Large scale phenotyping of methane for genetic evaluation is possible with 'Sniffers'

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Abstract

Our objective was to demonstrate that the ongoing recording of methane of individual cows on 100 dairy farms in the Netherlands will provide meaningful breeding values for methane mitigation. Previously we conducted a power calculation that used the available literature, which predicted that recording on 100 dairy farms, 15,000 cows, and two years of recording, would provide a high enough reliability of prediction, to allow for practical direct selection for lower methane emissions. To determine what reduction in methane could be achieved by 2050, a methane trait with genomic prediction was included in the Dutch national selection index, showing that methane intensity could be reduced by between 14% and 24% (depending on the strategy). To be able to achieve these gains, a large scale phenotyping strategy needed to be implemented. We have commissioned 100 infrared spectrometry methane sensors, or 'sniffers', to be used to fulfil the data need. To date, 15 sensors have been installed, and at the time of writing, installation of the remaining sensors is ongoing and will be completed in the second half of 2022. The benefit of using sniffers is that it allows for a high throughput of cows and continuous recording for extended periods of time. With the data already available we have calculated traits referred to as mean visit, daily, and weekly methane concentration (ppm). These methane concentration traits are moderately heritable (0.13 to 0.32) and repeatable (0.30 to 0.68). The downside of using sniffers is that it records the methane concentration and not the methane production (g/day). We have also temporarily installed GreenFeeds on 16 farms (four overlapping with sniffers). There are 1,800 cows with sniffer recorded weekly methane concentration, and 822 cows with GreenFeed recorded weekly methane production (184 cows with both). All of the cows are linked via the pedigree and there are 1,655 which are also genotyped. A preliminary genetic correlation between Sniffer methane concentration and GreenFeed methane production is high at 0.71, indicating that selection for methane concentration as recorded with sniffers will in fact reduce methane emissions. We have learned a number of valuable lessons in the large scale rollout of methane sniffers which will be useful for future industry application. Most importantly, is that suitably reliable genomic breeding values for methane are closer to being a reality than ever before.

Keywords: Greenhouse gas, environment, dairy cows, ruminant, CH_4, CO_2

Introduction

The Dutch government has committed to reducing greenhouse gas emissions by 55% in 2030 compared to year 1990, and by 2050 to be carbon neutral (Communication from the Directorate-General for Climate and Energy, 2022). The Dutch dairy industry is a large contributor to greenhouse gases in the Netherlands (Van der Maas *et al.*, 2009). We have been investigating how to use animal breeding as a methane mitigation tool, to help achieve these goals and reduce the environmental impact of the Dutch dairy industry.

To achieve a reduction in methane with breeding, accurate breeding values are required. To obtain accurate breeding values large scale recording of methane is needed. The use of various infrared spectrometry sensors have been used in various studies to estimate genetic parameters of methane (Lassen and Difford, 2020). Collectively these sensors have been referred to as 'sniffers'. Sniffers offer a comparatively cheap method of phenotyping a large number of commercial cows (Madsen *et al.*, 2010; Garnsworthy *et al.*, 2019).

We have reviewed our decision process in selecting sniffers as the most suitable method of large scale recording and how we determined that 100 farms would need to have a sniffer installation, to obtain reliable genomic breeding values (de Haas *et al.,* 2021). We summarise the parameter estimates obtained from large scale methane recording with sniffers, including the trait definitions and genetic correlations with methane traits measured with GreenFeed (C-lock Inc. Rapid City, SD, US (Zimmerman, 2011)). Then using the current knowledge and lessons learned during the upscaling to 100 farms, we outline the next steps towards genomic breeding values and implementation in breeding programs. This demonstrates the progress made towards accomplishing our objective, of large scale phenotyping with sniffers in the Netherlands to provide meaningful breeding values for methane mitigation.

Materials and methods

Current projects

Wageningen University and Research has ongoing research on the application of breeding as a strategy for methane mitigation. The results presented here are summaries of the work done during the projects Climate Envelope (The Klimaatenvelop is supported by the Dutch Ministry of Agriculture, Nature and Food quality), and Climate Smart Cattle Breeding (Public-private partnership with the cooperative cattle improvement organization CRV, Friesland Campina, and the Dutch government). We have focused only on recording and outcomes of ongoing projects directly related to animal breeding.

