Genetic Correlations Between Daily Dry Matter Intake, Body Weight, and Enteric Methane in Norwegian Red

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

Selecting for reduced enteric methane emissions and improved feed efficiency in cattle is of interest. These are important traits both considering climate and utilization of feed resources on farm. Before genetic selection on new traits can be implemented, a base population with phenotypes on the desired trait(s) must be established. This study collected and analyzed data on feed intake, methane emissions, and body weight on Norwegian Red dairy cows in commercial dairy farms in Norway. Our goal was to estimate genetic parameters and breeding values for the three traits, and to estimate genetic correlations amongst them. We also calculated correlations to current breeding indices in Norwegian Red dairy cows. The relevant traits were daily dry matter intake (dDMI), average daily body weight (dBW), and average daily methane emissions (dCH4). There were 452 055 daily records on 2 074 cows in the dataset. Bivariate linear animal repeatability models were used. The model included fixed effects of parity week, age at calving, and herd in addition to permanent environmental effects of herd testday, additive genetic effects and residual as random effects. The pedigree was traced 8 generations back and contained 18 697 animals. The estimated heritabilities were 0.29, 0.39, and 0.57 for dDMI, dCH4, and dBW, respectively. Standard errors were low (0.04 to 0.05). Genetic correlations among all three traits were significant and strong, and ranged from 0.50 to 0.65. The strongest correlation (standard error) was found between dDMI and dCH4 of 0.65 (0.10). Positive and relatively strong genetic correlations imply that selection for lower level of one trait also will reduce the level of the other two traits. The correlation between the breeding values of the three novel traits to current indices from routine genetic evaluations of Norwegian Red ranged from (-0.26 to 0.16), and the fertility index had strongest favorable correlation to the three traits with -0.19, -0.22, and -0.26 for dBW, dCH4, and dDMI, respectively. This indicate that higher feed intake, larger cows and more methane emissions are associated with lower genetic merit for fertility. Further research is needed to investigate the consequences of selecting for reduced methane emissions or reduced body weight and how this will affect cows' ability to utilize grass. For Norwegian Red it remains to define the feed efficiency trait, but we started to analyze traits that are key ingredients of a future feed efficiency trait.

Key words: Novel traits, phenotype on farm, greenfeed, body size, index correlations

Introduction

Improving feed efficiency and at the same time reduce the methane produced by Norwegian dairy cows have gained increased focus in recent years. Norway is committed to reduce greenhouse gas emissions from agriculture by 55 % of 1990 levels before 2030 according to the agreement made between government and the farmers organization. Selection and breeding for climate friendly cows are suggested as one of the most important solutions to achieve the reduction goal in the climate agreement.

Norwegian Red (NR) dairy cattle has a broad breeding goal, where beef traits are part of the breeding goal and weighted in the total merit index (www.norwegianred.com). Before we can implement new traits in the breeding goal we need knowledge on how feed efficiency and enteric methane can be improved and how this will affect current traits in the breeding program. Direct measurements of feed intake and methane phenotypes are costly, despite this collecting data on the actual traits are necessary as the cost of implementing new traits without considering the effect on current breeding goal can be more expensive in the long run. Hence, Geno have established a project collecting data both on daily feed intake, methane, and body weight for cows in 14 commercial herds, ongoing since 2021.

Some breeding organizations have recently published breeding values for feed efficiency traits based on feed intake records from commercial herds (CRV 2023, Manzanilla-Pech et al. 2023, Viking genetics 2021), while others publish breeding values based on phenotypes measured at research farms (Jamrozik et al., 2021). Heritability of feed intake and methane traits in Nordic Red dairy breeds range from 0.18 to 0.20 for feed intake (Bakke and Heringstad 2023, Manzanilla-Pech et al. 2023) and from 0.22 to 0.44 for enteric methane (Chipondro 2024, Wethal et al. 2022), respectively. Methane and feed efficiency are reported to be genetically correlated with estimates ranging from 0.05 to 0.76 (López-Paredes et al. 2021, Manzanilla-Pech et al. 2022). In the study by Manzanilla-Pech et al. (2022) they reported favorable and positive genetic correlations between two definitions of feed efficiency with methane intensity and methane production in Holstein cows. This suggests that genetic selection for both improved feed efficiency and reduced enteric methane at the same time, is feasible.

