Data collection and preparation for genetic analysis of methane emissions in Danish dairy cattle

T.M. Villumsen[1], P. Løvendahl[1], V. Milkevych[1] R. Krogh[1], H. Schneider[1], M. Bjerring[2] and G. Sahana[1]

[1]Center for Quantitative Genetics and Genomics, Faculty of Science and Technology,
Aarhus University, C. F Møllers Allé 3, DK-8000 Aarhus C, Denmark
[2]Department of Animal and Veterinary Sciences at Aarhus University, Blichers Allé 20,
8830 Tjele, Denmark
Corresponding Author: tmv@qgg.au.dk

Abstract

In Denmark, a carbon emission tax in the agricultural sector will be implemented to meet the 2030 greenhouse gas reduction target (Skm.dk, 2024). Enteric methane (CH_4) from cow digestion is a significant contributor, leading to interest in genetic selection for low CH_4 emitting dairy cows. Developing a genetic model for methane emission in dairy cattle requires a comprehensive database of individual CH_4 measures from many cows. This requires affordable, farm-installable equipment with high measurement capacity. Sniffers based on the Guardian NG CH_4 and CO_2 sensors, measuring gas concentrations in robotic milking systems (AMS), are used for this purpose in Denmark.

Currently, (September 2024) we have collected methane records from 15.000 dairy cows in 40 herds based on records from 38 sniffers with a two-channel multiplex setup. Installation and maintenance require ongoing technical support and daily data monitoring. Due to the high volume of daily data, an automated pipeline is needed to monitor, clean, and ensure high-quality data for CH_4 phenotypes. Equipment errors are detected based on data streams from AMS and sniffer, and measurements are matched to individual cows, using a CO_2 concentration-based filter which is also used to correct for potential time drift.

To filter environmental noise, data is split into baseline readings, based on empty periods in AMS and cow data where a cow is milked in the AMS. Both baseline readings and cow data are pruned. Reliable gas concentrations during milking are adjusted for baseline levels, and a head lifting criteria is added to discard records where a cow most likely does not have the head in the feed bin. Phenotypes such as CH_4 concentration and CH_4/CO_2 ratio are calculated. Additional information, such as milk yield, can be used to compute other methane traits. These phenotypes facilitate the development of genetic models for reducing methane emissions in dairy cattle.

Keywords: Methane emission, dairy cows, genetic selection, sniffer, data pipeline.
Presented at the ICAR Anual Conference 2024 in Bled at the Session 11: Methane Emission-Free Communications: Genetics, Environmental, and Life Cycle Assessment Studies

Introduction

In Denmark a carbon emission tax for the agricultural sector increasing toward € 100 per ton CO2e by 2035 has been agreed on by the Danish Government and key stakeholders to meet the Denmark's 2030 climate goals. Methane (CH_4) released from dairy cows' enteric digestion constitute a substantial portion of greenhouse gas emissions (Beach *et al*., 2015, Charmley *et al*., 2016). There are many methane mitigation options such as production intensification, dietary manipulation and selection of low CH_4 producing animals (Beauchemin *et al*. 2022). There is a major focus on feed additives aimed at reducing enteric methane (e.g. Honan *et al*, 2022, Majgaard *et al*., 2024). Also, genetic selection of cows with low CH_4 emission pr produced unit of milk and meat has been investigated (for review see Lassen and Difford, 2020).

To facilitate the development of a genetic model and conduct genetic evaluations for methane emission in dairy cattle it is necessary to have access to large-scale recording of methane emissions, to establish a comprehensive database with individual CH_4 and CO_2 measures. Sniffers, installed in automatized milking systems (AMS) at private farms have a high capacity to measure CH_4 and CO_2 concentrations in the exhaled air continuously during milking. The sniffer is a relatively cost-efficient system to measure gas emissions, that can easily be upscaled. Although sniffer data are valuable for the development of genetic models, they often present challenges in its raw form and require substantial processing and filtering. Currently, sniffers are not integrated with AMS software synchronization with cow-ID from milking system and potential synchronization of time is required. In addition, early detection of equipment errors and filtering for environmental noise is essential. The following text will shortly describe how we measure methane with the sniffer in a Danish setup, our current data, and cleaning of data used to form methane phenotypes

The Danish sniffer

The sniffer units consist of a CH_4 sensor (Guardian NG, Edinburgh Instruments, UK) and a CO_2 sensor (Gascard, Edinburgh Instruments, UK). Air and cows' breath is led into the sensors from the feed-bins in the AMS through a de-humidifier tube (Nafion, https://www.permapure.com/environmental-scientific/products/gas-sample-dryers/md-gas-dryers/) using the pump in the Guardian CH4 unit. Concentrations of CH_4 and CO_2 are recorded in volume percent units. As dust may block the inlet pipe a "sneezer" system is retrofitted, so as to clean the inlet filter (Festo, Pneumatic silencer, Festo, UC-QS-6H, 6mm)) by back-flushing part of the inlet pipe with compressed air from the AMS. The sneezer valve (Pneumatic control valve, SMC, SYJA712-01F) is triggered by the "exit gate" pressure so that the filter is cleaned for a few seconds when the cow exits the AMS. The instrument runs continuously giving one record of CH_4 and CO_2 concentrations per second. The sniffers are equipped with a two-channel multiplex setup that makes it possible to switch between measurements in two AMS with a pre-defined intervall.

