Genetics of enteric methane emissions of Dutch dairy cows

Climate Envelop project 2019

Yvette de Haas, Michael Aldridge, Anouk van Breukelen

Report 1318

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Wageningen Livestock Research

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Abstract NL De Nederlandse landbouw staat voor de uitdaging om methaanuitstoot in 2030 met 2,1 Mton te verminderen en nog verder in 2050. Omdat methaanuitstoot van melkkoeien het belangrijkste onderdeel is van deze voetafdruk, hebben boeren dringend behoefte aan efficiënte en kosteneffectieve opties om de methaanuitstoot verminderen. Fokkerij, waarbij gebruik wordt gemaakt van de natuurlijke variatie van dieren in methaanemissies, is een strategie die kosteneffectief, permanent en cumulatief is. Het doel van deze studie was om het potentieel te onderzoeken van het fokken op dieren met een lage uitstoot. De resultaten laten zien dat er fenotypische (709 ppm) en genetische variatie (474 ppm) is in methaanemissies tussen koeien gemeten door sniffers. De erfelijkheidsgraad van methaanemissies was 0,23, wat aangeeft dat het mogelijk is om genetische vooruitgang te bereiken met behulp van selectie.

Abstract UK The Dutch agricultural sector is facing the challenge to reduce the methane emissions by 2.1 Mton by 2030, and even further by 2050. As methane emission of dairy cows is the main component of this carbon footprint, farmers urgently need efficient and cost-effective options to reduce methane emissions. Animal breeding that exploits natural animal variation in methane emissions is a mitigation strategy that is cost-effective, permanent, and cumulative. The aim of this study was to explore the potential of animal breeding to reduce methane emissions. The results show that there is phenotypic (709 ppm) and genetic variation (474 ppm) in methane emissions between cows measured by sniffers. The heritability of methane emissions was 0.23, which indicates it is possible to achieve genetic progress by selection.

Wageningen Livestock Research Report

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Foreword

The long-term global climate goals of the Paris Agreement, adopted by nearly 200 countries in December 2015, imply the necessity for enhanced efforts for greenhouse gas emissions reductions in the Netherlands. Compared to the reference year 1990, the Dutch greenhouse gas (GHG) emission has to decrease by 49% by 2030, and 95% by 2050. The translation of the goals of the international climate regime into the context of the Netherlands was based on the comparison of different emissions reduction scenarios. These scenarios included reduction goals for the dairy sector and revealed that reducing methane (CH_4) emissions is important. Several technical solutions to reduce enteric methane emissions have been, and continue to be, extensively researched (e.g., feed additives or manure digesters). Animal breeding that exploits natural animal variation in methane emissions is an additional mitigation strategy that is cost-effective, permanent, and cumulative. The study described is an exploration of the potential of animal breeding to reduce enteric methane emission.

This research was conducted by Wageningen Livestock Research and commissioned and funded by the Dutch Ministry of Agriculture, Nature and Food Quality. The data were collected 13 practical farms and the research farms ‘De Marke’, ‘Dairy Campus’, and ‘KTC Zegveld’. Together they represent the Dutch national dairy herd.

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Samenvatting

De Nederlandse landbouw staat voor de uitdaging om methaanuitstoot in 2030 met 2,1 Mton te verminderen en nog verder in 2050. Omdat methaanuitstoot via de ademlucht van melkkoeien het belangrijkste onderdeel is van deze voetafdruk, hebben boeren dringend behoefte aan efficiënte en kosteneffectieve opties om de methaanuitstoot te verminderen. Het fokken van dieren, waarbij gebruik wordt gemaakt van de natuurlijke variatie tussen dieren, is een strategie die kosteneffectief, permanent en cumulatief is. Het doel van deze studie was om het potentieel van het fokken van dieren om methaanemissies te verminderen te onderzoeken.

Individuele methaanemissie van koeien kan op verschillende manieren worden gemeten. Om fokwaarden te kunnen schatten, is het van belang dat een grote hoeveelheid data wordt verzameld. Het meten van grote aantallen koeien kan met behulp van sniffers, dat zijn sensoren die concentraties methaan en koolstofdioxide in de ademlucht van koeien meten in de voerbak van melkrobots. Sniffers zijn relatief goedkoop in gebruik, maar het systeem meet geen omgevingsfactoren waarvan bekend is dat ze de meting kunnen beïnvloeden (bijvoorbeeld: temperatuur, windsnelheid en -richting, en de afstand tussen de aanvoerleiding en de neus/bek van de koe). Een systeem dat deze factoren wel meet is de GreenFeed (C-lock Inc. Rapid City, SD, US). GreenFeed units zijn echter niet geschikt voor het verzamelen van grote hoeveelheden data, een vereiste voor de fokkerij. In deze studie hebben wij onderzocht of GreenFeed units en sniffers tot dezelfde rangschikking van laag naar hoog methaan producerende koeien komen. Eerst is een vergelijking gemaakt tussen GreenFeed metingen als concentratie (ppm) en GreenFeed metingen omgerekend naar gram/dag. Het is namelijk gebruikelijk dat de fabrikant van de GreenFeed de concentraties omrekent naar gram/dag. Deze correlatie was 0.51, wat betekent dat koeien die een hoge methaan uitstoot hebben in ppm ook een hoge emissie hebben in gram/dag, maar dat de rangschikking van de koeien gemeten met hetzelfde apparaat op hetzelfde moment niet geheel gelijk is (dan zou de correlatie namelijk 1 zijn geweest). Door het corrigeren van de data, op basis van o.a. de bovenstaande factoren, kan de rangschikking van de koeien dus veranderen. De correlatie tussen sniffer- en GreenFeed-metingen op dezelfde dag varieerde tussen 0.059 en 0.529. Deze correlaties zijn allemaal positief, wat wil zeggen dat voor koeien waarvan een hoge emissie wordt gemeten door sniffers, ook een hoge emissie wordt gemeten door de GreenFeed units. Echter is ook hier een verandering in de rangschikking van koeien geobserveerd, afhankelijk van welke meetmethode wordt gebruikt. Dit betekent niet dat één van beide methoden niet geschikt is voor het meten van methaan. In genetische modellen kunnen beide methoden worden gebruikt, waar een correctie wordt gemaakt voor de methode en het moment van meten.

