

Implementation of Feed Saved evaluations in the U.S.

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Abstract

Feed efficiency is a trait of significant economic and environmental importance in the dairy industry, and feed accounts for half of the costs of dairy production. Improvements in feed efficiency have the potential to reduce manure and methane outputs, as well as crop and land inputs. Measurements of feed efficiency rely on individual feed intake data however, these data are expensive and time-consuming to collect, resulting in an insufficient phenotyped population. A concerted effort has been underway in the United States for 10 years to collect data for genomic evaluations of feed efficiency. As a result of this effort, the Council on Dairy Cattle Breeding (CDCB; Bowie, MD) provided official evaluations for Feed Saved beginning in December 2020. Feed intake was measured for 4 to 6 wk in individual cows between 50 and 200 days-in-milk in 9 research herds; to date, we have amassed 655,000 daily records of intake and milk production. From these data, residual feed intake (RFI) is estimated with a linear model accounting for milk energy, metabolic body weight, change in body weight, and cohort effects. Current phenotypic data include 6,221 RFI records from 5,023 U.S. Holsteins born 1999 to 2017 (as of December 2020). Phenotypic RFI are used to estimate traditional PTA in a linear animal repeatability model. Deregressed traditional PTA are then used to calculate genomic evaluations of RFI. These evaluations are combined with evaluations for body weight composite (BWC) to provide Feed Saved evaluations to the dairy industry. Progeny-tested bulls have an average genomic reliability of 38% for Feed Saved. Comparatively, young bulls have an average genomic reliability of 28%. Given the expectedly low reliabilities, a primary goal continues to be collecting additional phenotypes. Emphasis is also directed towards ensuring that phenotyped cows have close ties to current bulls actively used by the dairy industry. International collaborations will further expand the reference population. As an example, the next official evaluation (April 2021) will include phenotypic data from Canada for 650 cow-lactations. Preliminary testing has indicated a 1 to 2% increase in genomic reliability from these additional data. Feed Saved is currently published by the CDCB as an individual trait. Future plans include incorporating the trait into an economic selection index.

Key words: feed efficiency, genomic evaluation, Holstein, residual feed intake

Introduction

Feed efficiency can be defined as the fraction of feed energy captured in products – typically in the case of dairy cattle as milk (VandeHaar et al., 2016). The ability of a dairy cow to produce milk efficiently has improved greatly throughout the past century, largely as a

result of selection for increased production, along with improvements in management and nutrition. However, there is an approaching limit to the improvement that can be achieved by only increasing production. The dairy industry must also focus on identifying animals that have superior metabolic efficiency.

Numerous aspects of dairy production are impacted by feed efficiency. Feed is the largest single expense in dairy production (Connor, 2015). Improving feed efficiency is also one approach to decreasing the environmental impact of dairy production. More efficient animals may produce less manure and greenhouse gases (Bell et al., 2012; Connor, 2015). Additionally, animals that require less feed also result in less land utilization (Connor, 2015).

One measurement of feed efficiency commonly used is residual feed intake (RFI; Koch et al., 1963). Very generally, RFI measures the difference between expected feed intake and actual feed intake, after accounting for factors such as body size and production. Favorable animals are those consuming less feed than expected, resulting in a negative RFI value.

Using RFI as a measure of feed efficiency requires daily feed intake measurements on individual animals for a period of time, in addition to milk production. Regular measurements of milk composition and body weight are also required. Collecting these data is time consuming, laborious, and expensive. This limits the amount of data available worldwide, despite the importance of improving feed efficiency for the aforementioned reasons.

The availability of genomic data for dairy cattle has made the development of an evaluation for feed efficiency feasible. Largely based on data collected across multiple U.S. university research herds, an evaluation of feed efficiency is now published in the U.S. by the Council on Dairy Cattle Breeding (CDCB; Bowie, MD) since December 2020.

Materials and Methods

Phenotypes

The majority of data used for the U.S. evaluations were collected as part of two large national research projects. The initial project collected feed intake and associated data from 2010 to 2017, laying the foundations for the

current database (VandeHaar et al., 2016). A subsequent on-going project aims to collect phenotypes for an additional 3,600 lactating cows. As of April 2021, these two projects have resulted in over 770,000 daily records of intake and milk yield in addition to over 150,000 milk composition records across 9 research herds. Data are collected on individual cows for a minimum of 28 days, with most trials collecting data for at least 42 days. In addition to regular analysis of milk composition (approximately weekly), body weights, body condition scores, health events, and diet composition are recorded regularly. Data are collected mid-lactation anywhere from 50 days in milk (DIM) up to 200 DIM, in order to avoid the period of extreme negative energy balance that occurs at the beginning of lactation.

Additional North American data is also available through a data exchange agreement for genetic evaluations between CDCB and Lactanet (Ontario, CAN). These data are sourced from three Canadian herds and are edited to conform to the previously described constraints.

