Towards breeding for lower enteric methane emissions of dairy cows in the Netherlands

A.E. van Breukelen[1], M.N. Aldridge[2], Y. de Haas[3], C. Schrooten[4], J.M.L Heck[5], M.H.P.W. Visker[5] and R.F. Veerkamp[1]

[1]Wageningen University and Research, Animal Breeding and Genomics, 6700AH Wageningen, the Netherlands
[2]Animal Genetics and Breeding Unit, A joint venture of NSW Department of Primary Industries and University of New England, University of New England, Armidale, NSW 2351 Australia
[3]Animal Health and Welfare Group, Wageningen University and Research, 6700AH Wageningen, the Netherlands
[4]Cooperative CRV u.a., 6842 BD Arnhem, the Netherlands
[5]FrieslandCampina, Stationsplein 4, 3818 LE Amersfoort, The Netherlands / PO Box 1551, 3800 BN Amersfoort, the Netherlands
Corresponding Author: anouk.vanbreukelen@wur.nl

Abstract

Various strategies have been proposed to reduce enteric methane (CH_4) emissions from ruminants, focusing on areas such as management, feeding strategies, feed additives, vaccination, and animal breeding. Among these, animal breeding currently shows the largest long-term potential, due to its low implementation costs, and permanent and cumulative effect. Nonetheless, implementing CH_4 mitigation in breeding programs is still in its infancy. An important limitation to practical application has been the lack of phenotyping of CH_4 emissions on individual cows, to estimate sufficiently reliable genetic parameters, which are required for breeding decisions. However, recent innovations have accelerated the collection of CH_4 phenotypes. We describe the outcomes of a four year project in the Netherlands, that aimed to record CH_4 emissions on 100 dairy farms, to be used in genetic parameter estimations. This dataset will be the basis for future national breeding value estimations for enteric CH_4 of Holstein dairy cows, which will be implemented by the cooperative cattle improvement organization CRV. In the project, enteric CH_4 emissions were measured by 'sniffers' that sample air from the feed bin of milking robots. The latest dataset included 110,188 weekly mean CH_4 concentration (ppm) records on 7,749 cows from 72 farms, but data recording is ongoing. Several analyses have been performed already, with the following objectives:

1. Define a CH_4 trait from the raw concentration measurements.
2. Estimate heritabilities and repeatabilities.
3 Investigate different recording schemes.
4. Investigate the relationships between CH_4 and other breeding goal traits.

To date, the research output of the project showed that the phenotype for weekly mean CH_4 concentration has a moderate heritability of 0.17 ± 0.04 and a repeatability of 0.56 ± 0.03. As the sniffers only measure concentrations, and not the total grams of CH_4 emitted by breath, genetic correlations were estimated between the weekly mean CH_4 concentration phenotype and a weekly mean CH_4 production (g/day) phenotype. The latter was recorded by GreenFeed units on 797 cows from 16 farms (4 overlapping with sniffers). The genetic correlation was 0.76 ± 0.15, indicating that selection for lower concentrations will result in a reduction of total CH_4 production output in g/day.

Furthermore, with the novel dataset we confirmed that the genetic variance changed over a lactation. This has implications for recording schemes, and we showed that short recording of CH_4 during the first or last weeks of recording can result in lower genetic gains than predicted from the reliability, when modelled without using random genetic and permanent environmental regressions over the lactation. In the last stage of the current project, genetic relationships among CH_4 concentration, DMI, bodyweight, and milk yield traits were estimated, which are required to set up the selection index that includes CH_4 mitigation. The results show low genetic correlations between CH_4 and: dry matter intake (0.06 ± 0.10), body weight (-0.04 ± 0.10), and milk yield (-0.04 ± 0.08). The developed dataset and models, are currently used to set up national breeding value estimation for CH_4 emissions of dairy cows in the Netherlands. Furthermore, the dataset will be used in additional research projects in the coming years, that aim to

1. Investigate the relationship with the microbiome.
2. investigate the impact of selecting using the developed phenotype(s).
3. Investigate incentives for farmers to use the CH_4 breeding values.
4. Proof the impact of change in breeding values at farm and national level.

This comprehensive approach not only improves our understanding of breeding for lower enteric CH_4 emissions, but also integrates this knowledge into practical breeding strategies for sustainable dairy farming.

