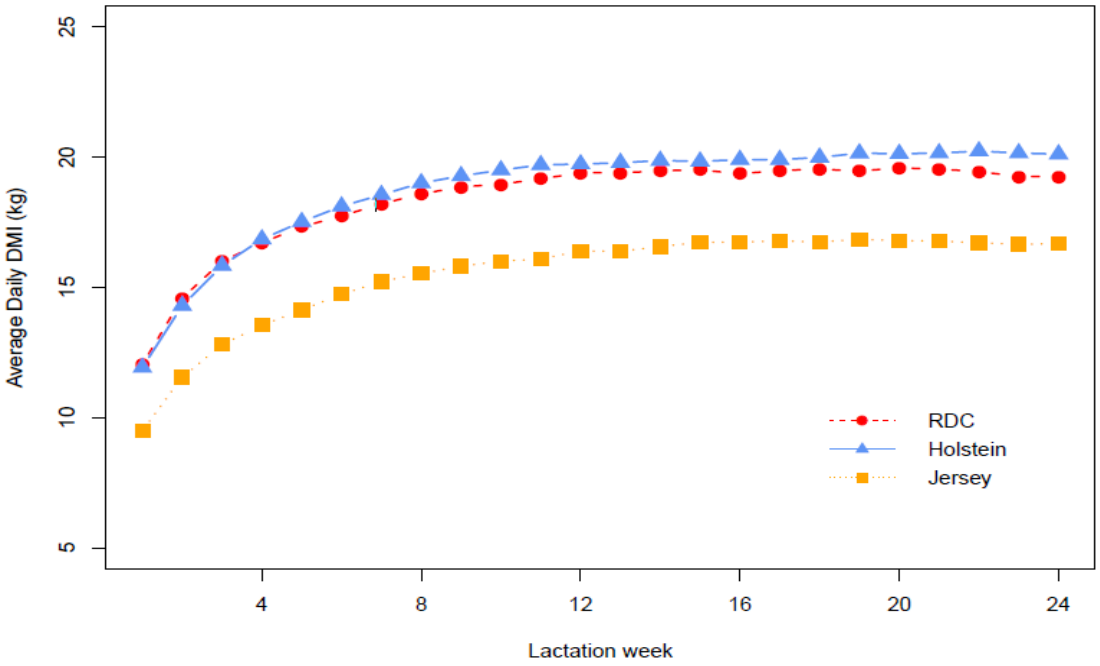

Figure 4. Average daily DMI during first 24 lactation weeks given for Nordic Rec cows (RDC), Holstein and Jersey.

Genetic analyses of dry matter intake

Multiple trait linear mixed models and random regression linear mixed models were fitted to access genetic correlations between DMI observations among different lactation weeks, changes in heritability across lactation stage and genetic differences between breeds. For the multiple trait analyses observations from the same lactation month were considered as the same trait, resulting in 6 different periods. Bivariate REML analyses were carried out for the estimation of correlations among these periods. The applied statistical model included the fixed effects breed, herd, calving age, trial × recording year × season and lactation week, and as random effects permanent environment, additive genetic animal and residual.

Task 2.4.3 Accuracy of feed efficiency breeding values when data collection is sparse

Enyew Negussie, Päivi Mäntysaari, Peter Løvendahl, Britt Berglund, Martin Lidauer

Motivation

Almost all feed efficiency traits need information on DMI. So far reliable DMI observations are resourced from research farms. DMI records collected from research farms are expensive and therefore collection of large data is limited. To allow any meaningful genetic and genomic analysis DMI observations are needed from a large number of animals. This calls for an on-farm DMI measurement method. However, even if such a method can be developed, optimal sampling strategy is needed to keep costs at minimum.

So far there is very limited information on the accuracy of estimated breeding values (EBV) for DMI based on observations from on-farm recording, and particularly studies that simulated a realistic on-farm DMI recording conditions are lacking. Moreover, different studies have demonstrated that DMI is not the same trait along the course of lactation. Therefore it is valuable to assess an optimal sampling strategy for DMI during the course of lactation to achieve highest possible accuracy when DMI observations are limited.

The main objectives of this task were first to estimate genetic parameters for daily DMI using random regression models and secondly to test the accuracy of EBVs for feed intake when dry matter intake recording becomes sparse under different on-farm recording scenarios. The outcome of this will provide optimal future DMI sampling strategies for use in commercial farms that takes associated cost, logistics and accuracy of sire breeding values into consideration.

Data for genetic analyses

The data used for the estimation of variance components and associated genetic parameters was from Luke's experimental dairy farm maintaining the Nordic Red dairy cows nucleus animals. The data is from several, consecutive and continuous feeding trials held since 2009 when automated feed intake, body weight and milk production data collection systems have been employed with the main purpose of studying the animal variation in the components of feed efficiency. The whole data was from 225 primiparous Nordic Red dairy cows of which an edited sample of the data was used for the estimation of variance components and associated genetic parameters. The actual data used for the estimation of the variance components included 38 421 daily dry matter intake observations recorded from the second to the 40th week of lactation. Feed intake was not recorded during the pasture period resulting in gaps in the feed intake data for animals which were in lactation during the summer months. The data from first week of lactation was also discarded due to the big variability in studied traits, and the possibility that it may compromise the subsequent genetic analyses. The final data included records on DMI (kg), ECM (kg), REI (MJ/d) and ECE which is calculated as milk energy output/energy intake as kg ECM/MJ ME intake. The mean DMI was 19.9 kg/d with standard deviation of 2.9 kg. The pedigree had in total 2409 animals, pruned to five generations back from the animals with observations. Traits included in the study were: DMI, REI and ECE.

Model for genetic analysis

Variance components and the corresponding genetic parameters for the daily DMI was estimated using random regression models fitting Legendre polynomials as time variable functions. The random regression model used for the estimation of variance components can be described as:

$$y_{d:ijpklmo} = Age_i + cys_j + rd_k + \sum_{r=o}^{4} D_{lr}\phi_{\pi}(d)_r + \sum_{r=o}^{2} pe_{mr}\phi_{\pi}(d)_r + \sum_{r=o}^{2} a_{mr}\,\phi_{\alpha}(d)_r + \varepsilon_{d:ijpklmo},$$

where: $y_{d;ijpklmo}$ is daily DMI observations of cow *m* recorded at age *i* within calving-year*season *j* and on recording day *k*. *Age* is age at calving in months, *cys* is the calving-year*season, where a calving year was divided into four seasons November to February, March to April, May to July and August to October; *rd* is a random effect of recording day, $\boldsymbol{D}_{lr}$ is a vector of fixed regression coefficient on stages of lactation day *d* modelled with $\boldsymbol{\o}_{\pi}(\mathrm{d})_{\mathrm{r}}$ Legendry polynomials order 5 to describe the shape of the dry matter intake curve during lactation, pe_{mr} is the r^{th} regression coefficient of the Legendre polynomial for the permanent environmental effect of the m^{th} cow, a_{mr} is r^{th} Legendre polynomial for the additive genetic effect of the m^{th} cow, $\boldsymbol{\o}_{\alpha}(\mathrm{d})_{\mathrm{r}}$ is the term of the second-order Legendre polynomial for *pe* and *a* and ε_{ijklmo} is random residual.

Simulation of different recording scenarios

For assessing the accuracy of breeding values associated with different frequency of on-farm recording, as simulation study with several different DMI on-farm recording scenarios (SCN) was carried out. For this, five different on-farm DMI intake recording scenarios were studied. For each scenario the accuracy of breeding values for the different traits were calculated. The five scenarios were: daily DMI is recorded once every week (SCN1); once every month (SCN2); once every second month (SCN3); once every third month (SCN4); and once every fourth month (SCN5).

The simulated data sets for SCN1 were based on a true data set from the combined Nordic feed efficiency data (see Task 2.4). The extracted data set (FUNC data set) contained of 53 000 records in weekly intervals from 900 Holstein cows. For each record a daily observation was simulated based on the variance component parameters estimated from Luke’s daily feed efficiency data as explained above. Phenotypic values ($\mathbf{y}_h$) for each trait were generated for each cow *h* of FUNC data set. Observations were simulated based on the model given above, by sampling from normal distributions and applying Cholesky decompositions of the estimated variance component matrices as implemented into the MiX99 software (Stranden and Lidauer, 1999). Values of fixed effects do not affect the distribution of random variables (Garcia-Cortes et al., 1995) and thus are simulated with values of zero. Phantom parent group effects were set to zero and each animal’s true breeding values was generated as the parental average plus a Mendelian sampling deviation. Simulated observations were finally generated by summing for each record the corresponding effects and adding a random error term. Five data set replicates were simulated for SCN1. The data sets for SCN2, SCN3, SCN4 and SCN5 were extracted from SCN1 dataset replicated by dropping records to increase data recording intervals. This resulted in a data structure as given in Table 3.

Table 3. Size of data sets and number of observations per cow given for different recording scenarios.

Scenario	*Dry matter intake recording Interval: once in*	*Observations per cow*	*Total number of observations*
SCN1	7 days	34.7	25 636
SCN2	1 month	9.5	6 986
SCN3	2 months	4.4	3 239
SCN4	3 months	3.1	2 299
SCN5	4 months	2.3	1 691

Assessment of accuracy of estimated breeding values

Breeding values were estimated for each replicates of the simulated dataset in each of the five different scenarios. The model used for the estimation of breeding values was the same as the model that was used for the estimation of variance components fitting random regression models. The resulting random regression coefficients of the breeding value solutions were compiled to calculate 280-day breeding values for both true ($TBV_{7\text{-}280d}$) and estimated breeding values ($EBV_{7\text{-}280d}$) as follows:

$TBV_{Ti} = \sum_{d=7}^{280} \text{ø}(d)\hat{a}(d)$, and $EBV_{Ei} = \sum_{d=7}^{280} \text{ø}(d)\hat{a}(d)$, where, TBV_{Ti} and EBV_{Ei} are true breeding values and estimated breeding values, respectively.

Within each scenario, for each replicate the correlation between true and estimated breeding values was calculated for different animal groups and obtained correlations were averaged over scenarios.

Reference

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WP3. Development of a method for recording dry matter intake on-farm

Task 3.1 Assessment of required accuracy for an on-farm dry matter intake measurement

Pekka Huhtanen, Abdulai Guinguina, Kevin Shingfield, Seppo Ahvenjärvi

Motivation

The objective of the current work package was to develop models for predicting feed intake and feed efficiency in dairy cows using single external marker or double markers (both internal and external).

Meta data from digestion trials

Calculations were done using data sets on measurements from cows used in digestion trials. All digestion trials were conducted as either Latin square or cyclic change-over designs. The data set comprised 442 individual cow/period observations originating from 29 trials conducted in Denmark (10), Finland (18) and Sweden (1). Diets were fed as TMR in forage to concentrate ratio of 60:40 on average. Grass silage was the main forage component for all diets, but in 2 trials, grass silage was partially replaced with red clover or whole-crop barley silages. Hay was used in 2 trials. Concentrate supplements contained oats (dehulled, starch or bran) and barley (starch or bran), protein supplements, typically soybean meal, rapeseed meal or rapeseed expeller.

All studies used one or more external and/or internal markers and reported actual DMI, faecal dry matter (FDM) output, total tract dry matter digestibility (DMD), ECM, live weight (LW), and dietary and faecal marker concentrations. In studies where ECM was not reported, it was calculated from milk yield and milk composition as:

ECM (kg) = Milk yield (kg) × (383 × fat% + 242 × protein% + 165.4 × lactose% + 20.7) / 3140 (Sjaunja et al., 1991).

Predicting faecal output and dry matter intake

FDM predictions (pFDM) were made using external marker and where more than one external marker was used, the marker of choice was based on retention time in the order, Cr-mordant > Yb > Fluid marker (Cr and Co EDTAs, PEG). FDM was calculated by the equation:

pFDM = external marker dose (g/d)/ faecal external marker concentration (g/kg DM).

DMD prediction (pDMD) was made from internal markers iNDF and AIA and was calculated as:

pDMD = 1-(dietary internal marker concentration /faecal internal marker concentration).

However, in 3 trials where only external markers were used, the one with the longer retention time and the one with higher rate of passage were used for FDM and DMD predictions respectively. The external markers used for pFDM and pDMD were Yb and Co-EDTA, Cr-mordant and Yb and Cr-mordant and PEG respectively. DMI was predicted first from external markers i.e. (pDMI1= p FDM/1-DMD) and then from double markers i.e. (pDMI2= pFDM/1-pDMD).

Assessment of accuracy

Estimates of variance components were made using the PROC MIXED procedure of SAS (version 9.4; SAS Institute Inc., Cary, NC) with experiment, diet within experiment, period within experiment, and cow within experiment as random factors. Covariance structure was specified using the TYPE = VC option in the RANDOM statement. From these estimates, repeatability values for DMI, pDMI1 and pDMI2 were calculated as the ratio of cow within experiment variance to the sum of cow within experiment variance and residual variance. Repeatability values provided an estimate of the correlation between values from consecutive samples on the same cow, on the same diet, and within the same period of the same experiment. The standard deviation and coefficient of variation for each factor were calculated as the square root of the variance estimate and standard deviation divided by the corresponding mean value of each factor respectively.

Also relationship between DMI and pDMI1 and pDMI2 were explored by regression analysis within the MIXED procedure of SAS. Subsequently, mixed procedure in SAS was used to develop models for predicting feed efficiency defined as observed kg ECM/observed kg DMI. The method = ML (maximum likelihood) statement was used in the PROC MIXED model syntax. Only one random independent (experiment) variable was used to avoid over parameterized models and improve convergence. The models were evaluated on the basis of Akaike's information criterion (AIC) and residual variance.

Task 3.2 Examination of external candidate markers

Seppo Ahvenjärvi, Laura Nyholm, Esa Mäntysaari, Martin Lidauer

Motivation

The aim of this task was to screen and evaluate a range of potential external markers to determine faecal dry matter output in dairy cows. Finding a suitable candidate marker was the first step in developing an on-farm measurement technique to determine faecal dry matter output. Dry matter intake could be estimated based on faecal output and either cow or diet specific digestibility coefficient.

Screening of candidate markers

Novel candidate markers were selected for initial screening based on three main criteria. Firstly, a potential marker compound had to be inert, i.e. non-degradable and non-absorbable, in the digestive tract of ruminants. Secondly, a potential compound had to be quantified using NIRS method. Thirdly, the compound had to be compatible with EU regulations on the use of feed ingredients for animal nutrition. The second criterion limited the choice of potential markers to organic compounds because mainly covalent bonds in organic substances are known to absorb near infrared wavelengths. Five different compounds charcoal, graphite, polyethylene glycol (PEG), chitin and galalith met the above mentioned criteria and were selected for evaluation as external markers. For NIRS calibration purposes incremental amounts of each marker were mixed with dairy cow faeces to obtain 27 samples with a wide range of marker concentrations. These samples were scanned using NIRS to identify specific spectral areas that exhibit correlations with known marker concentrations. When the relationship between marker concentrations estimated using NIRS and those determined in the lab were examined, the smallest standard error of prediction was noted for PEG and chitin. With galalith the precision of NIRS analysis was lower than that observed with PEG and chitin. With charcoal and graphite the results from NIRS calibrations failed to identify spectral areas specific to these compounds. Based on these results PEG and chitin were selected as the most promising candidate markers that could be used to determine faecal dry matter output in dairy cows.

Physiological experiment

Two physiological experiments with 6 lactating dairy cows were carried out to evaluate PEG and chitin as marker compounds. The first experiment was conducted between October and December 2014. The experiment consisted of two experimental periods and two different diets that were offered to experimental cows to introduce differences in feed intake and faecal output. PEG was administered twice daily into the rumen to determine daily faecal output. Direct measurements of daily feed intake and faecal output were carried out to assess the accuracy of indirect measurements attained using PEG. The second physiological experiment similar to that described above was conducted between December 2014 and February 2015 to evaluate chitin as an alternative marker to PEG. Unlike PEG chitin is an insoluble compound that is associated with particulate matter and, consequently, is likely to have considerably slower passage rate than that of PEG.

Task 3.3 Assessment of the administration of the external marker

Seppo Ahvenjärvi, Laura Nyholm, Esa Mäntysaari, Martin Lidauer

Motivation

The aim of this task was to address the question how frequently external markers should be introduced into the rumen. The extreme alternatives are either continuous administration or a single dose per day but a pragmatic choice is likely to be found somewhere between the extremes.

Administration of markers

This issue was studied in two physiological experiments with 6 lactating dairy cows described above under Task 3.2. The markers (either PEG or chitin) were dosed into the rumen of experimental animals either twice daily over a period of 11 days and as a single dose followed by frequent collection of faecal grab samples over 96 h post dose. Time required reaching equilibrium between PEG intake and faecal output was determined based on marker concentration patterns in faeces observed over the first 7 days after the onset of marker administration. Diurnal variation in faecal marker concentrations over days 8 to 11 after the onset of marker administration was determined based on hourly collection of faecal spot samples between morning and evening meals (i.e. between 0600 to 1700 h). Marker passage kinetics was determined based on a single dose and observed marker excretion pattern in faeces. Passage kinetics was used to model the effects of alternative marker administration protocols on diurnal variation in faecal marker concentrations.

Task 3.4 Validation of the dry matter intake measurement method

Marketta Rinne, Päivi Mäntysaari, Laura Nyholm, Seppo Ahvenjärvi, Esa Mäntysaari, Martin Lidauer

Motivation

The aim of this task was to get information about the feasibility of the marker methods in estimating feed intake under circumstances that resemble practical farms. Two external markers, PEG and chitin, were used in separate dairy cow experiments. In both experiments, markers were given either as part of the basal concentrate delivered from kiosks (marker group: PEG-K and Chi-K), or mixed with the concentrate given at the milking parlour (marker group: PEG-MP and Chi-MP).

Feeding trial

The experiments were conducted in Luke Minkiö dairy research barn during spring 2016 using 40 primiparous cows in both experiments. A dilute concentrate mixture was prepared to be used as the main concentrate feed of the cows the other one being a fortified mixture, which was offered in the milking parlour. This way we could compare a more stable marker intake to a method where the marker was received in two separate meals. Both experiments had 2 periods and cows were divided into two groups, which switched treatments for the second period. Both methods were planned to result in a 300-g intake of the marker per day. The reference feed intake measurements were obtained using routine methods at Minkiö barn, and faecal grab samples were collected on 3 days after morning and evening milking.

Processing of results

Faecal samples were analysed by NIRS for PEG, chitin and iNDF. Also the silage samples of each faecal sampling period were analysed by NIRS for iNDF. The iNDF concentration of the concentrates on each period was analysed by rumen incubation. The predicted DMI of the cows were calculated based on faecal output and digestibility of the diet.

3.2 Results

WP1. Phenotypic measuring of feed efficiency and metabolic functions

Task 1.1 Measurement protocol for cow-specific digestibility

Marketta Rinne, Terhi Mehtiö, Päivi Mäntysaari, Auvo Sairanen, Laura Nyholm, Timo Pitkänen, Esa Mäntysaari, Martin Lidauer

Organic matter digestibility

The statistical analyses for OMD showed that digestibility increased as lactation progressed. The repeatability estimates between different lactation stages were low which suggests that several faecal collections during lactation are beneficial. Higher repeatability estimates of composite samples compared to lower repeatability estimates between individual samples indicate that collecting of composite samples is preferable. The obtained variability in OMD across cows and the estimated repeatabilities give evidence that genetic improvement of dairy cattle digestibility might be possible. However, the accuracy of NIRS predictions for OMD should be higher to be able to predict small differences in OMD between the cows. These results were published in the proceedings of 10th World Congress on Genetics Applied to Livestock Production (WCGALP) in Vancouver, Canada August 2014 and presented as a poster.
https://asas.org/docs/default-source/wcgalp-posters/566_paper_9128_manuscript_437_0.pdf?sfvrsn=2

Dry matter digestibility

Alternatively, the trait $\mathrm{DMD}_{\mathrm{iNDF}}$ was studied: For this digestibility trait iNDF is used as an internal marker where concentration of iNDF in feed and faeces was obtained by NIRS scans. Hence, DMD can be calculated:

$$DMD_{iNDF} = 1 - \frac{iNDF_{feed}}{iNDF_{faeces}}.$$

We applied the same statistical model to the observations of the different digestibility traits under study to estimate the phenotypic correlations between the different traits definitions. As expected, obtained correlations were high between reference traits ($\mathrm{DMD}_{\mathrm{AIA}}$ and $\mathrm{OMD}_{\mathrm{AIA}}$) and iNDF-based predictions ($\mathrm{DMD}_{\mathrm{iNDF}}$ and $\mathrm{iNDF}_{\mathrm{faeces}}$). However, correlations between digestibility measures predicted by NIRS and corresponding reference digestibility measures by AIA were only moderate (Table 4).

Table 4. Phenotypic correlations between digestibility measures (dry matter digestibility by AIA, DMD_{AIA}; organic matter digestibility by AIA, OMD_{AIA}; DMD_{iNDF}, OMD, and iNDF predictions by NIRS from faeces, OMD_{faeces} and $iNDF_{faeces}$).

	50 DIM	150 DIM	250 DIM	All
DMD_{AIA}, DMD_{iNDF}	0.44	0.50	0.43	0.45
OMD_{AIA}, OMD_{faeces}	0.30	0.62	0.58	0.57
DMD_{AIA}, OMD_{AIA}	0.98	0.98	0.98	0.97
DMD_{iNDF}, $iNDF_{faeces}$	0.97	0.99	0.99	0.97
DMD_{AIA}, $iNDF_{faeces}$	0.35	0.50	0.36	0.41
$iNDF_{faeces}$, OMD_{faeces}	-0.06	0.13	0.01	0.04

The reason for these moderate correlations might be manifold. When correlating the raw observations we obtained correlations over 0.70 between DMD_{AIA} and DMD_{iNDF}, which is very positive as also the DMD_{AIA} measurements include measurement errors. However, when fitting environmental effects, correlations decreased, which can be expected as remaining variation between cows is smaller. This indicates that NIRS predictions for iNDF or OMD from faeces are associated with a large standard error. Therefore, we increased the reference data to come up with more reliable prediction for all following analyse in this project. Another complication was in predicting $iNDF_{feed}$, because the NIRS reference data is based on silage and the feed used in this study was total mixed ration, which could have reduced prediction accuracy.

Predictor trait for dry matter digestibility

The high correlation between DMD_{iNDF} and $iNDF_{faeces}$ proves that $iNDF_{faeces}$ is a promising trait for cow-specific digestibility given that $iNDF_{faeces}$ observations are modelled for the statistical analysis in a way that all cows in the same comparison group were also fed the same feed. Choosing $iNDF_{faeces}$ as a predictor trait for cow-specific digestibility is supported by the repeatability estimates we obtained (Table 5).

Comparison of digestibility data from two herds with different feeding regimes

In a pilot study we also studied the data collected from Minkiö research farm and compared these results with those from Maaninka. In Minkiö data there were 45 primiparous Nordic Red Cattle (RDC) cows and for each cow one observation from approximately 50, 150 and 250 days in milk and one from dry period was available. From each lactation stage three samples were collected from consecutive days and then composed as one composite sample prior to the NIRS scan. Predicting iNDF in feed was not straight forward for feed samples from Minkiö because other studies require a feeding regime where silage and concentrates are fed separately. Thus, iNDF in silage was predicted by NIRS and table values were used for the iNDF concentration in the cow-individually fed concentrates to calculated cow-specific iNDF concentrations. Positively, iNDF prediction for silage suited better the iNDF reference data base, but individual concentrate feeding increased pre-processing work of observation. For this comparison analysis from the Maaninka data the average of three individual consecutive morning measurements (Tuesday to Thursday) formed one observation, whereas one observation from the Minkiö data was obtained by three individual consecutive morning spot samples (Tuesday to Thursday), which were mixed prior to NIRS scanning.

