Genomic prediction of residual feed intake in the Nordic breeds using data from research herds and 3D cameras in commercial herds

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Abstract

Nordic Cattle Genetic Evaluation NAV (Denmark, Finland, Sweden) has published an index for Saved feed, which comprises maintenance and metabolic efficiency indices. The genetic evaluation for maintenance has been introduced in 2019. Metabolic efficiency, also known as residual feed intake, is more difficult to evaluate genetically because of lack of records for individual feed intake. Breed specific genetic evaluations were developed for residual feed intake in Holstein, Red Dairy Cattle and Jersey. The data for Holstein was repeated feed intake data from the Efficient Dairy Genome Project with data from 2,543 Holstein research farm cows and 420 cows (1st to 6th parity) from a commercial herd with the 3D camera system CFIT. The data for Red Dairy Cattle was repeated feed intake data from 725 1st parity research farm cows and 196 cows (1st to 6th parity) from a commercial herd with the 3D camera system CFIT. The data for Jersey was repeated feed intake data from 1,077 cows (1st to 6th parity) from five commercial herds with the 3D camera system CFIT.

The genetic evaluation was constructed as a two-stage model. In the first stage a least squares model was fit to calculate residual feed intake phenotypes. The residual feed intake phenotype was calculated with partial regressions on energy sinks (energy corrected milk, metabolic body weight and change in body weight). The residual feed intake phenotypes were corrected for heterogeneous variance with respect to herd, year and season. In the second stage the repeated residual feed intake phenotypes were modelled by a single-trait (Red Dairy Cattle and Jersey) or multiple-trait (Holstein) single-step genomic prediction model. Common for all breed-specific evaluations a heritability of 15% was modelled. For the Holstein evaluation a genetic correlation of 0.6 was assumed between countries. The developed index for residual feed intake was uncorrelated or has low correlation to the Nordic Total Merit index and Nordic Total Merit sub-traits for all breeds. Use of genomic information increased the reliability of breeding values. However, results from cross validation indicate that reliability of genomic breeding values for metabolic feed efficiency in candidate animals is still low.

Key words: Residual feed intake, Saved feed, genomic prediction, Holstein, Red Dairy Cattle, Jersey

Introduction

Improving feed efficiency in dairy cattle has been a hot topic for decades in dairy cattle breeding and requires several traits to be included for selection. The major reasons to select for feed efficiency are 1) reducing costs related to feed, which account for approximately 70-80% of variable farm costs, and 2) reducing emission of greenhouse gasses. Several studies in dairy cattle have been carried out to develop selection tools for improving feed efficiency (Berry and Crowley, 2013). The preferred approaches to include feed efficiency in the breeding goal are 1) residual feed intake

(**RFI**), 2) dry matter intake (**DMI**) or 3) feed conversion ratios.

In the recent years a common approach for evaluation centers is to include feed efficiency in the breeding goal with an index for Saved feed, firstly described by Pryce et al. (2015). The Saved feed index comprises feed expenses for both maintenance and metabolic efficiency in dairy cattle. In this article metabolic efficiency will be referred to as RFI.

Nordic Cattle Genetic Evaluation (NAV) in Denmark, Finland and Sweden has develop an index for Saved feed which has been published since 2019 and included in NTM since 2020 (NAV, 2020). The definition of Saved feed in the Nordic countries was described by Sørensen et al. (2018) as

$$EBV_{\text{Saved feed =}}\, EBV_{\text{maintenance}} + EBV_{\text{Metabolic efficiency}}$$

The genetic evaluation of maintenance in the Nordic countries for Holstein (**HOL**), Jersey (**JER**) and Red Dairy Cattle (**RDC**) was described by Lidauer et al. (2019). The aim of this research was to estimate genomic breeding values for RFI in all three Nordic breeds using data from research- and commercial herds with 3D cameras.

Materials and methods

The basis for the RFI genetic evaluation is individually measured feed intake data. Data from three major feed intake datasets were used for this study.