Keywords: methane emissions, sniffers, dairy cows, quantitative genetics, animal breeding.
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Introduction

In the Netherlands, a pledge has been made to reduce greenhouse gas emissions by 55% in 2030 compared to the year 1990, and to be carbon neutral by 2050 (Communication from the Directorate-General for Climate and Energy, 2022). A large contributor to national emissions is agriculture, from which a part of the emissions stem from ruminants, such as dairy cows (Van Bruggen *et al*., 2023). Dairy cows produce CH_4 during enteric fermentation of feed in the rumen, which is released through breath and belching. That animal breeding can play a role in reducing the environmental impact of dairy farming is becoming increasingly recognized. Here, we describe the outcomes of a four year project in the Netherlands, that aimed to record CH_4 emissions on 100 dairy farms, to be used in genetic parameter estimations. This dataset will be the basis for future national breeding value estimations for enteric CH_4 of Holstein dairy cows, which will be implemented by the cooperative cattle improvement organization CRV.

To enable selective breeding, phenotypes for CH_4 were recorded with ‘sniffers’. Sniffers are a comparatively cheap method to record large numbers of cattle, that are increasingly used to phenotype cows for genetic improvement (Garnsworthy *et al*., 2019; Madsen *et al*., 2010). Nonetheless, because CH_4 recorded with sniffers is a relatively new trait, many questions remain on how to apply the recorded emissions in genetic evaluations. For example, the measurements are faced with inaccuracies, which should be accounted for by taking repeated measurements and appropriate modelling (Bovenhuis *et al*., 2018; Wu *et al*., 2018), and the relationships with other economically important breeding goal traits are still unclear (Hossein-Zadeh, 2022).

In our four year project, we have collected over 100,000 weekly mean CH_4 concentration (ppm) measurements on 7,749 cows from 72 farms. Here, we summarise the genetic parameters that were estimated from this dataset, including genetic correlation estimates with other breeding goal traits. This demonstrates the progress made towards accomplishing our objective, which is to provide meaningful breeding values for methane mitigation in the Netherlands.

Material and methods

The latest dataset included 110,188 weekly mean CH_4 concentrations (CH_4c) records from 7,749 cows from commercial dairy 72 farms in the Netherlands. Data were collected between 2019 and 2023, and previously described in (van Breukelen *et al*., 2024). In short, non-dispersive infrared sensors, called sniffers (WD-WUR v1.0 and v2.0, manufactured by Carltech BV), were installed with a tube leading into the feed bin of the milking robot (AMS), and continuously recorded CH_4 (0 to 2,000 ppm) and CO_2 (0 to 10,000 ppm) concentrations. The recorded data was filtered to exclude biologically improbable records, and then matched with AMS visit information to determine the cows' IDs. Thereafter, the data was averaged per AMS visit, including records from the first up to the fifth minute of milking..

Genetic analyses

Various phenotypes defined from the sniffer concentration measurements were analysed, including visit, daily, and weekly means, on: the mean, median, log, and CH_4/CO_2 ratio. From the data, genetic parameters were estimated using univariate fixed repeatability models and a random regression repeatability model with ASReml 4.2 (Gilmour *et al*., 2015), and genetic correlations were estimated using pairwise bivariate models. All cows used for the genetic analyses had pedigree information, and most cows were genotyped. Several genetic analyses were performed, with the following objectives: 1) estimate heritabilities and repeatabilities (from various CH_4 traits), 2) investigate different recording schemes, including changes in genetic parameters over a lactation, and 3) investigate the phenotypic and genetic relationships between CH_4 and other breeding goal traits.

The estimated heritabilities and repeatabilities were used to calculate the reliability of breeding values, which was used to determine the number of daughter records needed to reach breeding value publication thresholds. For details on the datasets and methods used see van Breukelen *et al*. (2022) and van Breukelen *et al*. (2024).

Genetic correlations with GreenFeed recorded cows

To determine the applicability of CH_4c as an indicator for the reduction of total CH_4 emissions in grams/cow/ day, genetic correlations were estimated with CH_4 measurements from the more accurate GreenFeed, as GreenFeed units are considered the gold standard for on-farm recording of individual cow CH_4. Methane was recorded by GreenFeed units at 16 farms (of which four also had sniffer recording), and the analysed dataset included GreenFeed measurements in 822 cows [of which 184 cows also had sniffer records, for details see van Breukelen *et al*. (2023)].