Variability of $\text{OMD}_{\text{faeces}}$ and $\text{iNDF}_{\text{faeces}}$ across cows was higher in Minkiö data compared to Maaninka (Table 5). This is most likely explained by the low number of cows included from the Maaninka trail (20 cows) that were suitable to be included for this analysis. Repeatability estimates for the different digestibility traits were more consistent across the different traits in the Minkiö data and on an expectable level. Data from the Minkiö trial were from one breed only and all cows were fed the same diet, and hence the design of the trial (still ongoing) is closer to usual feeding and herd management at commercial farms.

Table 5. Variation in different digestibility measurements across cows and repeatability of measurements for observations of 20 cows of the Maaninka trial and 45 cows of the Minkiö trial.

	Maaninka DMD_{iNDF}	Minkiö DMD_{iNDF}	Maaninka $\text{iNDF}_{\text{faeces}}$	Minkiö $\text{iNDF}_{\text{faeces}}$	Maaninka $\text{OMD}_{\text{faeces}}$	Minkiö $\text{OMD}_{\text{faeces}}$
σ^2_{animal}	96.9	150.6	53.3	71.8	13.5	39.5
σ^2_{error}	442.0	790.5	62.0	227.0	230.3	170.7
r	0.18	0.16	0.47	0.24	0.06	0.19
CV	1.50	2.04	3.69	4.30	0.51	0.86

Development of a faecal sampling protocol

Based on all analyses of the Maaninka and Minkiö data DMD_{iNDF} and $\text{iNDF}_{\text{faeces}}$ were found to be the most promising traits to assess the digestive ability of an individual cow and therefore we decided to focus on DMD_{iNDF} and $\text{iNDF}_{\text{faeces}}$ when developing the sampling protocol for research farms in the Nordic countries.

The sampling protocol was developed based on the study of the 20-cow subset data from Maaninka. First, we calculated the correlations between composite samples and means of different combinations of individual samples for DMD_{iNDF}. The results showed that the correlations are stronger when the number of individual samples increases. However, after three samples the increase was clearly lower. Repeatability estimates for DMD_{iNDF} showed that repeatabilities nearly doubled when going from one single sample to composite sample of three spot samples. There was only very little or no gain in repeatability estimates when composite samples were made from four or five spot samples.

Based on the obtained estimates we assessed the expected accuracy of a future cow breeding value for digestibility depending on the accuracy of one single digestibility measurement and number of measurements per lactation. For this assessment we chose repeatability estimates of 0.15, 0.25 and 0.30 based on the results from this study and heritability estimates of 0.05 and 0.10 based on obtained repeatability estimates and on literature (Berry et al. 2007). The accuracy was calculated as: $\sqrt{\frac{nh^2}{1+(n-1)r}}$.

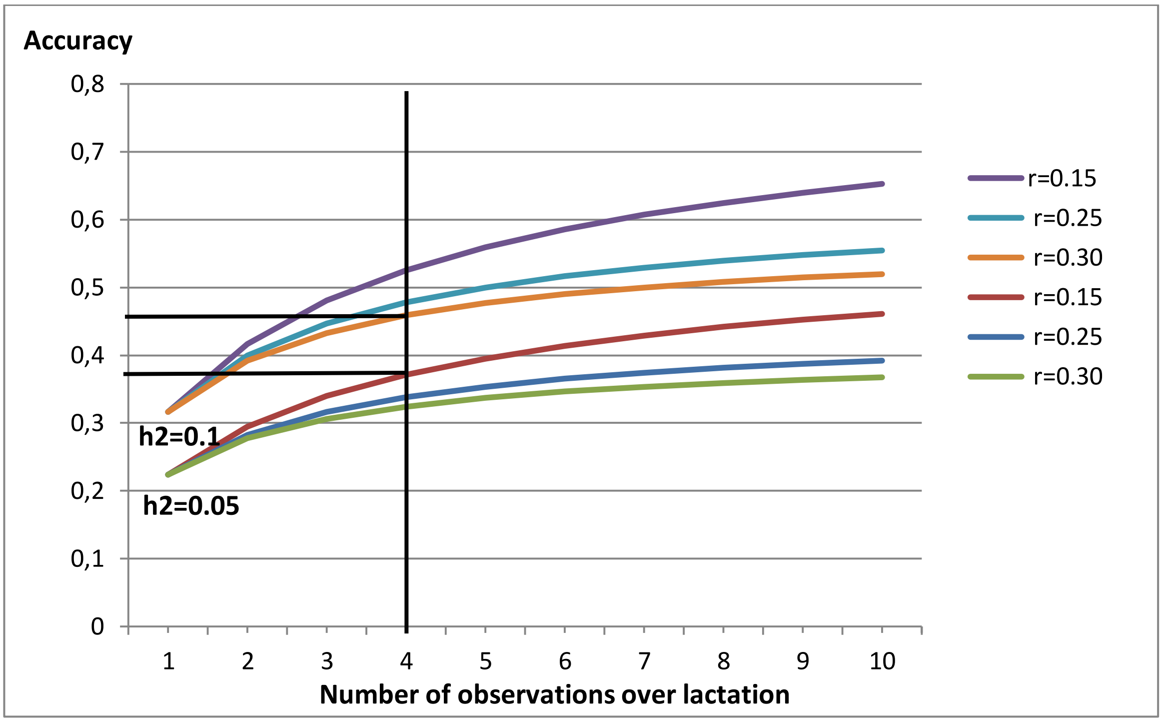

Figure 5: Increase in accuracy of breeding values by increasing number of observations for different heritabilities (h2) and repeatabilities (r).

As shown in Figure 5, a protocol with four observations per cow over lactation gives an accuracy of 0.38 to 0.47 depending on the “true” heritability and repeatability estimates. For on-farm measuring the number of observations will be small to keep cost at a minimum. Given spot samples are taken four times a year, a cow will have between 2 to 3 digestibility observations, which would equal breeding value accuracy between 0.30 and 0.40 and this equals for a sire with 50 daughters to accuracy between 0.70 and 0.80.

Based on these results, a protocol for faecal sampling at Nordic research farms was established. Faecal samples are collected every second month for three consecutive mornings after milking from all primiparous cows that milk in lactation week 4 or later (DIM>28) to lactation week 42. This sampling protocol was applied on all three Finnish research farms. It also has been proposed to Nordic collaborators but was only adopted by NOR just in connection with a specific trial of a certain project.

A description of the collected data is given under Task 1.2. The study has been published in J. of Animal Breeding and Genetics (Mehtiö et al., 2016).

Increasing of the NIRS reference data

We have realized that good progress in this task is only possible if we increase the NIRS reference data. During spring 2014, 72 faecal samples from previous Maaninka experiments were included into the existing calibration data and obtained calibration equations have been used in the work described above.

At the end of 2016 new calibration equations for faecal iNDF were developed at Valio. The new calibration equation is based on additional reference samples collected from Luke herds (Jokioinen and Maaninka) and from Norway. Suitable samples from all available samples were analysed for iNDF after rumen incubation at Minkiö research farm. The updated reference data includes 476 iNDF records with corresponding NIR spectra. Mean iNDF concentration was 219.6 g/kg FDM and standard deviation was 40.5 g/kg FDM. Best fit was obtained with derivative treatment 2,4,4,1, which resulted in a standard error of cross validation of

16.5 g/kg FDM and a coefficient of determination of cross validation of 0.83. Faecal iNDF concentrations of all faecal samples collected in the Feed Efficiency project were updated based on the new prediction equations.

Conclusions

Measuring cow-individual differences in digestibility accurately enough using faecal NIRS is challenging. However, based on the outcome of Task 1.1, the sampling protocol created for research farms has been implemented on the Finnish research farms to collect enough data to carry out genetic analyses for digestibility (see WP2).

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Task 1.2 Measurements to analyse feed efficiency

Päivi Mäntysaari, Anna-Elisa Liinamo, Sari Kajava, Annu Palmio, Auvo Sairanen, Tuomo Kokkonen

Feed efficiency data

The final Finnish feed efficiency data (FE-data) of primiparous Nordic Red cows was composed from the measurements collected in current project and the data of previous projects. The data from Seosrehu, ASMO and GREENDAIRY projects (Mäntysaari et al., 2003; 2004; 2005; 2012; Liinamo et al. 2015) were reworked and merged together to be used in the statistical analyses. Historical data included 39273 daily records (years 1998 – 2012) from 416 primiparous RDC cows. By end of 2017, in total the FE-data includes measurements from 622 cows with 100 670 records (Table 6).

Data description

The average ECM yield for the cows in FE-data is 28.1 kg/d, the total intake of DM and ME are 19.0 kg/d and 209 MJ/d, respectively (Table 7). Because all cows were in their first lactation, the milk and DM intake curves were flat, as is typical for primiparous cows (Figure 6). The development of calculated EB is presented in Figure 6. It was at the lowest on the second week of lactation, being -29.6 ME MJ/d. Thereafter EB turned positive on lactation week 12.

Table 6. Available Finnish feed efficiency data by end of 2017.

Herd	**Years**	**Cows**	**Daily observations**
Rehtijärvi	1998-2001	145	5508
Rehtijärvi	2006-2009	146	4233
Minkiö	2009→	261	75950
Maaninka	2013→	36	7850
Viikki	2013→	34	7129
Total (in calculations)		622	100670

Table 7. Mean, standard deviation and range (min, max) of cow-wise average milk production, feed intake and body weight and condition during lactation days 3-280 (N=586[#]).

	Mean	SD	Min	Max
Milk yield, kg/d	27.0	3.64	14.2	37.3
ECM yield, kg/d	28.1	3.58	15.7	39.5
Milk composition, %				
Fat	4.28	0.399	3.23	5.84
Protein	3.55	0.199	3.00	4.26
Lactose	4.60	0.122	3.93	5.00
Intake				
Forage, kg DM/d	9.9	1.26	5.7	14.3
Concentrate, kg DM/d	9.2	1.12	4.9	12.3
Total intake, kg DM/d	19.0	2.24	10.5	26.6
Energy, ME MJ/d	208.6	22.3	123.1	284.7
Crude protein, kg/d	3.28	0.42	1.73	4.41
Body weight, kg	586	51.0	443	752
Body condition score	3.11	0.28	2.26	4.36

[#] At the time analysed were carried out 36 out of 622 cows had still missing results from chemical analyses

The average BW of the cows was 586 kg varying from 443 kg to 752 kg. Cows lost BW during the first 6 weeks of the lactation, after which BW turned into increase. The total BW loss in the beginning of lactation was only modest being an average 25 kg. Because all the cows were primiparous, the cows grew BW; on the second week of lactation the BW was on average 577 and on week 40 it was 627 kg. The changes in BCS agree with the changes in BW. At calving the BCS was 3.30, on average, reaching the nadir (3.08) on lactation week 13.

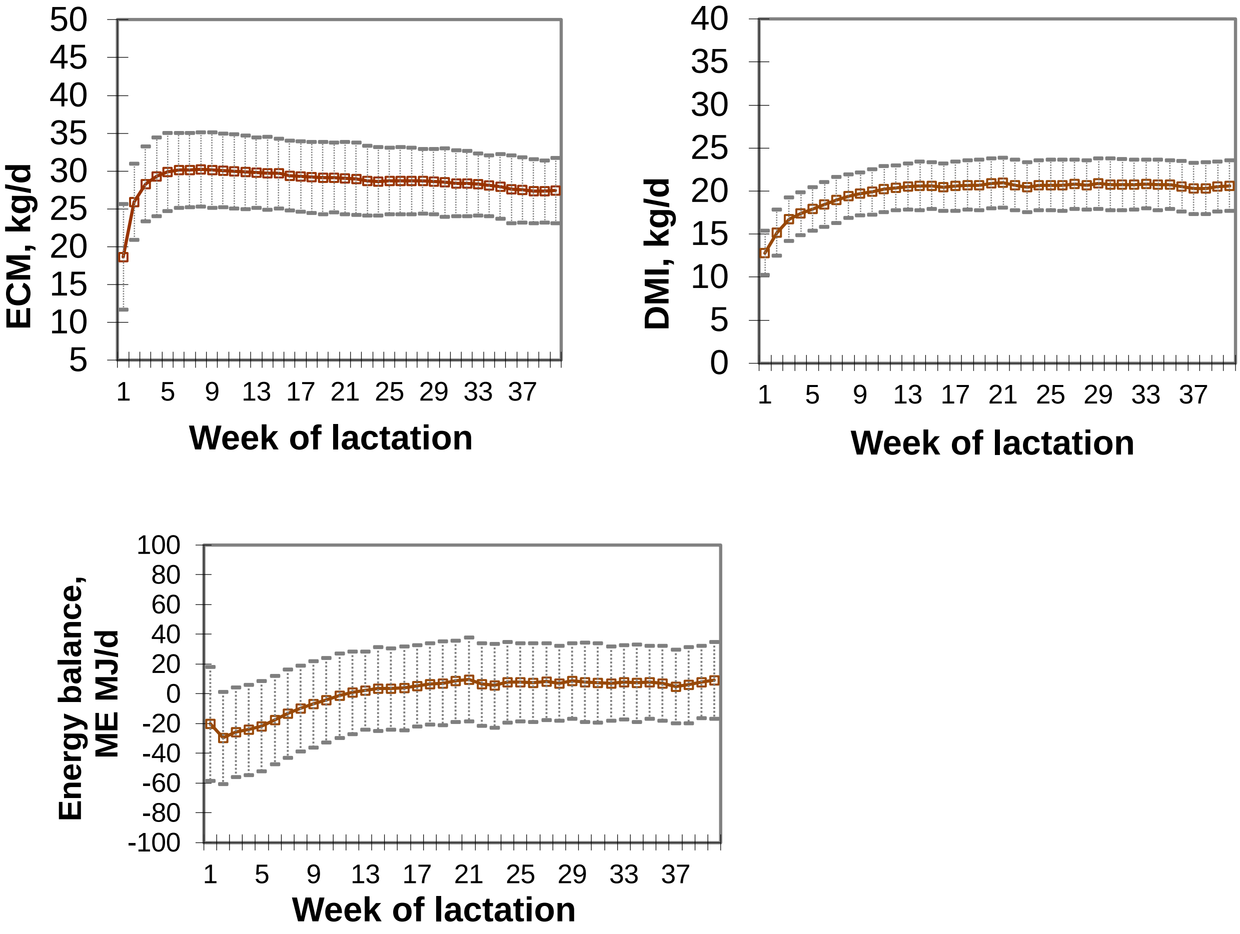

Figure 6. Daily average (± standard deviation) ECM yield, DMI and EB by week of lactation of the primiparous cows in Feed Efficiency data (N=586).

Feed efficiency traits

Feed efficiency was described either by ECE (ECM, kg/ME MJ/d) or by REI calculated using the requirements derived from the current data. The average of REI was, as expected, close to zero (0.00±25.2 ME MJ/d). The energy conversion efficiency was an average 0.137±0,027 kg ECM/ME MJ. The ECE was the highest during the second week of lactation and was decreasing slowly thereafter. Also the mean REI was lower (better efficiency) in the beginning of lactation than in the later lactation. In the case of ECE this is explained by the increased use of body reserves during the first weeks of lactation. In the calculation of REI the use of body reserves is taken into account. However, the differences in REI during lactation may be related to the difficulties in estimating the BW change and its composition during the first weeks after calving (Tamminga et al., 1997). It is also possible that there are differences in ME utilization for separate functions during lactation. The milk fat content is higher during the first weeks of lactation, which may influence the utilization of ME for the production (Chwalibog, 1991). These findings indicate that when comparing REI values of different cows, the values should either be based on the same period of lactation or in modelling a reliable estimation for the effect of stage of lactation is required.

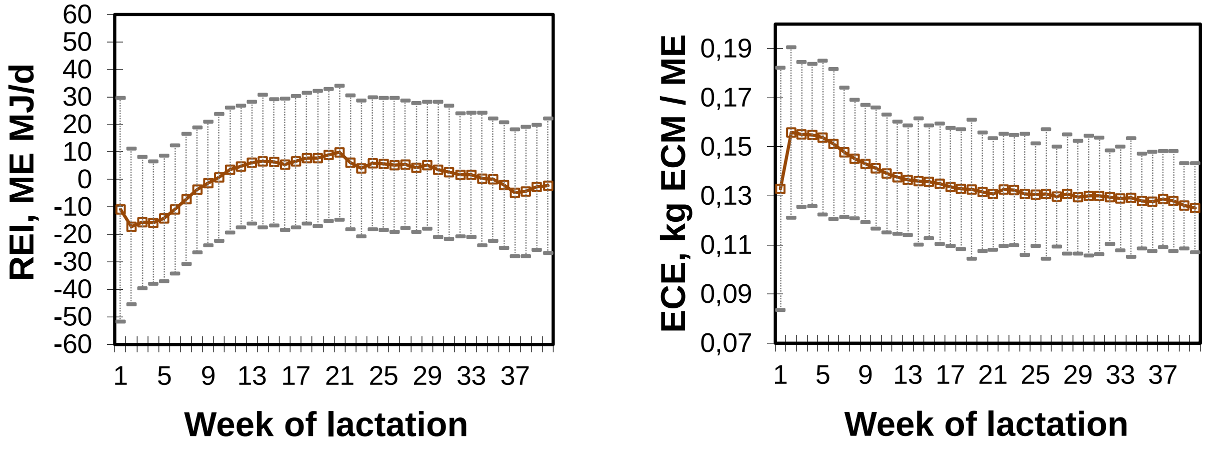

Figure 7. Mean (± standard deviation) residual energy intake and ECE by week of lactation of the primiparous cows in Feed Efficiency data (N=586).

Table 8. Mean, standard deviation (SD), the within animal standard deviation (SE) and between animals variance as a proportion of total variance (C^2) for energy efficiency and energy balance during lactation weeks 2-40.

Item	Mean	SD	SE	C^2
ECM/ME, kg/ME MJ	0.137	0.027	0.022	0.35
REI, ME MJ/d	0.00	26.1	21.2	0.34
Energy balance, ME MJ/d	-0.57	29.8	24.0	0.35

There was a notable variation in efficiency between the cows although the average efficiency measurements were very close to what was expected (Figure 7 and Figure 8). In FE-data the proportion of total variance due to animals (C^2) was 0.34 for REI and 0.35 for ECE (Table 8). In the case of ECE the variation arises partly from its inability to distinguish between the energy used for maintenance, milk and BW loss or gain. The genetic selection based on ECE could therefore lead to favouring of cows with long and deep energy deficiency in the beginning of lactation. With REI the use of energy for different functions is considered and the use of body reserves is taken into account. Nonetheless, a large variation in REI was observed among the cows. Partly the phenotypic variation in REI can be associated with errors in the measures of production, intake or BW, even if the current data was collected accurately in experimental conditions, but partly it reflects the true differences in the energetic efficiency between cows. In FE-data the proportion of total variance due to animals for REI was 0.34, which corresponds to 9 MJ/d. This is about 4.5 % of the average daily energy intake of the cows. To quantify the significance of cow differences, the average REI during the weeks 2-40 of lactation was calculated for each cow. Based on this average the cows were divided into 2 groups: the most (25%; n = 146) and the least (25%; n = 146) efficient cows. The difference in feed efficiency in these two groups is presented in Figure 8. Our findings indicate that there is true phenotypic between-animal variation in the energy efficiency among Nordic Red Dairy cattle cows. So the FE-data show that there exist phenotypic grounds for the selection on energetic efficiency.

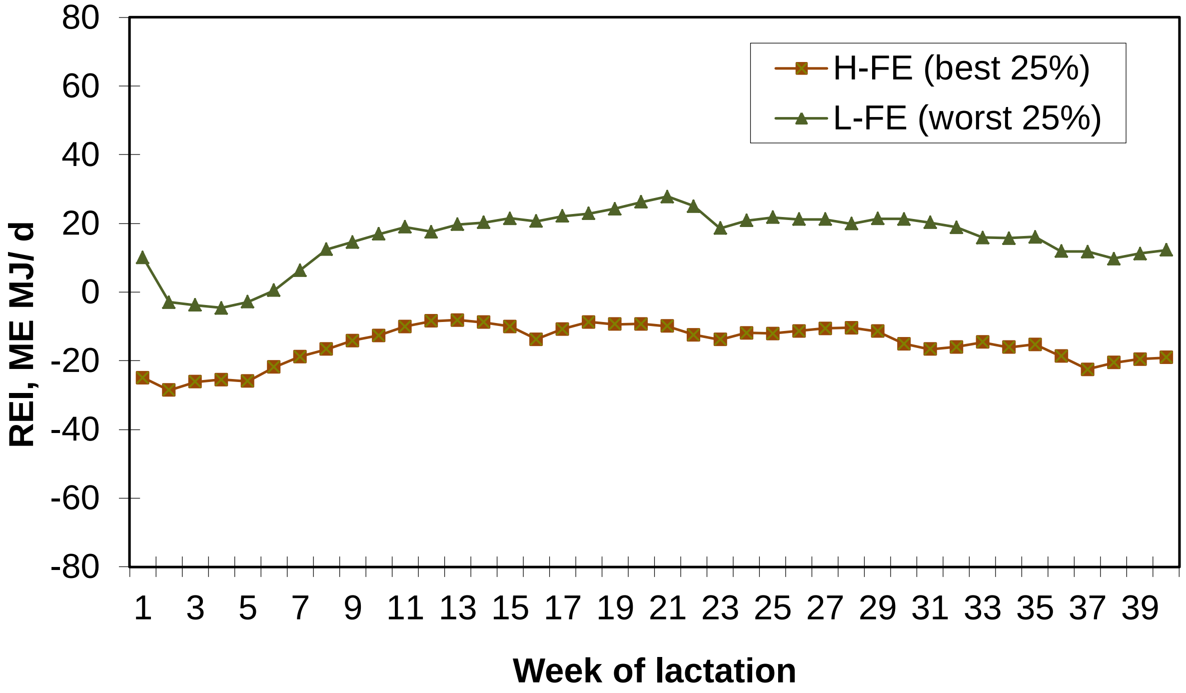

Figure 8. Residual energy intake of the most efficient (H-REI) and the least efficient (L-REI) cows in the Feed Efficiency data divided based on average residual energy intake (N=586).

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Task 1.3 Prediction of energy loss through methane exhalation

Enyew Negussie, Anna-Elisa Liinamo

Collection of methane measurements

Until spring 2017, a total of about 200 cows have been measured during their first lactation and a total of 350,000 raw measurements of the gases have been collected. These measurements and the data generated over the years on CH_4, CO_2, and acetone emissions will provide a rare and unique dataset for future association or genetic studies to clearly understand the genetic basis of dairy system emissions.