Feed intake data

Efficient Dairy Genome Project

The Efficient Dairy Genome Project (EDGP), is a consortium for exchange of research farm data from four different countries. The consortium provides access to each other’s feed intake data with the purpose of promoting a genetic evaluation for feed efficiency. This project uses data from the research farms Elora (CAN), DRTC (CAN), Foulum (DNK), Beltsville (USA) and Ellinbank (AUS). The dataset included 2,543 HOL cows with data from 1st to 6th parity. From some of the research facilities data was measured only during some periods of the lactation.

Finnish research farms

This project had access to the feed intake dataset from the Natural Resources Institute Finland (Luke) research farms (Rehtijärvi, Minkö, Maaninka) and Helsinki university research farm (Viikki), which contains feed intake on daily level for 725 1st parity cows.

3D camera system CFIT

The Cattle Feed Intake (CFIT) system from VikingGenetics measures individual feed intake in all three Nordic breeds HOL, RDC and JER. The system uses 3D camera technology and artificial intelligences to identify the individual cow and to estimate the daily feed intake level (Lassen et al., 2018). In the NAV May 2021 RFI evaluation, there were 420, 196 and 1,077 cows for HOL, RDC and JER respectively with CFIT data.

Data editing

Only data from 1st to 6th parity from the first 330 days in milk was utilized in the genetic evaluation of RFI. Data delivered from Finland was edited according to research criteria and therefore was not edited further. Outliers were defined as greater than the range mean±4×SD for the single phenotypes. Outliers were set missing.

Milk production, DMI and body weight (BW) data were interpolated by animal and parity to maximize the number of records. This was important for milk production data in CFIT data, since production data was measured monthly by milk recording and feed intake was summed on weekly basis based on CFIT measurements. Milk recording at research farms was measured on weekly basis. Scale measurements were at most research farms taken along with milking; however, few research farms measured BW every second week or on monthly basis. Subsequently, weeks with missing phenotypes for production, DMI or BW were deleted.

The majority of HOL and RDC cows at research farms in the most recent birth years have all been genotyped; however, in some of the more historical data, not all cows are genotyped. Production herds with the CFIT system genotyped all young females and also cows including at least 2nd parity.

Breeding values for residual feed intake

Breeding values for RFI were estimated with a two-stage model. The first stage was the calculation of the RFI phenotypes and the second stage was the estimation of the breeding values.

1st stage – calculation of the phenotype

The RFI phenotypes were calculated with partial regressions on energy sinks (energy corrected milk, metabolic body weight and change in body weight). The model used to calculate the phenotypes for all breeds was as follows:

$$\mathbf{DMI = CA + CA^2 + LACP + HYS + YS_{LACP} + ECM + MBW + \Delta BW + e}$$

where:
DMI is the average daily dry matter intake,
CA is the linear regression for age at calving nested within parity (1, 2, ..,6),
$\boldsymbol{CA^2}$ is the quadratic terms for age at calving nested within parity (1, 2, ..,6),
LACP is the fixed effect lactation period (1,2,..,11) nested within parity class (1st or later lactations)
HYS is the fixed effect of Herd x Year x Season (quarters for date of observation)
$\boldsymbol{YS_{LACP}}$ is the fixed effect of Year x Season x Lactation period,
ECM is the regression on energy corrected milk nested within lactation month (1,2,..,11) and 1st or later lactations,
MBW is the regression of metabolic body weight nested within 1st or later lactations,
$\Delta\boldsymbol{BW}$ is the regression of change in body weight nested within lactation month (1,2,..,11) and 1st or later lactations,
e is the residual and was used to form RFI observations for the genetic evaluation.

The formed RFI phenotypes were repeated observations across lactation and parities and it would be obvious to model them as different traits. Instead, because of the low number of records, all records were considered as the same trait and therefore phenotypes were corrected for heterogeneous variance with respect to breed, herd, year, season and parity.

The fixed effect model solutions of HYS and YS_{LACP} were added to the residual e to form a RFI observation. The reason for doing that was to avoid additive genetic variance being lost in herd and seasonal effects. The effect of HYS and YS_{LACP} was included in the genetic model.

