Heritability of Methane Emission in Young Norwegian Red Bulls Estimated from GreenFeed Measures at the Test Station

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Abstract

The aim of this study was to estimate heritability of methane (CH_4) emissions for young Norwegian Red bulls. Measures of CH_4 from a GreenFeed (GF) unit at Geno's test station for young bull was available. Bull calves arrive the test station 3-4 months old and are grouped in pens with on average 10 calves. Methane is measured the last 1-2 months before they leave the test station, at 11-12 months age. On average each bull had 40 days with CH_4 data. We used data recorded from September 2020 to April 2023 and the final dataset had records from a total of 76 094 GF visits from 212 bulls. The mean (standard deviation) was 218 (50) gram CH_4 per bull per day. The traits analyzed were gram CH_4 per day, measured per GF visit or computed as the average of the bull's individual visits each day. A linear animal repeatability model with fixed effects of age and group test-day, and random effects of animal and permanent environment were used to estimate variance components. The estimated heritability (standard error) was 0.24 (0.10) for CH_4 per visit and 0.56 (0.20) for CH_4 mean per day, with repeatability of 0.32 and 0.71, respectively. The predicted breeding values for bulls with phenotype varied from -37 to +60, with standard errors ranging from 12 to 15. Results so far are promising, the genetic variation for CH_4 in the Norwegian Red breed indicates that breeding for lower methane emission is feasible.

Key words: breeding values, methane, genetic evaluation, young stock, bulls

Introduction

One way of reducing environmental footprint from dairy production is by breeding. Selection for lower methane (CH_4) emission is possible (Lassen and Difford, 2020). Most of the research on CH_4 emissions in dairy cattle has been on lactating cows, and so far few genetic studies of CH_4 emissions in young stock and bulls are published. Geno, the breeding organization for Norwegian Red, has installed a GreenFeed (GF) unit at their test station for young bulls. Measures of CH_4 from this test station is now available and the aim of this study was to estimate heritability of CH_4 emissions for young Norwegian Red bulls.

Materials and Methods

Measures of CH_4 from the GF unit at Geno's test station for young bull was available. Each year the best 8 000 bull calves in the Norwegian Red population are genotyped, among these around 150 are selected and brought to the test station, and 50-60 of them will be recruited to be AI bulls. Bull calves arrive the test station 3-4 months old and are grouped in pens with on average 10 calves. Methane is measured the last 1-2 months before they leave the test station, at 11-12 months age. On average each bull had 40 days with CH_4 data. We used data recorded from September 2020 to April 2023. The number of GF visits per bull varied from 1 to 798, with an average of 356, and the number of recorded GF visits per test-day varied from 1 to 155, with mean 77. For the genetic analyses we kept records from test-day with at least 10 records, and bulls with at least 10 GF visits. The final dataset had records from a total of 76 094 GF visits from 212 bulls. The traits analyzed were gram CH_4 per day, measured per GF visit or computed as the average of the bull's individual visits each day.

Model

Variance components were estimated with DMUAI (Madsen and Jensen, 2013) using a linear animal repeatability model with fixed effects of age and group-test-day, and random effects of animal and permanent environment. Age was the bulls age in weeks at the day of phenotyping, grouped in 23 classes where <40 weeks is the first and >60 weeks is the last class. Group test-day had 964 levels. The pedigree of the bulls was traced back 4 generations and the pedigree file included 4 233 animals.

Correlations between breeding values

To give an indication of strength and direction of genetic correlations between CH_4 and other traits, correlations between predicted breeding values were calculated for the 212 bulls with a CH_4 phenotype. Correlations between the bulls EBV for CH_4 and their indexes for all other traits included in the routine genetic evaluations of Norwegian Red were calculated. Indexes for all traits from June 2023 were provided by Geno.