Analyses results

Concordance analysis of measurements from same animals measured in the respiration chamber and by the PAS-F10 methods were in satisfactory agreement. The concordance correlation coefficient between combined weekly CH_4 output estimates of PAS-F10 and chamber was 0.84 with lower and upper confidence limits of 0.65 and 0.93, respectively. When chamber CH_4 measurements were predicted from PAS-F10 measurements, the mean of two separate weekly PAS-F10 measurements gave the lowest prediction error variance than either of the separate weekly PAS-F10 measurements alone. This suggests that every other week PAS-F10 measurements of CH_4, when combined, improve the estimation of CH_4 output with PAS-F10 technique. Therefore, analysis of repeated CH_4 observations from same animals is preferable when assessing between animals variation. The comparison with the respiration chamber method showed that estimates from PAS-F10 can be used to provide CH_4 output estimates on an individual animal basis in a large scale.

The daily methane output of cows measured by PAS-F10 technique and respiration chamber were 555l/d and 585l/d, respectively. Accordingly, the estimated energy output (loss) by CH_4 exhalation as percentage of gross energy intake was 5.9 and 6.2%, respectively.

A linear mixed model was used for the analysis of the large continuously collected CH_4 data by PAS-F10 technique. The mean daily methane output of cows was 555l/d and ranged from 330-800 l/d. Dry matter intake, level of milk production, lactation stage and diurnal variation had significant ($P<0.001$) effects on daily CH_4 output. The obtained repeatability estimates of 0.40 - 0.46 indicated that there exists significant between-animal variation in CH_4 output traits.

For more details to the results from this study, refer to the paper titled “Non-invasive individual methane measurement in dairy cows” published in Animal, 2017: https://doi.org/10.1017/S1751731116002718.

Task 1.4 Prediction of energy retained in or mobilized from body tissue

Päivi Mäntysaari, Esa Mäntysaari

We examined the accuracy of different models to predict BW of the cows based on daily BW measurements, and investigated the usefulness of modelling in increasing the value of BW measurements as management and breeding tools. In un-modelled BW data, the within animal variation was 6.4% of the total variance. Modelling decreased the within animal variation to levels of 2.9-5.1 %. The smallest day to day variation and thereafter highest day to day repeatabilities were with PER and MIX models.

The usability of modelled BW as energy balance indicator was evaluated by estimating relationships between EB, or EB indicators, and modelled BW change on the beginning, mid and late lactation. The BW modelling increased considerably the correlation between BW change and calculated EB (Figure 9). The correlation was higher in the beginning and late lactation than the correlation in the mid lactation. In all time periods, the BW change based on MIX-model gave the highest correlation with the EB, followed by the BW change prediction based on FIX-model. However, in the beginning of the lactation the BW change based in the PER-model gave higher correlation than the BW change based on FIX-model.

The BW change based on weighted un-modelled BW correlated less to the change in BCS and milk FP ratio than the BW changes based on the BW models. The correlation between modelled BW change and change in BCS was moderate in the beginning of lactation, lower in mid lactation and in the late lactation; only BW change based on FIX- and MIX- models gave meaningful correlation. In the case of milk FP ratio only the BW change based on FIX-, MIX- and PER- models had low correlation during lactation weeks 4 to 7 but, as expected, hardly any correlation in the later lactation was found.

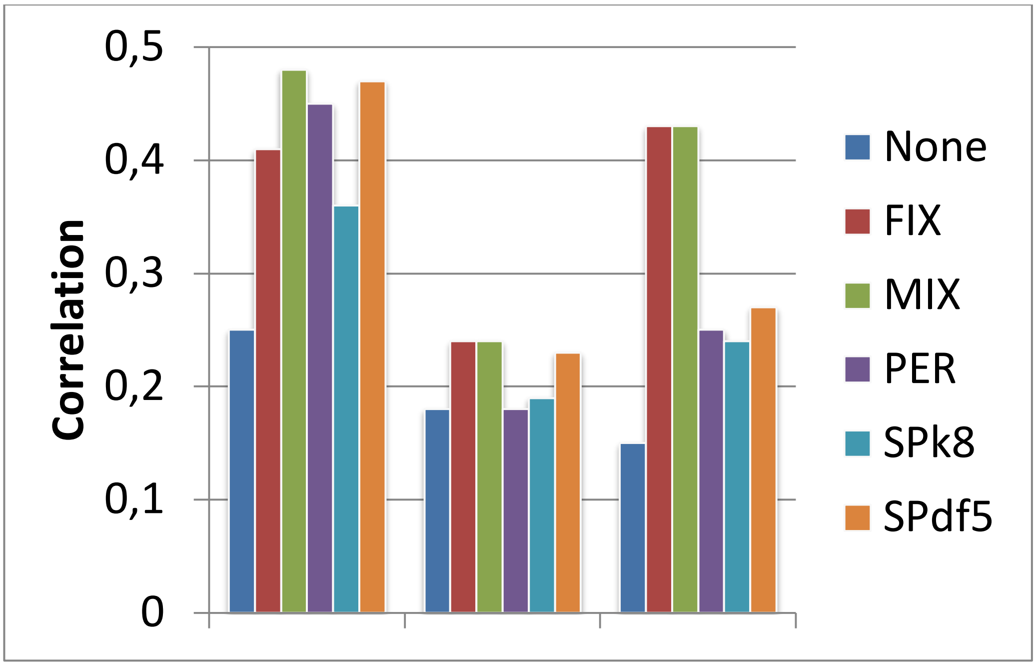

Figure 9. Correlations between EB on BW change based on different smoothing models.

The value of different BW predictions were addressed by fitting MEI on ECM, BW and BW changes as is done in the REI modelling. The model fit statistics (BIC and AIC) using BW from different models showed, that the highest accuracy of prediction for the REI was achieved when MIX – model was used in BW modelling. The predictive value of REI model was increased by using any of the modelled BW compared to un-modelled BW.

Conclusions

Our calculations showed that there was a clear diurnal change in the BW of the cows even if they had feed available 24 hours. Based on our findings, the modelling of BW increases significantly the usefulness of BW as EB and management indicator. From all tested models the random regression model with fixed and random animal lactation stage functions was found as a best-fit model. The results from Task 1.4 are published by Mäntysaari and Mäntysaari (2015).

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Task 1.5 New indicator traits for tissue energy mobilization based on MIR spectral data

Tuomo Kokkonen, Päivi Mäntysaari, Sari Kajava, Annu Palmio, Terhi Mehtiö, Clément Grelet, Laura Nyholm, Esa Mäntysaari, Martin Lidauer

Relationship between NEFA, energy balance and fatty acid concentrations

Simple correlations indicated a clear negative relationship (-0.47) between NEFA concentration in the plasma samples collected in the morning and calculated energy balance at the sampling day. On lactation weeks 2 and 3 the average NEFA concentrations were 0.61 (±0.33) and 0.46 (±0.25) mmol/l for first-parity cows, and 0.47 (±0.18) and 0.39 (±0.16) mmol/l for second-parity cows. The higher concentration in first-parity cows was unexpected, based on earlier studies and less negative energy balance of first-parity cows. This discrepancy can be, at least partly, explained by the stress induced by handling at blood sampling, since younger animals may be less accustomed to experimental procedures. At lactation week 20 NEFA concentrations were clearly lower being 0.13 mmol/l for both parities, in line with positive EB.

Correlation analysis based on data from lactation weeks 2 and 3 showed moderate to strong positive correlations between plasma NEFA and several parameters describing milk fatty acid composition in the morning milking : C18:1 cis-9 ($r = 0.53$), total C18:1 ($r = 0.52$), C16:1 cis-9 ($r = 0.47$), total mono-unsaturated fatty acids ($r = 0.50$), total unsaturated fatty acids ($r = 0.49$) and long-chain fatty acids ($r = 0.47$). The correlation between plasma NEFA concentration and milk fat-protein ratio was 0.38. There were moderate negative correlations between plasma NEFA concentration and concentrations of medium-chain fatty acids (MCFA) C10, C12 and C14 at lactation weeks 2 and 3. Correlations were very similar in first- and second parity cows, suggesting that milk fatty acid composition determined by MIR can predict plasma NEFA concentration and energy status irrespective of parity.

Predicting NEFA

In the whole data (weeks 2, 3 and 20) best linear multiple random regression models with one LCFA parameter and DIM explained 60 – 63% of the variation of plasma NEFA concentration. Using DIM as a single predictor of plasma NEFA concentration explained 41%, and both fat-protein ratio and DIM explained 49% of the variation of plasma NEFA concentration. The effect of parity was not statistically significant in the analysed models, and the lack of interaction between parity and LCFA parameters indicated equal slopes among parities.

When only lactation weeks 2 and 3 (i.e. period of negative energy balance) were included in the analysis, best models with single LCFA parameter and DIM explained 45 – 48% of the variation of plasma NEFA concentration, DIM 15% and combination of fat-protein ratio and DIM 42%. Models containing single LCFA (C18:1 cis-9) and MCFA (C14), and DIM explained 55% of the variation of plasma NEFA concentration. A further improvement to 60% was achieved by the inclusion of fat-protein ratio in the model. Using a model including C18:1 cis-9, C14, DIM and fat-protein ratio, the correlation between predicted and observed NEFA was 0.89, suggesting that energy status of dairy cows can be predicted more reliably based on milk composition predicted from MIR data than based on estimated average energy requirements and calculation of energy input and output.

Including also body measurements when predicting NEFA

The data collected in Minkiö research farm including measurements from 103 cows on the 1st and 43 cows on the 2st lactation were used in the study were the cow's energy status were predicted by body and milk traits. The NEFA concentration (mmol/l) on sampling days were on average 0.65 (±0.32) and 0.55 (±0.31) on lactation week 2, 0.47 (±0.24) and 0.45 (±0.22) on week 3 and clearly lower 0.14 (±0.06) on lactation week 20. The ΔBW and NEFA concentrations on sampling days are presented in Figure 10.

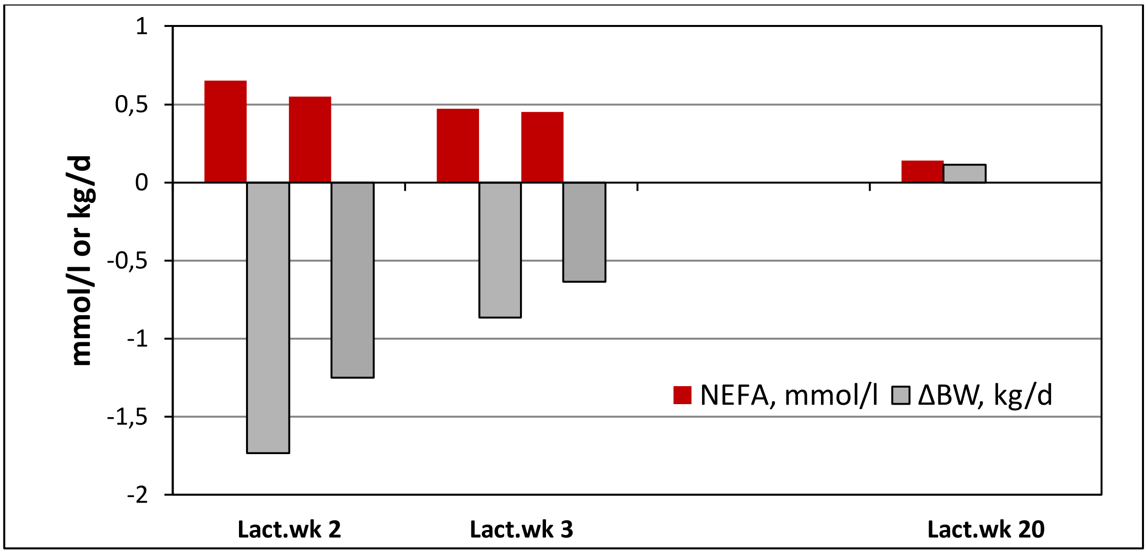

Figure 10. Average body weight change and plasma NEFA concentration on lactation weeks 2, 3 and 20 in energy status prediction data (N=146).

First, a multiple linear regression model to predict NEFA was developed without milk FA. The best fit model (Model 1) included ΔBW, FP, ΔBCS, BCS*ΔBCS, parity and days in milk. Then, for the second model, five milk FA or FA (C10, C16, C18:1, monounsaturated, and saturated FAs) groups were chosen by step-wise regression on NEFA. With FAs included, the best model (Model 2) contained ΔBW, ΔBCS, BCS*ΔBCS and FAs. The correlations between predicted and observed NEFA were 0.75 (Model 1) and 0.80 (Model 2) (Figure 11). Thus the results show that cow's ES can be predicted well, better than by calculated EB, with body and milk indicators and reliability was further increased with milk FAs inclusion.

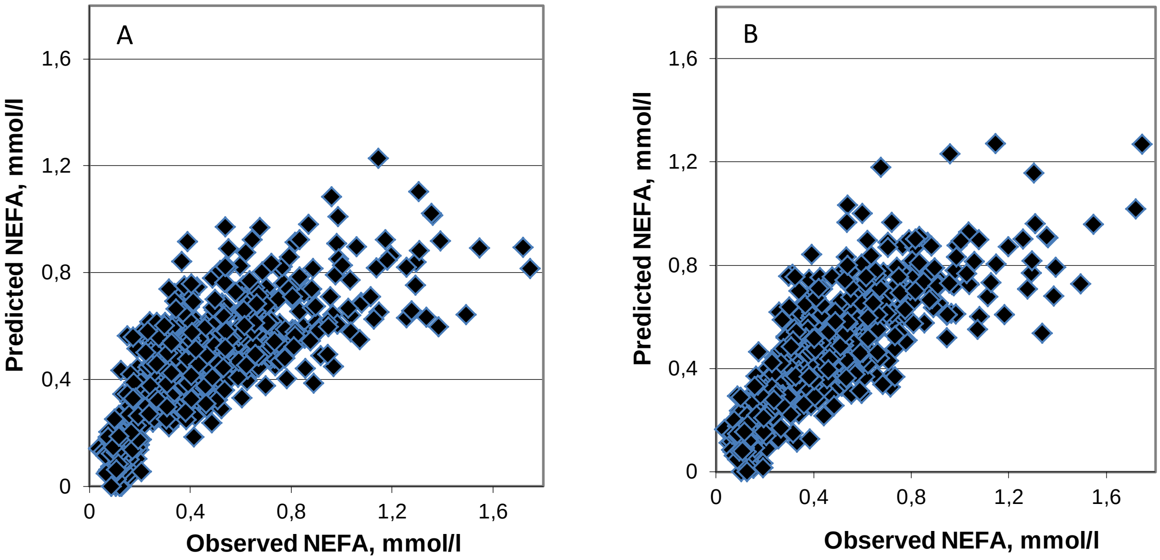

Figure 11. Observed and predicted plasma NEFA (mmol/l) based on model 1 (A) or model 2 (B).

Predicting NEFA directly from milk MIR spectral readings

The statistics for two different models for NEFA and EB are presented in Table 9. Following McParland et al. (2012), alternatively, also milk yield was included in the model as predictor variable. This failed to improve the accuracy when predicting NEFA, but clearly improved the accuracy when predicting EB. However, the correlation between observed NEFA and EB predicted with MIR spectra was -0.65 and the correlation between observed NEFA and EB predicted with MIR spectra and milk yield was only -0.56. This indicates that including milk as a prediction variable to predict EB, actually makes a weaker predictor for energy status. Cross validation results from leaving randomly 20% of cows out were slightly lower than from leave-one-out cross validation, probably because observations used for leave-one-out cross validation were not independent.

Table 9. Partial least squares regression fitting statistics[1] for NEFA and energy balance (EB) using MIR spectra (a.m. and p.m.) or MIR spectra and milk yield (my) as prediction variables in the model (809 NEFA observations), validated by leave-one-out or leave 20% cows out cross validation.

		NEFA			EB		
		N fac	R^2cv	RMSE (mmol/l)	N fac	R^2cv	RMSE (MJ/d)
Leave-one-out	Spectra	20	0.64	0.18	18	0.46	25.82
	Spectra+my	20	0.59	0.18	16	0.64	21.24
Leave 20% cows out	Spectra	9	0.58	0.19	11	0.45	25.94
	Spectra+my	10	0.56	0.19	12	0.62	21.22

[1] N fac = No of factors used (restricted to 20), R^2cv = coefficient of determination of cross validation, RMSE = root mean square error

Predictions based on evening milk samples yielded higher coefficient of determination (R^2cv=0.67) than predictions based on morning samples (R^2cv=0.59) (Table 10). This supports Blum et al. (2000) findings on diurnal variation in plasma NEFA concentration, and suggests that prediction of morning NEFA should be based on evening milk sample spectra.

Table 10. Partial least squares regression fitting statistics[1] from predicting morning blood NEFA from morning and evening milk MIR spectral data.

MIR spectra	N rec	N fac	R^2cv	RMSE (mmol/l)
Morning	809	20	0.59	0.18
Evening	778	20	0.67	0.17

[1] N rec = No of records, N fac = No of factors used (restricted to 20),
R^2cv = coefficient of determination of cross validation, RMSE = root mean square error

In many studies on utilizing MIR spectral data it is shown that the variation in the validation data set must be represented in the calibration data set (McParland et al., 2012; De Marchi et al., 2014). The three research herds in our study differed in the mean levels of milk yield, dry matter intake, EB and NEFA, and had differences in feeding and management. When we calibrated the equations with leave-one-out cross validation with evening MIR spectral readings and NEFA records from Viikki and Maaninka herds and then predicted NEFA for cows in Minkiö herd, we found a R^2 of 0.58 and a RMSE of 0.19 mmol/l in Minkiö data set. We compared the spectral variability of Minkiö data with the data from two other herds and the spectral variability was higher in Minkiö data.

The overall mean for observed value of NEFA in early lactation was 0.52 (minimum value 0.10 and maximum value 1.95). Dórea et al. (2017) applied a threshold of > 0.60 mmol/l to classify cows with high level of NEFA concentration. Thus, the RMSE of 0.17-0.20 mmol/l seems to be on a reasonable level for distinguishing cows with normal or very high level of NEFA.

This study was presented as oral presentation in Maataloustieteen Päivät in Helsinki, Finland Jan 2018. The abstract: http://www.smts.fi/sites/smts.fi/files/MTP2018_Abstraktikirja.pdf (p. 137)

This study was also presented as a poster in World Congress on Genetics Applied to Livestock Production (WCGALP) in Auckland, New Zealand Feb. 2018. The peer-reviewed paper: http://www.wcgalp.org/proceedings/2018/developing-indicator-body-fat-mobilisation-using-mid-infrared-spectrometry-milk.

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WP2. Modelling of feed efficiency and its economic and environmental value

Task 2.1 Economic and environmental value of total feed efficiency

Timo Sipiläinen, Päivi Akkanen

We assumed that the farms could improve their feed efficiency in milk production by 5 percent. We first assumed that there were no other changes in returns or costs. In principle there are three options: the farmer may increase the milk production per cow but keep the total amount produced at the earlier level. This means that the farmers have to reduce the number of cows. If we assume that the original total number of cows is 250 000 the number would go down by almost 11 000 heads. The increase in the surplus of milk production would be 153 euros per head and in total 23.2 million (taking into account the loss of gross margin of cows (less cows) and the gain in sales of crop products). This option would also follow a reduction in methane emissions by 1.9 million kg. This methane emission is approximated by using average emission coefficients of IPCC (2006, 10.29). If we calculate the value of the emission according to emission trading contracts of CO_2 its value would be at current low prices (5-10 €/t) about 200 000 – 400 000 euros. At the same time almost 15 500 hectares could be allocated to other crops instead of barley and silage. In addition, the farmers loose a part of the per cow payment in the AB region, which brings an additional loss of 513 euros per head. On the other hand, labour demand would also decrease.

The second option is to keep the current yield level and use less concentrates in feeding. If the yield level is 31.3 kg ECM per cow and day before the feed efficiency improvement, the yield level could be achieved by using 1.5 kg DM less concentrates after the improvement. This means the concentrate intake of 10 kg DM and 12 kg DM of silage per day. The concentrate cost reduces by 111 euros per cow and in total by 27.7 million euros. This would also follow lower methane emissions when a larger share of total feed intake is directed to milk production. The total feed intake goes down by 6.4 percent. If we assume that the effect is similar to an output increase but its inverse, we could approximate that the methane reduction is about 540 000 kg per year.

The third option to improve feed efficiency is to increase milk production by 5 percent when keeping the feed input and the number of cows constant. Thus, there is no change in production otherwise but a larger share of intake is utilized for production. This also follows that the field use remains unchanged. The value of total output would increase by 38.3 million euros. We could approximate that the methane emissions could reduce to some extent (540 000 kg per year) when feed efficiency in production increases.

From the farmers perspective the best option would be to increase production along with the genetic improvements. However, the milk increase comes at cost. We have not taken into account possible increase in e.g. mastitis or infertility. Other costs than feed are not included either. Feed efficiency affects excretion of N, too.

Task 2.2 Justification of feed efficiency traits and predicted economical genetic response

Martin Lidauer, Esa Mäntysaari, Terhi Mehtiö, Enyew Negussie, Anna-Elisa Liinamo, Paulina Kokko, Jarmo Juga

This task was divided in three sub-tasks with the aims of 1) evaluating different feed efficiency traits, 2) find applicable indicator traits, and 3) assess genetic response when considering feed efficiency in selection.

Task 2.2.1 Evaluation of different feed efficiency traits for development of a breeding goal

Terhi Mehtiö, Anna-Elisa Liinamo, Esa Mäntysaari, Enyew Negussie, Martin Lidauer

Literature on feed efficiency

Defining feed efficiency in lactating animals is more complicated than defining feed efficiency in growing animals, because dairy cows undergo a cycle through lactation. In particular early lactation is an important stage for dairy cows, because rapidly increased milk production results in an increase in dry matter intake and at the same time, when body reserves are mobilized to meet the requirements, an abrupt reduction in body weight happens (Prendiville et al., 2011). If the resulting metabolic challenge cannot be met, cows will suffer from metabolic stress (Buttchereit et al., 2011, Roche et al., 2009).

Feed efficiency, often expressed as some measure of gain per unit of dietary intake, is dependent on the magnitude of intake and the efficiency with which nutrients are digested, absorbed, and metabolized to maintenance, growth or milk production. The percentage of absorbed nutrients used to maintenance functions versus production or growth clearly shapes the efficiency of whole animal nutrient use for product formation. In dairy cattle it is influenced by diet and other environmental factors, genetic ability and physiological state of the cow to utilize nutrients for milk yield (Hill, 2012).

Selection for feed efficiency in dairy cattle has up to now been indirect due to the difficulties in trait definition and costs associated with measuring feed efficiency in large populations. Selection for higher milk yield has improved feed efficiency in dairy cattle. It has been estimated that correlated response to direct selection for increased milk yield probably results in 75-90 % of the potential improvement that could be achieved through direct selection for feed efficiency (Korver, 1988). Due to the complexity of a cows' feed efficiency a wide range of feed efficiency traits are reported in the literature.

Ratio traits. Gross energetic efficiency (Veerkamp and Emmans, 1995; Vallimont et al., 2011), gross feed efficiency (Korver, 1988; Spurlock et al., 2012; Van Arendonk et al, 1991), energy conversion efficiency (Mäntysaari et al., 2012) and feed conversion efficiency (Coleman et al., 2010). Ratio traits are relatively easy to quantify, but by definition, they are correlated with their component traits and expected responses to selection are difficult to predict (Gunsett, 1984).