Voor de fokkerij is het belangrijk dat er variatie is tussen koeien in methaanemissies en dat het effect van omgevingsfactoren wordt gescheiden van de genetische component met behulp van statistische modellen. Hierbij is het van belang zowel metingen van een grote hoeveelheid koeien te verzamelen, als meerdere metingen per koe. Aan de hand van de methaanmetingen kan de erfelijkheid worden bepaald door een koppeling te maken met de afstamming van de koe, op basis van stamboom en genotype (DNA) informatie. In dit onderzoek is de erfelijkheidsgraad bepaald aan de hand van herhaalde sniffermetingen van 1,698 koeien, van wie ook genotype informatie beschikbaar was. De resultaten geven een erfelijkheidsgraad voor methaanemissie van 23%, gedefinieerd als de gemiddelde emissie per week. Vergeleken met de erfelijkheidsgraad van melkproductie (40%) of de meeste gezondheid en vruchtbaarheid kenmerken (2% tot 8%), is de erfelijkheid van methaanemissie middelmatig. Een lage of middelmatige erfelijkheid betekent dat data van een groter aantal koeien verzameld moet worden om betrouwbare fokwaarden te schatten dan wanneer de erfelijkheid hoog is. Een indicatie van het verschil dat met behulp van fokkerij gemaakt kan worden, kan worden weergeven met de genetische standaard deviatie. Het genetische verschil tussen de koeien met de laagste en hoogste uitstoot was 474 ppm. Dit laat zien dat door middel van het selecteren van koeien en stieren met een lage uitstoot, een reductie in enterische methaanemissie een reële mogelijkheid is in de nabije toekomst.

Summary

The Dutch agricultural sector is facing the challenge to reduce methane emissions by 2.1 Mton by 2030 and even further in 2050. As methane emissions through breathing of dairy cows is the most important part of this footprint, farmers urgently need efficient and cost-effective options to reduce methane emissions. Animal breeding that exploits natural animal variation is a mitigation strategy that is cost-effective, permanent, and cumulative. The aim of this study was to investigate the potential of animal breeding to reduce methane emissions.

Individual methane emissions from cows can be measured in different ways. In order to estimate breeding values, it is important that a large amount of data is collected. Large numbers of cows can be measured with sniffers, which are sensors that measure the breath of cows in feed bins of milking robots. Sniffers are relatively inexpensive to use, but the system does not measure environmental factors that are known to influence the measurement (for example: temperature, wind speed and direction, and the distance between the air tube and the cow's nose). A system that does measure these factors is the GreenFeed (C-lock Inc. Rapid City, SD, US). However, GreenFeed units are costly and not suitable for collecting large amounts of data on a large number of cows, which is a requirement for breeding. In this study, we investigated whether GreenFeed units and sniffers achieve the same ranking from low to high methane producing cows. The measurement values of the GreenFeed have a different unit, these are converted by the manufacturer of the GreenFeed to grams/day. That is why we first made a comparison between GreenFeed measurements as concentration (ppm) and GreenFeed measurements converted to grams/day. The correlation was 0.51, which means that cows that have a high methane emission in ppm also have a high emission in grams/day, but the ranking of the cows is not completely equal, even if they were measured with the same device at the same time. By correcting the data, based on the above factors, the ranking of the cows can therefore change. The correlation between sniffer and GreenFeed measurements on the same day varied between 0.059 and 0.529. This means that for cows with high emission measured by sniffers, a high emission is also measured by the GreenFeed units. However, there is a change in the ranking of cows, depending on which measurement method is used. This does not mean that either method is not suitable for measuring methane. In genetic models, both methods can be used, where a correction is made for the method and the moment of measurement.

For breeding it is important that there is variation in methane emissions between cows and that the effect of environmental factors is separated from the genetic component by means of statistical models. To do so, measurements should be collected from a large number of cows as well as several measurements per cow. With the methane measurements, the heritability can be determined by making a link with the ancestry of the cow, based on pedigree and genotype (DNA) information. In this study, the heritability was determined of repeated sniffer measurements of 1,698 dairy cows, of which genotype information was also available. The results show that the heritability for methane emission is 23%, defined as the average emission per week. Compared to the heritability of full lactation milk production (40%) or most health and fertility traits (2% to 8%), the heritability of methane emission is moderate. A low or moderate heritability means that data from a larger number of cows must be collected to estimate reliable breeding values than when the heritability is high. An indication of the difference that can be made by breeding can be represented by the genetic standard deviation. The genetic difference between the cows with the lowest and highest emissions was 474 ppm. This shows that by selecting cows and bulls with low emissions, a reduction in enteric methane emissions is a real possibility in the near future.

1 Introduction

A lower carbon footprint of dairy products has become a key element of sustainable dairy production. The Dutch agricultural sector is facing the challenge to reduce the methane (CH_4) emissions by 2.1 Mton by 2030, and even further by 2050. As methane emission of dairy cows is the main component of this carbon footprint, farmers urgently need efficient and cost-effective options to reduce methane emissions. Technical solutions to reduce enteric methane emissions have been, and continue to be, extensively researched (e.g., feed additives or manure digesters). Animal breeding that exploits natural animal variation in methane emissions is an additional mitigation strategy that is cost-effective, permanent, and cumulative. Selective breeding can be an option as variation in emission is heritable. Breeding can also easily be included in the day-to-day herd management at low costs. With the recent successful incorporation of genomic information into breeding schemes, the reliance on very large populations of phenotyped animals is somewhat relaxed. However, a reference population of a few thousand animals is still required to estimate the contribution of each genomic region to expression of the phenotype under investigation (Calus et al., 2013).