Genetic correlations with other breeding goal traits

In addition, genetic correlations were estimated for first parity cows between CH_4c, and: milk yield (MY), protein yield (PY), fat yield (FY), protein percentage (P%), fat percentage (F%), body weight (BW), and dry matter intake (DMI). The number of weekly records and cows for each trait were: 8,891 cows with 179,469 records for MY, 8,889 cows with 139,295 records for PY, 8,889 cows with 139,328 records for FY, 5,919 cows with 119,523 records for BW, and 4,998 cows with 87,306 records for DMI. The traits P% and F% were calculated as PY or FY, respectively, divided by MY. The genetic correlations were estimated using pairwise bivariate models, including fixed effects for: an interaction between farm, year and week of measurement for the CH_4 and CO_2 traits only, an interaction between farm and experimental treatment for all traits except CH_4 and CO_2, a second order Legendre polynomial on age at calving in days, a third order Legendre polynomial on DIM, and an interaction between the second breed with a second order Legendre polynomial on the fraction of the second breed, and a random genetic and permanent environmental effect. The residual and permanent environmental covariances were fixed to zero for the runs including DMI and a CH_4 or CO_2 trait, because of the small number of cows with records on both DMI and a greenhouse gas trait.

Results and discussion

Genetic parameter estimates

The research output of the project showed that the phenotype for weekly mean CH_4 concentration has a moderate heritability of 0.17 ± 0.04 and a repeatability of 0.56 ± 0.03. As the sniffers only measure concentrations, and not the total grams of CH_4 emitted by breath, genetic correlations were estimated between the weekly mean CH_4 concentration phenotype and a weekly mean CH_4 production (g/day) phenotype. The latter was recorded by GreenFeed units on 797 cows from 16 farms (four overlapping with sniffers). The genetic correlation was 0.76 ± 0.15, indicating that selection for lower concentrations will result in a reduction of total CH_4 production output in g/day. Other phenotypes that were defined from sniffer measurements (i.e. median concentrations, log transformed concentrations, and traits defined from the maximum concentrations or peaks in concentrations) had high genetic correlations with mean CH_4 concentrations ($\geq$0.78), apart from the genetic correlations with the CH_4/CO_2 trait, which was negative.

Recording schemes

Furthermore, a comparison was made between genetic parameter estimates for CH_4 emission from a fixed regression repeatability model and a random regression (RR) model. The RR model, allowed for varying genetic variances and covariances over a lactation. The results showed that the heritability was highest mid lactation (on average 0.17 ± 0.04), and genetic correlations between lactation stages were high (0.34 ± 0.36 to 0.91 ± 0.08). Permanent environmental correlations deviated greatly over a lactation and ranged between -0.73 ± 0.08 and 1.00 ± <0.01, which highlights that it is most appropriate to model CH_4c with a RR model including a random permanent environmental effect. With a large number of full-lactation daughter CH_4 records for each bull, the reliability was similar for the fixed and RR models. However, when data were only available for shorter recording periods at the beginning and end of lactation, using the fixed regression model led to up to a 28% reduction in reliability for bulls. Assuming the fixed model when the true (co)variance structure is reflected by the RR model, more than twice as long recording from the start of lactation was required to achieve maximum reliability for a bull. Therefore, applying an overly simplistic model could lead to insufficient recording and lower than predicted genetic gains based on the estimated reliability. If all cows would only be recorded for a small period of time, for example three weeks, it is preferred to record cows in mid lactation as this would yield the highest reliabilities. In addition, to reach the Dutch breeding value publication threshold of 50% for sires, it is recommended to record at least 25 visits or 5 weeks, from 10 daughters per sire.

Genetic correlations with breeding goal traits

In the last stage of the current project, genetic relationships among CH_4c and important breeding goal traits were estimated. Results show low genetic correlations between CH_4c and: MY (-0.04 ± 0.08), PY (<0.01 ± 0.08), FY (0.12 ± 0.08), P% (0.10 ± 0.09), F% (0.21 ± 0.08), BW (-0.04 ± 0.10), and DMI (0.06 ± 0.10). This indicates that it is possible to breed for reduced CH_4 concentrations, while continuing to improve, for example, milk production or fat yield.

Continuation

The results coming from this project, will be used to set up national breeding value estimation for CH4 emissions of dairy cows in the Netherlands, from which first breeding values are expected in 2025. Furthermore, the dataset will be used in additional research projects in the coming years, that aim to 1

1. Investigate the relationship with the microbiome.
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4. Proof the impact of change in breeding values at farm and national level.

Conclusion

Animal breeding is an effective approach to reduce agricultural emissions, that can contribute to reaching greenhouse gas targets. To phenotype large numbers of cows on commercial dairy farms for breeding programs, sniffers provide a cost-effective method of measuring gas concentrations. In our four year project, we have shown that CH_4 concentration traits have a moderate heritability, have a favourable high genetic correlation (0.76) with CH_4 production recorded by Greenfeed units, and the CH_4 concentrations measured with sniffers have low genetic correlations with milk production traits, BW and DMI. The results coming from the project not only improve our understanding of breeding for lower enteric CH_4 emissions, but are also used to integrate this knowledge into practical breeding strategies for sustainable dairy farming.

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