Traits based on residual from regression models. Residual feed intake (Van Arendonk et al., 1991), energy balance (Buttchereit et al., 2010), residual energy intake (Mäntysaari et al., 2012) and residual solids production (Coleman et al., 2010). Residual traits rely on correctly modelling of the component traits which is difficult. Also the assumption that residual traits are biologically independent of the component traits may not hold and genetic correlation with the component traits may exist (Pryce et al., 2013). Berry and Crowley (2013) suggested that 1) the appropriate statistical model for RFI must be used that properly accounts for body tissue mobilization, and 2) a sufficiently long time period must be used to quantify RFI, which accounts for the necessity of cows to replenish lost body condition.

Index from component traits. Lu et al. (2015) suggested multiple-trait modelling strategy that exploits the Cholesky decomposition of the component traits to come up with more robust measures of feed efficiency. A similar idea was adopted by Pryce et al. (2015) in developing a selection index for feed saved in Australian dairy cows.

Analyses of own feed efficiency data

The literature study was underpinned by analysing feed efficiency data recorded at Rehtijärvi and Minkiö research farm. For traits, which describe different aspects of feed efficiency were chosen: residual energy intake, energy conversion efficiency, energy balance, and dry matter digestibility. The first one describes overall efficiency of a cow, the second one the efficiency of a cow in using metabolizable energy for

producing milk, third the ability of a cow the avoid severe negative energy status, and the last one the efficiency of a cow in digesting feed. The first three traits were more closely studied using Finnish feed efficiency data collected earlier and during this project. Work on DMD is reported under Task 2.2.2.
Results from the analyses of REI, ECE and EB demonstrated that variance ratios between model effects change significantly across lactations. This resulted heritabilities being moderate at the beginning of lactation, low during early-mid lactation, and from there on increasing towards end of lactation (Figure 12).

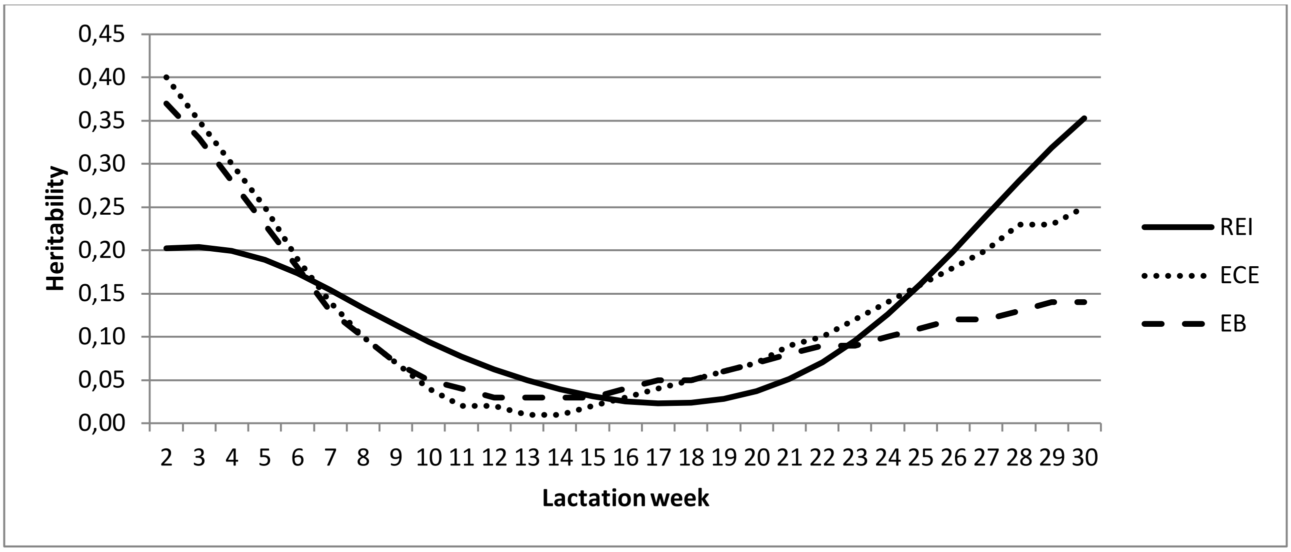

Figure 12. Heritability estimates for residual energy intake (REI), energy conversion efficiency (ECE) and energy balance (EB) in first lactation by lactation week.

Within a trait, the genetic correlation between beginning of lactation and mid- and end-lactation was low indicating that early stage of lactation is either a different trait or difficult to model, or both. The same pattern was found for all three traits. Genetic correlations of REI were positive with DMI, ECM and BW. Genetic correlations of ECE were positive with DMI and ECM but negative with BW. For REI genetic correlations were negative with DMI, positive with ECM and negative with BW (Figure 13). These analyse have been carried out in a previous "*Lehmien rehunkäyttökyky*" project and within here finalized and published. Detailed results are given in Liinamo et al. (2015).

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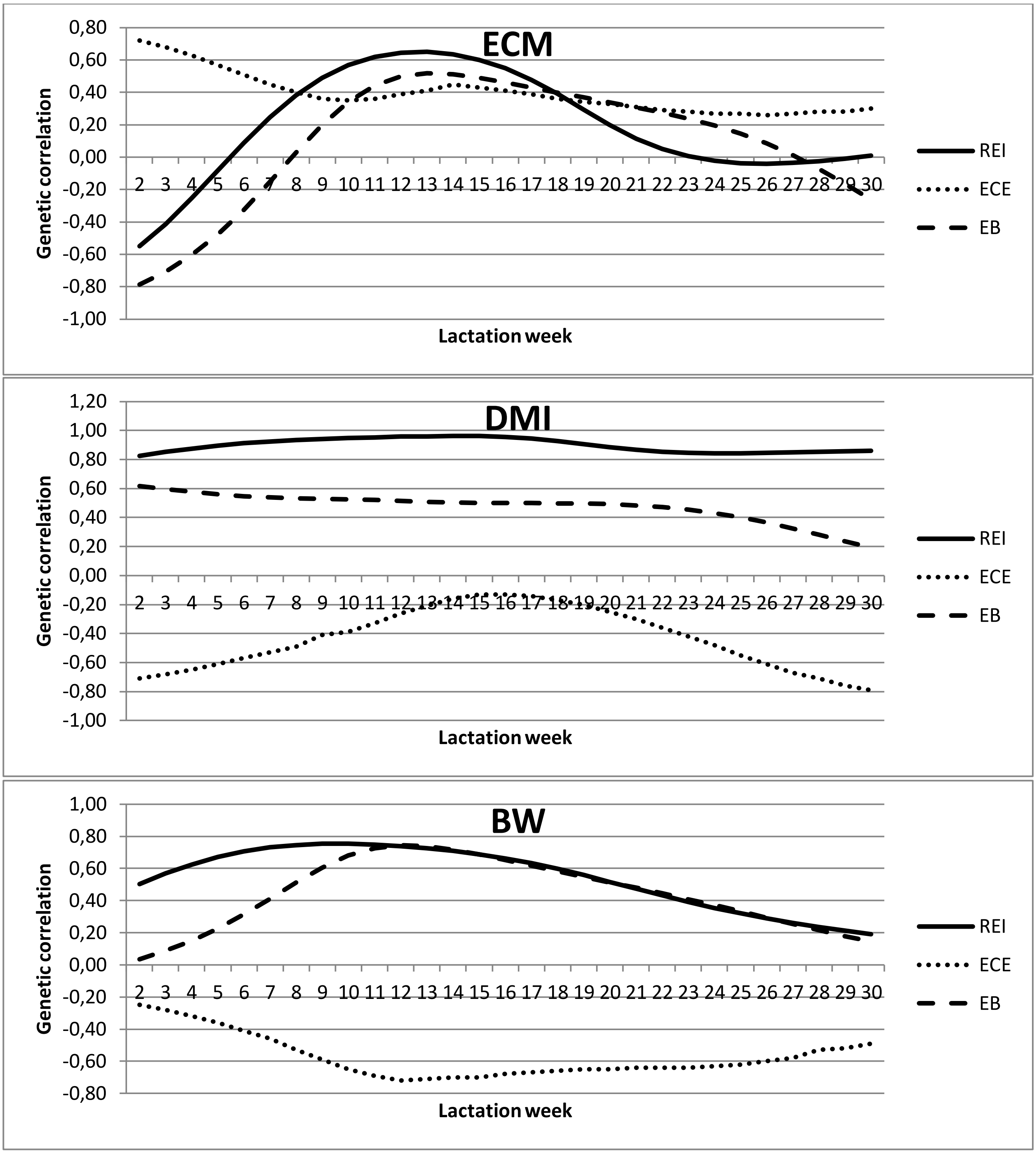

Figure 13. Genetic correlations of residual energy intake (REI), energy conversion efficiency (ECE) and energy balance (EB) with energy corrected milk (ECM), dry matter intake (DMI) and body weight (BW).

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Task 2.2.2 Feed efficiency indicator traits measureable on-farm

Terhi Mehtiö, Enyew Negussie, Esa Mäntysaari, Martin Lidauer

Indicator traits for energy conversion efficiency or energy conversion ratio.

As expected, heritabilites were moderate to high, which indicates that all these whole-lactation traits are highly heritable. Estimated heritabilities for the component traits were: 0.36 (MEI), 0.37 (ECM), 0.42 (MBW). Estimated heritabilites for the direct feed efficiency traits ECE and ECR were 0.37 and 0.32 respectively. The obtained heritabilities for the ECE indicator traits were 0.48 and 0.55 for EE and EE_M, respectively, and for the ECR indicator traits 0.35 and 0.43 for ER and ER_M, respectively. The genetic standard deviation for ER_M, the trait with the highest correlation to ECR, was 0.19 MJ/ kg ECM indication that there is significant genetic variation between animals in that amount of energy allocated to maintenance.

Estimated genetic correlations between ECE and EE or ECE and MAE, were 0.70 or 0.73, respectively. Estimated genetic correlations between ECR and ER or ECR and MRR were, 0.73 or 0.89, respectively. Especially MRR, for which the highest genetic correlation was found, may be a potential indicator trait. This indicator trait can be described as a cow's maintenance costs per kg ECM produced. The genetic correlation of MRR with MBW, ECM and MEI was 0.58, -0.91 and -0.18, respectively. In contrast, genetic correlation of ECR with corresponding traits was 0.82, -0.62 and 0.39, respectively. The high genetic correlation of MRR with ECE (-0.86) and ECR (0.89) and its reasonable correlations with BW, ECM and MEI, makes MRR a candidate trait to be considered for inclusion into dairy cows' efficiency index.

Selection index analyses showed that including MRR into the yield index improves net merit of the yield index by 18% compared to current situation where only milk yield, protein yield and fat yields are included in the index (Table 11). Highest improvement in net merit (+28%) was achieved when MBW and residual energy intake were included into the current yield index. Then, also genetic response in feed efficiency (defined as ECE) was improved most (+45%) compared to the current index. When including MRR, which does not require knowledge about feed intake, the genetic response in feed efficiency was improved by 23%. However, genetic response in feed efficiency increased by 31% when including MBW in to the index. MBW is not a feed efficiency trait as such, but breeding for smaller cows reduces feed requirements, which showed a positive effect on net merit.

Table 11. Additional net merit (current index 100%) and genetic response in production and efficiency traits (in units of genetic standard deviation) when improving the selection index by one standard deviation, given by criteria.

Criterion	Net Merit	Milk	Protein	Fat	MBW	MEI	ECE	REI	MRR
1	100%	0.68	0.61	0.63	-0.18	0.26	0.45	0.04	-0.61
2	128%	0.61	0.58	0.57	-0.58	-0.07	0.65	-0.17	-0.75
3	124%	0.63	0.62	0.61	-0.57	0.03	0.59	-0.06	-0.76
4	118%	0.67	0.64	0.67	-0.39	0.16	0.55	-0.01	-0.73

Selection based on: 1) milk, protein and fat (current index); 2) milk, protein, fat, BW and REI; 3) milk, protein, fat and MBW; 4) based on transformed linear index for MRR.

This study was presented in more detail at the World Congress on Genetics Applied to Livestock Production (WCGALP) in Auckland, New Zealand Feb. 2018. The peer-reviewed paper: *http://www.wcgalp.org/system/files/proceedings/2018/improving-feed-efficiency-and-net-merit-including-maintenance-requirement-selection-dairy-cattle.pdf*

Indicator trait for cow-specific dry matter digestibility

Heritability estimates of data set A varied clearly between different protocols (Table 12). The permanent environmental variance (σ^2_{pe}) was very small for both digestibility variables and genetic variance explained almost all of animal variance. Heritability estimates were lower for data collected according to the old sampling protocol. This is because of too small contemporary groups of animals consuming the same feed, which results in high residual variance. Also in Norway data the iNDF concentration in feed within the same contemporary group was varying noticeably, which resulted in high residual variance and lower heritability estimates. There were more clearly contemporary groups in C10 and new protocol data which resulted in lower residual variances and noticeably higher heritability estimates. The heritability estimates for $iNDF_{feces}$ and DMD_{iNDF} were on a same level. Using the new protocol even higher heritability estimates were found for $iNDF_{feces}$. However, the heterogeneous data set used was very small and the residual variance classes are even smaller. The standard deviation for permanent environmental variance was over 13 times larger than the estimate for $iNDF_{feces}$ and almost 15 times larger than the estimate for DMD_{feces}, indicating the uncertainty related to the estimated variance components.

Table 12. Estimates of genetic parameters* with standard errors (se) in different protocols (Old C3, redesigned B3, NOR=Norway, C10) for dry matter digestibility (DMD_{iNDF}) and for iNDF concentration in feces ($iNDF_{feces}$) using the data set A (328 cows with 931 observations).

	σ^2_{pe} (se)	σ^2_g (se)	σ^2_e (se)	h^2
DMD_{iNDF}	2.96 (43.53)	110.66 (50.34)		
C3			687.32 (78.01)	0.14
B3			281.44 (24.98)	0.28
NOR			609.24 (116.17)	0.15
C10			102.55 (22.29)	0.51
$iNDF_{feces}$	1.08 (14.66)	38.67 (16.17)		
C3			239.90 (25.82)	0.14
B3			74.65 (6.93)	0.34
NOR			255.88 (50.01)	0.13
C10			40.76 (8.07)	0.48

* σ^2_{pe} = permanent environmental variance, σ^2_g = additive genetic variance, σ^2_e = residual variance, h^2 = heritability estimate

Repeatability and heritability estimates of data set B are presented in Table 13. Repeatability estimates were smallest in B1 and largest in B3 data sets in both DMD_{iNDF} (0.17 to 0.34) and iNDF $iNDF_{feces}$ (0.19 to 0.39). This was a result of smaller residual variance as there were more spot samples in the composite sample. Also heritability estimates were smallest in B1 (0.03 for DMD_{iNDF} and 0.08 for $iNDF_{feces}$) and largest in B3 data (0.18 for DMD_{iNDF} and 0.28 for $iNDF_{feces}$). In addition to lower residual variances the additive genetic variances (σ^2_g) were clearly larger in B3 data set. However, the convergence characteristics were poor in genetic analysis of B1 and B2 data sets, and also for B3 data set the standard errors for σ^2_{pe} and σ^2_g were large. Both repeatability and heritability estimates were again larger for $iNDF_{feces}$ than for DMD_{iNDF}.

Table 13. Variance components* and repeatability estimates (r) using linear mixed model and variance components with standard errors (SE) and heritability estimates (h^2) using animal model for dry matter digestibility (DMD_{iNDF}) and iNDF concentration in feces ($iNDF_{feces}$) in B1, B2 and B3 data sets (441 observations from 144 animals).

	σ^2_a	σ^2_e	r	σ^2_{pe} (SE)	σ^2_g (SE)	σ^2_e (SE)	h^2
DMD_{iNDF}							
B1**	108.97	530.74	0.17	87.62 (101.44)	18.34 (101.36)	534.05 (44.45)	0.03
B2**	106.57	336.77	0.24	88.30 (71.92)	20.06 (70.50)	334.97 (27.91)	0.05
B3	139.85	271.20	0.34	69.71 (94.79)	73.30 (100.67)	268.95 (22.39)	0.18
$iNDF_{feces}$							
B1**	33.27	145.32	0.19	19.38 (30.96)	14.28 (32.61)	146.02 (12.15)	0.08
B2**	36.19	91.91	0.28	22.94 (24.24)	14.38 (25.46)	91.70 (7.67)	0.11
B3	46.10	72.74	0.39	13.63 (29.98)	33.92 (32.90)	72.33 (6.04)	0.28

* σ^2_a = animal variance, σ^2_{pe} = permanent environmental variance, σ^2_g = additive genetic variance, σ^2_e = residual variance

**Poor convergence in the genetic analysis

The heritability estimate for REI was 0.21, and the estimated breeding values (EBV) of REI for 129 primiparous RDC cows with digestibility observations in data set B varied between -6.89 and 9.41 (mean 1.19 and SD 3.20). The correlation between phenotypic DMD_{iNDF} and $iNDF_{feces}$ was very high (0.95) and the correlations between REI EBV's and digestibility traits were negative and rather low (DMD_{iNDF} -0.18 and $iNDF_{feces}$ -0.16; Table 14). The mean of repeated digestibility measurements of the high (EBV mean -4.47, meaning more efficient) and low genetic merit (EBV mean 7.48, meaning not so efficient) cows based on REI EBV's were compared to assess the response of genetic selection (Table 6). The high genetic merit cows had slightly higher DMD_{iNDF} (mean 630.15 g/kg) than the low genetic merit cows (mean 625.52 g/kg). Moreover, the iNDF concentration in feces was higher for low genetic merit cows (mean 211.11 g/kg) than for high genetic merit cows (mean 203.95 g/kg).

Table 14. Correlations with corrected iNDF concentration in feces ($iNDF_{feces}$), corrected dry matter digestibility (DMD_{iNDF}) and residual energy intake (REI) estimated breeding values (EBV) using B3 digestibility data including 129 cows.

	DMD_{iNDF}	$iNDF_{feces}$
DMD_{iNDF}		0.95^{***}
REI_EBV	-0.18^{***}	-0.16^{***}

*** P <.001

Conclusion

Heritability estimates ranged from 0.13 to 0.51 depending on the sampling protocol indicating that, despite the small data size, there was genetic variation in digestibility that could be improved by selection. However, our results confirmed that contemporary groups of cows consuming the same feed have to be large enough for statistical analyses to get reliable results. Moreover, in the case of proper contemporary groups, $iNDF_{feces}$ can be used directly as an indicator trait for digestibility.

Results of this study will be presented as an oral presentation in EAAP 2018 and scientific article is under preparation.

Task 2.2.3 Prediction of economical genetic response

Paulina Kokko, Jarmo Juga

The discounted costs of the modelled breeding program containing the variable costs connected with the selection process of sires were 10.1 € per cow for the investment period of 15 years. Measuring RFI in bull test stations made only a marginal contribution to the costs of the breeding program when focusing on a population-wide perspective. This was because the additional costs (13.5 € per tested bull) related to testing 200 bulls for RFI were spread over all 300 000 cows in the population.

In the studied scenarios the inclusion of additional traits in the breeding goal when introducing all new traits simultaneously (Sce. 4, Table 10) the discounted profit of the breeding program was 5.1% higher than in the reference scenario. Among the other studied scenarios, the use of a selection index including growth and carcass traits, while preventing higher LW of cows (Sce.1b, Table 10), generated the greatest improvement in the discounted profit of the breeding program (+3.7%). The use of the previous selection index instead of excluding LW of cows (Sce.1a, Table 10) increased the profit (+0.8%) although not nearly as much as when selecting for growth and carcass traits together with LW of cows. Under the scenarios evaluating the inclusion of feed efficiency related traits only, the profit of the breeding program decreased by -3.1% with the breeding goal including LW of cows (Sce.2, Table 10). However, adding RFI traits only to the breeding goal slightly increased the profit of the breeding program (1.4%) (Sce.3, Table 10).

Table 15. Discounted profit of the breeding program and discounted monetary genetic gain for the sets of traits over 15 years investment period in the different scenarios.

Scenario[1]	Profit, €/cow/period	Change in profit, %	Discounted monetary genetic gain, €/cow/period					
			Production	Functional	LW	Growth	Carcass	RFI
Reference	345.3	-	372.5	-30.2	-7.9	21.3	-0.4	0.0
Sce.1a	348.2	+0.8	357.7	-30.3	-29.3	56.9	3.3	0.0
Sce.1b	358.1	+3.7	371.6	-30.1	-1.1	25.5	2.3	0.0
Sce.2	334.7	-3.1	349.7	-28.6	35.5	-10.3	-1.6	0.0
Sce.3	350.1	+1.4	366.5	-29.7	-7.8	21.1	-0.5	10.9
Sce.4	362.8	+5.1	366.5	-29.7	-1.1	25.2	2.3	10.1

[1]Additional breeding goal traits in the different scenarios: **Sce.1.** a) Average daily gain of animals in the rearing and fattening periods and carcass traits b) with mature live weight (LW) of cows; **Sce.2.** LW of cows; **Sce.3.** Residual feed intake (RFI) traits; **Sce.4.** LW of cows, growth, carcass and RFI traits.

The results showed that including beef traits while preventing higher LW of cows would be the most promising option to improve the profitability of the combined milk and beef production systems under the Finnish market conditions. In addition, in Finland, where the majority of produced beef originates from dairy herds and beef production falls below consumption, the intensification of beef production based on dairy breeds by selecting for improved beef traits could be the most profitable and sustainable way to increase the level of self-sufficiency in beef.

When considering feed efficiency related traits, the inclusion of LW of cows in the breeding goal containing growth and carcass traits seems to be more profitable than the inclusion of RFI traits given the current pricing of outputs and inputs. This is also supported by its faster availability for selection and lower recording costs because selection for lower LW of cows could be implemented immediately for example by using highly correlated linear conformation traits. However, with the breeding goal that excludes growth and carcass traits, adding LW of cows alone to the breeding goal had a negative effect on the profit. Therefore, in production systems that exclude growth and carcass traits from their breeding goal, selection for RFI traits could be more profitable even with small economic benefits. However, to assess more carefully the consequences of selecting for RFI, information on the genetic correlations between RFI traits and other breeding goal traits as well as on the most cost-effective selection methods are needed.

Finally, it may be concluded that the inclusion of beef traits in the breeding goal for RDC should be considered. In addition, the simultaneous prevention of the increase in LW of cows seems advisable. As genetic evaluations for growth, carcass, and linear conformation traits are already routinely calculated for RDC, selection for beef traits and LW of cows could be readily implemented without extra costs.

Conclusions

Similar as in breeding for other trait complexes in dairy cows (e.g. production, fertility) also breeding for feed efficiency should involve several traits to address different aspects of efficiency. These traits could be: REI for describing general efficiency, ECE or ECR for describing the efficiency in using energy for milk production, DMD for describing the efficiency in digesting feed, predicted energy status for describing the ability to avoid severe negative status at the onset of lactation. Traits should be recorded bi-monthly but not less than every fourth month to get enough reliable observations from cows under recording. As long there is no affordable on-farm feed intake measuring available, inclusion of BW and also beef traits into the selection index could be considered.

