

Heritability of methane emission in Norwegian Red cows based on measures from GreenFeed in commercial herds

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Abstract

The aim of this study was to estimate heritability of methane emissions for Norwegian Red dairy cows. Methane measured by GreenFeed was available from 12 commercial herds. Data was collected from February to October 2021 and the final dataset had a total of 62,057 records from 252 cows. Methane emission from individual visits was analysed. The average methane emission was 441 gram per day. A linear animal repeatability model with fixed effects of parity and lactation week, and random effects of herd-testday, animal, and permanent environment was used to estimate variance components. The estimated heritability was 0.22 and repeatability 0.36.

Introduction

International agreements and commitments to reduce greenhouse-gas emissions imply that all sectors have to contribute to meet climate targets. One way to reduce the environmental footprint of dairy production is by breeding for reduced methane (CH_4) emissions. Implementing reduced CH_4 emission in the breeding program would have a direct and long-term environmental impact. Previous studies have reported genetic variation for methane emissions in Holstein dairy cattle (Lassen and Difford, 2020). In order to assess the genetic potential for reduced CH_4 emission in the Norwegian Red population, Geno breeding and A.I. association (www.norwegianred.com) implemented collection of measures of cows CH_4 emissions in commercial dairy herds. So far most genetic research on methane emission has been conducted in small and tightly controlled research herds which cannot encompass the full genetic variation of the population and tend to have multiple dietary treatments which complicate genetic evaluations (Tempelman *et al.*, 2015). For selection to be viable and genetic parameters to be relevant, large scale phenotype collection is needed in the commercial environments in which animals are expected to perform. To this end, Geno has installed GreenFeed (www.c-lockinc.com) equipment for CH_4 recording for individual cows at commercial dairy farms in the mid- and south-eastern part of Norway. The aim of this first initial genetic analyses was to estimate heritability of methane emissions for Norwegian Red dairy cows.

Material & methods

The GreenFeed unit measure gas fluxes of CH_4 (and other gases) from individual cows. The cows visit the unit voluntary, where they are offered a small amount of concentrate to entice visits. Each cow may have multiple daily visits, but maximum five feedings per day. Each visit results in an estimate of daily CH_4 emission. Only visits of at least 2 minutes with “good data”, defined based on head position or proximity inside the crib, were defined as reliable and retained for further analysis.

Methane emission data was collected from February to October 2021 in 12 herds with loose housing and automatic milking systems (Lely or DeLaval). Additional information on the cows were from the Norwegian Dairy Herd Recording System. Norwegian Red cows that had at least 5 GreenFeed records were included, and data from the period from calving to 350 days in milk were used. The final dataset had a total of 62,057 records (1 record per visit) from 252 cows. The trait analyzed was daily CH₄ emission, gram per day (Each visit results in an estimate of daily CH₄ emission).

A linear animal repeatability model was used to estimate variance components using the DMU software (Madsen and Jensen, 2012). The model included fixed effects of parity (1, 2, 3, and >3) and lactation week (from 1 to 50) and random effects of herd-testday, animal, and permanent environment. The pedigree of cows with data was traced as far back as 6 generations and included a total of 3791 animals.

Results

The average (standard deviation) methane emission was 441 (114) gram per day. The distribution of the phenotypic records followed an approximate normal distribution (Figure 1).

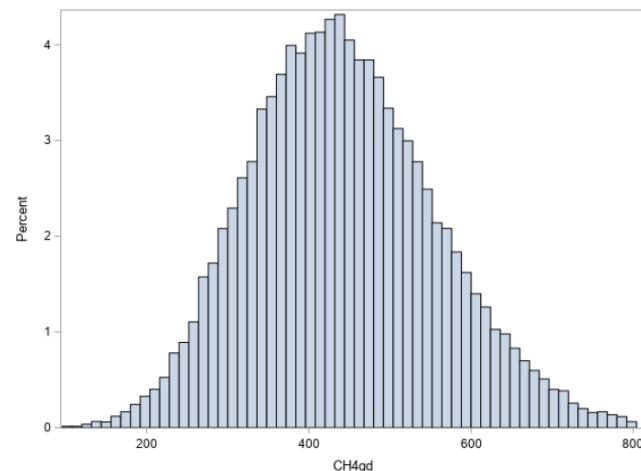


Figure 1. Distribution of phenotypic records of methane emission (CH4gd) for Norwegian Red cows (1 record per visit at the GreenFeed unit, each visit gives an estimate of daily methane emission)

Methane emissions vary with stage of lactation. Figure 2 shows the solutions for fixed effect of lactation week and illustrates how CH₄ emissions by lactation stage follows the same shape as a lactation curve for milk yield.