Results & Discussion

The distribution of CH_4 measures are given in Figure 1. The mean (standard deviation (SD)) of CH_4 production was 218 (50) gram per bull per day. In comparison, the average for Norwegian Red dairy cows in lactations was 420 gram per day (Wethal et al., 2022). The phenotypic level of CH_4 for our young bulls was very similar to reports by Callegaro et al. (2022) who analyzed methane data from GF on 111 young Italian Holstein bulls. The average (SD) in their study was 220 (41) gram CH_4 per day.

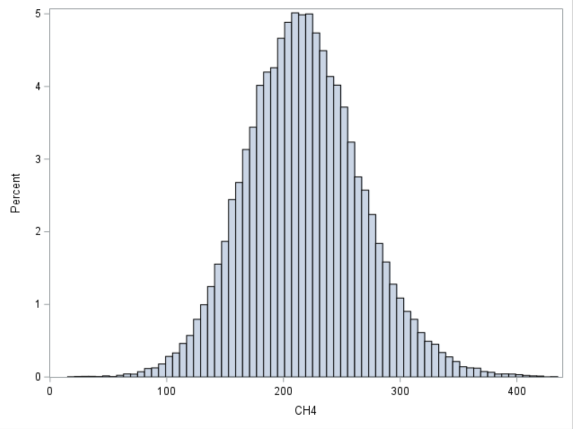

Figure 1. Distribution of phenotypic records of methane (CH_4) emissions for young Norwegian Red bulls, measured as gram per day from GreenFeed

Figure 2 shows the solutions for fixed effect of age and indicate an almost linear increase in CH_4 with increasing age. Solutions for fixed effect of group test-day in Figure 3 illustrates variation over time, seasonal variations, and group effects. The bulls stay in the pen with the GF the last 1-2 months before they leave the station. There may therefore be a large shift in mean CH_4 level from one test-day to the next, when one group leaves the station, and a new group of younger bulls start recording in the GF pen.

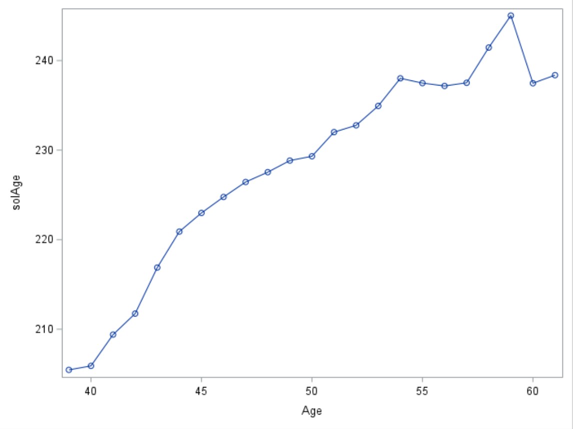

Figure 2. Fixed effect solutions for effect of age on methane emission in young bulls

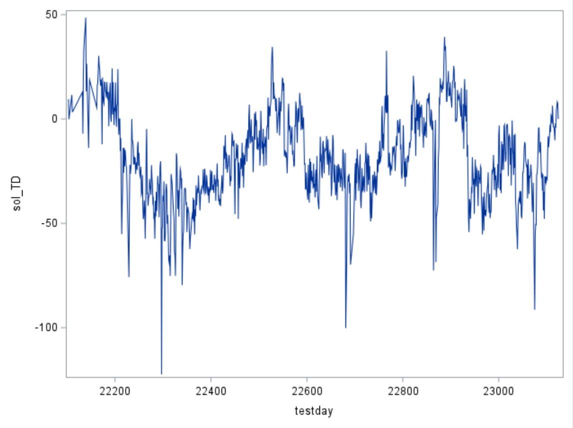

Figure 3. Fixed effect solutions for effect of group-test-day on methane emission in young bulls

Estimated variance components are given in Table 1. The corresponding heritability (standard error (se)) was 0.24 (0.10) for CH_4 per visit and 0.56 (0.20) for CH_4 mean per day, with repeatability of 0.32 and 0.71, respectively.

