Breeding Values for Daily Dry Matter Intake in Norwegian Red Dairy Cows and Correlation to Other Traits

***K.A. Bakke*[1] *and B. Heringstad*[1,2]**

[1] *Geno Breeding and A.I. Association, Norway.*

[2] *Department of Animal and Aquacultural Sciences, Faculty of Biosciences, Norwegian University of Life Sciences, Ås, Norway.*

Abstract

The current study aimed to estimate genetic parameters of feed intake in Norwegian Red (NR) dairy cows. Data from eight commercial herds with equipment for monitoring individual roughage intake was available. Our aim was also to predict breeding values (EBVs) for feed intake in lactating cows and calculate index correlations to other traits in the Total Merit index (TMI) for NR. Data on daily feed intake from roughage and concentrates together with results from weekly feed analyses were used to compute daily dry matter intake (dDMI) kg. A total of 557 NR cows with 61 321 records on feed intake from January to October 2022 were analyzed. The mean dDMI was 20.37 kg. A linear animal repeatability model was used to estimate variance components. The estimated heritability (standard error) of dDMI was 0.18 (0.04). The EBV's for dDMI varied from -3.32 to 3.65 (±1.2), with significant differences between individuals. Index correlations between cows EBV's for dDMI with other traits in the breeding goal of NR were calculated. The index correlations were in general low, ranging from -0.21 to 0.34, the strongest correlation was between 305-day protein yield and EBV for dDMI. Milk yield and body exterior traits had positive index correlations to dDMI. On the contrary, indexes for health and fertility were negatively correlated with EBV for dDMI. Although index correlations between dDMI and other traits for NR cows were not strong, our results indicate that dry matter intake are correlated with production, body exterior, fertility and health traits. We need more knowledge on the effects of selecting for novel feed intake traits, and how we best can define feed efficiency in Norwegian Red needs to be addressed. Our results so far show individual variation of feed intake capacity amongst Norwegian Red dairy cows. More phenotypes on more cows are needed to estimate genetic correlations, as well as increased knowledge on how to balance feed efficiency with production, health and fertility in the current breeding goal of Norwegian Red.

Key words: Feed intake, heritability, dairy cows, index correlations

Introduction

Feed efficiency of dairy cows is one of the most complex traits to work with in breeding programs and have gained a lot of focus for decades (Berry et al. 2007, Veerkamp 1998). The complexity lies both in the physiological processes behind utilization of gras in the rumen, as well as the fact that it is time consuming and costly to monitor individual feed intake in dairy cows. Direct measures on feed intake are necessary for establishing basic knowledge on the nature of this relative new trait in breeding context. Although challenging to measure, equipment for recording of individual feed intake exists. Data on feed intake have mainly been collected from research herds (Pryce et al. 2014), but in more recent years breeding organizations have also started collecting data from commercial herds routinely for genetic evaluation of feed efficiency (de Jong et al. 2019, Negussie et al. 2019). Equipment for monitoring actual individual feed intake in dairy cows may constitute of large mangers or feed bins where the amount of roughage or gras each cow eats during a visit are recorded, and the system provides data on kg of roughage eaten per visit in the manger. This can provide phenotypic data on feed intake throughout the lactation. Although some extra maintenance and calibration of the system are required, time consumption are manageable as part of a daily routine for farmers. Alternative methods to predict roughage intake are also available e.g., 3D cameras, although they are less disturbing for animals in their daily routine and offers an opportunity to phenotype a large number of cows at lower costs (Lassen et al. 2023), it might be a less accurate alternative.

In order to establish a reference population of cows with direct and actual individual feed intake measures, Geno the breeding organization of Norwegian Red, have installed equipment to monitor intake of roughage and concentrates in commercial herds. Feed mangers to record daily and accurate feed intake throughout the lactation under commercial settings are now in place in fourteen herds. The feed efficiency project aims to collect phenotype and genotype data on 1000 Norwegian Red dairy cows yearly and enables Geno to implement future selection for feed efficiency in our breeding goal. This study aimed to perform the first genetic analysis of feed intake in Norwegian Red as a novel trait by using data from the first commercial dairy farms with equipment for monitoring daily roughage intake. As a secondary aim, the relationship between feed intake and traits in routine genetic evaluations was investigated.