Daily data are compiled by each participating institution and uploaded securely to CDCB using consistent formats at the conclusion of each trial. Data are further compiled and edited, checking for missing and outlying data at CDCB. Summary statistics of the phenotypic data are calculated and returned to the contributing institution prior to calculation of RFI.

Calculation of RFI

Daily records for each animal were used to form a single 28-day average phenotype for dry matter intake (DMI), milk energy, metabolic bodyweight (MBW, defined as bodyweight raised to 0.75), and change in bodyweight (Tempelman et al., 2015). RFI is calculated using an energy sink model following the 2-stage methodology presented in Tempelman et al. (2015). The model is provided as equation (1) below:

$$DMI = par \times \sum DIM + b_1 MilKE + b_2 MBW + b_3 \Delta BW + ration(exp) + testwk + RFI \quad (1)$$

where *DMI* represents dry matter intake, $par \times \sum DIM$ represents the effect of parity class (1st versus later) by 5th order polynomial of dry matter intake on days in milk, $b_1 MilKE$ is the partial regression on milk energy, $b_2 MBW$ is the partial regression on metabolic body weight, $b_3 \Delta BW$ is the partial regression on change in bodyweight, *ration(exp)* is the random effect of the experiment-specific ration, *testwk* represents the random effect of test week, and *RFI* is the residual of the model, representing residual feed intake. Calculated RFI values are then combined and cross-checked with the associated data already present in the CDCB Cooperator database including pedigree, birthdate, calving date, etc. Table 1 includes number of RFI phenotypes from both U.S. projects currently available in the CDCB database as of April 2021.

Table 1. – US RFI phenotypes by contributing institution as of April 2021

Institution ¹	NIFA	FFAR/CDCB	TOTAL
Miner	58		58
VA Tech	96		96
PANC	184		184
DFRC	624		624
UW	1,054	623	1,677
MSU	315	251	566
ISU	1,006	207	1,213
AGIL	834	370	1,204
UF	582	338	920
Total	4,753	1,789	6,542

¹ Miner = Dairy Research Facility at the Miner Institute (Chazy, NY); VA Tech = Virginia Polytechnic Institute and State University (Blacksburg, VA); PANC = Purina Animal Nutrition Center (Gray Summit, MO); DFRC = Dairy Forage Research Center (ARS, USDA; Madison, WI); UW = University of Wisconsin (Madison, WI); MSU = Michigan State University (East Lansing, MI); ISU = Iowa State University (Ames, IA); AGIL = Animal Genomics and Improvement Laboratory (ARS, USDA; Beltsville, MD); UF = University of Florida (Gainesville, FL)

Canadian records included in the CDCB April 2021 evaluation totaled 660 RFI records from 568 cows across 3 herds. Thus, the total phenotypes used for the April 2021 evaluation including both domestic and international sources was over 7,200.

Genotypes

Genotype records were available for 6,382 animals that also had RFI phenotypes. Animals were genotyped on various available chips and imputed to the standard set of 79,060 SNP included in CDCB evaluations using FindHap version 3 (VanRaden et al., 2011). Genomic evaluations predicted RFI PTA for all 3.8 million genotyped Holsteins available in the CDCB Cooperator database.

Genetic evaluation

Multi-step genetic and genomic evaluations are performed following a similar pipeline as most other traits evaluated at CDCB. First, pedigree-based evaluations are calculated modelling RFI with effects including age by parity group, management group, trial date, herd by sire interaction, breeding value, permanent environment, and regressions on the genomic predictions for milk net energy and body weight composite (BWC). The regressions on genomic predictions for milk net energy and BWC are included to remove present genetic correlations with RFI (VanRaden et al., 2018). Body weight composite combines five type traits to estimate body weight including stature, strength, body depth, dairy form, and rump width (Holstein Association USA, 2016). Records based on 42-d trials were given full weight; records based on 28-d trials were weighted by 0.92 (VanRaden et al., 2018). Genomic evaluations then use deregressed values from the pedigree-based evaluation to predict RFI for all genotyped Holsteins. Estimated heritability for RFI is 0.14 (VanRaden et al., 2018).

The official trait published by CDCB is Feed Saved (FSAV), similar to that described by Pryce et al. (2015). RFI and BWC are combined

into a single value indicating the expected pounds of feed saved per lactation compared to the breed average. Positive values are desired, indicating more feed saved, i.e., less feed consumed. PTAs for Feed Saved were calculated as

$$PTA_{FSAV} = -138 \times PTA_{BWC} - 1 \times PTA_{RFI}$$

pounds/lactation.

Reliability for Feed Saved was calculated as $REL_{FSAV} = 0.35 \times REL_{BWC} + 0.65 \times REL_{RFI}$.

Results & Discussion

Phenotypic RFI was calculated for 7,202 cows from 12 herds in the April 2021 CDCB official evaluation. Of these, 6,829 records were based on 42-day trials and the remaining 373 records were based on 28-day trials. Phenotypic RFI had a mean of -1.2 kg/lactation with a standard deviation of 531 kg/lactation.