A relatively strong genetic relationship between methane production and body weight of 0.65 was reported for Holstein cows across-country (Manzanilla-Pech et al. 2021), and a genetic correlation of 0.69 was estimated for Nordic Red (Manzanilla-Pech et al. 2023), which imply more methane are produced with increasing cow size.

Body weight is accounted for in some definitions of feed efficiency. In RFI, a popular way to define feed efficiency in dairy cattle, energy sinks used for production, maintenance of body weight and loss or gain in body weight are usually accounted for (Stephansen et al., 2021). Hence, collection of longitudinal data on cows' body weight are important for calculating individual feed efficiency. Genetic correlations between body weight and methane are scarcely investigated, and previous studies have reported strength and direction of the correlations ranging from non-significant, negative, to a strong positive correlation (Breider et al. 2019, Lassen and Løvendahl 2016, Manzanilla-Pech et al. 2021). This suggests that more research are needed on how cows body weight might affect the other traits.

Limited research on genetic associations between methane, body weight and feed intake in Red dairy breeds is published. Therefore, the current study aimed to analyze these traits genetically based on data from commercial herds with NR and examine how they correlate with some of the traits in the current breeding goal of NR dairy cattle.

Materials and Methods

Data

Data was collected by Geno's feed efficiency project and included records from fourteen Norwegian dairy herds with equipment from BioControl for individual feed intake recording, as well as weight scales from BioControl. In addition, were methane data from 25 herds with GreenFeed included in the study. We had records from GreenFeed from more herds because these units were moved during the period of data collection. Feed samples of silage was collected weekly and feed analyses gave information for calculation of daily dry matter content of the feed consumed. The dataset had data from 2020 to 2024 and a total of 452 055 observations. The number of cows measured for one or more of the traits methane, feed intake, or dry matter intake was 2 074.

Edits of data

Before genetic analysis of the novel traits was performed, data was checked and edited for logical values. Average body weight for six parity and lactation stages was calculated, and observations within 3 standard deviations of the mean was considered a logical body weight record for the cow and used in further analyses. All records out of this range were excluded from the genetic analysis. 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 silage and concentrates intake in order to be included in the genetic analysis. Additional information on birth info and calving data was collected from the national herd recording system and pedigree information used to construct relationship matrix. The pedigree was traced eight generations back, and cows with a known NR A.I. sire was included in the analysis. Lastly, breeding values on current established traits from Genos database for the routinely breeding value estimation was collected.

Traits

Feed intake was defined as daily dry matter intake (dDMI) from both grass (silage) and concentrate. Methane production was measured as gram per day for each visit in GreenFeed. The phenotype for methane was calculated as daily average methane emission (dCH4) for each cow. Body weight was collected from each visit on the scale and the final phenotype included for further analysis was the daily average body weight (dBW). Descriptive statistics for the traits are given in Table 1. Daily dry matter intake (dDMI) ranged from 7 to 35.9 Kg, Methane (dCH4) from 100 to 799 gram per day and daily body weight (dBW) from 400 to 850 kg. The number of records for each trait combination were 3 162 for dDMI and dCH4, 40 284 for dDMI and dBW, and 49 290 for dCH4 and dBW (Table 1).

Table 1. Descriptive statistics of daily dry matter intake (dDMI), methane produced (dCH4), and body weight (dBW) after editing the data.

Trait			
	dDMI	dCH4	dBW
Cows, n	557	1 370	1 011
Mean (SD)	20.4 (4.4)	418.4 (104)	607 (77)
Maximum	35.9	799	850
Minimum	7.0	100	400
N obs. dDMI	61 321		
N obs. dCH4	3 162	220 932	
N obs. dBW	40 284	49 290	260 132

Statistical model

Bivariate mixed linear repeatability animal models were used to estimate (co)variance components and breeding values (EBV). Variance components were estimated with DMUAI (Madsen and Jensen, 2013). The following mixed model was used for all 3 traits:

$$Y = Herd + Week + Parity/CAge + htd + a + pe + e$$

where the effect of herd, lactation week, and parity and age at calving were fixed effects, while the effect of testday within herd (htd), additive animal genetic effect (a), permanent environment of animal (pe), and residual (e) were random effects.