Materials and Methods

Data

The data used in this study was extracted from the feed efficiency database and included records from eight herds with data from January to October 2022. Daily roughage intake registered in the BioControl software (CRFI) were merged with daily intake of concentrates collected from automatic milking systems (Lely or DeLaval). Feed samples on roughage were sampled by farmers every week, and we used information on dry matter content from the feed analyses. The analyzed trait was daily dry matter intake in kg (dDMI), as a sum of dry matter from roughage and concentrates eaten at a specific test-day. For the genetic analyses only Norwegian Red dairy cows with a known sire (Norwegian Red) were included. The final dataset included 557 cows, and 61 321 daily records on kg dDMI in total.

Edits of data

Restrictions on logical feed intake values were set between seven and 36 kg dDMI per test-day. Test-days with records out of this range were excluded. Records from 6 to 350 days in milk were included. Cows had to have a minimum of eight days with feed intake data and information on both roughage and concentrates in order to be included in the genetic analysis. Pedigree information were collected from the Norwegian dairy herd recording system, and sire and dams were traced eight generations back.

Statistical model

A mixed linear repeatability animal model was used to estimate variance components and breeding values (EBVs). Variance components were estimated with DMUAI (Madsen and Jensen, 2013). The model included fixed effects of herd, days in milk and age-parity, and random effects of animal, herd-test-day and permanent environment. Days in milk ranged from 6 to 350, and herd had eight classes. First parity cows were grouped in six groups according to their age in months at calving: ≤ 22, 23, 24, 25, 26 and ≥ 27, while second parity and third or later parities were in two separate groups (age-parity had eight classes). The random effect of herd-test-day had 1 203 levels in total. The pedigree contained 12 291 animals. The relationship matrix (A) was constructed assuming no inbreeding between animals and without genetic groups for animals with unknown parents.

Correlations between breeding values

Correlations between EBV for dDMI and other traits were calculated to give an indication of strength and direction of possible genetic correlations between traits. For the 557

Norwegian Red cows with phenotypes on feed intake, correlations between their EBV for dDMI and indexes for all other traits included in routine genetic evaluations of Norwegian Red were calculated. Indexes from the routine evaluation performed in June 2023 are provided by Geno.

Results & Discussion

The phenotypic mean dDMI was 20.37 kg per day with a standard deviation of 4.35 kg. Daily dry matter intake displayed an approximately normal distribution and large phenotypic variation amongst cows and test-days (Figure 1). These are the first results on feed intake of Norwegian Red based on data from commercial herds but are in line with what previous studies from research-facilities have reported (Salte et al. 2020, Wallén et al. 2018). Li et al. (2016) presented feed intake in Nordic Red to be close to 20 kg dry matter intake/day 24 weeks after calving in primiparous cows.

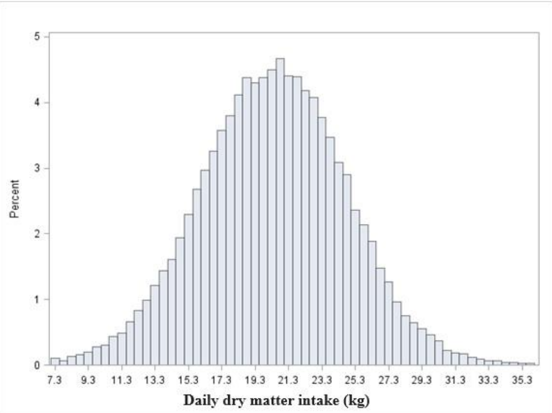

Figure 1. Phenotypic distribution of daily dry matter intake in kg for 557 Norwegian Red cows in commercial herds.

Variance components estimation

Estimated variance components for dDMI were significant different from zero (Table 1) with heritability 0.18 (0.04) and repeatability 0.34 (0.02). Our results were in the same range as a study on feed intake in Nordic Red cattle by Liinamo et al. (2012) who reported heritabilities ranging from 0.18 to -0.33 for DMI in primiparous Nordic Red cows based on data from one research herd. Li et al. (2016) analyzed DMI from 872 Nordic Red cows from four herds and estimated heritability ranged from 0.25 to 0.41 for six different periods of the first 24 lactation weeks for primiparous cows. These authors showed that heritability of DMI varies throughout the lactation, and that it should be accounted for in genetic evaluation of feed efficiency. Our results confirms that significant genetic variation in feed intake exists, despite a relatively small dataset with few animals, the standard error on our heritability estimate was low. This is promising for the further work.

Table 1. Estimated variance components for daily dry matter intake (kg) and the corresponding heritability and repeatability.