Tabe 1. Number of cows with individual methane records in the Danish methane database.

Breed	Cows
Holstein	~8,000
Jersen	~3,000
Red	~2,000
Crossbreds	~1,000

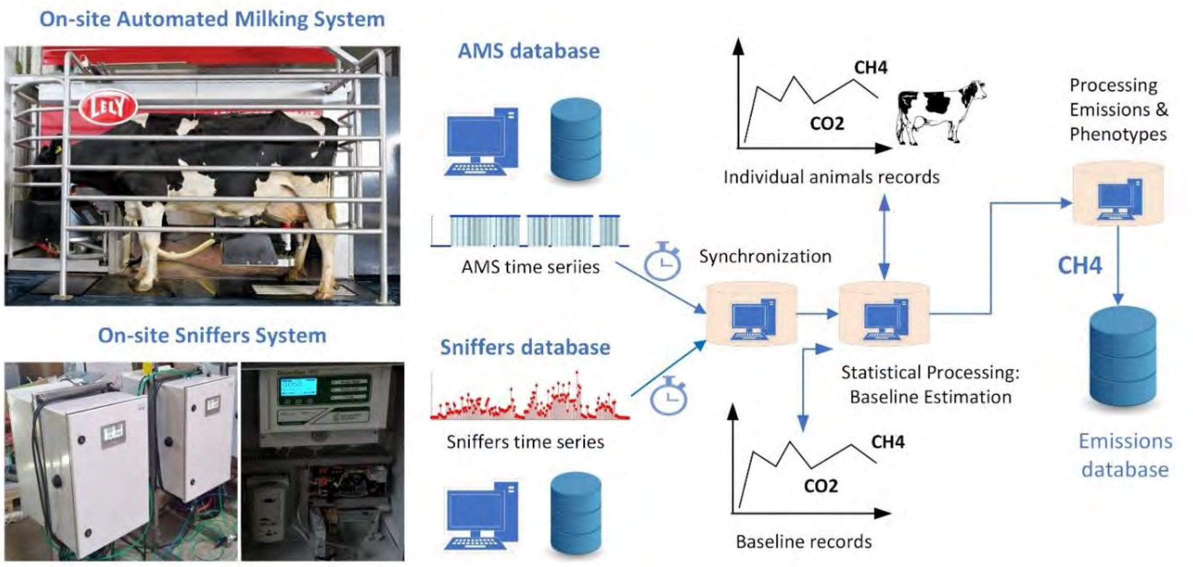

Figure 1. Fig. Diagram of experimental data acquisition system and processing pipeline. Top-left, AMS Milking unit where all measurements occur and milking data is acquired. Below, the sniffers where CH4 and CO2 is measured. Data processing follow the arrows, and the pipeline end-product is the phenotypes stored in the emissions database.

Animal data

By September 2024 the database with methane records consists of about 15.000 dairy cows from 40 herds with methane records. Models must be developed for all major dairy breeds in Denmark, therefore gas concentrations are measured in more breeds as summarized in table 1.

Data acquisition and processing pipeline for milking and emission phenotypes

The data system comprises two distinct pipelines for each milking unit, processing time series from both the AMS milking unit and the gas sniffer. The AMS pipeline collects cow identification data, milking details, and gate status to track the start and end of milking sessions. This data is downloaded weekly from the farmers' management system. The sniffer pipeline, operating on its own server, records CH_4 and CO_2 concentrations.

Data from the AMS milking unit and the sniffer are combined into a single processing pipeline, where key operations are executed. This integrated pipeline carries out critical tasks, including monitoring data flow, detecting and correcting equipment errors, cleaning data, estimating background gas concentrations, and analyzing cow data. These steps result in the calculation of condensed phenotypes, which are then stored as a single record for each milking event. This streamlined approach ensures that data from both the AMS system and gas sniffers is processed efficiently and consistently, as illustrated in Figure 1.

Monitoring of dataflow

Daily monitoring ensures smooth connection and reliable data transfer, with continuous tracking of cow visits in the AMS, maximum and mean gas values, as well as standard deviations for gas concentrations.

Detection of equipment error and cleaning of data

Several key issues arise with the sniffer techniques, including data association and synchronization, reliability detection, and significant embedded noise levels in measurements. To address these challenges, we employed the methods proposed by Milkewych *et al*. (2022), which utilize a matched filter approach based on milking times and CO2 gas concentrations to estimate potential time discrepancies and identify reliable data. These methods are grounded in the principles of linear filtering theory. The algorithmic implementation of this approach enables rapid and efficient automated data processing, resulting in an assessment of the proportion of reliable data. A high percentage of unreliable data may indicate equipment malfunction, necessitating a thorough check-up of the sniffer.