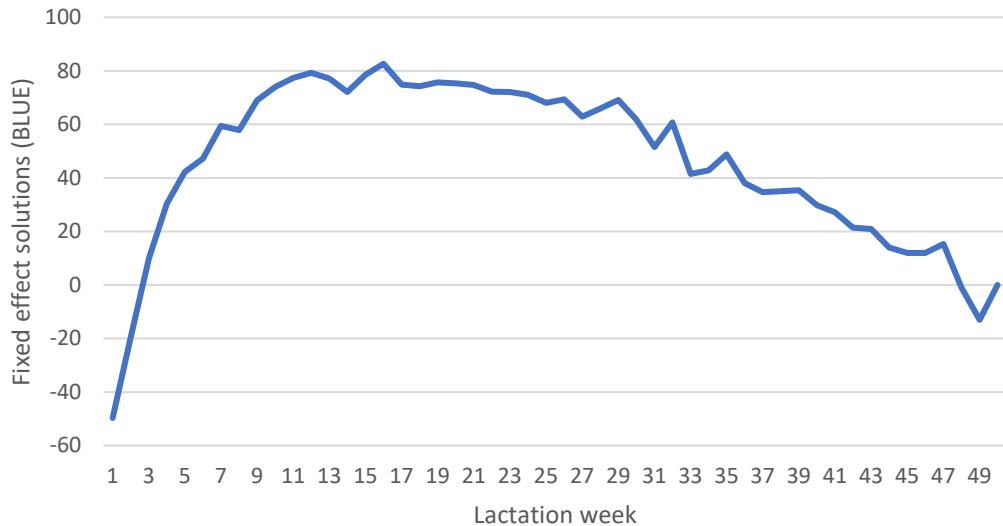


Figure 2. Fixed effect solutions for lactation week, effect on daily methane emission (gram per day) (standard errors were between 7 and 9)

The estimated variance components are given in Table 1. The corresponding heritability of CH₄ emission in Norwegian Red was 0.22 and repeatability 0.36.

Table 1. Estimated variance components with standard error (SE) for daily methane emission.

Variance component	Estimate	SE
Herd-testday	1024.5	47.4
Additive genetic	2693.7	1002.1
Permanent environment	1670.9	836.9
Residual	6809.9	39.3

Discussion

Due to challenges related to large scale recording of CH₄ there are so far relatively few estimates of genetic parameters for direct CH₄ emission in dairy cows. This is, as far as we know, the first heritability estimate based on data from GreenFeed in commercial herds, and the first for the Norwegian Red breed. Our heritability estimate agrees well with previous published results, although not directly comparable due to differences in breed and phenotyping method/equipment. A review by Lassen and Difford (2020) showed that heritability estimates of CH₄ emissions measured by “sniffer” in Holsteins varied from 0.11 to 0.45, with most estimates from 0.21 to 0.27. Our heritability estimate is larger than previous estimates of 0.15 and 0.11 for daily CH₄ emission in 100 Finnish Ayrshires and 409 grazing Italian Holsteins, respectively, both recorded using GreenFeeds in research herds (Wallace *et al.*, 2019). However, it is lower than 0.31 ± 0.15 reported for weekly averaged CH₄ production in 305 Holstein cows from research herds in Canada and Switzerland in a joint evaluation (Manzanilla Pech *et al.*, 2021).

This initial analysis of CH₄ emissions in Norwegian Red cows shows that there is substantial genetic potential for reducing CH₄ emissions from dairy cows by breeding. With GreenFeed units installed in collaborating commercial herds and a system for data collection in place, we will soon have access to larger datasets for further genetic studies of CH₄ emissions. We will estimate genetic correlations between methane production and important traits in the breeding goal. Zetouni *et al.* (2018) found low genetic correlations between methane production and health, fertility and body type traits in Danish Holstein. However, they concluded that further studies based on larger dataset are needed to understand these relationships. Increased knowledge of the genetic relationship between traits related to climate, traditional efficiency traits, including feed efficiency, but also animal welfare and health traits is needed before reduced methane emission can be implemented in Norwegian Reds' future breeding goal.

Acknowledgements

We want to thank the dairy farmers hosting the GreenFeed units and providing data, Geno and Tine for access to data, and the Norwegian Research Council for funding of research project (project 309451).

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