Genetic residual feed intake and its genetic association to other breeding goal traits

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Abstract

Selecting for improved feed efficiency in dairy cows is relevant for optimising the utilization of local feed resources, improving sustainability, while reducing the climate footprint from dairy production. The current study analyses feed efficiency based on real data on feed intake and methane in Norwegian Red cows (NR). The goal is to include feed efficiency in the current NR breeding program. Genetic residual feed intake (gRFI) is a measure of the difference between actual an expected feed intake. It has been proposed as a promising feed efficiency trait as it is genetically uncorrelated with the energy driving processes such as milk production and body weight of the cow. Therefore, the objective of this study was to calculate gRFI, predict breeding values (EBVs) and estimate genetic associations between gRFI and other traits. Daily feed intake, body weight, milk yield, and methane emissions from 2,412 NR cows, with on average 433 repeated records, from 14 herds were measured between 2019 and 2024. Two multivariate linear animal repeatability models in DMU were used for estimation of (co)variance components between all traits. Genetic (co)variances for daily traits such as feed intake measured as daily dry matter intake (dDMI) or daily energy intake (dEI), milk yield or energy-corrected yield (ECM), and bodyweight were further used to obtain regression coefficients of the energy sinks (milk and bodyweight on feed intake) and compute gRFI. Heritability of gRFI was low, 0.07. The EBVs for gRFI showed variation and there were differences between animals, with BLUP breeding values ranging from -10.9 to 12.5 for dEI (daily energy-intake from both roughage and concentrate). The correlation between EBVs of gRFI and EBVs of daily body weight and milk yield were close to 0, as expected. The EBVs for gRFI was not standardized, low gRFI was therefore desirable. The correlation of gRFI EBVs to indexes from Geno's routine genetic evaluation ranged from -0.1 to 0.19 and were in general low. The strongest unfavourable correlations were found between gRFI and 305-days milk production traits and exterior. Somatic cell count, calving ease, calf size, silent heat, and number of inseminations had favourable correlations with gRFI (-0.10 to -0.06). These results indicate that improving feed efficiency defined as gRFI in the Norwegian Red population are possible, but before implementing gRFI as a novel trait in the breeding program the genetic correlations must be established and the definition should be improved in order for gRFI to be uncorrelated with current production traits in the TMI.

Key words: Feed efficiency, EBV, methane, residual feed intake

Introduction

Improving feed efficiency of dairy cows has been of great interest for many years and improving cows individual feed utilization is possible by improving the diet composition (management) or by improving genetics for feed efficiency of a population. As routine phenotype collection of feed intake is already implemented in many countries and dairy breeds, knowledge about the associations to traits of economic importance is necessary before feed efficiency or feed intake are to be included in a breeding goal. Along with this, different definitions of cows' ability to utilize feed are also important to investigate. Genetic

residual feed intake (gRFI) is an example of a trait that might be a good alternative to include in the breeding goal for improving feed efficiency of dairy cows. It is a promising efficiency trait for selection because it is genetically uncorrelated to energy driving processes in the cow and thus has no genetic correlation to milk yield and body weight. By calculating breeding values for gRFI, we can get information about cows eating less than expected according to their body weight and milk production, and they are then expected to have higher EBVs for this trait.

The aim of current study was to compute gRFI for Norwegian Red (NR) cows. The secondary aim was to predict gRFI EBVs and estimate genetic associations between gRFI and traits included in Geno's routine genetic evaluation for the NR population.

Materials and Methods

Data

The data used in this study was collected from Geno's feed efficiency database and included records from fourteen herds with daily feed intake, body weight and enteric methane records. Daily milk yield was collected from the automatic milking system. For the genetic analysis only NR dairy cows with a known proven sire from the official breeding program were included.

From the national herd recording system we collected calving dates and pedigree, and information on fat, protein and lactose content in milk from routine test days. Energy corrected milk was calculated after Sjajuna et al. (1990).

Traits

All the traits included for further analysis were defined with one record per day per cow and they were the following:

- Feed intake as sum daily dry matter intake from silage and concentrate in kg per day (dDMI)
- Feed intake as sum daily energy intake from silage and concentrate in MegaJoule NEL per day (dEI)
- Daily milk yield from AMS in kg per day (dYield)
- Average methane in grams per day (dCH_4)
- Energy corrected milk (dECM) in kg per day
- Average daily body weight in kg per day (dBW)

Feed intake records were from direct measurements of silage intake from feed bins provided by BioControl, body weight were measured either by weight scales in the milking robot or by additional scales also provided by BioControl. Methane was measured by GreenFeed provided by C-Lock inc. Milk yield was collected from either a DeLaval or Lely AMS.