Task 2.3 Modelling of energy pathways in the cow

Terhi Mehtiö, Päivi Mäntysaari, Enyew Negussie, Esa Mäntysaari, Martin Lidauer

Least squares analysis resulted in significant differences between energy sink regression coefficients of different lactation stages. The overall estimate for ME use for lactation was 2.67 MJ/kg ECM across lactation and estimates increased from 1.27 MJ to 3.70 MJ as lactation progressed. The overall estimate for maintenance was 0.81 MJ/kg $BW^{0.75}$ decreasing from 1.09 MJ to 0.48 MJ during lactation. The estimates for body weight loss and gain across lactation were 8.05 MJ/kg and 13.80 MJ/kg, respectively. For body weight loss there were observations only from week 2 to week 14 and estimates increased from 5.52 MJ/kg to 14.95 MJ/kg during this period. Estimates for body weight gain varied between 6.35 MJ/kg and 23.01 MJ/kg during lactation. Thus, regression coefficients estimated in this study for the various energy sinks were somewhat different than the values from Finnish feed table recommendations (metabolic body weight: 0.515 MJ/kg $BW^{0.75}$; energy corrected milk production: 5.15 MJ/kg ECM; body weight gain: 34.0 MJ/kg; body weight loss: 28.0 MJ/kg; Luke, 2015).

Variance component estimation based on the repeatability models resulted as lower genetic and residual variances and higher permanent environment variance for MEE compared to REI (Table 16). Thus, heritability estimate was higher for REI (0.33) than for MEE (0.26). The heritability estimate for REI from this study was slightly higher than most estimates reported in the literature (Liinamo et al., 2015; Tempelman et al., 2015; Pryce et al., 2014).However, fitting regressions for energy sinks simultaneously with all other model effects yielded not only a smaller heritability and residual variance, but also a slight increase in repeatability, which indicates that the model for MEE may have a better predictability compared to the model for REI.

With the partial MEE models, we obtained heritability estimates that are in line with the repeatability model analysis of MEE (Table 16). Most of the variance was explained by the intercept, for which heritability estimates ranged from 0.13 to 0.23 depending on the applied random regression model. The heritability estimates for partial ME efficiency for milk production ranged between 0.04 and 0.06. The heritability estimates for partial ME efficiency with respect to maintenance and growth were 0.02 and 0.04, respectively. The variance explained by BWL was practically non-existent, and because of this model pMEE3 was not studied any further.

Table 16. Variance component estimates and heritability (h^2) given by different models.

Model	Additive Genetic Animal Effects	σ^2_a	σ^2_{pe}	σ^2_e	h^2
REI	Intercept	187.99	115.57	268.57	0.33
MEE	Intercept	137.23	148.81	246.68	0.26
pMEE1	Intercept, ECM	141.91	244.05	223.81	0.23
pMEE2	Intercept, MBW, ECM, BWG	249.53	705.16	167.37	0.22
pMEE3	Intercept, MBW, ECM, BWG, BWL	225.61	685.55	165.50	0.21

Genetic and permanent environmental variances for regression coefficients from models pMEE1 and pMEE2 are presented in Table 17. The estimated genetic variances were highest for the intercepts in both models, whereas estimated genetic variances were clearly smaller for the linear regression coefficients $BW^{0.75}$, ECM and BWG. Variance estimates obtained by pMEE1 or pMEE2 for the same genetic (intercept and ECM) and permanent environmental (intercept and ECM) effects differed considerable. The genetic variances, estimated with model pMEE2 for the linear regression coefficients on $BW^{0.75}$ and BWG, were smaller than their associated standard errors, which indicate large uncertainty associated with estimates for energy efficiency for maintenance and growth. However, analyses with model pMEE1 resulted in combined variance component estimates, which resemble with the estimates from MEE (Table 16). Based on pMEE1 the genetic standard deviation estimate for the intercept was 10.8 MJ MEI /d and the genetic standard deviation estimate for the regression coefficient for milk production was 0.75 MJ MEI/kg ECM. The genetic standard deviation estimates for regressions on maintenance and growth, obtained with model pMEE2, were 0.47 MJ MEI/kg $BW^{0.75}$ and 18.0 MJ MEI/kg, respectively, but associated standard errors were large.

Table 17. Genetic (σ^2_a) and permanent environmental (σ^2_{pe}) variance estimates with SE for regression coefficients from two random regression model including random regression on intercept andECM (pMEE1); and intercept, MBW, ECM and BWG (pMEE2).

Regression	σ^2_a		σ^2_{pe}	
coefficient	pMEE1	pMEE2	pMEE1	pMEE2
Intercept	116.74 ± 48.52	78.18 ± 54.37	174.46 ± 40.78	320.47 ± 58.63
$BW^{0.75}$		15.21 ± 71.68		627.92 ± 90.95
ECM	10.60 ± 8.91	12.21 ± 7.63	48.90 ± 9.58	25.18 ± 7.65
BWG		17.07 ± 27.83		219.35 ± 33.11

Genetic correlations between regression coefficients were positive, except between energy efficiency for maintenance and for growth which was practically zero (Table 18). The genetic correlation between energy efficiency in milk production and maintenance was 0.44, and the genetic correlation between energy efficiency in milk production and growth was 0.53. However, the standard errors for genetic correlations were high, which again is an indication of uncertainty associated with the genetic covariance estimates. Mostly permanent environmental correlations were weakly negative except that the correlation between energy efficiency in growth and maintenance was -0.71, and the correlation between energy efficiency in growth and intercept was 0.24.

Table 18. Genetic (upper triangle) and permanent environmental (lower triangle) correlations with SE between genetic values for partial efficiencies for intercept [pMEE(int)], maintenance [pMEE(MBW)], milk production [pMEE(ECM)], and growth [pMEE(BWG)] based on the pMEE2 model.

	pMEE(int)	pMEE(MBW)	pMEE(ECM)	pMEE (BWG)
pMEE(int)		0.182 ± 1.26	0.523 ± 0.48	0.753 ± 0.70
pMEE(MBW)	-0.040 ± 0.11		0.441 ± 1.75	-0.006 ± 2.20
pMEE(ECM)	-0.084 ± 0.17	-0.207 ± 0.147		0.526 ± 0.71
pMEE (BWG)	0.243 ± 0.11	-0.712 ± 0.06	0.096 ± 0.15	

Conclusion

In this study metabolizable energy intake was modelled by including regressions on energy sinks resulting in an efficiency trait that is analogue to residual feed intake. Metabolizable energy efficiency improved modelling of the data and resulted in better properties for prediction of breeding values compared to residual feed intake. Moreover, the model for metabolizable energy efficiency can be expanded to include random regressions on different energy pathways to model genetic variation in efficiency with respect to specific energy pathways. In this study we found evidence for genetic variation among cows in how efficiently cows are using metabolizable energy for specific energy pathways and also that there is a positive genetic correlation among these partial efficiencies. By fitting random regression models we were able to model cow-specific partial efficiency breeding values for milk production and growth. However, modelling partial efficiency breeding values for maintenance was difficult and will require additional research.

Results have been presented on Maataloustieteen Päivät 2016 and EAAP 2016, and are published in Mehtiö et al. (2018).

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Task 2.4 Modelling of the genetics of feed efficiency and energy status

Enyew Negussie, Bingjie Li, Terhi Mehtiö, Päivi Mäntysaari, Peter Løvendahl, Britt Berglund, Martin Lidauer

Task 2.4.1 Combining of feed efficiency data across Nordic countries (required for the Nordic cooperation)

Enyew Negussie, Päivi Mäntysaari, Peter Løvendahl, Britt Berglund, Martin Lidauer

The validated combined data included on average 49 weekly records per cow. This sums to a total of 144 360 records. A descriptive statistic of the data for the three main breeds Holstein (HOL), Nordic Red Cattle (RDC) and Jersey (JER) is given for the first three lactations in Table 19.

Table 19. Number of observations and means for average daily dry matter intake (DMI), milk yield, protein, fat and lactose percentages, body weight (BWT) body condition score (BCS) and residual feed intake (RFI) by breed and parity.

Parity	Breed	Obs	DMI(kg)	Milk(kg)	Protein(%)	Fat(%)	Lactose(%)	BWT(kg)	BCS	RFI
1	HOL	26120	19.0	27.9	3.5	4.2	4.9	599.9	3.2	-0.7
	RDC	22241	18.6	25.9	3.5	4.3	4.7	587.2	3.2	-0.8
	JER	9650	15.8	18.8	4.3	6.1	4.8	434.8	3.2	0.0
2	HOL	17420	22.1	34.1	3.5	4.2	4.8	659.2	3.1	0.4
	RDC	4722	21.2	28.9	3.6	4.3	4.8	637.8	3.4	0.5
	JER	6770	18.3	22.2	4.4	6.1	4.8	477.2	3.2	1.2
3	HOL	10451	22.2	34.6	3.5	4.2	4.8	693.0	3.1	0.1
	RDC	2740	21.5	31.0	3.5	4.3	4.7	667.7	3.4	-0.2
	JER	4241	18.9	23.2	4.3	6.1	4.8	493.1	3.1	1.3

Observations from for second and third lactation were only available from Denmark. Therefore, analyses carried out with this data focused mainly on first lactations records. The extracted combined pedigree included 28,002 animals. The joint Nordic feed efficiency database and its associated pedigree file provided a rare and unique dataset that has been used for both genetic and nutritional studies in feed intake and efficiency traits.

Task 2.4.2 Genetic analyses of dry matter intake in Nordic Red, Holstein and Jersey

Bingjie Li, Britt Berglund, Päivi Mäntysaari, Martin Lidauer, Peter Løvendahl

Estimated heritabilities for DMI across first lactation varied between 0.2 and 0.4, which is consistent with the literature. Heritabilities differed between the breeds however, differences were within the standard errors (Figure 14). For RDC and unexpected high heritability was found for lactation month 3. As expected, genetic correlation decreased the more lactation weeks were apart from each other (Figure 15). Genetic correlations were higher for Holstein and Jersey compared to RDC. Furthermore, for RDC the genetic correlations pattern differed significantly for lactation month 3 and 4, which was unexpected.

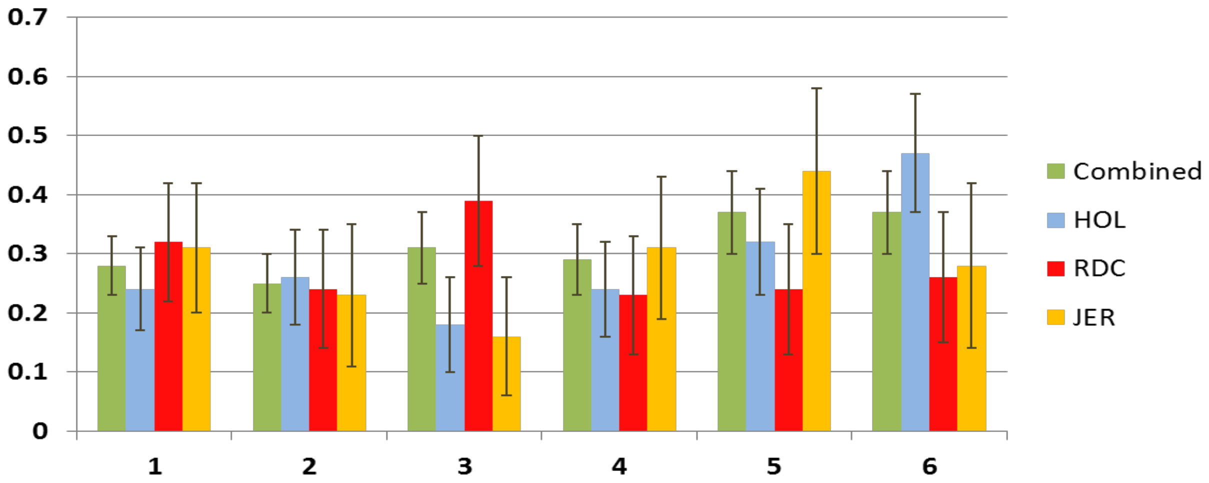
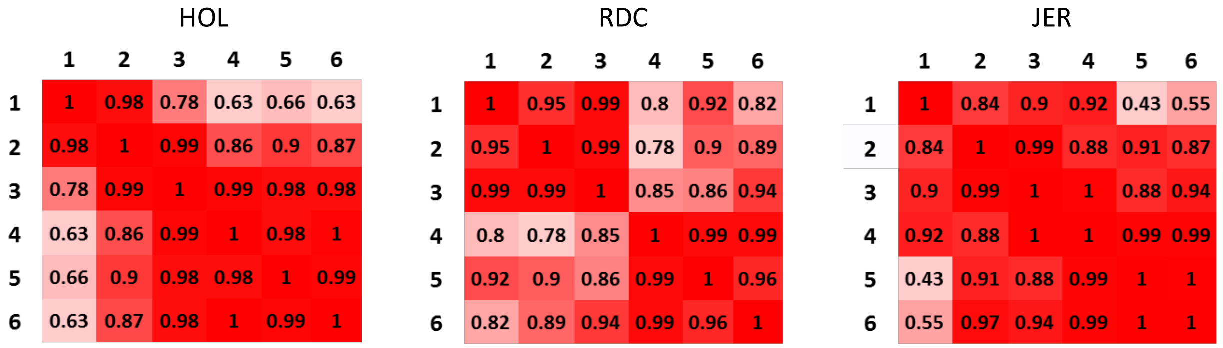


Figure 14. Heritabilites of dry matter intake in the first 6 lactation months given by breeds.



HOL

	1	2	3	4	5	6
1	1	0.98	0.78	0.63	0.66	0.63
2	0.98	1	0.99	0.86	0.9	0.87
3	0.78	0.99	1	0.99	0.98	0.98
4	0.63	0.86	0.99	1	0.98	1
5	0.66	0.9	0.98	0.98	1	0.99
6	0.63	0.87	0.98	1	0.99	1

RDC

	1	2	3	4	5	6
1	1	0.95	0.99	0.8	0.92	0.82
2	0.95	1	0.99	0.78	0.9	0.89
3	0.99	0.99	1	0.85	0.86	0.94
4	0.8	0.78	0.85	1	0.99	0.99
5	0.92	0.9	0.86	0.99	1	0.96
6	0.82	0.89	0.94	0.99	0.96	1

JER

	1	2	3	4	5	6
1	1	0.84	0.9	0.92	0.43	0.55
2	0.84	1	0.99	0.88	0.91	0.87
3	0.9	0.99	1	1	0.88	0.94
4	0.92	0.88	1	1	0.99	0.99
5	0.43	0.91	0.88	0.99	1	1
6	0.55	0.97	0.94	0.99	1	1

Figure 15. Within breed genetic correlations between first 6 lactation months.

About 15% of the feed intake data for RDC was from Swedish feeding trials. For these trials recording was done for certain, shorter periods of the lactation whereas in Danish and Finnish trials feed intake was recorded during the whole lactation period. Removing the Swedish data resulted into estimates, which were consistent with those for Holstein and Jersey. Based on these analyses we can conclude that currently we have high quality data for Holstein, Nordic Red Cattle and Jersey that was recorded at Foulum KCF research farm in Denmark and Jokioinen Rehtijärvi and Minkiö research farm in Finland.

For feed intake we obtained similar results as for other breeding traits, which is, that estimated genetic parameters are similar for the Holstein and Nordic Red cattle breed but for the Jersey breed estimated parameters are somewhat different.

Task 2.4.3 Accuracy of feed efficiency breeding values when data collection is sparse

Enyew Negussie, Päivi Mäntysaari, Peter Løvendahl, Britt Berglund, Martin Lidauer

Parameter estimates for daily dry matter intake

The daily heritability estimates for DMI on the other hand ranged from 0.18 to 0.40 across the different stages of lactation with higher heritability of about 0.4 observed at the beginning which then declined to

0.18 in mid lactation at which point the heritability curve started to increase towards late lactation (Figure 16). Combined 280-d heritability for DMI was 0.33 indicating that based on the cow's own information from weekly recording only, the cows' EBV accuracy cannot be higher than 0.57. The genetic correlation of DMI ranged from -0.5 to 0.98 at different stages of lactation.

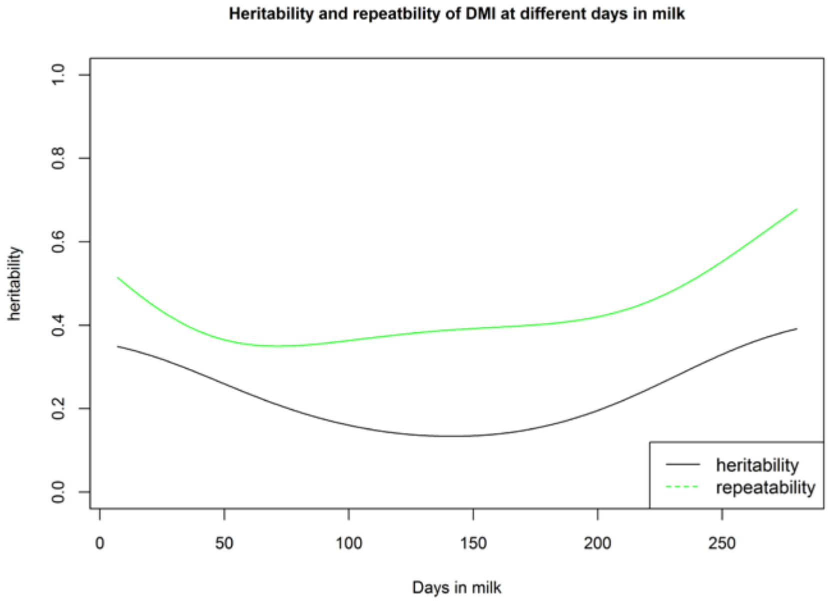


Figure 16. Estimates of heritability and repeatability of DMI at different stages of lactation from random regression model.

The correlations of DMI at 15, 90, 150 and 274 DIM with all the other days in lactation are in Figure 17**.** Genetic correlations of DMI at all DIM with DMI recorded on DIM 15 was close to unity in early lactation but declined quickly to 0.5 at DIM 100 and was negative after DIM 160 and onwards. The genetic correlation of DMI at all DIM with DMI recorded at DIM 90 was 0.6 in early lactation which increased gradually to 0.95 by DIM 100 and decreased to below zero by DIM 230. On the other hand, genetic correlations between DIM 150 in mid-lactation with all the other days were close to zero at DIM 20 which peaked at DIM 150 before it started declining to 0.3 at DIM 280. The genetic correlation of DMI at DIM 280 with all the other days was close to unity at 260 to 280 and quickly decreased to below zero by DIM 140.

A clear understanding of the genetic associations between DMI at different days in milk is helpful in deciding the optimal DMI recording strategies. Genetic correlations for selected DIMs of 15, 90, 150 and 280 with all the other days in this study clearly showed that except for adjacent DIMs, correlations between different DIMs were less than unity and ranged from -0.5 to 0.9. Several studies have found similar genetic correlation patterns (Hüttmann et al., 2009; Liinamo et al., 2012; Tetens et al., 2014, Li et al. 2016). In general, that indicates that DMI at early stages of lactations is not a good predictors of DMI at mid and late lactation stages. The most ideal strategy would therefore be to sample DMI records from most representative stages of lactation, which should be considered in any future DMI recording on-farm from commercial farms.

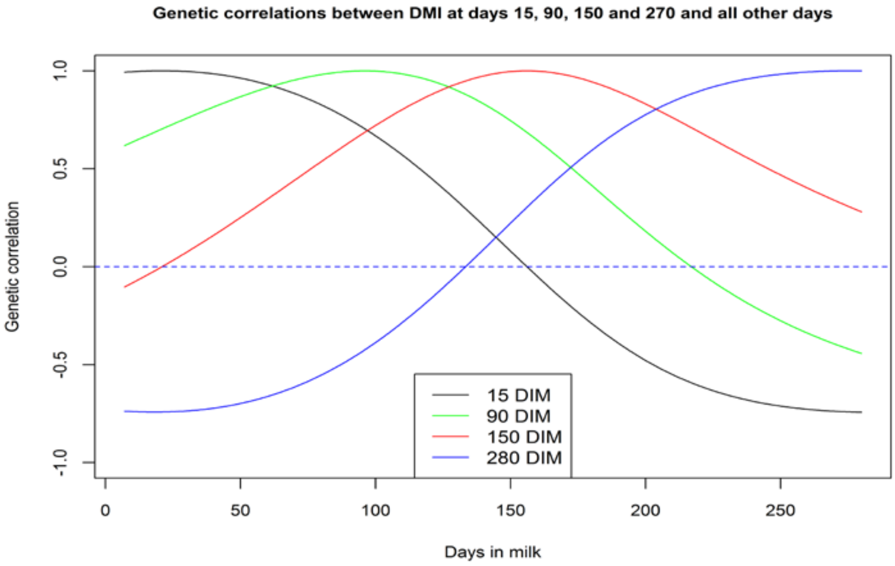


Figure 17. Genetic correlations between DMI at 15, 90, 150 and 280 days with all other days during lactation.

Reliability of EBVs for DMI, RFI and ECE for different on-farm sampling scenarios

The result shows that the reliability of cows EBVs was highest for ECE and lowest for RFI (Table 20). The result shows that with the increase in the sampling interval the reliability of EBVs is declined. For instance, for DMI the reliability of cows EBVs was 0.32 when DMI was collected once a week but this has declined to 0.18 when intake was recorded once every fourth month (SCN5). Especially for RFI, reliability was declining rapidly indicating that RFI is much more sensitive to larger sampling intervals than ECE.

Table 20. Reliability $\left(r_{TBV,EBV}\right)^2$ of cow EBVs for dry matter intake (DMI), residual feed intake (RFI) and energy conversion efficiency (ECE) by recording scenarios. Cows with observations (n=485)

Data sampling scenarios	DMI	RFI	ECE
SCN1	0.32	0.26	0.40
SCN2	0.28	0.13	0.36
SCN3	0.24	0.09	0.31
SCN4	0.23	0.06	0.26
SCN5	0.18	0.05	0.21

Results from the five different DMI sampling scenarios shows that reducing the frequency of on-farm measuring will significantly reduce required samples to achieve certain reliability and by this saves sampling costs (Table 21). However, this comes at the cost of higher number of cows included in the sampling scheme. Given there would be 2000 cows under recording and that the reliability of bull EBVs should reach at least 0.6, then 117, 105, 86 and 83 bulls could be tested with scenario SCN1, SCN2, SCN3 and SCN4, respectively.

Table 21. Reliability of cow EBVs for DMI and number of daughters and corresponding number of observations required for sire EBV reliability of 0.4, 06 and 0.8 given by sampling scenarios.

Data sampling scenarios	**DMI** $(r_{TBV,EBV})^2$	**No. of daughters per sire**			**No. of DMI observations per sire**		
		Reliability of sire EBVs			Reliability of sire EBVs		
		0.4	**0.6**	**0.8**	**0.4**	**0.6**	**0.8**
SCN1	0.32	7	17	46	261	588	1564
SCN2	0.28	9	19	53	84	189	503
SCN3	0.24	10	23	62	45	103	272
SCN4	0.23	11	24	65	34	76	201
SCN5	0.18	14	31	84	32	73	193

Achievable accuracy under genomic selection

For continuous traits with effective chromosome segments of 1000 following Wientjes et al (2013), and genomic prediction accuracy based on Daetwyler et al . (2008), required number of genotyped cows under feed efficiency recording can be calculated. Considering 2000 cows, the achievable genomic prediction accuracy for selection candidates by genomic selection and considering DMI would be between 0.50 and 0.65 depending on the chosen recording scenario (Figure 18).