Days in milk ranged from 6 to 350 and was grouped in 50 classes according to week after calving. Age at first calving and parity were merged in contemporary groups due to limited records in the tails of the dataset. For dDMI we grouped first parity cows in six contemporary 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. For dCH4 age at first calving were grouped as ≤ 21, 22, 23, 24, 25, 26, 27, and ≥ 27 while parity 2 and ≥ 3 was in a separate group. For dBW age of calving in first and second parity was in different groups, while cows in parity ≥ 3 were in one group. The pedigree was traced 8 generations back and contained 18 697 animals. A relationship matrix

(A) was constructed assuming no inbreeding between animals and without genetic groups for animals with unknown parents.

Correlations between breeding values

We calculated the spearman correlations between EBV for the novel traits in this study to other traits in the breeding goal of NR. For the cows with phenotypes on dDMI, dCH4, and dBW correlations between their estimated EBV's and indexes included in routine genetic evaluations of NR were calculated.

Results and Discussion

The phenotypic mean (standard deviation, SD) for dDMI and dBW was 20.3 (4.4) and 607 (77) kg per day, respectively. For dCH4 the mean (SD) was 418.4 (104). The phenotypic distribution for dBW (Figure 1) did not follow a perfect normal distribution. This can be explained by different mean weights for cows in first and second parity compared to older cows.

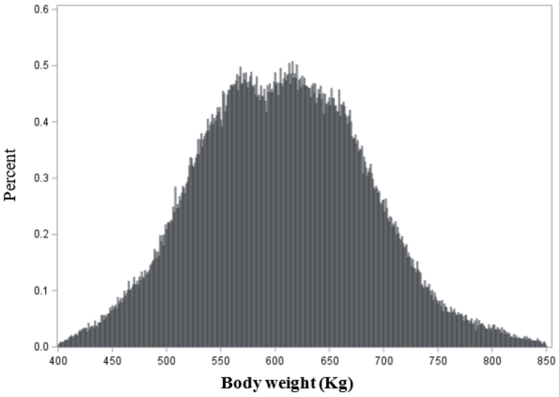

Figure 1. Phenotypic distribution of daily body weight for 1 011 Norwegian Red cows in commercial herds.

Body weight can vary a lot between two visits and high standard deviation is expected. Body weight is largely influenced by time from eating, milking, and drinking before weighing. The cows were either weighed in the concentrate feeding station, or before they entered or after they left the milking unit. Current results are the first to report longitudinal records on feed intake, body weight and methane in commercial herds with NR. The average dBW was higher than the average body weight reported to be 557 kg for NR cows in a previous study by Wallén et. al (2018). However, their study was from one research facility at the Norwegian University for Life Sciences and might not be representative for the population as a whole.

Variance components

There were significant genetic variation for all three traits, and the variance components differed from zero. Estimated variance components are given in Table 2.

Table 2. Variance components (standard errors), heritability and repeatability for daily dry matter intake (dDMI) (kg), daily methane (dCH4) (gram), and daily body weight (dBW) (kg)

Variance components			
	dDMI	dCH4	dBW
	Estimate (SE)	Estimate (SE)	Estimate (SE)
Herd-testday (σ^2_{htd})	4.4 (0.2)	1891.7 (28.5)	836.5 (17.2)
Additive (σ^2_a)	4.7 (0.9)	3971.9 (419.3)	3057.5 (374.6)
Permanent (σ^2_{pe})	1.5 (0.6)	522.6 (272.3)	911 (245.5)
Residual (σ^2_e)	5.6 (0.02)	3707.4 (11.5)	540.8 (1.5)
Repeatability*	0.38	0.45	0.74
Heritability**	0.29	0.39	0.57

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

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

Heritability of dDMI was 0.29 (0.05) which is larger than the estimate from previously analyses of the trait in a univariate model (Bakke and Heringstad, 2023). The heritability of dry matter intake is in line with results reported in Holstein (Li et al. 2016). Heritability of daily methane production on 0.39 (Table 2) corresponds with what Wethal et al. (2022) estimated based on a subset of the data used here. Body weight had the highest heritability of 0.57, and this is comparable to heritability estimates for body weight in Holstein from another study on using electronical weight measurements from scales (Toshniwal et al., 2008).

Our results confirms that significant genetic variation for dry matter intake, body weight, and methane production in NR dairy cattle exists. The relatively high heritabilites of dDMI, dCH4, and dBW are promising for the further work of defining feed efficiency in NR. The repeatabilities for dDMI and dCH4 was low compared to dBW, we need to find good solutions to improve repeatability for these traits. Good quality controls of data are important, and filtering and editing of data at feed bin level, testday level or cow level is important in order to improve the repeatabilities.