Genomic PTA were calculated for 3.8 million genotyped Holsteins (April 2021). Mean RFI PTA was 2.1 kg/lactation with a standard deviation of 24.2 kg/lactation. Genomic reliabilities for all genotyped Holsteins averaged 18.4%, reaching a maximum of 93.0%.

Feed Saved PTAs were calculated as previously described for genotyped Holsteins, combining RFI and BWC. Feed Saved PTAs had a mean of 12.5 kg of feed saved per lactation with a standard deviation of 57.6 kg/lactation. The distribution of Feed Saved PTAs is shown in Figure 1. Reliability of Feed Saved for all genotyped animals averaged 38%, ranging from 10 up to 95%. For reference, the average reliability for BWC among genotyped Holsteins is approximately 77%, ranging from 30 up to 99%. Among bulls with Net Merit \$ (NM\$) reliability of at least 90%, average Feed Saved reliability was 49%. Comparing proven and young AI sires, average reliability was 47% and 39%, respectively, in the April 2021 evaluation.

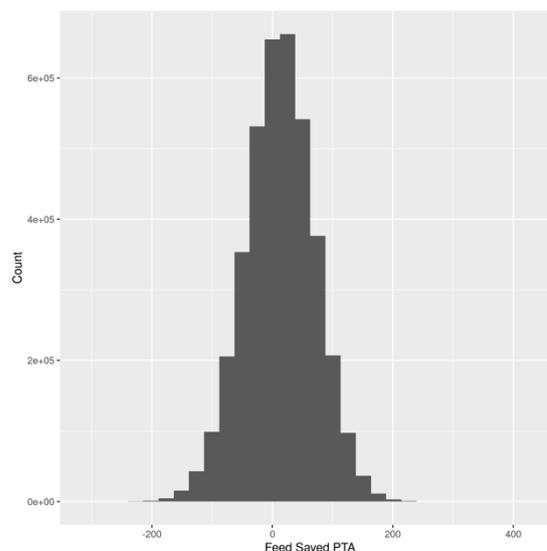


Figure 1. Feed Saved genomic PTA distribution among all genotyped Holsteins

Low reliabilities for Feed Saved reflect the small size of the reference population with RFI phenotypes. Among the top 100 Net Merit bulls with at least 10 milking daughters, only 6 had daughters with an RFI phenotype in the April 2021 evaluation. Among bulls with at least 50 daughters with an RFI phenotype (n=12), the average reliability is 89%, ranging from 86 to 95%. This emphasizes the need for continued collection of phenotypes, identification of available proxy variables, and international collaboration.

Since December 2020, Feed Saved evaluations are published by the CDCB as a stand-alone trait. Beginning with the August 2021 evaluation, the Net Merit indices (Net Merit \$, Cheese Merit \$, Fluid Merit \$, Grazing Merit \$) will be revised, with one of those revisions being the inclusion of RFI. Relative emphasis on RFI in NM\$ beginning in August 2021 will be -3.8%. While the relative value of RFI is -14%, the smaller relative emphasis reflects the lower standard deviation for young animals due to lower reliability. The relative emphasis of BWC in the revised NM\$ will be -9.4%. Increased negative emphasis is placed on BWC because larger maintenance costs have been estimated from the collected feed intake data (VanRaden et al., 2021). Thus, total

relative emphasis on Feed Saved in NM\$ 2021 will be 13.2%.

Since April 2021, there have been slight revisions to the calculations of Feed Saved PTAs and reliability. Current formulas are as follows and will be implemented in the August 2021 evaluation. PTAs for Feed Saved will be calculated as $PTA_{FSAV} = -151.8 \times PTA_{BWC} - 1 \times PTA_{RFI}$ pounds/lactation. Reliability for Feed Saved will be calculated as $REL_{FSAV} = 0.367 \times REL_{BWC} + 0.633 \times REL_{RFI}$.

Conclusions

Feed costs constitute at least 50% of dairy production. One approach to reduce the feed costs required for production is to select for those animals that are more feed efficient. These animals may also have a decreased environmental impact, which is an increasingly important issue for the sustainability of the dairy industry. Feed Saved evaluations allow producers to identify animals with higher feed efficiency and lower maintenance costs.

The current limited size of the reference population for RFI, and subsequent low reliability, emphasizes the importance of continued data collection. Along with this, the identification of proxy variables or new methods to collect these data that are less labor-intensive could aid in growing the reference population. Lastly, international collaboration is another important strategy by which to grow the number of phenotyped animals at a global level.

Acknowledgments

The authors acknowledge the financial and/or technical support of the Council on Dairy Cattle Breeding, the Animal Genomics and Improvement Laboratory, ARS, USDA, and the Foundation for Food and Agriculture Research.

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