	Estimate	Standard error
Herd-test-day (σ^2_{htd})	4.28	0.18
Additive genetic (σ^2_a)	2.65	0.69
Permanent environment (σ^2_{pe})	2.40	0.57
Residual (σ^2_e)	5.62	0.03
Repeatability* (r)	0.34	0.02
Heritability** (h^2)	0.18	0.04

* $r = (\sigma^2_a + \sigma^2_{pe}) / (\sigma^2_a + \sigma^2_{pe} + \sigma^2_{htd} + \sigma^2_e)$
** $h^2 = \sigma^2_a / (\sigma^2_a + \sigma^2_{pe} + \sigma^2_{htd} + \sigma^2_e)$

Breeding values estimation

The EBVs for dDMI ranged from -3.32 to 3.65 with standard errors of 1.2. In figure 2, EBVs for the 557 Norwegian Red cows are sorted from lowest to highest, and this illustrates that there were significant differences between the animals in the tails of the distribution. Breeding values for dDMI were not standardized but given as kg/d. Our result indicates that genetic variation for feed intake capacity exists and genetic selection for feed efficiency in Norwegian Red is possible, as dDMI are the main component trait in various definitions of feed efficiency.

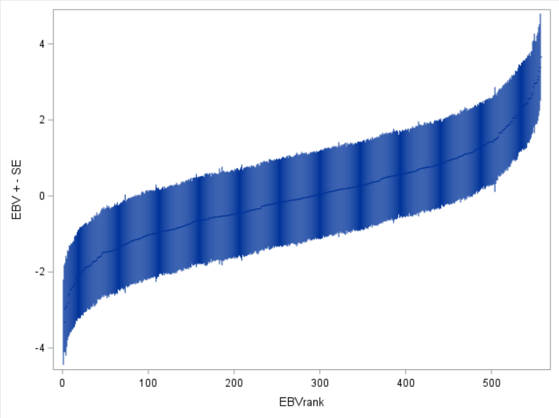

Figure 2. Breeding values (EBV) for daily dry matter intake in kg for 557 Norwegian Red cows. Standards error (SE) illustrated with blue bars. EBVs are sorted from lowest to highest rank (x-axis) and illustrated with EBV +/- SE (y-axis).

Index correlations

Correlations between indexes for all traits from routine genetic evaluations of Norwegian Red and EBVs for dDMI ranged from -0.21 to 0.34. Many correlations were low and not significantly different from zero. Only the strongest correlations are presented here. In Table 2 positive correlations are presented. Production and body exterior traits had the strongest positive index correlations with dDMI, ranging from 0.15 to 0.34, and the strongest was to 305-days protein yield. A positive index correlation means that high EBV for dDMI is associated with high index for other traits. The correlations are logical indicating a high stature, milking type cow with high milk yield will have a larger intake capacity of the rumen.

Table 2. Index correlations to daily dry matter intake (dDMI) in kg.

Trait	Correlation to EBV for dDMI
Kg protein 305-days	0.34
Kg milk 305-days	0.30
Angularity*	0.26
Kg fat 305 days	0.24
Stature body*	0.21
Rump width*	0.18
Body depth*	0.15
Foot angle*	0.15

*Trait not included in the Norwegian total merit index

The traits with the strongest negative index correlations to EBV for dDMI are given in Table 3. Here we find health and fertility traits with correlations ranging from -0.12 to -0.21. Number of inseminations and interval from calving to first insemination had the strongest negative correlations (Table 3). Clinical mastitis in different lactations had an index correlation to dDMI ranging from -0.12 to -0.15. Although the correlations were not strong, they were significantly different from zero. Top line with correlation of -0.14 indicates a weaker top line associated with higher EBV for dDMI. The correlation to calf size (direct), indicates that higher EBV for dDMI may increase calf size, and small calf size are preferable in the current index. Although these correlations are relatively weak, they are interesting and indicates the direction of the genetic correlations to dDMI.

Table 3. Index correlations to daily dry matter intake (dDMI) in kg.

Trait	Correlation to EBV for dDMI
No. of inseminations (1-4 parity)	-0.21
Interval calving to 1st ins. (1-4 parity)	-0.16
Top line[1,*]	-0.14
Calf size, direct[2] (Parity 1)	-0.14
Bone structure[3,*]	-0.13
No. of inseminations, heifers	-0.13
Clinical mastitis (1-3 parity)	-0.12 to -0.15
Silent heat (3-5 parity)	-0.12 to -0.14

[*]Trait not included in the Norwegian total merit index
[1] Top line: Scored from 1 to 9. 1 = weak, 9 = upward
[2] Calf size, direct: High score is small calf
[3] Bone structure: High score is very fine and thin bones, low score for coarse bones (broad and thick)

This study shows that genetic variation in feed intake in Norwegian Red exists and that dDMI is moderately heritable. These results are promising for the further work of defining feed efficiency as a novel trait. There are still many unanswered questions that must be addressed before selection for feed efficiency can be implemented. We need more knowledge on genetic correlations to other important traits in our breeding goal. Feed intake can be measured as energy or protein intake and seen in the context of energy mobilization (body condition or body weight) to capture the energy sinks in the cow. This will be part of our further work on feed efficiency in Norwegian Red dairy cattle.