Genetic correlations

The genetic correlations between the traits were strong and positive, ranging from 0.50 to 0.65 (Table 3). The highest correlation was between dDMI and dCH4.

Table 3. Estimated genetic correlations between daily dry matter intake (dDMI), average daily methane (dCH4), and body weight (dBW) in Norwegian Red cows. Standard errors of correlations in parenthesis.

Genetic correlations		
Trait	dDMI	dBW
dCH4	0.65 (0.10)	0.50 (0.09)
dBW	0.59 (0.11)	

Our results for dDMI and dBW are comparable with what Manzanilla-Pech et al. (2023) reported in Nordic Red and Holstein cattle who estimated correlations from 0.58-0.65 with phenotypes from 3D-cameras. Genetic correlation between dCH4 to dBW and dDMI are a little higher compared with what Breider et al. (2018) estimated. The direction and level of the genetic correlations was logical. Body weight (adult), methane production, and dry matter intake can be reduced when selection pressure is put on one of the traits. Our results support that the level of methane production and feed intake will be reduced if selecting for lower body weight.

Fixed effects

The significance of effects included in our models were tested. For all 3 traits there was a significant effect of weeks in milk, parity and age at calving. For dDMI and dCH4 the fixed effect solutions for lactation week followed a lactation like curve, as illustrated for dDMI in figure 1, with largest effect around peak lactation.

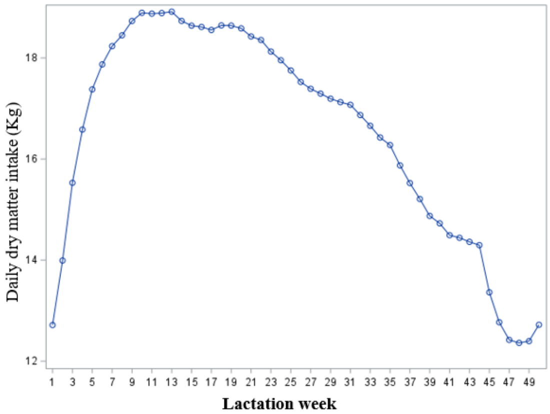

Figure 1. Best linear unbiased estimates of fixed effect of lactation week on daily dry matter intake for Norwegian Red cows.

For dBW we discovered the opposite pattern for the effect of weeks in milk (Figure 2). Here the body weight drops after calving, before increasing almost linearly throughout the lactation. Cows are losing weight after calving for biological reasons and on average 20 kg of weight loss are within the first 7 weeks of the lactation. The phenotypic change of body weight throughout the lactation showed a different curve for different parities (not shown).

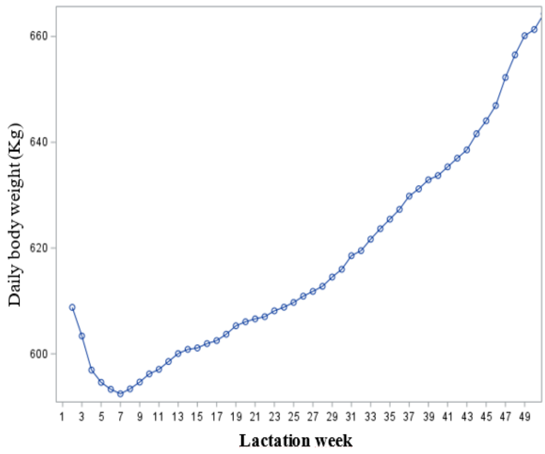

Figure 2. Solution of fixed effect of lactation week on body weight (Kg) for Norwegian Red cows.

Breeding values estimation

The EBVs for dDMI ranged from -4.01 to 6.49 kg dry matter per day (±1.5). For dCH4 the EBVs ranged from -124.5 to 150 gram per day (± 40.5), for dBW from -178. 5 to 190.9 kg of body weight. There was a large variation in EBVs for alle tree traits as illustrated for dBW in figure 3. This shows the differences between animals with high and low breeding values.