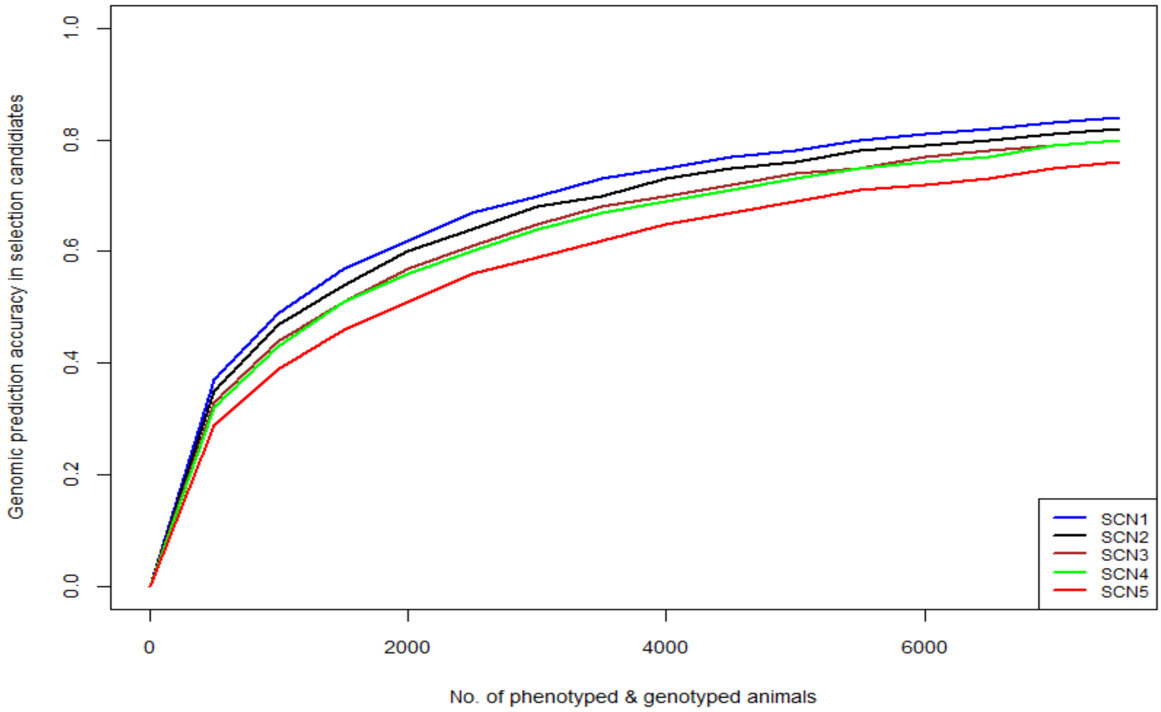


Figure 18. Accuracy of genomic breeding values for selection candidates for dry matter intake depending on female reference population size given by scenarios.

Conclusions

Recording feed intake every second or third month compared to weekly recording resulted only in minor reduction of accuracy which can be compensated by having more cows under recording. However, it resulted in a significant reduction in number of samples (over 80%) and by this reduces cost of recording. Considering genotyping of cows, it has to be noticed that all first lactating cows of a herd that participate in the on-farm recording have to be genotyped and have to be under recording. Under a bimonthly milk content recording scheme, like in Finland, SCN3 (bimonthly) and SCN5 (every fourth month) would be preferable, so it would allow that feed intake recording would be connected to the milk recoding test-day. However, every fourth month recording would lower accuracy for RFI considerably.

A scientific paper about this study is under preparation. Negussie et al. "Reliability of breeding values for feed intake efficiency traits when feed intake recordings are sparse under different scenarios".

Reference

Hüttmann, H., E. Stamer, W. Junge, G. Thaller, and E. Kalm. 2009. Analysis of feed intake and energy balance of high-yielding first lactating Holstein cows with fixed and random regression models. Animal 3:181–188.

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Liinamo, A.-E., P. Mäntysaari, and E. A. Mäntysaari. 2012. Short communication: Genetic parameters for feed intake, production, and extent of negative energy balance in Nordic Red dairy cattle. J. Dairy Sci. 95:6788–6794.

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WP3. Development of a method for recording dry matter intake on-farm

Task 3.1 Assessment of required accuracy for an on-farm dry matter intake measurement

Pekka Huhtanen, Abdulai Guinguina, Kevin Shingfield, Seppo Ahvenjärvi

The current results showed repeatability values, co-efficient of variations and residual variances of 0.65, 0.58 and 0.47, 8.0%, 8.1% and 9.2%, 1.17, 2.37 and 3.03 for DMI, pDMI1 and pDMI2 respectively. The lower repeatability and high CV and residual variance estimates for pDMI2 could be related to the sensitivity of laboratory procedures involved for analysing samples of indigestible markers especially when calibrations have to be made for each set of conditions. Moreover, problems with incomplete marker recovery (particularly internal markers) results in variation in digestibility values and consequently lower repeatability of measurements. R^2 and mean square prediction errors for the prediction of DMI (adjusted for experimental effect) from pDMI1 and pDMI2 were 0.81 and 0.82, 1.16 kg/d and 1.08 kg/d respectively. This indicates that, predicting DMI from external markers is as good if not better than calculating it from double markers. A residual plot was also made by regressing the residuals (DMI- pDMI) on centered predicted values (calculated by subtracting the mean pDMI value from each pDMI). There were linear biases of -0.49 and -0.44 for DMI predicted from pDMI1 and pDMI2 respectively, i.e. residual DMI = –0.493*centered pDMI1 –1.304 and residual DMI = –0.440*centered pDMI2 + 0.850. pDMI1 over predicted DMI at lower intakes while pDMI2 under predicted DMI.

Table 22. The results from the models developed where LW represents live weight in kg.

Model	AIC	Residual variance
basal model FE = 0.966+0.034*ECM–0.0007*LW	-541.0	0.0100
FE= 1.177+ 0.041*ECM–0.0006*LW–0.090*pFDM	-671.1	0.0072
FE= 0.820+0.034*ECM–0.0007*LW–0.0002*pDMD	-540.6	0.0101
FE= 1.208+0.041*ECM–0.0005*LW–0.027*pDMI1	-614.9	0.0074
FE= 1.103+0.040*ECM–0.0005* LW–0.022*pDMI2	-638.3	0.0076

Table 22 shows that although predicted DMD is positively related to feed efficiency it does not improve the predictions. Also predicting FDM output from external markers has a potential to improve ranking of cows according to feed efficiency.

Task 3.2 Examination of external candidate markers

Seppo Ahvenjärvi, Laura Nyholm, Esa Mäntysaari, Martin Lidauer

The results from the first animal experiment indicated that faecal dry matter output was accurately determined using PEG when compared with the results obtained by total collection method (8.02 kg/d vs. 8.05 kg/d). Dry matter digestibilities determined using PEG were in agreement with those determined by total collection of faeces. The mean recovery of PEG in faeces was 100.5% (SD 4.79) of the dose administered into the rumen (Table 23).

Table 23. Diet effects on measured and estimated faecal output and nutrient digestibility

	TRM-40[1]	TMR-60[2]	SEM[3]	P-value
Faecal DM output, kg/d				
Measured	7.75	8.35	0.243	<0.01
PEG	7.67	8.36	0.198	0.01
Digestibility				
Measured	0.689	0.693	0.0039	0.16
PEG	0.692	0.692	0.0044	0.95
PEG recovery	1.01	1.00	0.020	0.54

[1] Total mixed ration consisted of 40% of concentrates.

[2] Total mixed ration consisted of 60% of concentrates.

[3] Standard error of the mean.

Similar to PEG the recovery of chitin in faeces was complete (99.5%) but more variable with PEG (SD 9.1). Faecal DM output estimated using chitin was close to that measured by total collection (8.05 vs. 7.97 kg/d; Table 24). These results suggest that both PEG and chitin are quantitatively excreted and recovered in faeces and their concentrations can be accurately determined using NIRS.

Table 24. Diet effects on measured and estimated faecal output and nutrient digestibility

	TRM-40[1]	TMR-60[2]	SEM[3]	P-value
Faecal DM output, kg/d				
Measured	7.61	8.33	0.231	<0.01
Chitin	7.67	8.42	0.274	0.11
Digestibility				
Measured	0.688	0.696	0.0044	0.18
Chitin	0.685	0.692	0.0109	0.65
Chitin recovery	0.998	0.991	0.041	0.90

[1] Total mixed ration consisted of 40% of concentrates.

[2] Total mixed ration consisted of 60% of concentrates.

[3] Standard error of the mean.

Task 3.3 Assessment of the administration of the external marker

Seppo Ahvenjärvi, Laura Nyholm, Esa Mäntysaari, Martin Lidauer

Passage rate

The passage rate of chitin was considerably slower than that of PEG as indicated by the mean retention time in the mixing compartments of the digestive tract (23.9 vs. 9.4 h for chitin and PEG, respectively). As a water soluble compound PEG is associated with rumen liquid phase and, consequently, has a rapid passage rate out of the rumen. In contrast, chitin is an insoluble compound, which associates with rumen particulate matter and has considerably slower passage rate than PEG. Differences in passage rate have direct effects on marker excretion patterns in faeces. PEG reaches equilibrium between marker intake and faecal output in two days, whereas for chitin it takes approximately three days to approach equilibrium (Figure 19). With a safety margin these results suggest that collection of faecal spot samples can be started 3 and 4 days after the onset of PEG and chitin administration into the rumen.

Rapid passage rate in combination with twice a day administration into the rumen was associated with substantial diurnal variation in faecal PEG concentrations. The minimum and maximum PEG concentrations in faeces ranged between 66 and 139% of the daily average (Figure 20). Such variation in faecal PEG concentrations indicates that, in practise, either frequent collection of faecal spot samples or frequent administration of marker into the rumen is required to ensure accurate faecal output measurements. Owing to slower passage rate, daily variation in faecal chitin concentrations was considerably lower than that observed for PEG. The minimum and maximum chitin concentrations ranged between 92 and 112% of the daily average (Figure 20).

Simulation of marker administration

Simulations of PEG excretion patterns in faeces demonstrated that administration of PEG twice daily into the rumen represents the minimum frequency of marker doses that restricts the variation within a reasonable range and decreasing the interval to 8 hours further decreases the diurnal variation. Simulations of chitin concentration in faeces demonstrated that twice a day administration is advisable to provide accurate estimates of faecal output with the smallest number of faecal spot samples. In practice, dairy cows exhibit substantial variation between days in feed intake and faecal output such that the minimum number of faecal spot samples needed for reliable estimates of faecal output is between three and five. Such a number of spot samples is also sufficient to account for the diurnal variation in marker concentrations when spot samples are collected at different hours relative to the time of marker administration.

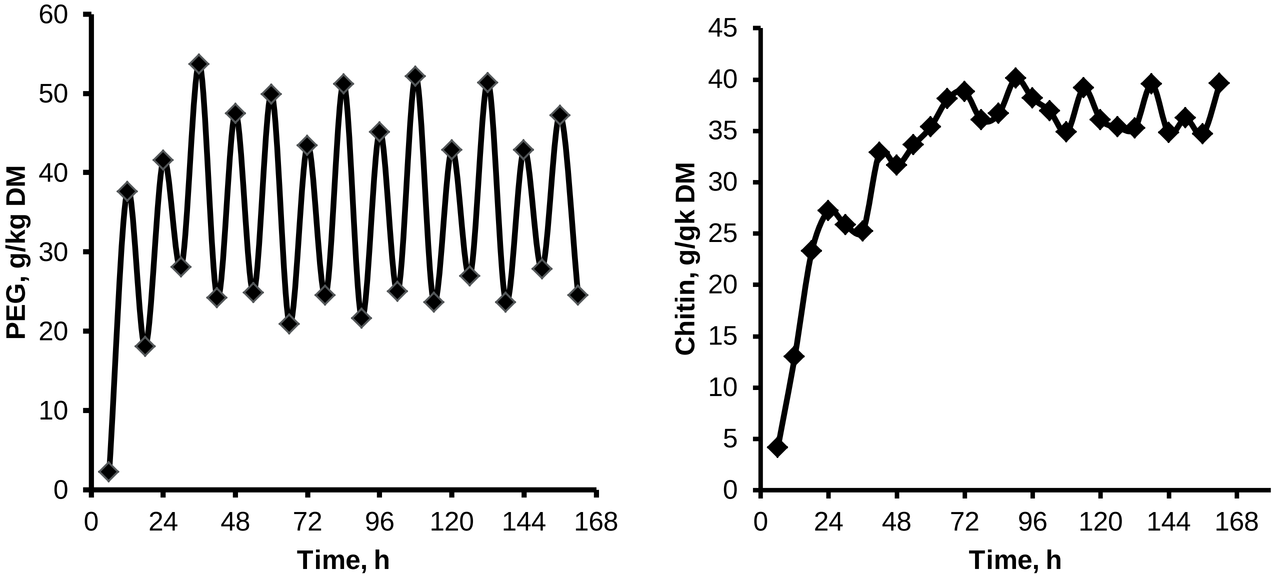

Figure 19. Diurnal variation for PEG and chitin during first 7 days.

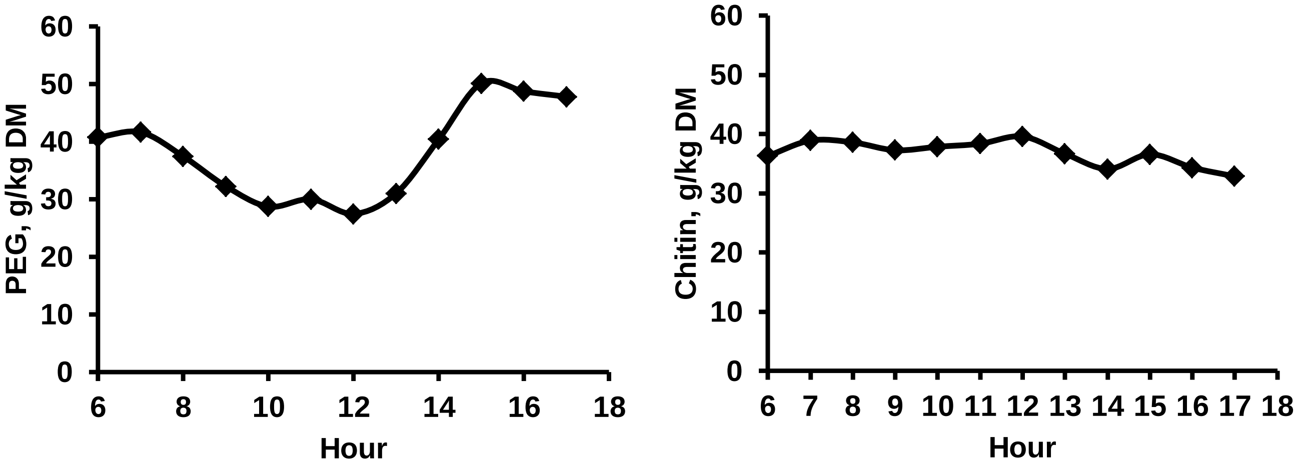

Figure 20. Diurnal variation for PEG and chitin when marker was administrated twice a day.

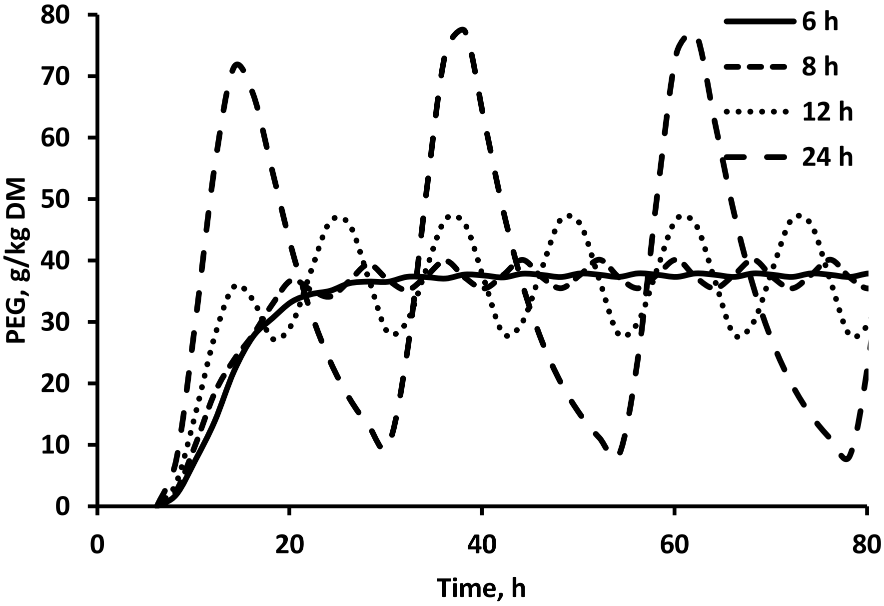

Figure 21. The effects of PEG dosing interval on marker excretion pattern in faeces.

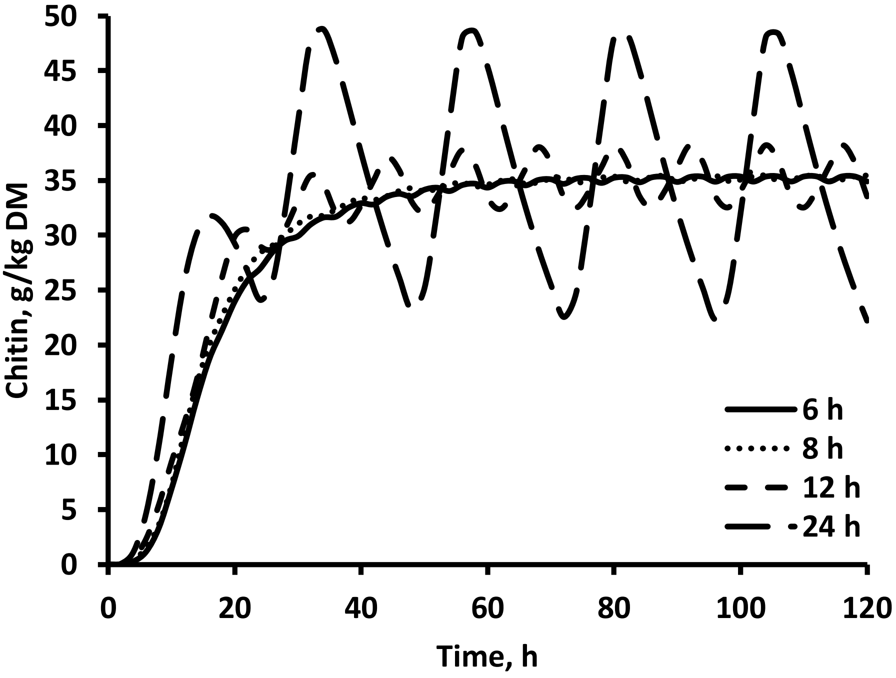

Figure 22. The effects of chitin dosing interval on marker excretion pattern in faeces.

Conclusion

The current results suggest that both PEG and chitin are promising markers to quantify faecal output in dairy cows. However, there are some issues that need to be assessed further. The recovery of chitin was more variable than that of PEG and the precision of DM digestibility estimates was lower for chitin than for PEG. A larger calibration data set may improve the precision of chitin measurements using NIRS method.

Alternative sources of chitin may prove to be more suitable for a marker application than the product that was used in the current experiment.

Results are published in Ahvenjärvi et al. (2018).

Task 3.4 Validation of the dry matter intake measurement method

Marketta Rinne, Päivi Mäntysaari, Laura Nyholm, Seppo Ahvenjärvi, Esa Mäntysaari, Martin Lidauer

Preparation of the pelleted feeds containing markers and conduction of the experiments went without practical problems. There was e.g. no reduction in feed intake although the concentrations of the markers were rather high particularly when administered at the milking parlour (10 %). The marker concentrations in the concentrate were assumed to be as planned. Based on concentrate intakes the marker doses were an average 271 ±51.4, 297±13.9, 279±32.7 and 298±3.2 g/d for cows on PEG-K, PEG-MP, Chi-K and Chi-MP groups. The faecal samples were analysed for marker concentrations by NIRS, which resulted in a rather high number of unrealistic values. The average markers concentration in faecal grab samples on PEG-K, PEG-MP, Chi-K and Chi-MP groups were 34.6±10.1, 35.5±11.8, 33.4±5.3 and 31.5±8.9, respectively. Giving marker only twice a day in milking parlour increased the variation of marker concentration in grab samples a little.

Based on faecal marker concentration and daily marker dose, the faecal output of the cows was calculated either using marker concentration of each grab sample separately (FO1), or calculating daily average concentration of marker in faeces (FO2=average of daily two grab samples) or by calculating the average concentration over all three sampling days (FO6=average of six grab samples). Because of the unrealistic marker concentrations in individual faecal samples, the faecal output resulted in several unrealistic values when judged against true dry matter intake (DMI) and DM digestibility of the diet. The diet digestibility was calculated using diet and faecal iNDF concentrations (DMDindf). Thus, faecal marker concentrations resulting in faecal output lower than 5 kg DM/d or higher than 15 kg DM/d were excluded from the data. Totally 10.5 % of the observations were excluded.

The daily DMI predicted (DMIpred) based on faecal output (FO1, FO2 or FO6) and DMDindf were calculated. The means of DMI observed and DMIpred using FO6 were 26.4 and 23.4 kg on PEG-K, 25.9 and 23.9 kg on PEG-MP, 25.8 and 26.5 kg on Chi-K and 25.4 and 27.7 kg on Chi-MP. The correlations between observed and predicted DMI are presented in Figure 23. The correlation was the highest when PEG was used as marker and when it was given as a part of the basal concentrate from kiosk. The results indicate that the method needs improving. Probably the most critical point to be improved is the accuracy of marker determination from faecal samples.

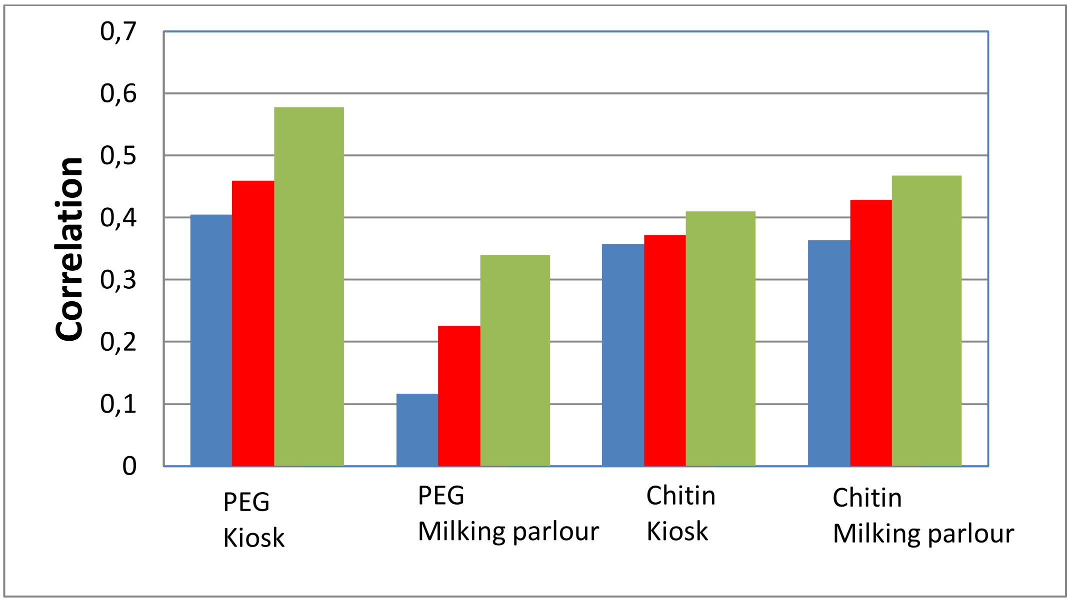

Figure 23. The correlations of observed and predicted DMI using faecal marker concentration of one grab sample (blue), average of daily two grab samples (red) or average of six grab samples during three days (green). The markers (PEG or Chitin) were given either twice a day in milking parlour (high concentration of marker in a small concentrate allowance) or continuously from concentrate kiosk (low concentration of marker in the whole concentrate allowance) so that the total amount of the markers was the same for all groups.