2nd stage – single-step genomic model

The genomic relationship matrix was formed following Mäntysaari et al. (2020) applying a 10% residual polygenetic effect and using QP transformation. For computational reasons, a ssGTaBLUP model was used, that allows to include all genotyped animals of the particular breed, and the model was solved by MiX99 (MiX99 Development Team, 2019).

Pedigree of all animals with phenotypes were traced for 5 generations in RDC and JER, and 3 generations for HOL. The pedigree for HOL was traced for fewer generations because the EDGP project only included 3 generations pedigree. Genetic groups were formed by grouping unknow parents by 5-year birth year classes, country, and breed.

The single-step repeatability model used for the genetic evaluation of all breeds was as follows:

$$RFI = HYS + YS_{LACP} + pe + a + e$$

Based on various variance component estimates we assume a heritability of 0.15 for all Nordic breeds. For RDC and JER a single-trait model was applied, whereas for HOL a multiple-trait model with a genetic correlation of 0.6 between countries.

Validation of genomic reliabilities for production traits

The validation test (Mäntysaari et al., 2010) for RFI genomic breeding values (**GEBVs**) could not be performed, because of few data available. Instead production traits were used to evaluate the expected genomic reliability for RFI. This was done by comparing de-regressed proofs for production traits from the NAV evaluation with parent average (PA) and GEBVs calculated for production traits from using the HOL and RDC feed efficiency data as reference population, respectively. A Proc Reg procedure in SAS was used to calculate the gain in reliability from including genomic information.

Results and discussion

The biggest cow (HOL) consumed most dry matter and has the highest metabolic body weight (**MBW**; Table 1). The smallest cow (JER) consumed least dry matter and had the lowest MBW. As expected, the RDC breed was between the two other breeds. The reason for the breed pattern for ECM yield, was the distribution of parities. The majority of RDC data was from 1st parity. The JER breed had the highest ECM yield which was influenced by the high management level in the first CFIT herds.

Table 1. Descriptive statistics for Dry Matter Intake, Energy Corrected Milk and Metabolic Body Weight

	HOL		RDC		JER	
	Mean	**SD**	**Mean**	**SD**	**Mean**	**SD**
DMI	*21.8*	*3.6*	*20.2*	*3.6*	*17.4*	*2.6*
ECM	*34.0*	*8.2*	*29.7*	*5.4*	*34.8*	*6.7*
MBW	*128.4*	*11.3*	*119.2*	*8.8*	*101.3*	*6.5*

The validation results for production traits showed a gain in reliability from 1 to 8 percent points by adding genomic information (Table 2). It should be noticed that all production traits have a higher heritability than RFI. Therefore, the expected gain in genomic reliability of RFI in all breeds is expected to be approximately 3%.

Table 2. Gain in reliability from including genomic information for production data between research herds and the NAV evaluation. 1,303 HOL bulls and 498 RDC bulls

	Milk Yield	Fat Yield	Protein Yield
HOL	0.08	0.02	0.03
RDC	0.03	0.01	0.01

The correlations between the RFI index and NTM, fertility, udder health, type traits respectively show zero or low correlation for all breed trait combinations. The index for Saved feed was as expected strongly correlated to RFI (0.25-0.40) since RFI is a part of the Saved feed index. The expectation is that the correlation between NTM and RFI will increase with increasing reliability in RFI indices and if Saved feed will be given higher economic weight in NTM in the future. To increase the reliability on the genomic RFI indices, the number of cows with CFIT data is expected to increase to 3,000 HOL cows and 2,000 RDC and 2,000 JER cows by the end of 2021.

Conclusions

The NAV countries Denmark, Finland and Sweden have introduced a single-step evaluation for residual feed intake for the three main breeds Holstein, Red Dairy Cattle and Jersey. The evaluation models utilize feed intake measurements from research farms and commercial herds with the 3D camera system CFIT from VikingGenetics. The genomic validation reliabilities for residual feed intake were evaluated on productions traits using same reference population. The results for genomic reliabilities show as expected a small gain in reliability by using genomic information (1-8 percent points). The reliabilities are expected to increase soon when getting more feed intake data from commercial herds. GEBVs for residual feed intake are included in the Nordic Total Merit index through the Saved feed index to enhance resource efficiency in dairy cattle.

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