Within the Climate Envelop 2018 we started recording individual methane emissions on those farms that were selected for monitoring and had a milking robot (11 farms). Within the Climate Envelop 2019 the number of farms was extended with "Cows and Opportunity"-farms that have a milking robot (3 farms), and with the research farms 'De Marke' and 'KTC Zegveld'. In this report an exploratory study was described, where we investigate the potential of animal breeding to reduce enteric methane emissions of dairy cows. First, we compared the ranking of low to high emitting cows recorded by two methods, GreenFeed units and by the sniffer method. As large amounts of data need to be collected to use in animal breeding models, it would be helpful if data sets from these two methods can be combined. Second, we investigated if there is variation in enteric methane emissions between cows, recorded with a sniffer. For animal breeding, recording methane emissions with the sniffer method is most feasible because sniffers can measure a large amount of cows, while other measuring techniques are often restricted by the number of cows that can be recorded per herd. As a third objective, we investigated if there are differences in enteric methane emissions between breeds, recorded with a sniffer. To investigate if the variation between cows has a heritable component, in the fourth objective the heritability of enteric methane emission was determined. A final objective was to estimate a genetic correlation between enteric methane emission and milk yield, an important breeding goal trait. Thereby, we want to highlight if there can be an effect of selecting for low emitting cows on other breeding goal trait. So in the future they can be weighed accordingly in a breeding program.

2 Background

2.1 Methane emissions by dairy farming

Climate change induced by emissions of greenhouse gases is an urgent environmental issue. One of the gases that induces climate change is methane (CH_4), a greenhouse gas that is 200 times less abundant but 80 times stronger than carbon dioxide (CO_2) over a 20-year period (IPCC, 2014). In the Netherlands, approximately 75% of methane is emitted during agricultural practices (Rijksoverheid, 2019). The majority of this is produced by anaerobic fermentation in the rumen of cattle and emitted in the air through breathing and belching (van Bruggen et al., 2019; Cottle et al., 2011). Animal breeding offers an opportunity to achieve a permanent, cost effective, and cumulative reduction in enteric methane emissions, which can be implemented in addition to changes in nutrition and manure management, thereby lowering the environmental impact of dairy farming (Knapp et al., 2014). To reduce methane emissions with animal breeding techniques, major innovations are required in four areas: 1) large-scale automatic recording of methane emissions of individual cows, 2) suitable parameter estimates and breeding values, 3) knowledge of the impact of selecting for lower emitting cows on other breeding goal traits, and 4) implementation in practical and broadly accepted breeding tools.

2.2 Recording enteric methane emissions

The most precise measurements of methane emissions can be obtained by housing a single cow in a respiration chamber for several hours. The measurements on the airflow in a respiration chamber result in a direct measurement of the total methane emitted by that cow. However, respiration chambers have practical limitations including: they are low throughput, require a large amount of labour to measure individual cows, are expensive, and they possibly inhibit normal behaviour (Hammond et al., 2015). Because of these limitations respiration chambers cannot be used for large scale phenotyping of dairy cows.

Similar to respiration chambers, the GreenFeed system uses airflow to analyse methane emissions (C-lock Inc. Rapid City, SD, US). The system is placed in the barn and configured to offer small amounts of pelletized bait which lure individual cows to visit the GreenFeed unit multiple times a day, where breath measurements are taken in the feed bin of the unit. The GreenFeed measures CH_4 concentration, records head positioning, and uses an air flux method to provide CH_4 data in g/cow/day. Although the GreenFeed system is less costly than respiration chambers, the system is still too expensive to apply it for large scale phenotyping in a breeding program, because it can only record on average 30 cows per unit.

A system that is new and still in development are ‘sniffers’. Sniffers are a high-throughput, non-invasive method to measure gas concentrations from the breath and belching of cows, using infrared spectroscopy. The devices are installed in the feed bin of automated milking stations or concentrate feeders (Lassen et al., 2013; Negussie et al., 2017), where continuous measurements of the methane concentration in the air (ppm) are taken. Sniffers do not use an air flux, therefore they cannot measure the exact amount of methane emissions in g/cow/day, but the data can be used to rank cows from low to high emitting. A disadvantage of sniffers is that the precision of measurements can decrease by movement of the head of the cow or background barn gases (Difford, 2018). Studies have shown high correlations (0.77 ± 0.18 and 0.89 ± 0.07) between on-farm sniffers and respiration chamber measurements, demonstrating the potential of using sniffers as an indicator for methane emissions in dairy cattle (Difford, 2018; Garnsworthy et al., 2019). Sniffers are cost effective and show potential for use in breeding programs, but still need further validation.

2.3 Reducing methane emissions through animal breeding

Some steps need to be taken before methane emissions can be reduced through animal breeding. Large-scale recording of methane emissions of individual cows is required to determine if there is variation in emissions between cows. Afterwards genetic parameters can be estimated based on the individual measurements and pedigree information.

To estimate genetic parameters for animal breeding practices, it is common to use statistical models, which include fixed effects to account for biological and design related issues. For example, biological differences in methane emissions occur throughout different lactation stages of a cow (van Engelen et al., 2018). Enteric methane emissions are also influenced by diet composition and feeding pattern, resulting in fluctuations of the level of methane emitted during the day (Crompton et al., 2011). These factors may vary during the course of the year, for example, during the summer season fresh grass is often added to the feed ration. Long-term and large scale recording of methane emissions makes it possible to investigate different trait definitions for methane emissions in a statistical model, with repeated records for each cow to account for biological and management changes over a longer period of time.

Before integrating the mitigation of enteric methane emissions in a breeding program for dairy cows, phenotypic and genetic relationships with other traits must be analysed (Lassen et al., 2020). This includes traits from the following categories: production, feed efficiency, conformation, health, and reproduction. For example, studies have shown that methane emissions, measured with sniffers, correlated positively with milk yield (0.17 ± 0.39 to 0.54 ± 0.26, depending on the week of lactation) (Breider et al., 2019; van Engelen et al., 2018; Lopez-Paredes et al., 2020). Meaning that a cow that emits more methane, produces more milk. However, when we select for reduced methane emissions, we do not want milk yield to decrease. Therefore it is important to be aware of the relationships between methane emissions and other breeding goal traits, to weigh them accordingly in a breeding program. By using a broad breeding goal and multitrait selection, negative side effects can be reduced.

3 Are animals ranked the same with sniffers and GreenFeed?

3.1 Units of GreenFeed measurements

The main issue with trying to compare sniffer and GreenFeed records is the units used. While the sniffers record CH_4 as a concentration in ppm, the GreenFeed records are processed by the manufacturer to a flux in g/day, where undisclosed data processing steps are performed. Our expectation was that cows with a higher ppm recorded will also have a higher emission in g/day.