Table 1. Estimated permanent environment (σ^2_{pe}), animal (σ^2_a), and residual (σ^2_e) variance with standard error (se), and the corresponding heritability and repeatability for methane (CH_4), gram per day, for young Norwegian Red bulls measured per visit or computed as the average of the bull's individual visits each day.

	CH_4 per visit		CH_4 mean per day	
	Estimate	se	Estimate	se
σ^2_{pe}	153	194	141	188
σ^2_a	532	216	538	211
σ^2_e	1479	8	278	5
heritability	0.24	0.10	0.56	0.20
repeatability	0.32	0.02	0.71	0.02

The results for CH_4 per visit agree well with Wøyen Hamfjord (2022) who did the first genetic analyses on a subset of these data. Our heritability estimates correspond well with other published results, although they are not directly comparable due to differences in phenotyping equipment as well as breed. Donoghue et al. (2016) estimated heritability of CH_4 based on large scale methane measures from respiration chambers. Their study included data on 1 048 young bulls and heifers of Angus cattle in Australia. Methane production rate was measured in respiration chambers for 48 hours. Estimated heritability (se) was 0.27 (0.07). Johansen et al. (2022) estimated heritability (se) of methane concentration for beef x dairy crossbred (Belgian Blue and Holstein) slaughter calves of 0.44 (0.08) and 0.33 (0.06). They measured methane in feed boxes using an infrared gas sensor.

Figure 4 shows the distribution of EBVs for CH_4 emission for bulls with own phenotype. The EBV for CH_4 varied from - 37 to + 60, with SE ranging from 12 to 15. Here the EBVs were not standardized, the unit is gram CH_4 per day. Although the SE were relatively large this illustrates that there are significant genetic differences between bulls and potential for selection for reduced CH_4 emissions.

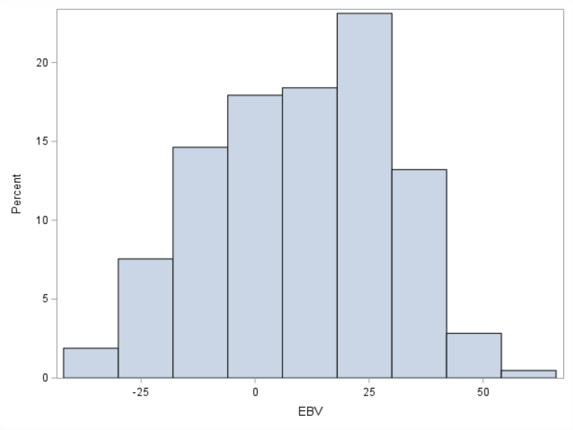

Figure 4. Distribution of predicted breeding values (EBVs) for methane for 212 young Norwegian Red bulls with phenotype. The unit of EBV is gram methane per day

Currently we do not have enough data for estimation of genetic correlations between CH_4 emissions in young bulls and other traits. Correlation between EBVs were therefore used to give an indication of strength and direction of genetic correlations between traits. The correlations between EBV for CH_4 and the bull's official indexes for all traits in routine genetic evaluation varied between -0.36 and 0.34. Many of the correlations, including the correlation to the total merit index, were close to zero. The traits with the strongest correlations to EBV (not standardized) for CH_4 are given in Table 2. The highest positive correlations were found to traits related to body size, while high genetic merit for direct calving traits were associated with lower EBV for CH_4.

Table 2. Correlations between predicted breeding values for methane (CH_4) and indexes for other traits from the routine genetic evaluations of Norwegian Red. The traits with the strongest positive and negative correlations with CH_4, respectively, are shown.

		Correlation to CH_4
Strongest positive	Carcass weight	0.34
	Angularity[1]	0.29
	Body depth[1]	0.27
	Body total score[1]	0.26
	Stature[1]	0.25
Strongest negative	Calf size, direct[2]	-0.36
	Calving ease, direct	-0.34
	Stillbirth, direct	-0.25
	Hock quality[1]	-0.23
	Bone structure[1,3]	-0.22

[1] Trait not included in the total merit index

[2] Calf size: High score is small calf

[3] Bone structure: High score is very fine and thin bones low score for coarse bones (broad and thick)

The correlation between EBV for CH_4 and the total merit index was not significantly different from zero, suggesting that no correlated selection response should be expected. No indication of indirect selection for, or against, CH_4 emission in young bulls with the current breeding goal is further illustrated in Figure 5 where the bulls EBV for CH_4 was sorted from lowest to highest and those selected as AI bulls marked with red color.