Conclusions

The validation trail resulted in rather low correlations between measured DMI and predicted DMI by the marker method. Investigation of the results suggests that the method should be improved twofold. First, the administration of the external marker needs to be improved to ensure 1) that a cow gets the whole daily marker dose and 2) that the marker dose concentration is more stable across different times of the day. Secondly, prediction of the marker concentration in faeces by NIRS needs a significant improvement. With respect to the latter point currently additional analyses are carried out with the aim to use the data from this validation trial for developing new prediction equations. An improvement of the results would indicate that there is potential in improving this method to be practically applicable.

3.3 Evaluation of the projects implementation

General set up of the project and surrounding circumstances

The *Finnish Feed Efficiency* project was not only exceptionally large and multidisciplinary with respect to necessary research facilities involved, size and complexity of data to be collected, amount of laboratory analyses to be carried out, size of research group and number of cooperating partners involved, but it was also embedded into a large Nordic researcher initiative (FUNC). The general set up of the project was based on two important conditions which were crucial for the success of the project. 1) The project activities were planned for five years with a progress evaluation after three years (the project continues after delivery of this end report). 2) There was significant funding by the industry, larger than the funding by MMM, which allowed conducting a project of this size.

The project was designed to carry out coordinated research together with the Nordic research partners to achieve highest possible cooperation and synergism. Despite the intensive cooperation among the Nordic countries during the whole project time, it was not always possible to address the originally commonly agreed Nordic research plan (“*Towards more sustainable dairy production in the Nordic countries through improved feed efficiency and reduced environmental impact*”) accepted by the Nordic dairy industry R&D. This was because research groups had to apply funding from national bodies, which obviously changed research goals within countries in order to meet national funding requirements. A common funding across Nordic countries would have significantly improved this situation. Moreover, coordination of work packages across countries was delegated to national level, which added unforeseen additional coordination and administration work to this project.

Other unforeseen circumstances affecting this project were the merge of MTT Agrifood Research Finland into Natural Resources Institute Finland (Luke) and the Russian import embargo for dairy products, which affected Valio Ltd. Consequently, both project partners were undergoing significant organisation changes with effect on the progress of the project. The latter circumstance forced Valo Ltd. to reduce the originally planned funding for the project. At the same time the R&D focus area of RAISIOagro Ltd was changed and therefore RAISIOagro Ltd terminated funding of the project after the third year. The original research plan for the last two years was adjusted in agreement with the industry funding partners due to these circumstances.

Project management

The complexity of the project required a string organization. Research was organized in three work packages and 15 work tasks, of which many tasks were rather large. Assigning for each task a responsible researcher was crucial to ensure progress and coordination among tasks. Progress of research was followed up in 10 research group video-link meetings, 5 Nordic FUNC workshops, 7 steering group meetings, 3 meetings with industry funding partners, 1 interims evaluation meeting, numerous task-specific national and Nordic video-link meetings and a countless number of spontaneous meetings, and phone and e-mail conversations.

Project management was challenged by continued changes in research and technical personnel beyond normal expectations. This was partially due to the reasons mentioned above. Several persons were on sick leave for longer time, two on maternity leave, one person twice on leave of absences, one resigned and numerous technical personnel was reduced due to research infra cost reduction targets. Unfortunately two invaluable colleagues, Kevin Shingfield and Anna-Elisa Liinamo, passed away during the project. The changes were compensated by reallocating data collection, laboratory and research tasks to technical and research personnel who was not involved in the project originally, by a significant increase in work load for researchers central for the project, which was often going far beyond normal working time, and some tasks had to be postponed until a suitable person was found to continue the work task.

Timetable

The required research farm data collection was carried out over the whole project period as has been planned originally for the majority of all data collection activities. Data collection was carried out in a professional manner as well as all analyses in the laboratories. This ensured to make high quality data available for later statistical analyse. Cows under feed efficiency data collection at the three research farms were selected based on their common genetic background, which required a careful selection procedure for Ayrshire cows at the Viikki research farm. Collection of feed efficiency data was ended at Maaninka and Viikki research farm, and collection of faecal spot samples was ended at all three research farms in August 2016 due to the reduction of industry funding. To establish the Nordic feed efficiency research for genetic analyses it was planned that data from seven research farms for the four Nordic countries will be merged. However, only Finland (Rehtijärvi, Minkiö), Denmark (KFC Foulum) and Sweden (Lövsta) was able to deliver data. During genetic analyses of data it was found that only the data from Rehtijärvi, Minkiö, and KFC Foulum fulfilled the quality requirement to obtain reliable results.

Establishing the MIR spectral data collection was started by Valio Ltd as planned, but many technical problems were encountered which were impossible to foresee. The whole system was finally established as planned but routine collection of MIR spectral data started 1.5 years later as planned. This delayed also the analyses of the MIR spectral field to the end of the project because a sufficient long recording period is needed to allow extraction of suitable data for genetic analyse. When storing MIR spectral data for the first time into the database, errors in storing the milk sample numbers occurred. The errors were detected when extracting data for the first time from the database. This was crucial because almost half of the samples for the NEFA trial were affected. Intensive work on this problem allowed to recover 80% of the MIR spectra needed for the NEFA trial. The data was still large enough to carry out this research task successfully.

All specific animal trials were carried out as planned and the data collection for these trials was successful, which is owed to the high skilled technical personnel involved in the project. Processing of samples involved massive amount of laboratory work and data preparation. For the marker-based dry matter intake validation study and for the digestibility study final data preparations a currently carried out and statistical analyses started in summer 2017. These studies could have been completed already by that time if there would have been fewer changes in personnel as explained above.

All planned research tasks were carried out except the analyses of field data and the pilot field test for measuring dry matter intake as was agreed with the funding partners. Data collection and analyses were often more demanding than originally anticipated.

3.4 Publications

Scientific articles:

Ahvenjärvi, S., Nyholm, L., Nousiainen, J., Mäntysaari, E.A., and Lidauer, M.H. 2018. Polyethylene glycol as an indigestible marker to estimate fecal output in dairy cows. J. Dairy Science 101: 4245-4258. https://doi.org/10.3168/jds.2017-13337

Hietala, P., Bouquet, P., and Juga, J. 2014. Effect of replacement rate, crossbreeding and sexed semen on the efficiency of beef production from dairy herds in Finland. Acta Agriculturae Scandinavica, Section A – Animal Science, 64: 199–209.

Hietala, P. and Juga, J. 2016. Impact of including growth, carcass and feed efficiency traits in the breeding goal for combined milk and beef production systems. Animal 11: 564-573.
http://dx.doi.org/10.1017/S1751731116001877

Liinamo, E.-E., Mäntysaari, P., Lidauer, M., Mäntysaari, E. 2015. Genetic parameters for residual energy intake and energy conversion efficiency in Nordic Red dairy cattle. Acta Agric. Scand. Section A. 65: 63-72. http://dx.doi.org/10.1080/09064702.2015.1070897

Li, B., Fikse, W.F., Lassen, J., Lidauer, M.H., Løvendahl, P., Mäntysaari, P., and Berglund, B. 2016. Genetic parameters for dry matter intake in primiparous Holstein, Nordic Red, and Jersey cows in the first half of lactation. J. Dairy Sci. 99: 7232–7239. https://doi.org/10.3168/jds.2015-10669

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Participation in FUNC annual researcher meeting in 3.-4., March 2014, Lövsta, Sweden (Martin Lidauer, Päivi Mäntysaari, Marketta Rinne, Juha Nousiainen, Enyew Negussie, Jarmo Juga, Seppo Ahvenjärvi, Laura Nyholm, Terhi Mehtiö, Sari Kajava).

The project was presented in agricultural exhibition, Okra, Oripää, Finland in 2.-5., July 2014 (Martin Lidauer, Terhi Mehtiö, Anna-Elisa Liinamo, Kirsi Muuttoranta and Anna-Maria Tyrisevä)

Participation in METHAGENE Training School, 29. September – 1. October 2014, Dummerstorf, Germany (Terhi Mehtiö).

Hosting the Annual meeting of FUNC researches at Luke, Jokioinen on 12-13 March 2015. Total number of participants 26. Finnish participants: Rinne Marketta, Lidauer Martin, Ahvenjärvi Seppo, Pauliina Hietala, Laura Nyholm, Mehtiö Terhi, Jarmo Juga, Mäntysaari Päivi, Mäntysaari Esa, Negussie Enyew, Anna-Elisa Liinamo, Timo Sipiläinen, Sairanen Auvo, Kokkonen, Tuomo, Annu Palmio.Participation in the "Final OptiMIR scientific and expert meeting", 16.-17. April 2015, Namur, Belgium (Martin Lidauer).

Participation in final FUNC seminar in 30. November – 1. September 2016, Helsinki, Finland (Paulina Kokko, Martin Lidauer, Enyew Negussie, Päivi Mäntysaari, Esa Mäntysaari, Tuomo Kokkonen, Jamo Juga, Timo Sipiläinen).

4. EVALUATION OF THE RESULTS

4.1 Practical applicability of results

The overall research aim of this project was to produce new scientific knowledge needed for developing genetic evaluations for feed efficiency in dairy cattle. The project continued research on feed efficiency initiated by the previous "*Lehmien rehunkäyttökyky*" project and addressed important research questions identified by that latter project and in the literature. Interdisciplinary research in this project has produced significant amount of new knowledge, which will allow initiating the development of a feed efficiency genetic evaluation for Finnish and Nordic dairy cattle.

There are many biological factors that determine the efficiency of a dairy cow and several traits are needed to describe the most important aspects. For describing the within lactation genetic variation of REI, which describes the overall efficiency of a lactating cow, it was found that appropriate modelling of the observations is crucial to obtain reliable breeding values. Best fit was achieved when modelling MEI observations instead of REI observations and fitting regressions on energy requirements simultaneously in the model (Table 16), which could be named "metabolizable energy efficiency" and for which a heritability of 0.26 was estimated for weekly observations. Nevertheless, modelling MEI or REI requires accurate and repeated recording of feed intake and body weight within lactation. The genetic correlation between REI and ECM was found to change from negative in early lactation to positive in later lactation (Figure 13), which should be studied more closely if REI is chosen as breeding trait. It was found the modelling ratio traits, like ECE, which describes the efficiency of using MEI for producing milk, results more stable genetic correlation with other traits along the different stages of lactation (Figure 13) and required less frequent recording to achieve same accuracy in breeding values compared to RFI (Table 20). This makes ECE an interesting trait to be considered for breeding. Estimated heritability for daily ECE was 0.16.

In this project we identify one indicator trait which may be of interest for building genetic evaluations in the absence of feed intake measurements. For this assessment, we formed whole-lactation feed efficiency observations for ECE and ECR and substituted the missing MEI observations by their expectations. The highest genetic correlation between a feed efficiency trait (ECR) and its indicator trait found was 0.89. This indicator trait was the ratio of expected lactation MEI for maintenance over lactation ECM, which could be named maintenance requirement ratio (MRR), and for which we estimated a genetic standard deviation of 0.19 MJ/kg ECM and a heritability of 0.43. This trait could be linearly transformed by Taylor series expansion into an index with weighted component traits (metabolizable body weight and ECM), which resembles the ratio trait. The trait MRR describes the amount of feed needed for maintenance per kg ECM produced. Selection index analyses showed that including MRR into the current yield index would increase the net merit of the yield index by 18 and would increase current progress in feed efficiency (i.e. ECE) by 23%. Including metabolic body weight into the current index would result even larger increase in net merit and progress of feed efficiency (Table 11). Assuming that inclusion of these traits into the breeding goal would result a genetic progress in the indicator trait of between 0.1 to 0.3 genetic standard deviation annually, then DMI would reduce annually between 0.25 to 0.75%. After seven years of genetic progress, the annual saving in feed would be between 1.8 and 5.4% which relates to cost savings of 6 M€ to 20 M€ for Finnish dairy farmers under current feed prices. The reduction in methane emission would be between 15 000 and 47 000 metric tons of CO_2 equivalents annually. Simulation of the effect of a 5% increase in feed efficiency showed that the expected increase of margins over costs is even larger (between 23 M€ and 38

M€) depending on how this efficiency increase is utilized on the farm. In contrast, when included only body weight as indicator trait into the total merit index, a decrease in discounted profit was found (Table 10). This was because also milk yield was reduced due to the positive correlation between body weight and milk yield. When adding RFI traits into the total merit index, the discounted profit of the breeding program increased only slightly (1.4%, Table 10) and largest increase in discounted profit was obtained when also beef traits were included while preventing higher body weights for cows (5.1% or 17.5€/cow).

Developing genetic evaluations will require recording of feed efficiency from genotyped cows. A simulation study carried out in the project showed that between 2000 to 3000 primiparous genotyped cows should be under feed efficiency record annually to achieve genomic prediction accuracy in selection candidates of 0.4 to 0.6 (Figure 18). Therefore, depending on the trait, between 5 000 to 28 000 feed efficiency records have to be collected annually. Our results indicated that at least 3 times more data has to be collected for RFI compared to ECE to achieve same accuracy (Table 3 & 20). So far, such records can only be collected at research farms. The feed efficiency data collected in Finland includes over 100 000 daily records from over 600 Nordic Red Cattle cows (Table 6) of which half are genotyped. Therefore, currently, the most obvious approach for developing a feed efficiency evaluation would be to develop a single-step genomic prediction model that combines the data from the research farms with feed efficiency component traits obtained from routine milk recording as explained earlier. The feed efficiency data collected at Luke research herds Rehtijärvi and Minkiö would be valuable for such an approach, because all cows under recording originate from the Nordic Red Cattle breeding nucleus herd. Such an approach would benefit by tripling the current annual number of research cows under recording to up to 110 cows.

Research on NIRS-analyse based methods to predict cow-specific digestibility and DMI showed that the approaches have the potential to be used for future on-farm recoding. Getting an indicator trait for digestibility by NIRS analyse of faeces for iNDF concentration seems feasible, but large contemporary groups of cows consuming the same feed are needed. The genetic analyses showed that there is genetic variation in cows' ability to digest feed and that could be improved by genetic selection. For a marker method to predict DMI based on NIRS analyses of feaces three suitable external markers (PEG, chitin and galalith) were found. Physiological studies resulted accurate recover of the external markers but significant diurnal variation of the marker concentration in the faeces (Figure 21 & 22). Latter will require developing of a marker administration protocol that ensures that the cow will almost continuously consume accurately known amounts of markers because collection of faeces in short intervals is not feasible. Using NIRS on faecal samples to determine feed intake and diet digestibility may open opportunities to on-farm collection of necessary data for animal breeding, but such methods could also be used for feeding experiments and as management tools. This would require a laboratory that could provide these measurements on commercial basis.

Research on developing a predictor trait for negative energy status based on MIR spectral data of milk samples resulted in new opportunities applicable for the practice. During the project time it was possible for Luke and Valio Ltd to join the European Milk Recording (EMR) consortium by signing a contract with the EMR partners. Cooperation with the EMR partners allows Valio Ltd and Luke to use prediction equations developed in the OptiMIR consortium to predict fatty acid profiles for milk samples from Finnish routine milk recording. A routine collection of MIR spectra and transfer to Mtech Digital Solutions Ltd has been established. This will allow future utilization of MIR spectral information for animal breeding, animal nutrition and milk quality purposes. Within this project, predicted milk fatty acids were used for predicting NEFA, which is an established biomarker for negative energy status. For the best prediction models the correlation between measured and predicted NEFA was 0.80 (Figure 11). When using directly milk MIR spectra to predict when cows' blood NEFA concentration the correlations between measured and predicted NEFA were on the same level (Table 9 & 10). Our results showed that this predictor has the potential to be implemented into genetic evaluations. We found that the developed predictor was by far better than using energy balance or fat/protein ratio as predictor. Including a predictor trait for NEFA into a genetic evaluation for feed efficiency will be important, because otherwise breeding for feed efficiency would favour animals which are in severe negative energy status at the onset of lactation.

4.2 Scientific significance of the results

One aim of the project was to publish all results with scientific significance according to the publication activities explained in the report. Results with significant interest for the scientific community are: the assessment of the genetic variance in cow-specific digestibility, which will be finalized this year; partitioning genetic variance of MEI, which showed that maintenance and production are the main components; modelling metabolizable energy efficiency instead of REI which yields better model fit of the data; accessing the required reference population size and amount of feed efficiency records needed to establish genomic predications for feed efficiency; modelling of body weight changes by random regression models; development of a predictions for NEFA based on model including milk MIR spectral information; discovery of new external markers suitable for NIRS analyses (chitin and galalith); the diurnal variation of external marker concentration in faeces of dairy cows; assessment of the accuracy of a marker-based DMI prediction methods, which will be finalized this year; genetic variation in various feed efficiency traits and the genetic correlations among lactation stages and other breeding traits; the value of including feed efficiency traits into the total merit selection index; and the economic and environmental effect of improving feed efficiency in dairy cows.

5. SUMMARY

TOWARDS GENETIC IMPROVEMENT OF FEED EFFICIENCY IN DAIRY CATTLE

Lypsylehmien rehuhyötysuhde paremmaksi eläinjalostuksella

FINNISH FEED EFFICIENCY PROJECT

Responsible organisation	Natural Resources Institute Finland (Luke) Green technology Myllytie 1 31600 Jokioinen
Principal investigator	Martin Lidauer martin.lidauer@luke.fi
Duration	2012 – 2017

Funding		
	Total costs of the project	2 108 000 €
	MMM	400 000 €
	Natural Resources Institute Finland (Luke)	881 000 €
	Valio Ltd	170 000 €
	Valio Ltd, in kind	100 000 €
	Faba co-op	200 000 €
	VikingGenetics	180 000 €
	Naudanjalostussäätiö	100 000 €
	RAISIOagro Ltd	60 000 €
	University of Helsinki	17 000 €

Key words breeding, dairy cow, body weight, body condition, feed intake, digestibility, milk fatty acids, methane, Nordic Red Cattle

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Summary

AIM OF THE PROJECT

The aim of the project was to assess the genetic variation in feed efficiency traits and their suitability for inclusion into the Nordic total merit index for achieving genetic response, to assess the economic and environmental importance of feed efficiency, to identify indicator traits for feed efficiency that are highly correlated with feed efficiency traits of interest, to perform research on developing measurement methods for such indicator traits and to dedicate significant effort on developing an on-farm method for measuring individual feed intake of cows.

RESULTS

During the time of the project feed intake, milk production, milk composition, body weight and body condition was measured on 136 Nordic Red Dairy Cattle (RDC) breeding nucleus cows at Minkiö Luke research farm, 36 RDC cows at Maaninka Luke research farm and 34 RDC cows at Viikki University research farm. These records were combined with corresponding 39 273 records from earlier studies (ASMO 1998-2001, Lehmän rehunkäyttökyky 2006-2009, GREENDAIRY 2010-2012) resulting in 100 670 daily feed efficiency records from 622 primiparous cows. On average energy corrected milk yield was 28.1 kg/d, dry matter intake (DMI) 19.0 kg/d, metabolizable energy intake 208.6 MJ/d, crude protein intake 3.28 kg/d and body weight 586 kg. The average energy conversion efficiency was 0.137 kg ECM/ME MJ and was highest during second week of lactation. There was notable variation in feed efficiency indicated by an animal variation of 17.4 MJ/d for residual energy intake. Difference in daily residual energy intake (REI) between 25 % most efficient and 25 % least efficient cows was over 20 MJ/d across lactation. For genetic analyses of diet digestibility data with 956 observations from 330 cows from three research farms in Finland and one in Norway were compiled. Blood and milk samples were collected on week 2, 3 and 20 after calving and were analysed for NEFA and fatty acid profile resulting 806 NEFA records with corresponding fatty acid profiles and feed efficiency data from 143 Nordic Red cattle cows. Average NEFA concentration in mentioned sampling weeks was 0.60, 0.46, and 0.14 mmol/l, respectively. A routine collection and storage of mid-infrared spectral data from Finnish routine milk recording milk samples has been established and meanwhile already over 5 million spectra have been stored at Mtech Digital Solutions database, which can be used to predict for each milk sample fatty acid profiles or any other in future predictable compound or quantity. Methane emission was recorded by PAS-F10 method from 136 cows at Minkiö research farm and records were merged with data recorded during the GREENDAIRY project resulting 350 000 raw measurements from 200 cows. Weekly feed intake records have been prepared and merged with corresponding records from the Nordic research partners establishing a Nordic feed efficiency data with 144 360 weekly records from 996 Holstein, 932 RDC, 388 Jersey and 177 Swedish local breed dairy cows.

At Maaninka research farm 47 cows were included in a feeding trial to access cow-specific diet digestibility. 1850 faecal grab samples were collected during weeks with lactation day 50, 150 and 250 as well as dry period on five consecutive days each. Organic matter digestibility increased from 736 g/kg on day 50 to 755 g/kg in the dry period and was on average 1 percent point lower for the high concentrate diet. Two physiological experiments with 6 lactating cows were conducted at Luke's physiological study research barn to evaluate polyethylene glycol and chitin as marker compound. Compounds were administrated by different protocols and full faecal collection was carried out to assess marker recovery and diurnal variation of markers in faeces. In a continuation trial marker substance enriched concentrate was fed to 40 cows at Minkiö research farm by different feeding protocols and 960 faecal spot samples were collected for validation of marker-based DMI prediction. For all trials and the feed efficiency recording representative and regular collection of feed samples for wet chemistry analyses was carried out.

Several traits are needed to describe different aspects of feed efficiency in dairy cattle. Traits based on model residuals, like residual feed intake (RFI), describe the general efficiency of utilizing feed whereas ratio traits, like energy conversion efficiency (ECE), describe the efficiency of converting feed into milk, or energy balance (EB) which describes the metabolic energy status of a cow during lactation but is less informative about the feed efficiency of a cow. These three traits are of close interest in genetic evaluations because they can be measured during first parity compared to traits like lifetime efficiency which is realized at the end of a cow's life. For all three traits we obtained heritability estimates which were high (0.2 to 0.4) at beginning of lactation, low (0.02 to 0.10) during early mid-lactation and afterwards increasing (towards 0.15 to 0.30) during later lactation. Correspondingly, estimated genetic correlations were below unity across lactation stages. Genetic correlations between beginning and later lactation stages were between -0.20 and 0.50, whereas genetic correlations between mid and later lactation stages were above 0.80. Genetic correlations of energy corrected milk with REI and EB were between negative (-0.70) and positive (0.50) and with ECE positive (0.30 to 0.70). Genetic correlations of DMI were with REI highly positive (>0.80), with ECE negative (-0.15 to -0.70), and with EB positive (~0.5). Genetic correlations of body weight were with REI positive (0.20 to 0.70), with ECE negative (-0.20 to -0.70), and with EB positive (0.10 to 0.70). Partitioning the genetic variance of metabolizable energy intake (MEI) showed that there is genetic variation among cows in how efficiently they are using ME for specific energy pathways and also that there is a positive genetic correlation between these partial efficiencies. By fitting random regression models, we were able to model cow-specific partial efficiency breeding values for milk production and growth. However, modelling partial efficiency breeding values for maintenance was difficult and will require additional research. Analyses of methane emissions data resulted cow-specific methane emissions of 236 to 571 g/d, which relates to an energy loss being on average equal to 5.9% of daily gross energy intake. Repeatability estimates for methane measurements were between 0.40 and 0.46. Heritability estimates for cow-specific diet digestibility were moderate, indicating that digestibility can be improved by genetic selection and that iNDF content in faeces may be used as an indicator trait, given that cows in the contemporary groups are consuming the same feed. Overall, analyses showed that feed efficiency is a heritable trait that can be genetically improved, but modelling daily feed efficiency within lactation is challenging.