To investigate this, we estimated correlations between the raw record in ppm and the record in g/day of the same measurement in the GreenFeed, to see if there was a change of the ranking of cows after the data processing steps by the manufacturer. The correlation we calculated between GreenFeed recorded in g/day and GreenFeed recorded in ppm was positive (0.51 ± 0.11), but the correlation was not one (Figure 3.11), which is expected when both traits are recorded perfectly and exactly the same. This shows us that cows that have a high methane emission in ppm also have a high emission in grams/day, but the ranking of the cows can be different, even if they were measured with the same device at the same time.

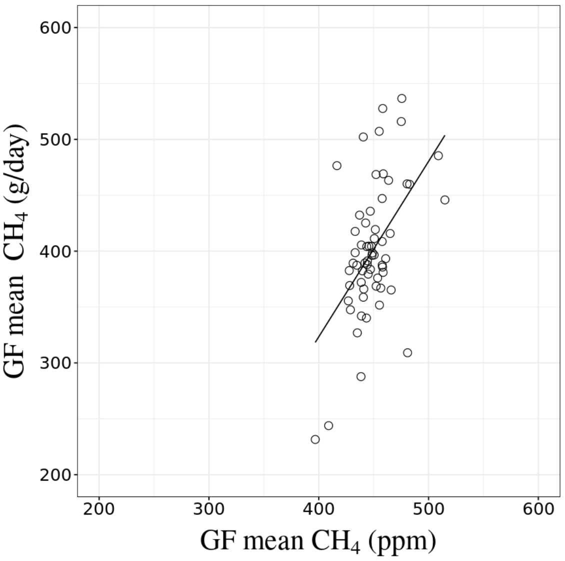


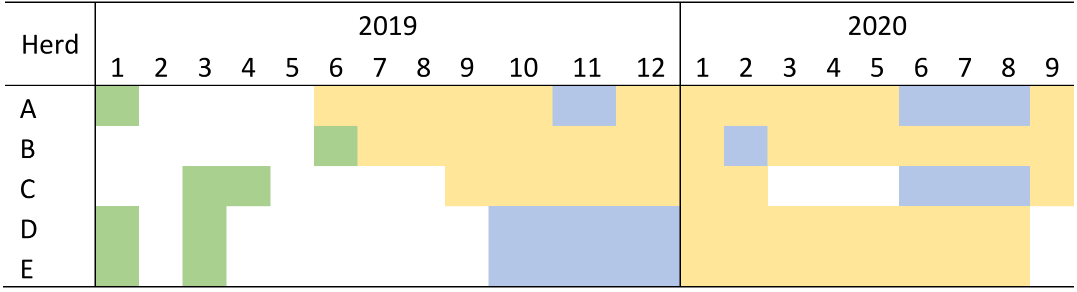
Figure 3.1 *Correlation between GreenFeed CH_4 in recorded in g/day and ppm during a two week period. Demonstrating the relationship between GreenFeed ppm and g/day is moderately positively correlated.*

The lower than expected correlation between ppm and g/day could be caused by corrections for background emissions, head position, proximity to sensor, temperature, airflow, wind speed or wind direction, or just by random noise because of inaccuracy in measurements. None of these corrections were made for the ppm records in the GreenFeed. However, which corrections have influenced the ranking of cows is unknown, as we do not have access to the data processing steps. The calculated correlation between the g/day and ppm records obtained from GreenFeed was an indication that calculating correlations between GreenFeed (g/day) and sniffers (ppm) would be difficult. We then namely compare two different devices, that are installed at different positions in the barn, and the times between moments of recording (in either the GreenFeed or in the milking robot) change continuously.

3.2 Data corrections of sniffer measurements

For sniffer records (unlike the GreenFeed), no corrections for head position, proximity to sensor, airflow, air pressure, wind speed, and wind direction were made. Basic data cleaning methods were applied, including filtering low concentrations of background level methane and carbon dioxide (200 ppm and 400 ppm, respectively). Furthermore the first minute of milking was discarded, to ensure that the cow has reached the feed bin and to account for a delay in the air sample entering the air intake and reaching the sensor. A record was at least two and a half minutes long, to capture not only breathing but also the belching of cows. Any records after the first five minutes of milking were discarded, because thereafter the chance becomes higher that the cow has eaten all of the pellets and does not come close to the feed bin with her nose. The final dataset contained six recording periods where both GreenFeed and sniffers were installed in a herd at the same time, which were periods of either 2 weeks or 3 months (Table 3.1).

***Table 3.1** Available data used in the comparison of GreenFeed and sniffers.*



Herd	2019												2020								
	1	2	3	4	5	6	7	8	9	10	11	12	1	2	3	4	5	6	7	8	9
A	🟩					🟨	🟨	🟨	🟨	🟨	🟦	🟨	🟨	🟨	🟨	🟨	🟨	🟦	🟦	🟦	🟨
B						🟩	🟨	🟨	🟨	🟨	🟨	🟨	🟨	🟦	🟨	🟨	🟨	🟨	🟨	🟨	🟨
C			🟩	🟩					🟨	🟨	🟨	🟨	🟨	🟨				🟦	🟦	🟦	🟨
D	🟩		🟩							🟦	🟦	🟦	🟨	🟨	🟨	🟨	🟨	🟨	🟨	🟨	
E	🟩		🟩							🟦	🟦	🟦	🟨	🟨	🟨	🟨	🟨	🟨	🟨	🟨	

Green, GreenFeed; Yellow, Milking robot and sniffer data; Blue, Overlapping GreenFeed and sniffer data.

3.3 Correlations between sniffer and GreenFeed measurements

The correlation between sniffer recorded methane (ppm) and GreenFeed (g/day) of measurements on the same day ranged between 0.06 and 0.53 (Table 3.2), and the relationships appeared to be weak (Figure 3.2). However, high correlations were not expected, because of the correlation of 0.51 that we calculated between the GreenFeed ppm and GreenFeed g/d records. We were not able to estimate a correlation between both sniffer and GreenFeed measurements in ppm at this time, because there was no GreenFeed data available in ppm that overlapped with sniffer recording periods.