Recording methane on commercial farms

Determining the number of farms to record with sniffers

We wanted to determine what the current genetic trends are for methane production (g/day) and methane intensity (g/kg), and what theoretical gain could be made if methane was added to the Dutch national breeding goal. To this end, we adapted a selection index that included 15 traits that are included in the current breeding goal. We tested various goals and economic weights placed on methane with or without genomic prediction. Concurrently a power analysis was performed to determine a recording strategy that would achieve a high enough reliability of genomic prediction that would facilitate the selection and genetic gain seen in the selection index. Published genetic parameters and preliminary data collected during the Climate Envelope were used as inputs for the selection index and power analysis. For full details on the selection index and power analysis see de Haas *et al.* (2021).

Previously 15 sniffers were purchased and installed on 14 commercial dairy farms across the Netherlands (WD-WUR v1.0, manufactured by Carltech BV), between March 2019 and September 2020. The sniffers were installed with the air intake located in the feeding bin of automated milking robots (AMS), where they measured methane concentration (0 to 2,000 ppm) and carbon dioxide concentration (0 to 10,000 ppm) continuously, for between 64 and 436 days (depending on farm). During the data collection and analysis, several practical and technical lessons were learnt. These lessons were used to develop a second generation of sniffers. Installation of an additional 90 units has begun using the new design. Methane data has continued to be collected after September 2020 and is expanding as new sensors are installed. The data collected from the sniffers is uploaded in near real time to a Microsoft Azure data cloud.

Developing a sniffer and installation

Using long-term and continuous recording with sniffers can be used to defined methane traits, but the raw sniffer requires processing for this purpose. A method similar to Garnsworthy *et al.* (2012) was used to match cow visits to the AMS with peaks in methane concentration. The data was then processed to remove background levels of methane and carbon dioxide and correct for cow behaviour. Across the farms there were 1,746 Holstein Friesian cows that visited an AMS a total of 308,968 times, during each milking event the methane concentration was measured.

Defining methane traits from sniffer recorded methane

The main considerations included, calculation methods (mean, median, log, ratio) and the period used per record (visit or weekly). Based on various combinations of trait definitions we wanted to estimate heritability and repeatability of various methane traits defined from the largest data set of long-term repeated cow records. All cows were linked via pedigree and 1,611 were genotyped. Parameter estimates were made using univariate animal models, that included repeated records, with ASReml 4.2 (Gilmour *et al.*, 2015). The heritabilities and repeatabilities were used to calculate reliability of the breeding values and determine the number of records per daughter that would be needed for implementation. For full details on matching AMS and sniffer data, data processing, parameter estimations, and determining reliability of estimated breeding values see van Breukelen *et al.* (2022a).

The application of sniffers for genetic selection is still in a development stage, and is why we explored the genetic relationship with traits recorded with GreenFeed, as GreenFeed are considered the gold standard for on-farm recording of individual cow methane. Since the univariate analysis with the sniffers, data collection has been ongoing and is expanding to measure methane on 100 dairy farms. There have also been GreenFeed units installed temporarily on 16 farms (four overlapping with sniffers). At the time of this analysis, there were 1,800 cows with sniffer recorded daily methane concentration, and 822 cows with GreenFeed recorded daily methane production (g/day) (184 cows with both). All of the cows are linked via the pedigree and there are 1,655 which are also genotyped. Bivariate animal models in ASReml 4.2 (Gilmour *et al.*, 2015) were used to estimate the genetic parameters for methane concentration (ppm recorded by sniffers) and methane production (g/day recorded by GreenFeed).

Sniffer and GreenFeed methane traits

Results and discussion

Why and how to record methane on commercial farms?