Conclusions

Genetic variation of feed intake in Norwegian Red dairy cattle exists, and results from this study shows that feed intake data from commercial dairy farms can be used for genetic evaluation.

Acknowledgement

We would like to acknowledge Norwegian Research Fund for Agriculture and Food Industry (FFL/JA, 309451), and Innovation Norway for funding the *"Feed Efficiency project*", as well as the farmers that are project partners for contributing with data.

References

Berry, D.P. Horan, B. O'Donovan, M. Buckley, F. Kennedy, E. McEvoy, M. and Dillon, P. 2007. Genetics of grass dry matter intake, energy balance, and digestibility in grazing Irish dairy cows. *J. Dairy Sci*. 90 (10), 4835-4845. Doi: https://doi.org/10.3168/jds.2007-0116.

de Jong, G. Bouwmeester-Vosman, J.J. van der Linde, C. de Haas, Y. Schopen, G.C.B. and Veerkamp, R.F. 2019. Feed intake genetic evaluation: progress and an index for saved feed cost. *Interbull Bulletin* 55, 1-4. https://journal.interbull.org/index.php/ib/article/view/171/171.

Lassen, J. Thomassen, J.R. and Borchersen, S. 2023. Repeatabilities of individual measure of feed intake and body weight on in-house commercial dairy cattle using a 3D camera system. *J. Dairy Sci. In Press.* Doi: https://doi.org/10.3168/jds.2022-23177.

Li, B. Fikse, W.F. Lassen, J. Lidauer, M.H. Løvendahl, P. Mäntysaari, P. 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 (9), 7232-7239. Doi: https://doi.org/10.3168/jds.2015-10669.

Liinamo, A.-E. Mäntysaari, P. and Mäntysaari, E. A. 2012. Short communication: Genetic parameters for feed intake, production, and extent of negative energy balance in Nordic Red dairy cattle. *J. Dairy Sci*. 95 (11), 6788–6794. Doi: https://doi.org/10.3168/jds.2012-5342.

Madsen, P. and Jensen, J. 2013. DMU Ver. 6, rel 5.2.https://dmu.agrsci.dk/DMU/Doc/Current/dmuv6_guide.5.2.pdf.

Negussie, E. Mehtiö, T. Mäntysaari, P. Løvendahl, P. Mäntysaari, E.A. and Lidauer, M.H. 2019. Reliability of breeding values for feed intake and feed efficiency traits in dairy cattle: When dry matter intake recordings are sparse under different scenarios. *J. Dairy Sci*. 102 (8), 7248-7262. Doi: https://doi.org/10.3168/jds.2018-16020.

Pryce, J. E. Wales, W. J. de Haas, Y. Veerkamp, R. F. and Hayes, B. J. 2014. Genomic selection of feed efficiency in dairy cattle. *Animal* 8 (1), 1-10. Doi: https://doi.org/10.1017/S1751731113001687.

Salte, R. Storli, K.S. Wærp, H.K.L. Sommerseth, J.K. Prestløkken, E. Volden, H. and Klemetsdal, G. 2020. Designing a replacement heifer rearing strategy: Effects of growth profile on performance of Norwegian Red heifers and cows. *J. Dairy Sci.* 103 (11), 10835-10849. Doi: https://doi.org/10.3168/jds.2020-18385.

Veerkamp, R.F. 1998. Selection for Economic Efficiency of Dairy Cattle Using Information on Live Weight and Feed Intake: A Review. *J. Dairy Sci*. 81 (4), 1109-119.Doi: https://doi.org/10.3168/jds.S0022-0302(98)75673-5.

Wallén, S.E. Prestløkken, E. Meuwissen, T.H.E. McParland, S. Berry, D.P. 2018. Milk mid-infrared spectral data as a tool to predict feed intake in lactating Norwegian Red dairy cows. *J. Dairy Sci.* 101 (7), 6232-6243. Doi: https://doi.org/10.3168/jds.2017-13874.