***Table 3.2** Correlations and standard errors (SE) between GreenFeed and sniffer records for CH_4 of measurements on the same day.*

Herd	Duration	Correlation (SE)	Number of cows
1	Two weeks	0.53 ± 0.25	14
2	Two weeks	0.39 ± 0.20	23
2	Three months	0.14 ± 0.21	24
3	Three months	0.08 ± 0.20	28
4	Three months	0.07 ± 0.13	65
5	Three months	0.06 ± 0.16	43

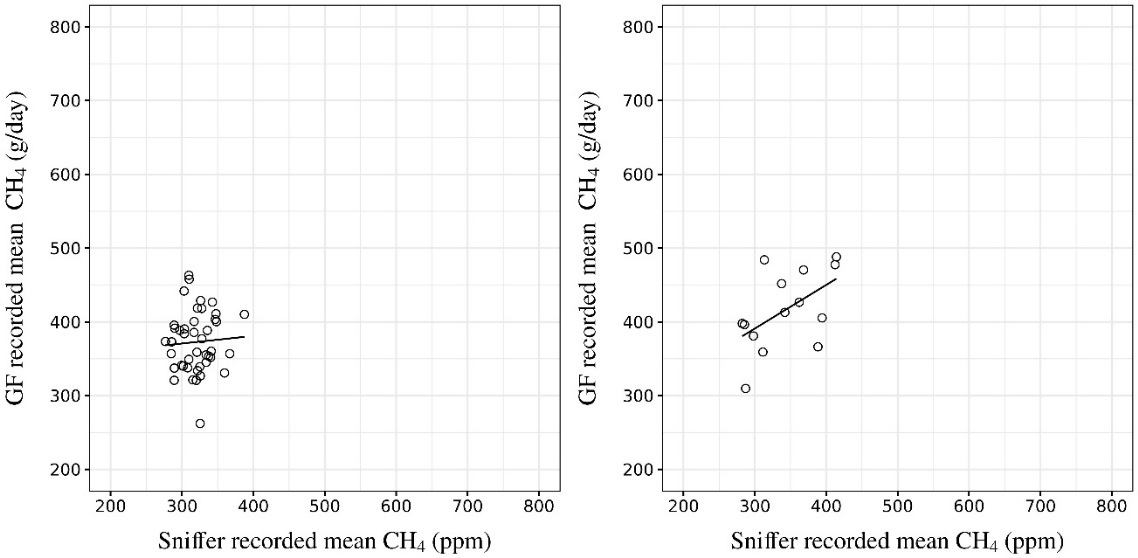


Figure 3.2 *Lowest correlation (left) and highest correlation (right between mean methane recorded by GreenFeed (g/day) and sniffers (ppm) of measurements on the same day.*

The low correlation between sniffer and GreenFeed measurements indicate that there is either some inaccuracy in the methods of recording, or that the two systems may measure a different part of the variation in methane emissions between cows. This can also be caused by differences in the moment of recording. Sniffer and GreenFeed records can still be combined in genetic models, where a correction can be included for a difference between measurement devices and moment of recording.

4 Differences in emissions between cows and farms

4.1 Summary of sniffer data

For animal breeding it is important that there is variation in the trait of interest and environmental effects can be accounted for. There are clear differences between cows, and between farms. Table 4.1 is a summary of the data used in this analysis which includes individual methane emissions on 17 herds (16 farms), with a total of 2,135 cows (Not all cows are genotyped and could be included in the genetic analysis). The average CH_4 concentration of all farms was 591 ppm, ranging from 342 ppm to 1,024 ppm. For the three farms with the lowest emissions, the average emissions was 342 ppm, 368 ppm, and 410 ppm, and the highest three 1,024 ppm, 869 ppm, and 745 ppm. Most farms participated in the herd test-day milk recording, showing an average daily milk yield of 31.2 kg, with a range of 27.4 kg to 35.2 kg. Two of the three lowest emitting farms had an average daily milk yield of 32.6 kg and 27.6 kg (the third herd had no herd test-day milk recording data available), and the three highest emitting farms had an average daily milk yield of 34.9, 29.1, and 30.3 kg. The recording period per farm differs, and so does the number of daily records that are available, because we started installing the devices at the end of 2018, and continued installing in 2019. Furthermore, this is the first time that such a large-scale recording with sniffers on multiple commercial farms has been undertaken, causing some hic-ups in the data recording, for example when the sensors drifted towards zero and could not measure sufficient variation.

Table 4.1 *Descriptive statistics per herd for number of cows, the mean CH_4 (ppm) and CO_2 (ppm), the average milk yield per test day (kg), the recording period and the total number of visits recorded after filtering on visit length and minimum CH_4 and CO_2 concentration (200 ppm and 400 ppm respectively).*

Herd	No. cows	Mean record per visit		Mean test day milk yield (kg)	Recording period	No. of visits
		CH_4 (ppm)	CO_2 (ppm)			
1	168	610	7,380	32.3	09/07/2019 – 31/10/2019[1]	9,507
2	299	680	4,694	32.7	15/03/2019 – 31/08/2020	53,545
3	104	368	3,508	32.6	12/07/2019 – 02/09/2020	19,955
4	115	1,024	6,503	34.9	08/08/2019 – 31/08/2020	15,146
5	192	647	9,294	27.4	07/03/2019 – 14/06/2020	12,160
6	201	745	5,595	30.3	09/07/2019 – 31/08/2020	35,207
7	84	671	1,513	31.0	18/09/2019 – 02/09/2020	2,140
8	124	714	3,766	34.1	09/08/2019 – 28/06/2020	12,860
9	95	528	6,262	35.2	11/06/2019 – 31/08/2020	3,501
10	124	696	6,669	-	04/10/2019 – 20/07/2020	3,533
11	51	424	7,521	34.8	21/09/2019 – 03/01/2020	1,364
12	206	410	3,975	27.6	05/04/2019 – 31/08/2020	9,304
13	93	484	5,445	28.9	01/06/2019 – 28/08/2020	18,173
14	152	869	6,523	29.1	18/09/2019 – 27/08/2020	12,266
15	63	411	5,342	-	18/09/2019 – 24/07/2020	3,669
16	64	342	3,849	-	20/11/2019 – 03/08/2020	978
17	176	420	7,380	35.1	18/09/2019 – 31/08/2020	9,507

[1] Herd one stopped shortly after starting recording with a sniffer on that farm.