Based on the current Dutch selection index, the genetic trend for methane production is unfavourable with a genetic trend of increasing methane by 5.79 g/day per generation. However, as the current index selects for traits that improve production efficiency, methane intensity will decrease by 13%. With active selection on lowering methane production and utilizing genomic prediction, the genetic trend for methane production can be decreased by 5.79 g/day, will still result in increasing milk production, and lower methane intensity by 24%. This was a clear justification for us to develop a recording scheme that will allow us achieve these theoretical improvements. We found, to achieve a desired reliability of genomic prediction of 0.40 within two years of recording, we would need to record methane on 100 farms with an average herd size of 150 cows (15,000 total cows). For full results of the selection index and power analysis see de Haas *et al.*, (2021).

During the data collection and analysis of the first 15 sniffers, we identified several technical requirements that should be considered when developing new sniffers. Due to the challenging environment of dairy barns and the sensitivity of methane sensors, the housing containing the sensor should be dust resistant, operate within a wide range of ambient temperatures and humidity, and exclude gases that can interfere within the measured wavelength such as water. Methane sensors can have a large range of detection limits, while most measurements are within 200 to 2,000 ppm, consider that the error should be minimized within the most common recording ranges (measurements closer to the mean per visit should be the most accurate). Some methane sensors are prone to drifting away from the calibration curve, limiting factors that affect the methane sensor can help to minimize the drift, regular checks of the incoming data can help identify when a sensor drifts and requires recalibration. If this is ignored it can limit the potential analysis, for example traits that use a ratio with carbon dioxide were limited because the methane sensor drifted and the carbon dioxide sensor did not drift. The methane data recorded in these projects is uploaded in near real time to a data cloud infrastructure, however there can be issues with communication due to interference with farm equipment or with poor connections via the telecommunication infrastructure, having built-in data storage options are a good redundancy. With these lessons learned, 90 new sniffers were purchased that implement these requirements. However, they are still in development and with limitations in global supply chains the full scale installation was inhibited. The installation on 100 farms is expected to be completed in 2022, in the meantime this still remains the largest and longest methane recording dataset on individual cows for genetic evaluations.

Methane traits can be measured with sniffers and used in genetic evaluations

We have found that mean methane per visit is heritable (0.13 $\pm$ 0.01) and repeatable (0.30 $\pm$ 0.01), but with lower estimates compared to weekly methane (0.32 $\pm$ 0.01 and 0.68 $\pm$ 0.01, respectively). However this has limited effect for the reliabilities of the breeding values. To achieve a reliability of 0.50, 25 mean methane records on 10 daughters is needed. For the full results of on the genetic parameters estimated with sniffers see van Breukelen *et al.* (2022a). The estimated heritabilities and repeatabilities, were within the parameter space of the estimates used in the selection index and power analysis, indicating the large scale methane recording currently in progress, will make the goal of providing meaningful breeding values for methane mitigation possible.

The previous parameter estimates were for methane concentration traits, while the desired trait change is placed on methane production. The preliminary results with the GreenFeed have been very encouraging. The heritability (0.20) and repeatability (0.34) for methane production are within the same parameter space as the sniffers (van Breukelen *et al.* 2022b, accepted). Importantly the genetic correlation between GreenFeed and sniffer methane is high and positive (0.71). This indicates that selection for lower methane concentration will reduce methane production and be a

useful methane mitigation option. This has given us confidence that by the end of the project there will be the required data for reliable breeding values for a methane trait that can be selected.

The work so far has mostly utilized data already collected. As the dataset from the full 100 farms becomes available there are several research objectives to be completed. Genetic and phenotypic correlations will be estimated with all of the traits included in the current national Dutch breeding goal. Subsequently a selection index that incorporates the new methane traits will be developed. Reliable breeding values for the methane trait to be included in the selection index need to be estimated. In the meantime, the full 100 sniffers need to be installed, the data processing is being refined, and methods to improve the accuracy of the methane traits are being explored such as standardising the methane measurements across devices and including the microbiome population as a random effect.

Genomic breeding values and implementation in breeding programs

Conclusion

Animal breeding is a promising method of methane mitigation that can be used to help reach greenhouse gas targets. Before breeding strategies can be implemented, there needs to be enough data to reliably predict breeding values. Long-term measuring with sniffers is a viable method of data collection. Results so far are encouraging and the traits developed could be used for selection purposes. With the expansion of sniffers to 100 farms we believe meaningful breeding values for methane mitigation will be available in the relatively near future.

Acknowledgement

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