Edits of data

All the traits had a phenotypic normal distribution, and records were deleted when they were outside four standard deviations from the mean. In addition to this, a visual inspection of data was done and non-logical records deleted. Each cow had at least five records for each trait. Test days within the herd with less than 10 cows with known phenotypes were removed from further analysis. The pedigree was constructed by keeping relatives on average 7 generations back in time, and only animals with breed code for Norwegian Red was included for constructing the A-matrix. The pedigree included 17 706 animals in total.

The final dataset included 1 046 629 daily records from 2019 to 2024, and 2 412 NR cows with data after data cleaning. Summary statistics of the final dataset are in table 1.

Statistical model

The statistical models used were mixed linear repeatability animal models to estimate (co)variance components and BLUP breeding values (EBVs). Two different rounds of multivariate models (containing four-traits) that differed for which feed intake and milk yield traits that were included. Variance components were estimated with DMUAI (Madsen and Jensen, 2013). The model included the fixed

Table 1: Summary statistics for traits used for calculating breeding values of gRFI for 2 412 Norwegian Red cows with records on feed intake, milk yield, body weight, and methane. The traits are measured as sum or daily average in kg.

Trait	Rec.	Avg	Sd	Min	Max
Dry matter intake (dDMI),	499 866	20.14	4.75	2	40
Yield (dYield)	814 527	28.63	10.18	5	65
Body Weight (dBW)	565 398	615	76.93	400	850
Methane (dCH_4)	257 973	411	102.2	100	800
ECM (dECM)	788 510	29.15	9.95	1.7	60
Energy Intake (dEI)	495 399	130	31.2	30	230

regression of days in milk (DIM), herd year (HY), calving age nested within parity (CA_p), and calving year and season (CYS).

We used two 4-trait models for the analysis and to estimate the (co)variance components and the heritability for the traits; dDMI, dYield, dBW, dCH_4 in the first analysis. The traits dEI, dECM, dBW, dCH_4 in the second analysis. All analyses were performed using DMU (Madsen and Jensen 2013). The model used was as follows:

$$y_{ijklm} = \mu + HY_i + DIM_j + CYS_k + CA_p_l + a_m + pe_m + htd_m + e_{ijklm},$$

where y_{ijklm} is the trait (dDMI or dEI, dYield or dECM, dBW, dCH_4), μ is the intercept, *HY* is the *i*th year within herd, *DIM* is the *j*th day in milk, *CYS* is the *k*th calving year season (2 seasons), CA_p_l is the *l*th age at calving nested within parity, a_l is the random additive effect of the *m*th animal, pe_l is the permanent environmental effect for the animal due to repeated records, htd_l is the herd-test day variance and *e* is the random residual.

The method we used to calculate genetic RFI and phenotypic RFI is similar to what is explained in Difford et al (2020), from the 4x4 additive genetic and phenotypic (co) variance matrices we retrieved genetic regression coefficients for the two "energy sinks" on feed intake: $\hat{b}_g dDMI|dYield, dBW|$ for the first model resulting in $\hat{b}_{g1}$ and $\hat{b}_{g2}$ for dYield on dDMI and dBW on dDMI, respectively. For the second model the multivariate genetic partial regression coefficients where computed for dECM on Energy intake (dEI) and for dBW on dEI: $\hat{b}_g dEI|dECM, dBW|$. The genetic regression coefficients were further used together with the phenotypic regression coefficients in a covariance function B, $B\hat{G}B'$ including *I dDMI* (or *I dEI*), *I dYield* (or *I dECM),* and *I dBW* where *I* means the identity matrix. Methane dCH_4 was not included in the gRFI calculation directly but included ascriptive to the (co)variance as a correlated or helping trait.

Genetic correlations between measured traits

The genetic correlations among the measured traits collected in this study were estimated by running multivariate model (two 4-trait models). From the multivariate models with measured traits, we calculated the heritabilities of the traits by dividing the additive genetic variance component for each trait on the total phenotypic variance that included the additive genetic variance, permanent environmental variance, and residual error variance.

