Improving dairy feed efficiency, sustainability, and profitability by impacting farmer's breeding and culling decisions

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Abstract

Enhancing feed efficiency should improve the profitability and sustainability of dairy farming due to reduced use of feed and land resources while potentially reducing emissions of greenhouse gas (GG) per liter of milk. The selection of animals that are genetically superior for feed efficiency requires precise measurements of feed energy intake and milk energy output from enough cows to predict genetic merit for feed efficiency with reasonable reliability. Previously, a consortium of dairy science experts from North America and Europe created a pool of data including 5,000 cows genotyped and phenotyped for feed intake and related traits. Using this database, the researchers showed that dry matter intake (DMI) and residual feed intake (RFI) had sufficient heritability to enhance genetic progress for feed efficiency. Data from that study projected that the US dairy sector could save $540 million/year with maintained milk production by breeding for more efficient cows. The project presented herein was launched in 2019 to build on previous results and is the next logical step for implementing the selection for feed efficiency in the US and to address concerns about greenhouse gas emissions. Specific objectives are to:

1. Increase the reliability of genomic predictions for feed efficiency.

2. Develop a feed intake index that uses sensors to predict feed intake on individual cows,

3. Initiate a long-term program for updating genomic predictions of feed efficiency, and

4. Determine if genomic predictions of feed efficiency can decrease methane emissions.

The project protocol calls for the acquisition of data related to feed intake, milk yield and composition, and body weight for 42 days in 3600 mid-lactation cows (50-200 DIM) over a 5-year period. Additionally, a subset of cows will be fitted with sensors to monitor body temperature, feeding behavior, and locomotion. Mid-infrared spectral profiles will be collected from all milk samples. Methane emission will be measured in 300 cows. Data collection is in progress at all research stations. These data will be used to develop a genomic evaluation for feed efficiency in U.S. Holsteins and support the development of management tools.

Introduction

Increases in population and consumption of dairy products will translate into a need for approximately 600 billion kg more milk in 2067 than is produced today (Britt *et al.*, 2018). This need might be constrained by environmental challenges. Scientists need to provide tools to farmers and their advisers to achieve their environmental sustainability goals in an economically viable manner. Genetic selection has yielded remarkable gains in the yield and efficiency in livestock production, bringing milk production of US Holstein cows from 5,904 to 13,015 kg/lactation in the period 1957-2019 (CDCB, 2021), 56% of this improvement was due to genetic selection. Over this time period, increased focus on "functional traits" has led to a breeding goal, the Lifetime Net Merit index, including non-production traits, such as female fertility, calving ability, udder health, and longevity. Genetic selection has been revolutionized by genomic selection (Meuwissen *et al.*, 2001), coupling low cost animal genotyping stored in large repositories housing thousands of DNA samples from dairy bulls, and milk-recording databases with millions of performance records from their progeny. As a result, US dairy farmers now carry out genomic testing on more than 90,000 calves per month, increasing genetic progress dramatically over the past decade (García-Ruiz *et al.*, 2016). Currently, the database of the US Council on Dairy Cattle Breeding (CDCB) contains more than 5 million dairy genotypes.

Genetic selection for higher milk production has increased efficiency of energy utilization in dairy cattle however, variation among cows in their ability to digest and metabolize nutrients and perform maintenance functions has not been exploited in genetic improvement programs. Residual Feed Intake (Fig 1) is a measure of the amount of feed energy a cow consumes each day relative to her expected energy requirement, computed from Dry Matter Intake (DMI), secreted milk energy, body weight (BW) and BW change measured over a period of time. Davis *et al.* (2014) and Yao (2016) showed that selection for RFI is feasible, and that low RFI values selection might impact feed costs. The key to improving feed efficiency through breeding programs is to establish a reference population of animals with performance data and genomic testing data. Reference genotypes and phenotypes can be matched with the genotypes from the
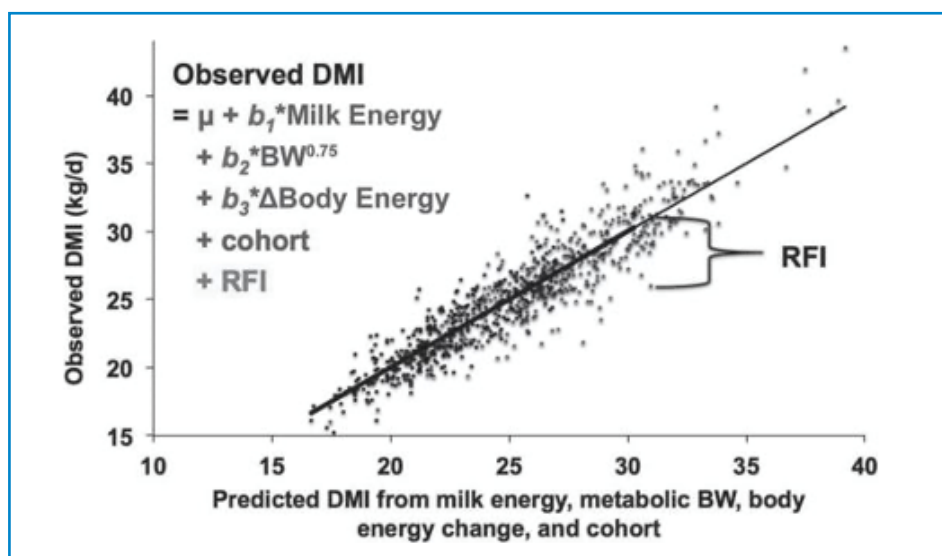