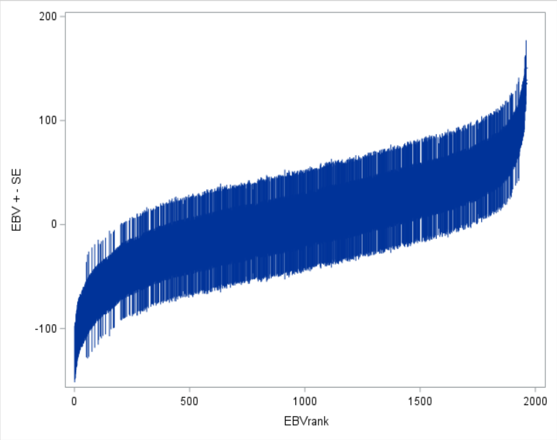

Figure 3. Breeding values (EBV) for body weight in kg for 1 960 Norwegian Red cows. Standards error (SE) illustrated with blue bars. EBVs are sorted from lowest to highest (x-axis) and illustrated with EBV +/- SE (y-axis).

Index correlations

Correlations between EBV for dDMI, dCH4, dBW and indexes for traits in the routine genetic evaluations of NR are given in table 4. In general correlations were low and ranged from -0.26 to 0.14 for dDMI, -0.22 to 0.14 for dCH4, and from -0.19 to 0.14 for dBW. Fertility came out as the sub-index with highest correlation to the EBVs for all the 3 analysed traits. The correlation was negative from -0.19 to -0.26, indicating higher EBVs are associated with lower genetic merit for fertility i.e. larger cows, with higher feed intake and more methane will have poorer fertility. The weak positive correlation between EBVs for dDMI and dCH4 to milk index (0.09-0.14) indicates that higher yielding cows tend to eat more and produce more methane.

Table 4. Index correlations to daily dry matter intake (dDMI), methane (dCH4), and body weight (dBW) in Norwegian Red cows.

Trait (index)	dDMI	dCH4	dBW
Milk yield	0.14 (<.001)	0.09 (<.001)	-0.00 (0.96)
Fertility	-0.26 (<.001)	-0.22 (<.001)	-0.19 (<.001)
Udder health	-0.10 (<.001)	-0.14 (<.001)	-0.13 (<.001)
Milk fever	0.13 (<.001)	0.14 (<.001)	0.16 (<.001)
Mastitis	-0.10 (<.001)	-0.08 (<.001)	-0.4 (0.05)
Claw health	-0.11 (<.001)	-0.11 (<.001)	-0.15 (<.001)
Ketosis	0.05 (0.03)	0.06 (<.01)	0.13 (<.001)
Carcass	0.00 (0.1)	0.07 (<.01)	0.14 (<.001)
Total Merit	-0.04 (0.07)	-0.07 (.001)	-0.13 (<.001)

Correlations between EBVs and the current total merit index (TMI) for NR were slightly negative for both dCH4 (-0.07) and dBW (-0.13). Negative correlation indicates lower TMI with increased genetic potential for more dry matter intake and more methane produced because the EBVs were not standardized. For dDMI the correlation to TMI was not significant different from 0.

We need estimates of genetic correlations to other traits before we can start selecting for feed efficiency or methane. It is important to have a make good decisions when defining feed efficiency and methane in the breeding goal. More research is needed to understand the genetic relationship between methane and feed efficiency traits. A definition of feed efficiency considering body weight changes, energy intake (from grass and silage versus concentrate), and milk production will be investigated further for the NR population. We aim to balance feed efficiency, climate effects, production, health and fertility in a sustainable breeding goal for NR.

Conclusions

Genetic variation for traits considered important for feed efficiency in NR exists. The new traits dDMI, dBW, and dCH4 measured in commercial dairy farms are genetically correlated. The results are promising for the further work on feed efficiency as a new trait to be included in routine genetic evaluations of NR.

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 all the farmers that are project partners for contributing data.

References

Bakke, K.A., and Heringstad, B. 2023. Breeding values for daily dry matter intake in Norwegian Red dairy cows and correlation to other traits. *Interbull Bulletin* 59, 89-94. https://journal.interbull.org/index.php/ib/article/view/1882/1908.

Breider, I.S, Wall, E., Garnsworhty, P.C., and Pryce, J. 2018. Genetic relationships between methane emission and milk yield, live weight and dry matter intake. *Proc. 11th World Congress on Genetics Applied to Livestock Production, Auckland, New Zealand.* Wageningen Academic Publishers, pp. 134.