Simulating the effect of a 5% increase in feed efficiency on the dairy farming economics indicated, that producing more milk based on the same production input and number of cows (cows production level has increased by 5% as well) is the most beneficial option and increases Finnish farmers margin over cost by 38.3 M€ annually, whereas keeping production level unchanged and using released field resources for crop production resulted a 39% lower increase in margin over costs (23.2 M€). Adding residual feed intake traits into the total merit index increased the discounted profit of the breeding program only slightly (1.4%) and largest increase in discounted profit (5.1%) was obtained when also growth and carcass traits together with body weight of the cows were included.

Studying possible feed efficiency traits, that can be recorded in the absence of feed intake measurements resulted two potential traits. One is an indicator for energy conversion ratio where MEI is substituted by the expected MEI for maintenance, which describes maintenance cost per kg ECM and could be named maintenance requirement ratio (MRR). The other one is a predictor for NEFA (pNEFA) which is not a feed efficiency trait as such but an important indicator for negative energy status at the onset of lactation. The estimated genetic correlation between MRR and energy conversion ratio (MEI MJ/kg ECM) was 0.89 and its genetic correlation with MEI, ECM and metabolic body weight was -0.18, -0.91 and 0.58, respectively. The correlation between pNEFA and observed NEFA was 0.80 when prediction model included regressions on body measurements and fatty acids, as well as using directly milk MIR spectra for prediction. However, the correlation between EB and NEFA was only -0.47.

Research on marker-based prediction methods based on near infrared reflectance spectroscopy (NIRS) to predict dry matter digestibility (DMD) using an internal marker (iNDF) and DMI using internal and external marker showed that NIRS analyses of faecal samples might be possible, but a larger reference data has to be established for the development of prediction equations. Reference data for iNDF was increased to 476 observations resulting in a standard error of cross validation of 16.5 g iNDF/kg faecal dry matter. Two suitable external markers, polyethylene glycol (PEG) and chitin were identified and prediction equations were developed based on 66 and 96 reference samples, respectively. Prediction equations also correct for confounding between external maker spectra and iNDF spectra, a problem observed in an earlier study. Under total faeces collection recovery of both markers from faeces by NIRS was close to 100% and predictions for faecal output accurate. However, diurnal variation of external marker concentration in faeces demonstrated that external markers should be administrated several times a day to increase predictability of faecal output from spot samples. Results from the meta-analysis of 21 feeding trials indicated that expected standard error of marker-based DMI predictions is expected to be at least 1.1kg DMI/d. Simulation of on-farm recoding schemes showed that expected reliability of cow breeding values for DMI, RFI and ECE is 0.24, 0.09 and 0.31 respectively when feed intake recording is carried out bi-monthly but as low as 0.18, 0.05 and 0.21, respectively when recording is carried out in 4-months intervals.

EVALUATION OF RESULTS

Results demonstrated that there is significant genetic variation in feed efficiency traits which can be utilized by dairy cattle breeding to improve productivity and increase environmental sustainability of dairy farming. Ratio traits (e.g. ECE) are easier to model and yield estimated breeding values with higher reliabilities compared to traits based on model residuals (e.g. REI), especially when recording of feed intake is sparse. However, selection based on ratio traits is less favourable and instead the component traits could be considered in the index. To establish genomic predictions for feed efficiency, between 500 to 1000 genotyped primiparous dairy cows should be preferable under bi-monthly feed intake recording annually to create a sufficiently large (N>5000) reference population.

Results obtained from marker-based methods give indications that these NIRS-based methods have the potential to be used for on-farm measuring given that prediction accuracy can be further improved by making the reference data even more comprehensive. Furthermore, administration of the external marker needs to be optimized to reduce diurnal variation and marker costs and an efficient sampling and analyses of faecal spot samples would have to be established. The use of mid-infrared spectral reading from routine milk samples for predicting negative energy status at the onset of lactation gave very promising results and this non-invasive information should be considered for developing genetic evaluations.

In the absence of a cheap feed intake measuring method a first genetic evaluation for feed efficiency could be based on a single-step genomic prediction model where feed efficiency traits, recorded on research farms, are combined with component traits obtained from routine milk recording. Predicted breeding values for component traits could be incorporated into the selection index in a way to resemble the indicator trait for energy conversion ratio as was found in this study. A trait to start with would be metabolic body weight. Developing a prediction model for metabolic body weight would benefit from revising current routine recording of body weight.

Publications Results from this project were published in 11 peer-reviewed scientific articles, 1 PhD-thesis, 24 scientific congress presentations (oral and poster), 3 professional publications and numerous Nordic workshop presentations. Furthermore, 6 scientific manuscripts are currently under preparation and of those at least 3 will be submitted during 2018. All publications are listed in the end report.

6. SUOMENKIELINEN TIIVISTELMÄ

TAVOITTEET

Tutkimuksen tavoitteena oli 1) arvioida perinnöllistä vaihtelua rehuhyötysuhde-ominaisuuksissa ja tutkia olisivatko ominaisuudet sopivia lisättäväksi pohjoismaiseen kokonaisjalostusarvoon (NTM), 2) arvioida rehuhyötysuhteen merkitystä taloudelle ja ympäristölle, 3) tutkia indikaattoriominaisuuksia, jotka korreloisivat vahvasti kiinnostavien, mutta hankalasti mitattavien rehuhyötysuhdeominaisuuksien kanssa, 4) kehittää indikaattoriominaisuuksien mittausmenetelmiä, ja 5) kehittää maatiloilla käytettäviä menetelmiä eläinkohtaisten rehunsyöntimäärien mittauksia varten.

TULOKSET

Tutkimusaineistossa oli mukana Luken Minkiön tutkimusnavetasta 136, Maaningan tutkimusnavetasta 36 ja Helsingin yliopiston tutkimusnavetasta Viikistä 34 punaisen rodun lehmän tiedot ensimmäiseltä lypsykaudelta. Lehmistä mitattiin ja kerättiin tiedot syönnistä, maitotuotoksesta, maidonkoostumuksesta, painosta ja kuntoluokasta. Tiedot yhdistettiin vastaavien edellisistä tutkimuksista (ASMO 1998–2001, Lehmän rehunkäyttökyky 2006–2009, GREENDAIRY 2010–2012) kerättyjen tietojen kanssa (39 273 havaintoa). Koko aineisto sisälsi 100 670 päivittäistä havaintoa 622 ensikosta. Energiakorjatun maidon (EKM) keskiarvo oli 28,1 kg/pvm, kuiva-aineen syönnin (dry matter intake, DMI) 19,0 kg/pv, muuntokelpoisen energian saannin (metabolizable energy intake, MEI) 208,6 MJ/pv, raakavalkuaisen saannin 3,28 kg/pv ja painon 586 kg. Keskimääräinen energian muuntotehokkuus (energy conversion efficiency, ECE) oli 0,137 kg EKM/ME MJ ja tämä oli korkeimmillaan lypsykauden toisella viikolla. Jäännösenergiankulutuksessa (residual energy intake, REI) eläinten välinen vaihtelu oli 17,4 MJ/pv eli varsin suuri rehuhyötysuhdeominaisuudelle. Päivittäisessä REI:ssa ero energian hyväksikäytön perusteella tehokkaimman ja heikoimman neljänneksen lehmien välillä oli yli 20 MJ/pv koko lypsykauden aikana. Geneettisiä analyysejä varten yhdistettiin aineisto, joka sisälsi 956 sulavuusmittausta 330 lehmältä kolmesta eri tutkimusnavetasta Suomessa ja yhdestä Norjassa. Veri- ja maitonäytteitä kerättiin lehmistä poikimisen jälkeen viikoilla 2, 3 ja 20 vapaiden rasvahappojen (NEFA) ja maidon rasvahappoprofiilin selvitystä varten. Yhteensä saatiin kerättyä 143 punaisen rodun lehmästä 806 NEFA-havaintoa, joille löytyi myös vastaava maidon rasvahappoprofiili ja muut rehuhyötysuhdetiedot. Keskimääräinen NEFA-pitoisuus viikolla 2 oli 0,60, viikolla 3 0,46 ja viikolla 20 0,14 mmol/l. Maidon tuotosseurantanäytteistä on aloitettu keräämään ja tallentamaan rutiininomaisesti keskialueen infrapunaspektriaineistoa (mid-infrared reflectance spectroscopy, MIR) ja nyt jo yli 5 miljoonaa spektriä on säilötty Mtech Digital Solutions Oy:n tietokantaan. Tätä tietokantaa voidaan käyttää ennustamaan maidon rasvahappoprofiilia tai muita tulevaisuudessa ennustettavissa olevia yhdisteitä tai määriä. Metaanipäästöjä mitattiin PAS-F10 menetelmällä Minkiön tutkimusnavetan 136 ensikosta ja havainnot yhdistettiin GREENDAIRY-projektissa kerättyyn aineistoon. Yhteensä tutkimusaineistoa kertyi 350 000 raakamittausta 200 lehmästä. Viikoittaiset syöntihavainnot käsiteltiin ja yhdistettiin vastaaviin tietoihin Pohjoismaisten tutkimuskumppaneiden kanssa ja näin saatiin muodostettua Pohjoismainen rehuhyötysuhdeaineisto, joka sisälsi 144 360 viikoittaista havaintoa 996 holsteinlehmästä, 932 punaisen rodun lehmästä, 388 jerseylehmästä ja 177 ruotsalaista alkuperää olevasta punaisesta lypsylehmästä.

Maaningan tutkimusnavetassa 47 lehmää oli mukana ruokintakokeessa, jossa tutkittiin lehmäkohtaista rehun sulavuutta. Sontanäytteitä kerättiin viikoittain 50, 150 ja 250 päivän kuluttua poikimisesta ja umpikaudella viitenä peräkkäisenä päivänä (yhteensä 1850 näytettä). Orgaanisen aineen sulavuus (organic matter digestibility, OMD) parani lypsykauden edetessä, sillä 50 päivää poikimisesta OMD oli keskimäärin 736 g/kg ja umpikaudella 755 g/kg. Väkirehun osuuden kasvattaminen ruokinnassa pienensi OMD:tä keskimäärin 10 g/kg. Kuudelle lypsylehmälle suoritettiin Luke Jokioisilla kaksi fysiologista koetta, joissa tutkittiin polyetyleeniglykolia (PEG) ja kitiiniä merkkiaineina. Merkkiaineita käytettiin erilaisten protokollien mukaan ja vertailumenetelmänä käytettiin kokonaissonnankeruuta, jotta yhdisteiden saanto ja päivittäinen vaihtelu sonnassa saatiin selville. Tutkimuksen seuraavassa osassa merkkiaineitta lisättiin väkirehuun ja syötettiin 40 lehmälle Minkiön tutkimusnavetassa joko perusväkirehussa tai lypsyasemalla annettavan houkutusrehun mukana. Lehmiltä kerättiin 960 sontanäytettä syönnin ennustamisen validointia varten. Kaikkia kokeita ja rehuhyötysuhdemittauksia varten kerättiin myös säännöllisesti edustavat rehunäytteet analyysejä varten.

Lypsylehmien rehuhyötysuhdetta kuvaamaan tarvitaan useita ominaisuuksia eri näkökulmista. Ominaisuudet, jotka perustuvat mallin jäännöksiin, kuten jäännösrehunsyönti (residual feed intake, RFI), kuvaavat yleistä rehun hyödyntämisen tehokkuutta. Suhdeominaisuudet, kuten energian muuntotehokkuus (ECE), taas kuvaavat tehokkuutta, jolla lehmä muuttaa syödyn rehun maidoksi. Energiatase (energy balance, EB) kuvaa lehmän metabolista energiastatusta, mutta ei kerro paljon lehmän rehunkäyttökyvystä. Nämä kolme ominaisuutta ovat suurimpana mielenkiinnon kohteena jalostusarvostelun näkökulmasta, koska ne ovat mitattavissa ensimmäisen lypsykauden aikana, toisin kuin ominaisuudet kuten elinikäinen tehokkuus, jonka saa selville vasta lehmän elämän päättyessä. Kaikille kolmelle ominaisuudelle olemme löytäneet periytymisasteet, jotka ovat melko korkeita (0,2 – 0,4) lypsykauden alussa, matalia (0,02 – 0,10) aikaisella keskilypsykaudella ja kasvavat taas tämän jälkeen lypsykauden loppua kohti (0,15 – 0,30). Vastaavasti geneettisten korrelaatioiden arviot lypsykauden vaiheiden välillä vaihtelivat. Geneettiset korrelaatiot lypsykauden alun ja loppulypsykauden vaiheiden välillä vaihtelivat välillä -0,20 ja 0,50, kun taas geneettiset korrelaatiot lypsykauden keskivaiheen ja myöhempien vaiheiden välillä olivat yli 0.80. Geneettiset korrelaatiot energiakorjatun maidon ja REI:n sekä EB:n välillä vaihtelivat negatiivisesta (-0,70) positiiviseen (0,50). Energiakorjatun maidon ja ECE:n väliset geneettiset korrelaatiot olivat positiivisia (0,30 – 0,70). DMI:n geneettiset korrelaatiot REI:n kanssa olivat positiivisia ja korkeita (>0.80), ECEn kanssa negatiivisia (-0,15 – -0,70) ja EB:n kanssa positiivisia. Painon geneettiset korrelaatiot olivat REI:n kanssa positiivisia (0,20 – 0,70), ECE:n kanssa negatiivisia (-0,20 – -0,70) ja EB:n kanssa positiivisia (0,10-0,70). Muuntokelpoisen energian saannin geneettisen varianssin osittamisen tulokset osoittivat, että lehmien välillä on perinnöllisiä eroja siinä, miten tehokkaasti ne käyttävät muuntokelpoisen energian maidontuotantoa ja kasvua varten, ja että näiden toimintojen välillä on positiiviset geneettiset yhteydet. Energiatehokkuus ylläpitoa varten oli vielä haastavaa mallintaa ja vaatii lisätutkimuksia. Metaanipäästöaineiston analyysien tuloksena lehmäkohtaiset metaanipäästöt vaihtelivat 236 – 571 g/pv, mikä tarkoittaa keskimäärin 5,9 % energiahävikkiä päivittäisestä kokonaisenergian saannista.

Toistumiskertoimet metaanimittauksille vaihtelivat välillä 0,40 – 0,46. Lehmäkohtaisen sulavuuden periytymisasteet olivat kohtalaisia, mikä osoittaisi että sulavuutta olisi mahdollista parantaa jalostuksen avulla. Sonnan iNDF-pitoisuutta voidaan käyttää sulavuuden indikaattoriominaisuutena, jos lehmät riittävän isoissa vertailuryhmissä syövät samaa rehua. Kokonaisuudessaan analyysit osoittivat, että rehunkäyttökyky on periytyvä ominaisuus, jota on mahdollista parantaa jalostuksella, mutta päivittäisen rehukäyttökyvyn mallintaminen lypsykauden aikana on haastavaa.

Simulaatiotutkimuksessa lypsylehmien rehunkäyttökykyyn oletettiin 5 % parannus ja katsottiin, miten maidontuottajien taloudellinen tilanne muuttuisi erilaisissa skenaarioissa. Tutkimuksen tulokset osoittivat, että paras vaihtoehto olisi tuottaa enemmän maitoa samalla tuotantopanoksella ja lehmämäärällä (myös lehmien tuotostaso nousi 5 %). Tämä kasvattaisi suomalaisten maidontuottajien taloudellista tulosta 38,3 M€/vuosi. Pitämällä maidontuotanto samalla tasolla ja käyttämällä vapautunut peltoala viljan viljelyyn saavutettiin 39 % pienempi tulos (23,2 M€/vuosi). Kun tutkimuksessa lisättiin RFI-ominaisuus kokonaisjalostusarvoon, nousi jalostusohjelman diskontattu voitto vain hieman (1,4 %). Suurin lisäys diskontattuun voittoon (5,1 %) saavutettiin, kun myös kasvu- ja ruho-ominaisuudet yhdessä lehmien painon kanssa lisättiin kokonaisjalostusarvoon.

Kaksi potentiaalista ominaisuutta löytyi, kun tutkittiin mahdollisia rehuhyötysuhdeominaisuuksia, joita voisi mitata ilman rehunsyöntitietoja. Toinen on indikaattori energian muuntosuhteelle (energy conversion ratio), missä MEI korvataan ylläpidon suhteen odotetulla MEI:llä, mikä kuvaa ylläpitokustannusta per kilo energiakorjattua maitoa, eli ”maintenance requirement ratio” (MRR). Toinen on NEFA:n ennustaja (pNEFA), joka ei ole varsinaisesti rehuhyötysuhdeominaisuus, mutta tärkeä indikaattori negatiiviselle energiataseelle lypsykauden alussa. Geneettinen korrelaatio MRR:n ja energian muuntosuhteen (MEI, MJ/kg EKM) välillä oli 0,89. Geneettiset korrelaatiot MRR:n ja MEI:n, EKM:n ja metabolisen painon välillä olivat -0,18, -0,91 ja 0,58. Korrelaatio pNEFA:n ja mitatun NEFA:n välillä oli 0,80, kun ennustemalli sisälsi myös painon ja kuntoluokan muutokset sekä maidon rasvahapot selittävinä muuttujina. Samansuuruinen korrelaatio saatiin myös ennustamalla NEFA suoraan maitonäytteen MIR-spektristä. Korrelaatio EB:n ja NEFA:n välillä oli melko alhainen, vain -0,47.

Tutkimus, jossa käytettiin merkkiaineiden avulla lähialueen infrapunaspektroskopiaan (near-infrared reflectance spectroscopy, NIRS) perustuvaa ennustetta kuiva-aineen sulavuudesta ja syönnistä osoitti, että NIRS-analyysit sontanäytteistä voivat olla käyttökelpoisia, mutta referenssiaineiston täytyy olla suurempi ennusteyhtälöiden kehittämistä varten. iNDF:n referenssiaineistoa kasvatettiin 476 havaintoon, jolloin ristiinvalidoinnin keskivirhe oli 16,5 g iNDF/kg sonnan kuiva-ainetta. Eläinkokeissa löytyi kaksi sopivaa ulkoista merkkiainetta, PEG ja kitiini, ja kehitetyt ennusteyhtälöt perustuivat 66 ja 96 referenssinäytteeseen. Ennusteyhtälöt myös korjasivat merkkiaine-spektrin ja iNDF-spektrin sekoittumisen, mikä oli havaittu aikaisemmassa tutkimuksessa. Kokonaissonnankeruussa molempien merkkiaineiden saanti sonnasta NIRS:llä oli lähes 100 % ja ennusteet sonnan määrästä olivat tarkkoja. Kuitenkin merkkiaineiden pitoisuuden päivittäinen vaihtelu sonnassa osoittaa, että merkkiainetta pitäisi syöttää useita kertoja päivässä, jotta sonnan määrän ennustettavuus yksittäisistä sontanäytteistä paranisi. Tulokset 21 ruokintakokeen meta-analyysistä osoittivat että merkkiaineperusteisen DMI-ennusteen odotettu keskivirhe on ainakin 1,1 kg DMI/pv. Erilaisten mittausjärjestelmien simulaatiotutkimus osoitti, että odotettu lehmien jalostusarvojen arvosteluvarmuus on DMI:lle 0,24, RFI:lle 0,09 ja ECE:lle 0,32, jos syönti mitataan tiloilla joka toinen kuukausi. Jos mittaus tapahtuisi neljän kuukauden välein, olisivat varmuudet matalampia (DMI 0,18, RFI 0,05 ja ECE 0,21).

TULOSTEN ARVIOINTI

Tulokset osoittivat, että rehuhyötysuhdeominaisuuksissa on merkittävää perinnöllistä vaihtelua, jota voidaan hyödyntää lypsykarjan jalostuksessa parantamaan tuottavuutta ja ympäristölle kestävämpää maidontuotantoa. Suhdeominaisuudet (esim. ECE) ovat helpompia mallintaa ja niihin perustuvilla jalostusarvoilla on korkeampi arvostelu-varmuus kuin ominaisuuksilla, jotka perustuvat mallien jäännöksiin (esim. REI), silloin kun syönnin mittaaminen tapahtuu harvoin. Suhtautuminen suhdeominaisuuksiin jalostusvalinnassa ei ole ollut myönteistä, mutta sen sijaan näiden ominaisuuksien osatekijöitä voisi käyttää indekseissä. Jos rehuhyötysuhde-ominaisuuksille halutaan genomisia ennusteita, tarvitaan vuositain 500 – 1000 genotyypitettyä ensikkoa, joilta mitattaisiin syönti joka toinen kuukausi.

Merkkiaineperusteisten menetelmien arviointi on vielä alustavaa, sillä lopulliset analyysit ovat kesken. Tulokset, jotka tähän mennessä on löydetty, osoittavat että NIRS-perusteiset menetelmät ovat potentiaalisia tiloilla käytettäväksi. Kattavampi referenssiaineisto tarvitaan kuitenkin parantamaan ennusteiden tarkkuutta. Ulkoisten merkkiaineiden optimaalinen anto lehmille tulisi selvittää, jotta päivittäistä vaihtelua ja myös kustannuksia saadaan pienennettyä. Lisäksi pitäisi perustaa tehokas näytteidenotto- ja sontanäytteiden analysointisysteemi. MIR-spektrien käyttö tuotos-seurantanäytteistä negatiivisen energiataseen ennustamiseen lypsykauden alussa antoi lupaavia tuloksia ja tätä tietoa tulisi harkita jalostusarvojen kehittämisessä.

Koska edulliset rehunsyönnin mittausmenetelmät puuttuvat vielä, voisivat ensimmäiset rehuhyötysuhteen jalostusarvostelut perustua genomiseen single-step malliin, jossa rehuhyötysuhdeominaisuudet mitattaisiin tutkimustiloilla ja yhdistettäisiin muihin komponenttiominaisuuksiin, jotka saadaan selvitettyä tuotosseurantanäytteistä. Jalostusarvojen ennusteet komponenttiominaisuuksille voisi sisällyttää valintaindeksiin siten, että se muistuttaisi tässä tutkimuksessa löydettyä energianmuuntosuhdetta (MRR). Tällainen malli vaatisi genotyypitettävien lehmien painon ja kuntoluokan mittaamisen rutiininomaisesti.

Julkaisut

Tämän projektin aikana valmistui 11 julkaisua tieteellisiin lehtiin, yksi väitöskirja, 24 kongressiesitystä, 3 ammattilehtiartikkelia, sekä lukuisia esityksiä Pohjoismaista workshopia varten. Lisäksi valmisteltavana on 6 tieteellistä artikkelia, joista ainakin kolme lähetetään tieteellisiin lehtiin vertaisarviointia varten vuoden 2018 aikana. Kaikki julkaisut on listattu loppuraportissa.