Figure 1. Residual feed intake (Van de Haar et al.*, 2016)*

national population that have economic test results but lack performance data for feed efficiency, to compute genomic estimated breeding values (GEBV) (Meuwissen *et al.*, 2001), and hence make informed selection decisions. GEBV of new animals can then be calculated at birth (or on embryos), allowing greater genetic gains over a shorter time interval (Boichard *et al.*, 2015). Previous studies with a 5000-cow database with feed efficiency phenotypes and SNP genotypes demonstrated that genomic selection for feed efficiency is possible and could improve dairy farm profitability (Van de Haar *et al.*, 2016; Yao, 2016). The heritability for RFI has been estimated at 0.16 (Tempelman *et al.*, 2015, 2020; Hardie *et al.*, 2017; Lu *et al.*, 2018; Li *et al.*, 2020), showing that genetic selection for RFI can improve feed efficiency. The reliability for EBV has been estimated at 34% and 13% for phenotyped and genotyped cows, respectively. These low reliability values are attributed to the limited data size (Li *et al.*, 2020). Increasing prediction reliability for RFI requires more feed intake data (van Raden *et al.*, 2018). Preliminary analysis of genomic evaluation of feed efficiency for US Holsteins indicated that, calculating the range in GEBV for 16,000 sires, the top 20 % most efficient cows require 635 kg of feed less per lactation than the least efficient cows (bottom 20%) (VanRaden *et al.*, 201; Yao, 2016) hence, RFI has economic value. The use of genomic selection for feed efficiency in US dairy will depend upon maintenance of a reference population to re-calculate marker effects and maintain GEBV accuracy. Currently, measures of feed efficiency, like RFI, are limited to research facilities that can determine individual cow feed intake, BW, body condition score, and milk energy output. Today, automated sensor technology is being used on many commercial dairies in the US, providing an opportunity to use this data for genetic improvement (Neethirajan *et al.*, 2017). Sensor data, combined with biological traits like milk spectra, may allow development of predictive models for feed efficiency traits like RFI (Pahl *et al.*, 2015).

Although economic benefits of selecting for improved feed efficiency are clear, the environmental impact is not. Enteric methane represents ~30% of US methane emissions from agriculture (US EPA, 2018). Predictions of cattle methane emissions are based primarily on DMI and are not very accurate (Ellis *et al.*, 2010). The relationships between feed efficiency and enteric methane emissions in dairy cows, have not been sufficiently studied. Some attempts have been made to use mathematical models to estimate a cow's enteric methane emissions from milk spectral data (Vanlierde *et al.*, 2018). Such models could allow enteric methane emissions to be estimated without direct measurement.

This project will allow direct selection for improved feed efficiency based on DMI data recorded on thousands of cows. In addition, it will allow indirect selection for improved feed efficiency based on predicted intakes of hundreds of thousands of cows, where these predictions are derived from sensors that record location, physical activity, and rumination data in real-time, as well as routine laboratory analyses that provide mid-infrared (MIR) spectral data of milk samples. The impact of this project is to increase the efficiency and sustainability of dairy production addressing the following identified gaps: 1) The reliability of the GEBV for RFI is too low, 2) The cost of measuring DMI of individual cows is too high, and measuring individual intakes on commercial farms for genetic or management purposes is infeasible at present, 3) The dairy industry needs leadership to translate research to practice in the form of a sustainable reference population for feed efficiency, and 4) The relationship of RFI to overall sustainability, and particularly enteric methane emissions is not known. The project presented herein has 4 specific aims:

1. to increase the reliability of genomic predictions for feed efficiency,

2. to develop a feed intake index that uses sensors to predict feed intake on individual cows,

3. to initiate a long-term program for updating genomic predictions of feed efficiency, and

4. to determine if genomic predictions of feed efficiency can decrease methane emissions.