4.2 Variation between herds

Differences can be observed the mean methane emission between herds (Table 4.1). These differences can be explained by biological differences between cows and herds, but also by environmental or calibration differences between sniffers. For example, herd 7 had a very low average CO_2 emissions, which is partly explained by an error in calibrating the sniffer. Whereas most sniffers recorded the full range of 0 to 10,000 ppm, the sniffer on farm 7 appeared to be less sensitive and recorded only a maximum of 7,000 ppm. Another example of a calibration issue with a CH_4 sensor on farm 12 is shown in Figure 4.1, where for the first three months of installation, records are within the calibration range but slowly drift towards zero over time. As long as the sensor records sufficient variation between cows, the data can be applied in genetic models with a correction for day or week to account for the drift of the sensor over time. This means that we do need a statistical model before interpreting the results, and cannot just look at the numbers and figures without correcting the data.

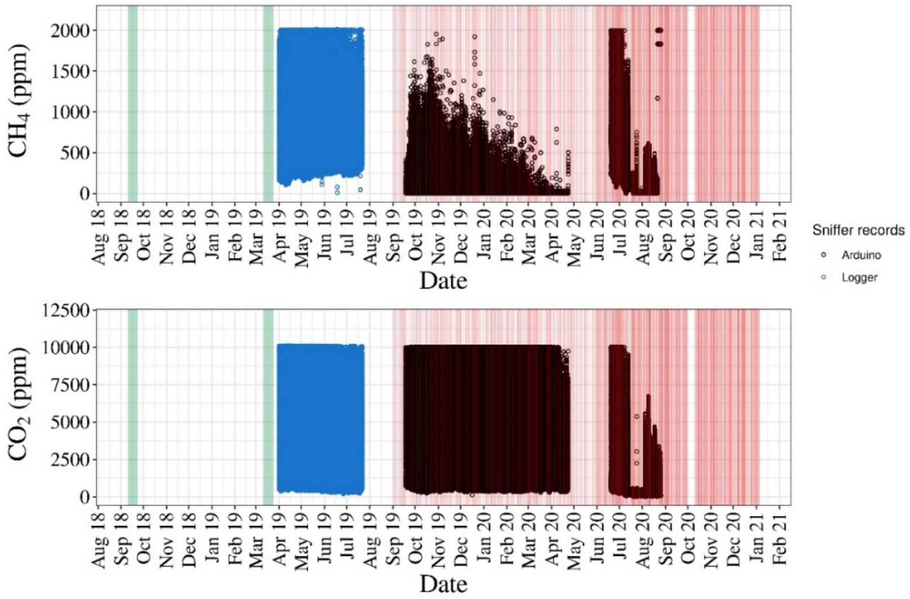


Figure 4.1 *An example for one farm and the available sniffer data (blue dots are stored on logger, black dots are stored on the cloud), milking robot data (red lines), GreenFeed data (green line).*

4.3 Variation between cows

During the full recording period a large variation was observed in mean emissions between cows (Figure 4.2). This also clearly shows us that cows can be ranked from low to high emitting.

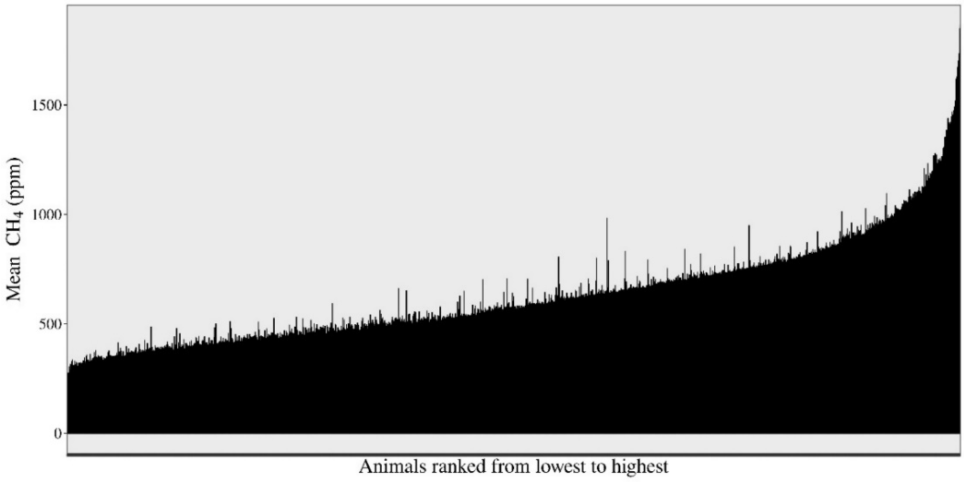


Figure 4.2 *Cows ranked based on their mean methane concentration of one week (ppm ± SE).*

A more detailed overview was made for the herd with the most variation and the herd with the least variation (Figure 4.3). For each figure one measuring week per farm is used and the cows are ranked by their mean methane concentration. The herd with the least variation had considerably lower methane concentrations compared to the herd with the most variation, (herd mean was 342 ppm and 1,024 ppm, respectively). The figures show us that there is variation, also within herds, and cows can be easily ranked based on a simple trait using mean methane concentration.