Associations with other traits

We calculated correlations between EBVs for gRFI to other traits included in Genos routine breeding value estimation. For the 2 412 cows with phenotypes for traits, we collected their breeding values and used the Proc Corr procedure in SAS (2013). Indexes from one of the routine genetic evaluations in February 2025 were provided by Geno and used for calculating correlations to all indexes for all cows included in the study.

Results & Discussion

Breeding values estimation for gRFI

The breeding values for gRFI showed a gaussian distribution and ranged from -10.9 to 12.5 when gRFI were calculated from dEI (figure 2) measured as daily NEL, and from -1.65 to 2.59 kg of daily dry matter intake when dDMI (figure 1 and 2) were used for gRFI calculation. The breeding values in figure 1 are not standardized and negative gRFI breeding values must be interpreted as being favorable (eating less than expected) and positive values as being unfavorable (genetic predisposed for eating more than the expectations). We did not calculate the standard error of the predicted gRFI breeding values.

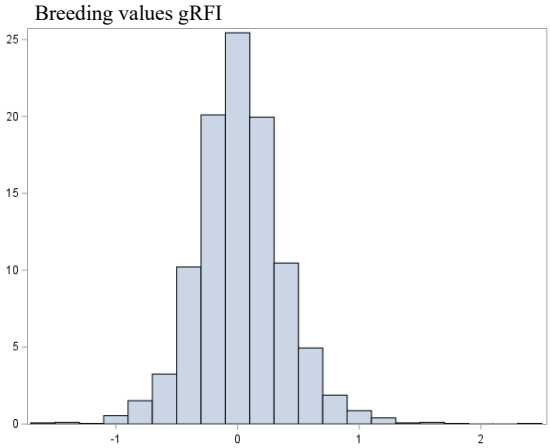


Figure 1. Distribution of BLUP breeding values of genetic residual feed intake (gRFI) for 2 412 Norwegian Red cows with feed intake records, given in kg of daily dry matter intake (dDMI).

Heritabilities

Estimated heritabilities are given in table 2. Heritability of gRFI was on 0.07. Comparing our results with reports from previous studies, gRFI heritability for NR cows was in line with other studies on other breeds. Our results are lower compared to a heritability of 14 % in the study by Difford et al. (2020), but similar to 5% in an older study by Veerkamp et al. (1995). A relatively high heritability of 0.30 to 0.38 was found in Veerkamp et al.'s (1995) study when they used the phenotypic level to estimate regression coefficients of energy requirement and calculate phenotypic residual feed intake. Our results were in the lower range of what Stephansen et al. (2023) presented in a across-country calculation with data on Holstein cows, when they used a random regression model and estimated heritabilities for gRFI within and across parities. One explanation for their higher heritability in other studies might be due to more controlled settings as cows were measured at research facilities, while our current study is based on data from commercial Norwegian farms with less standardized environments. Another explanation might be that they used non-linear (random regression) models compared to our linear models.

Table 1: Heritabilities for the measured traits, daily dry matter intake in kg (dDMI), daily energy intake (dEI), in addition to heritability for calculated daily genetic residual feed intake (gRFI).

Trait	Heritability
dDMI	0.14
dEI	0.13
gRFI	0.07

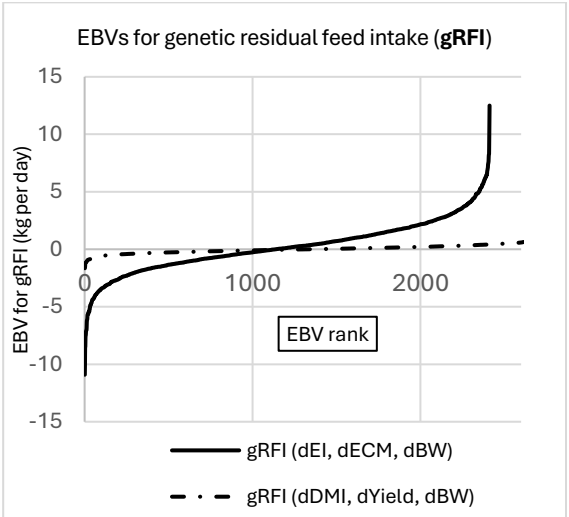


Figure 2. Breeding values (EBV) for gRFI for 2 413 Norwegian Red cows, sorted from lowest to highest rank (x-axis) and EBV on the y-axis. EBVs of gRFI calculated from daily energy intake (dEI) and energy corrected milk (dECM) - black line. EBVs of gRFI calculated from daily dry matter intake (dDMI) and "raw" milk (dYield) - dotted line.