Ultimately, feed efficiency would be improved by including genomic breeding values for feed intake in the US Net Merit Index.

Methods

A total of 3600 lactating Holstein cows will be assigned to the project for a period of 5 years (2019-2024) and will be studied for 42 days between 50 and 200 days of lactation in cohort groups (Fig 2). Only data between 50 and 200 DIM are collected in this project, BW is more stable within this window than outside it, minimizing errors in RFI determinations due to BW change. A cohort group of cows is fed the same diet at the same time at the same location. Diets are total mixed rations fed *ad libitum.* Briefly, Milk yields (**MY**), DMI, BW, Body condition score (BCS) fat (**FAT%**), protein (**PROT%**), and lactose (**LACT%**) components, and other sensor-based data are collected from Holstein cows on 5 research stations: Iowa State University (**ISU**; Ames), Michigan State University (**MSU**; East Lansing), the University of Florida (**UF**; Gainesville), the University of Wisconsin-Madison (**UW**), and the USDA Animal Genomics and Improvement Laboratory (**AGIL**; Beltsville, MD) as in Tempelman *et al.* (2015). Body temperature is recorded by sensors in the vagina (iButton thermosensor) and MIR milk spectra are collected during the experimental period. Methane emission will be measured on 300 cows using a GreenFeed system (C-Lock, Inc., Rapid City, SD). Cows visit the system throughout the day. Only cows with more than 36 methane measurements taken within a 24-hour will be included in the result analysis.

Results

Since the beginning of the project, feed intake phenotypes corresponding to a total of 1824 cows have been collected and added to the current CDCB feed intake database which contains a total 6577 records. From these records, 6,221 phenotypes of residual
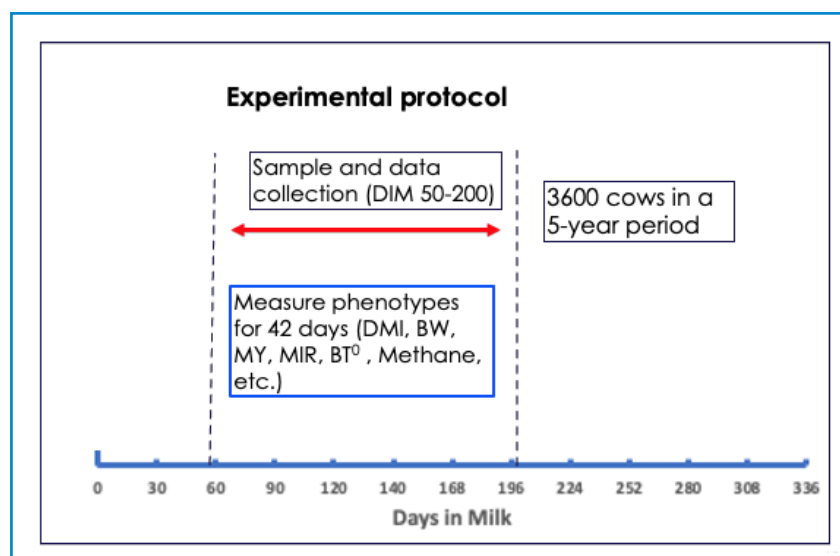

Figure 2. Experimental protocol.

feed intake (RFI), from 5,023 Holsteins born from 1999 to 2017, were included in the official predicted transmitting abilities (PTA) for Feed Saved in Holsteins, released by the CDCB in December 2020. Additionally, middle infrared (MIR) milk spectral data have been collected from 1149 cows, and methane emission were measured in 81 cows at the AGIL-USDA research station. During the year 2020 the CDCB-FFAR project has involved 16 undergraduate students, 8 graduate students, and 3 postdocs. In terms of visibility and technology transfer the project has generated 2 scholarly publications, 2 abstracts/conference presentations, 7 presentations, 3 extension trade articles, and various popular publications. This study is supported by the Foundation for Food and agricultural Research (FFAR) and the CDCB and will continue to add phenotypes to the US feed efficiency database until 2024.

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