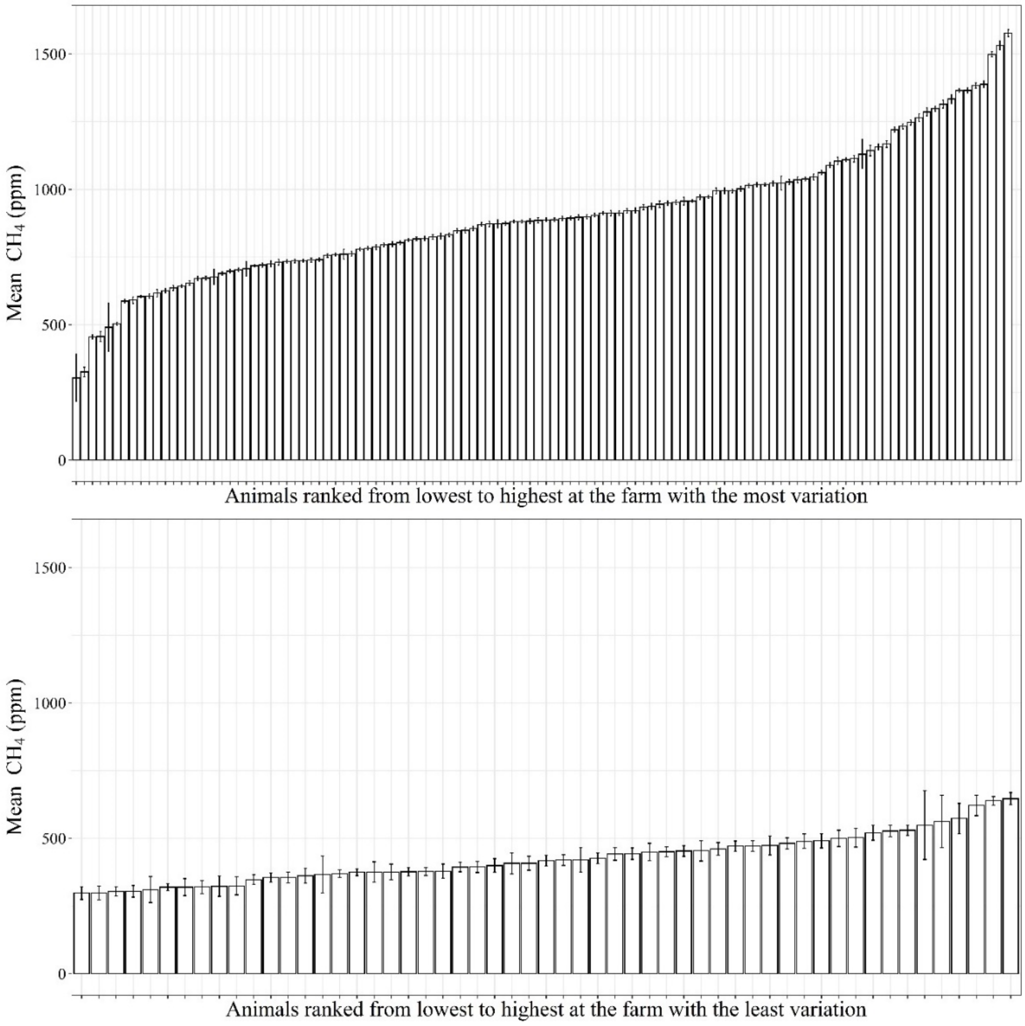


Figure 4.3 *Cows ranked based on their mean methane concentration of one week (ppm ± SE) for the herd with the most variation (top) and least variation.*

4.4 Variation between breeds

One of the farms has two herds of different breeds, one herd with Holstein Friesian cows (herd 15), and one herd with Jersey cows (herd 16). The two breeds are not managed together, and were milked in separate robots with in each robot a sniffer. The mean CH_4 and CO_2 emissions of the Jersey cows were lower (324 ppm) than the mean emissions of the HF cows (411 ppm). Although statistical models are needed to conclude if the breed differences are caused by breed, or by other effects such as differences between the sniffer devices, it does show us that it can be of interest to further investigate genetic differences between breeds.

4.5 Variation between seasons

On four farms where there was no clear change in the sensitivity of the sensor over time, the difference in emissions in the summer or winter season was investigated. Methane emissions appeared to be higher in the winter season than the summer season (Table 4.2). This highlights the importance to correct for seasonal differences in a genetic model. Although there was some reranking of cows, cows that had a high mean emissions in summer also had a high mean emission in winter (Table 4.3 and Figure 4.4).

Table 4.2 *Differences in minimum, maximum, mean, and the standard deviation of methane emissions between the summer and winter season, recorded on four farms without changes in calibration.*

	Summer				Winter			
Farm	Mean	Min	Max	SD	Mean	Min	Max	SD
3	344	236	437	37	356	289	509	38
2	618	299	978	125	806	527	1,266	148
9	451	283	651	98	501	327	752	85
14	408	276	616	69	498	357	674	64

Table 4.3 *Correlation between a cows mean emission in summer and in winter, recorded on four farms without changes in calibration.*

Farm	Correlation (SE)
3	0.62 (0.09)
2	0.49 (0.09)
9	0.43 (0.16)
14	0.44 (0.11)

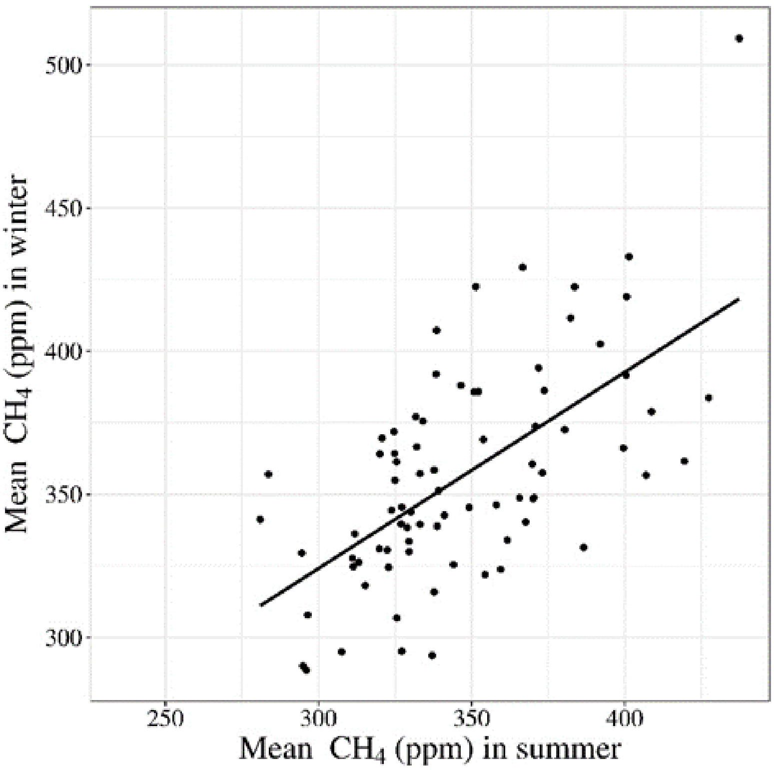


Figure 4.4 *Relationship between the mean methane emission (ppm) of a cow in winter and in summer on farm 3.*

5 Genetic parameters

5.1 Methane

For there to be any selection on a methane trait there needs to be a genetic component. The heritability is an estimation of the amount of variation caused by that genetic component, the higher the heritability the easier it is to achieve genetic progress. For this analysis we included 1,698 Holstein Friesian cows that had a methane phenotype and were also genotyped (i.e., actual DNA information was available). Using the relationships based on these cows, their ancestors in the pedigree (dams and sires), and genotypes of other related cows, the heritability can be estimated. The final relationship matrix, which combines genotyped and ungenotyped animals, included 34,599 animals. Only cows which were at least 75% Holstein Friesian were included in the analysis, as there was not enough (pedigree) data available from crosses with other breeds. Therefore, we could not entangle breed differences at this moment.