Breider, I.S., Wall, E., and Garnsworthy, P.C. 2019. Short communication: Heritability of methane production and genetic correlations with milk yield and body weight in Holstein-Friesian dairy cows. *J. Dairy Sci.* 102 (8), 7277-7281. Doi:https://doi.org/10.3168/jds.2018-15909.

Chipondro, L. 2024. Heritability of methane emissions in Swedish Red cattle in northern Sweden. MS Thesis. Faculty of Veterinary Medicine and Animal Science, Department of Animal Breeding and Genetics. Swedish University of Agricultural Sciences. https://stud.epsilon.slu.se/19720/1/chipondoro-l-240130.pdf.

CRV. 2023. Feed Efficiency. Assessed 05.06.2024. https://crv4all.com/en/service/feedefficiency.

Jamrozik, J., Kistemaker, G.J, Sullivan, P.G, Van Doormal, B.J., Chud, T.C.S., Baes, C.F., Schenkel, F.S., and Miglior, F. 2021. Genomic evaluation for feed efficiency in Canadian Holsteins. *Interbull Bulletin* 56, 153-161. https://journal.interbull.org/index.php/ib/article/view/68/68.

Lassen, J., and Løvendahl, P. 2016. Heritability estimates for enteric methane emissions from Holstein cattle measured using noninvasive methods. *J. Dairy Sci.* 99 (3), 1959-1967. https://doi.org/10.3168/jds.2015-10012.

Li, B., Fikse, W.F., Lassen, J., Lidauer, M.H., Løvendahl, P., Mäntysaari, P. and 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.

López-Paredes, J., Saborío-Montero, A., Charfeddine, N., Jiménez-Montero, J.A., and González-Recio, O. 2021. Dry matter intake, methane emissions and microbiome profiles as new traits for feed efficiency. *Interbull Bulletin* 56, 111-120. https://journal.interbull.org/index.php/ib/article/view/77/77.

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

Manzanilla-Pech, C.I.V., Løvendahl, P., Mansan Gordo, D., Difford, G.F., Pryce, J.E., Schenkel, F., Wegmann, S., Miglior, F., Chud, T.C., Moate, P.J., Williams, S.R.O., Richardson, C.M., Stothard, P., and Lassen, J. 2021. Breeding for reduced methane emission and feed-efficient Holstein cows: An international response. *J. Dairy Sci.* 104 (8), 8983-9001. Doi:https://doi.org/10.3168/jds.2020-19889

Manzanilla-Pech, C.I.V., Stephansen R.B., Difford G.F., Løvendahl P., and Lassen J. 2022. Selecting for feed efficient cows will help to reduce methane gas emissions. *Front. Genet.* (13). Doi: https://doi.org/10.3389/fgene.2022.885932

Manzanilla-Pech, C.I.V., Stephansen, R.B., and Lassen, J. 2023. Genetic parameters for feed intake and body weight in dairy cattle using high-throughput 3-dimensional cameras in Danish commercial farms. *J. Dairy Sci.* 106 (12), 9006-9015. Doi:https://doi.org/10.3168/jds.2023-23405

Stephansen, R.B., Lidauer, M.H, Nielsen, S., Pösö, J., Fikse, F., Manzanilla-Pech, C.I.V., and Aamand, G.P. 2021. Genomic prediction of residual feed intake in the Nordic breeds using data from research herds and 3D cameras in commercial herds. *Interbull Bulletin* 56, 166-162. https://journal.interbull.org/index.php/ib/article/view/66/66.

Toshniwal, J.K., Dechow, C.D., Cassell, B.G., Appuhamy, J.A.D.R.N., and Varga, G.A. 2008. Heritability of electronically recorded daily body weight and correlations with yield, dry matter intake, and body condition score. *J. Dairy Sci* 91 (8), 3201–3210. Doi: https://doi.org/10.3168/jds.2007-0627.

Viking Genetics. 2021. Feed Efficiency takes a major step forward. Assessed 05.06.2024. https://www.vikinggenetics.com/news/feed-efficiency-takes-a-major-step-forward.

Wallén, S.E., Prestløkken, E., Meuwissen, T.H.E., McParland, S., and 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.

Wethal, K.B., Difford, G.F., Winnberg, K., Norberg, E., and Heringstad, B. 2022. Heritability of methane emissions in Norwegian red cows based on measures from GreenFeed in commercial herds. Proc. 12th World Congress on Genetics Applied to Livestock Production, Rotterdam, the Netherlands, Wageningen Academic Publishers, pp. 176-178.