Table 3: Genetic correlations between the measured feed intake traits included in gRFI calculations, to body weight (dBW), methane (dCH_4), milk yield (dYield), and energy corrected milk yield (dECM).

Trait	dDMI	dEI
dBW	0.66 (0.07)	0.64 (0.07)
dCH_4	0.82 (0.06)	0.80 (0.06)
dYield	0.64 (0.07)	NA
dECM	NA	0.69 (0.08)

Genetic correlations

The two measured feed intake traits, dDMI and dEI, had relatively high genetic correlations to the other "ingredients" in the gRFI calculation ranging from 0.64 to 0.82 with strongest correlation to CH_4 (table 3).

Index correlations

The correlations between breeding values for gRFI (not standardized) to traits included in the routine genetic evaluation are in table 4. Because the index correlations showed similar trends for the two different gRFI calculations (dDMI / dEI), we only give the results on index correlations for gRFI based on dDMI including dBW and dYield explaining energy driving processes. The indexes for body (size), udder conformation traits, 305-days milk production traits, calving ease and milk fever showed the strongest unfavorable genetic associations to gRFI. Udder exterior traits and 305-days yield had highest correlation to gRFI ranging from 0.13 to 0.19.

Table 4: Index correlations to gRFI calculated from dDMI in kg, traits with strongest unfavorable correlation to gRFI in Norwegian Red cows.

Trait	Correlation to EBV for gRFI
Udder Exterior traits	0.13 to 0.19
Milk yield, kg fat 305d	0.19
Milk Protein % 305d	0.18
Milk Fat % 305d	0.17
Milk yield, kg protein 305d	0.16
Body Total Score*	0.14
Ketosis (Parity 1-5)	0.08 to 0.12
Angularity*	0.11
Stature*	0.11
Calving Ease (Maternal Parity 1)	0.10
Milk Fever (Parity 3-5)	0.06 to 0.08

*Trait not included in the Norwegian total merit index. P values < .001.

Table 5: Index correlations between gRFI calculated from dDMI in kg, and traits with strongest favorable correlation to gRFI in Norwegian Red cows.

Trait	Correlation to EBV for gRFI
Somatic Cell Count (305d)	-0.10
Silent Heat (Parity 1)	-0.06 to -0.10
Calf Size (Direct)[1,2]	-0.10
Milk Leakage	-0.10
Calving Ease (Direct)	-0.07
Nmbr Inseminations (Parity 1)	-0.07

[1]Trait not included in the Norwegian total merit index

[2] Calf size, direct: high score is small calf

P values < .0001

Although these correlations are relatively weak, they are interesting and can give us an indication of the genetic correlations we can expect between current indices to gRFI. Because we used milk yield from the AMS (daily trait) for gRFI, the trait was not uncorrelated to milk production in current breeding goal. Daily AMS yield was uncorrelated with gRFI, -0.02 (0.3), as expected.

The traits with strongest favorable correlation to gRFI are given in table 5, and were direct calving traits, cow fertility, and udder health. Indexes for somatic cell count, silent heat, calf size, and milk leakage had correlations ranging from -0.06 to -0.10. The correlations were not very strong but indicate a favorable association to improved feed efficiency, and might be related to the energy status of the cow. Low reliabilities of the gRFI EBVs might be one reason for relatively weak correlations, this uncertainty can be accounted for in future work with a "Calo" correction of the EBVs and to approximate the genetic correlations between gRFI to breeding goal traits.

Conclusions

We demonstrated that genetic variation for feed efficiency defined as gRFI in NR cows exists. Udder health, calving traits, and cow fertility had favorable associations with the calculated gRFI breeding values. Although selection for

improved genetic RFI is possible, the current definition are correlated with 305 days milk production traits. Further improvement to define gRFI as independent of production traits in the breeding goal is necessary but a potential for further refining gRFI is possible, once the genetic correlations to the current breeding goal traits are established.

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