Based on the available data, six methane traits have been defined and the heritability estimated. The methane traits were based on the average CH_4 concentration (ppm) per visit, per day, and per week, or the average CH_4/CO_2 ratio per visit, per day, and per week. These methane traits were all estimated using the entire recording period (which differs per farm). The model used was a univariate animal model, with repeated records for all cows. Furthermore the model corrected for differences between farms, year, seasons, days in milk, and parity. We observed a clear effect of days in milk on the level of methane emission, shown by a steep increase in emissions at the start of the lactation (Figure 5.1).

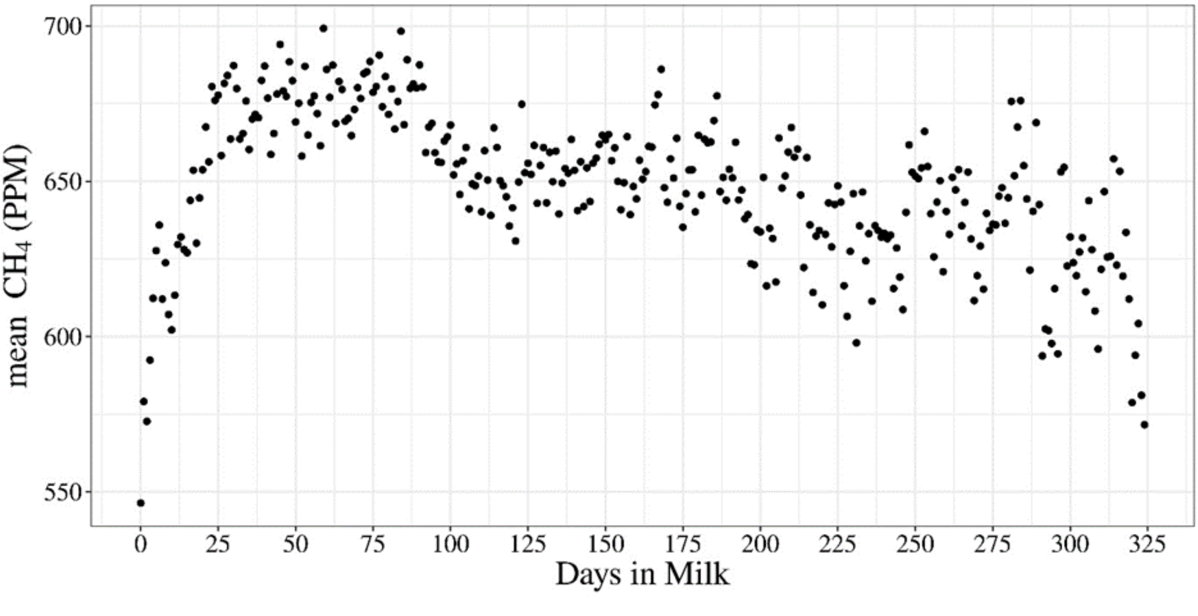


Figure 5.1 *The mean emission of CH_4 per visit on each day in milk after calving.*

The most heritable trait was the average methane emission per week (0.23 ± 0.02). The ratio traits were less heritable (0.01 to 0.03), and thereby less suitable for animal breeding purposes. When compared to heritabilities of other important traits in the Dutch breeding goal, a heritability of 23% is average. For example, full lactation milk production has a heritability of 40%, but health and fertility traits have heritabilities of 2 to 8%. A low to moderate heritability means that data of more cows needs to be recorded, and more repeated measurements per cow, to be able to be able to estimate reliable breeding values. The genetic difference between the 1% highest and lowest emitting cows has been estimated with the genetic standard deviation. The genetic standard deviation in our data was 95 ppm, and therefore the difference between the 1% highest and lowest emitting cows was 474 ppm. Indicating that by selecting your best cows and mating them with the best bulls, methane emission of cows can be lowered.

5.2 Milk yield

From all the genotyped cows with methane emissions recorded, we also had information on test day milk yield. These data were used to estimate genetic parameters for milk yield and a correlation with methane emission. The heritability of a test day milk yield trait with repeated records during the full recording period was 0.28 ± 0.04. The estimated genetic correlation between milk yield and methane emission is low and negative (0.09± 0.05), using the mean methane trait with repeated records (methane trait with the highest heritability). Indicating that cows that produce more milk emit more methane. When selecting low emitters, it will therefore be important to weigh methane emissions and milk yield accordingly in a breeding program. So that negative side effects can be reduced.

6 Conclusions

Sniffers have allowed for long term recording of methane emissions on a large number of cows and farms. We now have data of 1,698 individual cows available, of which all are genotyped. Within this project we have increased the number of herds where we collect individual methane emissions to 17. These data have been used to study the differences in methane emissions between farms and between cows within a farm. We compared the methane measurements with a GreenFeed and with a sniffer for four farms, and have shown that sniffer measurements are poorly correlated with GreenFeed measurements. However, they can be combined in genetic models where a correction is made for the method of recording. We have shown that the mean methane emissions between herds ranges from 342 ppm to 1.024 ppm. When ranking cows within a herd, we have shown that the lowest and highest emitting cow can differ up to 709 ppm (474 ppm when only looking at the genetic background). The estimated genetic parameters show that methane recorded with sniffers has a heritability of 0.23, high enough to achieve genetic progress. But before methane emission can be included in a breeding program, relationships with other breeding goal traits should be further studied with more data.

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