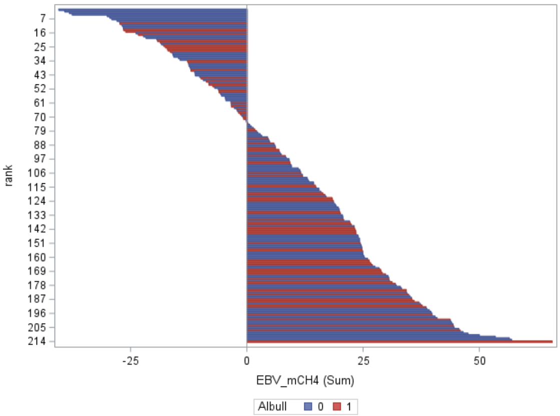

Figure 5. Predicted breeding values for methane for 212 young Norwegian Red bulls with methane phenotype, sorted from lowest to highest. Color indicates selected (red) or not (blue) as AI bull

This initial analysis of CH_4 emission in young Norwegian Red bulls shows that there is substantial genetic potential for reducing CH_4 emissions by breeding, also in young stock. It should be noted that estimates are based on few animals, standard errors of variance components are therefore large, and results should be interpreted with caution.

We need more knowledge on associations between CH_4 emissions and other important traits. In future research we will also examine whether CH_4 emission is the same trait genetically in young bulls and in lactating dairy cows.

Acknowledgements

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References

Callegaro, S., Niero, G., Penasa, M., Finocchiaro, R., Invernizzi, G. and Cassandro, M. 2022. Greenhouse gas emissions, dry matter intake and feed efficiency of young Holstein bulls. *Ital. J. Anim. Sci.* 21:1, 870-877, https://www.tandfonline.com/doi/full/10.1080/1828051X.2022.2071178

Donoghue, K.A., Bird-Gardiner, T., Arthur, P.F., Herd, R.M. and Hegarty, R.F. 2016. Genetic and phenotypic variance and covariance components for methane emission and postweaning traits in Angus cattle. *J.Anim.Sci* 94, 1438–1445. https://doi.org/10.2527/jas.2015-0065

Johansen, K., Kargo, M., Bjerring, M., Løvendahl, P. and Buitenhuis, A.J. 2022. Phenotypic differences and genetic parameters for methane concentration in BeefxDairy crossbred slaughter calves. Proceedings of the 12th WCGALP.

https://doi.org/10.3920/978-90-8686-940-_26

Lassen, J. and Difford, G.F. 2020. Review: Genetic and genomic selection as a methane mitigation strategy in dairy cattle. *Anim*, 14:S3,473–s483. https://doi.org/10.1017/S1751731120001561

Madsen, P. and Jensen, J. 2013. A user's guide to DMU. A package for analysing multivariate mixed models. Version 6, release 5.2. Center for Quantitative Genetics and Genomics, University of Aarhus, Tjele, Denmark. http://dmu.agrsci.dk/

Wethal, K.B., Difford, G.F., Winnberg, K., Norberg, E. and Heringstad, B. 2022. Heritability of methane emission in Norwegian Red cows based on measures from GreenFeed in commercial herds. Proceedings, 12th WCGALP. https://doi.org/10.3920/978-90-8686-940-4_32

Wøyen Hamfjord, I. 2022. Arvbarhet og avlsverdier for metanproduksjon hos unge okser av Norsk Rødt Fe (NRF), med målinger i GreenFeed. Master thesis, Norwegian University of Life Sciences. https://hdl.handle.net/11250/3038215