Analysis and estimation of background gas concentrations

The estimation of background gas concentrations is outlined in Løvendahl *et al*. (2024). Reliable data are categorized into baseline measurements taken when the AMS is unoccupied (idle), and emissions data recorded during cow usage. Idle periods of the AMS serve as the basis for calculating background gas concentrations. To mitigate potential carry-over effects from previous cows and address issues related to imperfect data synchronization, specific restrictions on the recording window are implemented to minimize edge effects. A baseline value is calculated for each restricted recording window, using data from 60 seconds after the start to 30 seconds before the end, with a minimum duration of 3 minutes. The diurnal effect of baseline is modelled using Fourier series as harmonics (Lassen and Løvendahl, 2016).)

Phenotypes

For cow visits, the recording window is limited to a range of 30 to 300 seconds. Concentration values that significantly exceed the baseline are used as indicators to ensure that the cows' heads are adequately positioned near the sniffer's air inlet.

The mean values of the selected gas records and their ratios form the basic response phenotypes. Additionally, other phenotypes can be generated when data such as milk yield (ECM) and dry matter intake (DMI) are available. These phenotypes include methane production (g/day), methane intensity (g/day/kg ECM), and methane yield (g/day/kg DMI), as described by Manzanilla-Pech *et al*. (2021).

Conclusions

Developing a genetic model for low-emission dairy cows requires a comprehensive database of individual CH_4 measures. Utilizing advanced sniffers integrated with automated milking systems (AMS), we have collected extensive methane emission data from 15,000 dairy cows across 40 herds.

By implementing automated pipelines for data processing, we ensure the maintenance of high-quality measurements through rigorous monitoring and error detection. The analysis of background gas concentrations, along with the establishment of key phenotypes for methane emissions, paves the way for effective genetic models and selection strategies aimed at reducing enteric methane emissions

List of references

Beauchemin, K.A., E.M. Ungerfeld, A.L. Abdalla, C. Alvarez, C. Arndt, P. Becquet, C. Benchaar, A. Berndt, R.M. Mauricio, T.A. McAllister, W. Oyhantçabal, S.A. Salami, L. Shalloo, Y. Sun, J. Tricarico, A. Uwizeye, C. De Camillis, M. Bernoux, T. Robinson, E. Kebreab, 2020. Invited review: Current enteric methane mitigation options. Journal of Dairy Science, 105, 9297-9326. https://doi.org/10.3168/jds.2022-22091.

Gerber, P.J., Steinfeld, H., Henderson, B., Mottet, A., Opio, C., Dijkman, J., Falcucci, A. and Tempio, G. 2013. Tackling climate change through livestock – A global assessment of emissions and mitigation opportunities. Food and Agriculture Organization of the United Nations (FAO), Rome. https://openknowledge.fao.org/server/api/core/bitstreams/e1afd815-5a76-4b88-beac-fb9bc0e92001/content

Honan M., Feng X., Tricarico J.M., Kebreab E. (2022) Feed additives as a strategic approach to reduce enteric methane production in cattle: modes of action, effectiveness and safety. Animal Production Science 62, 1303-1317. https://doi.org/10.1071/AN20295.

J. Lassen, G.F. Difford, 2020. Review: Genetic and genomic selection as a methane mitigation strategy in dairy cattle. Animal, 14 suppl 3, 473-483. https://doi.org/10.1017/S1751731120001561.

Løvendahl *et al***.** 2024. A data driven approach to processing sniffer-based gas emission data from dairy cattle -under revision.

Maigaard M, Weisbjerg MR, Johansen M, Walker N, Ohlsson C, Lund P. Effects of dietary fat, nitrate, and 3-nitrooxypropanol and their combinations on methane emission, feed intake, and milk production in dairy cows. J Dairy Sci. 2024 Jan;107(1):220-241. doi: 10.3168/jds.2023-23420.

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. Lassen, J. 2021. Breeding for reduced methane emission and feed-efficient Holstein cows: An international response. Journal of Dairy Science. 104, 8. https://doi.org/10.3168/jds.2020-19889.

Milkevych, V., Villumsen, T.M., Løvendahl, P., Sahana, G. 2022. Data synchronization for gas emission measurements from dairy cattle: A matched filter approach, Computers and Electronics in Agriculture, 201, 107299, https://doi.org/10.1016/j.compag.2022.107299.

Robert H. Beach, Jared Creason, Sara Bushey Ohrel, Shaun Ragnauth, Stephen Ogle, Changsheng Li, Pete Ingraham and William Salas (2015) Global mitigation potential and costs of reducing agricultural non-CO2 greenhouse gas emissions through 2030, Journal of Integrative Environmental Sciences, 12:sup1, 87-105, DOI: 10.1080/1943815X.2015.1110183.