Sustainable dairy breeding: reducing methane emissions in the Netherlands and Flanders

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Abstract

Dairy cows contribute to the emission of methane (CH4), a strong greenhouse gas, into the atmosphere. Reducing CH4 emissions from dairy cows will lower the impact of livestock on global warming. Breeding could be an effective reduction method, and estimating breeding values was the objective of this work. The CH4 emission of 11,595 dairy cows in 89 Dutch herds was measured with sniffers in parts per million (ppm) of exhaled air. The CH4 emission of 397 dairy cows from 1 Dutch herd was measured in grams per day (g/d) of exhaled air using GreenFeed. CH4 measurements took place from 2019 to 2025 (sniffer) and from 2022 to 2025 (GreenFeed). All observations during a week on a cow were averaged into week observations. There were 226,449 week observations for ppm and 11,824 week observations for g/d. Genetic parameters were estimated with ASReml 4.2 using an animal multi-trait repeatability model. Heritabilities (h2) were 0.14, 0.14 and 0.19 for ppm and 0.34, 0.37 and 0.37 for g/d, for respectively parity 1, parity 2 and parity 3 and later (3+). Genetic correlations between different parities for ppm were 0.74, 0.47 and 0.79, and for g/d 0.73, 0.38 and 0.69, between respectively 1 and 2, 1 and 3+, and 2 and 3+. An overall breeding value was calculated for g/d based on traits in parity 1, 2 and 3+. By using a selection index, extra information was added to the overall breeding value in g/d. Traits in the selection index were kg milk production, kg fat production, feed intake and body weight with genetic correlations of respectively 0.39, 0.19, 0.20 and 0.09. The average CH4 emission of a dairy cow was 435 gram per day with a genetic standard deviation of 36 grams per day. The heritability of the trait, the size of the genetic standard deviation, and the fact that genetic correlations with health traits were estimated to be small, makes breeding an effective and powerful tool to mitigate CH4 emissions from dairy cattle in the Netherlands and Flanders. The overall breeding value for CH4 in grams per day is published in the Netherlands and Flanders from April 2025 onwards.

Key words: methane, methane emissions, sustainable dairy breeding, dairy, genetics

Introduction

In Europe, 10.8% of total greenhouse gas (GHG) emissions is from agriculture (EEA, 2023). Methane (CH4) is the second most important GHG, with a warming effect that is about 28 times more powerful than carbon dioxide. CH4 has a half-life in the atmosphere of 12.4 years, and reducing CH4 production leads directly to less GHG in the atmosphere and is therefore an effective measure against climate change (Cottle et al., 2011; Pachauri et al., 2014).

Around 85% of the CH4 coming from cows is formed by enteric fermentation in the rumen, and is emitted by breathing and belching. The other 15% of CH4 coming from cows is from manure storage and management.

Breeding is one of the CH4 mitigation strategies to reduce emissions from dairy cows.

Selecting animals that emit less CH4 than average as parents for the next generation, leads to a future generation that emits less CH4 than the previous generation. To know which animals have the lowest CH4 emissions, phenotyping animals on their CH4 emissions is necessary.

Phenotyping dairy cows on their CH4 emissions is challenging, since those techniques are often expensive and have low-throughput. Recently developed air analyzers, so-called ‘sniffers’, made it possible to phenotype dairy cows on their methane emission on a relatively large scale. Sniffers measure the CH4 emission of cows in parts CH4 per million of analyzed air. GreenFeeds are another CH4 measurement system, and are relatively high-throughput, although they can measure less animals compared to a sniffer, but with more accurate measurements. GreenFeeds measure the CH4 emission of cows in grams CH4 per day.

Materials and Methods

Data

A total of 89 herds, located all over the Netherlands, were selected to phenotype their cows with sniffers (Carltech B.V., Maarheeze, the Netherlands). The sniffers were located in the milking robot (automatic milking system, AMS), so cows were phenotyped during milking. Each herd had only one sniffer installed, so on herds with more than one AMS, there was only one AMS equipped with a sniffer. Because there were not enough sniffers to phenotype on all herds at the same time, sniffers rotated between herds. The first herds started phenotyping in 2019, and by 2025, all herds had a phenotyping period of at least two years.

The sniffer was not connected with the AMS, so observations from the sniffer were merged with AMS data afterwards to assign the sniffer measurements to the correct cow, based on date and time.

Next to the 89 herds that phenotyped their cows with sniffers, data was used from one herd in the Netherlands that phenotyped their cows with GreenFeeds (C-Lock Inc., Rapid City, South Dakota, USA). Three GreenFeeds were installed in this herd, and measurements started in 2022.

There is diurnal variation in CH4 emissions. Cows emit more CH4 after eating, and CH4 emissions are decreasing after a long period without eating. The diurnal variation is dependent on the management/ feeding strategy, and is therefore herd specific.

All sniffer observations were corrected for diurnal variation (van Breukelen et al, 2023). In addition to correction for diurnal variation, GreenFeed observations were also corrected for GreenFeed unit since there were three units on the farm where measurements took place. The correction for diurnal variation and unit was based on the estimated effects for θ and $unit_i$ according to formula 1:

$$y_{ijklmnop} = \mu + \sum_{j=1}^{1}(\sin j\theta 2\pi + \cos j\theta 2\pi) + unit_i + year{*}season_p + animal_k + dim_l + par_m + afc_n + e_o \qquad (1)$$

where $y_{ijklmnop}$ is the measurement of CH4 emission, j is the order of regression, and in this analysis an order of 1 was used, θ is a decimal fraction of the time of measurement during the day following a 24-h diurnal cycle, $unit_i$ is the GreenFeed unit i within the herd, $year{*}season_p$ is year and season p, $animal_k$ is the kth animal, dim_l is days in lactation l, par_m is the mth parity, afc_n is age at first calving in months n and e_o is the residual error o.

The residual error was a random effect, the diurnal variation was a covariable using a fifth order polynomial, all other effects were fixed effects. The estimated effects for diurnal variation are shown in figure 1.

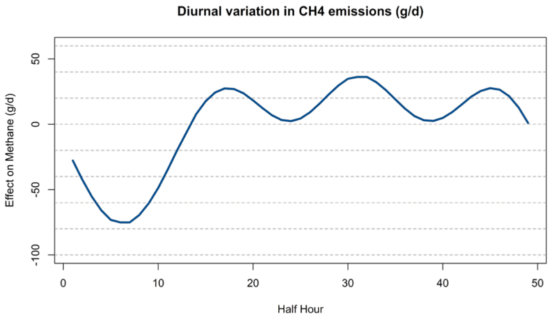

Figure 1. Diurnal variation in CH4 emissions (g/d) on herd with GreenFeed measurements relative to 0 a.m.

All measurements on a cow during a week were averaged into a week observation for both sniffer and GreenFeed.

In April 2025, 457,036 week observations for sniffer from 14,089 dairy cows on 89 different herds were available, and 11,889 week observations from the GreenFeed on 404 cows were available.

For the breeding value estimation, only herdbook animals were allowed and the minimum number of measurements in the week observation was four for sniffer and three for GreenFeed. After those selection criteria, 226,449 weekly sniffer observations from 11,595 cows with 1,380 different sires and 11,824 weekly GreenFeed observations from 397 cows with 154 different sires were selected for the breeding value estimation.

Parameters

Parameters were estimated for parity 1, parity 2 and parity 3+ (parity 3 and higher) and were based on 139,098 weekly sniffer observations and 9,974 weekly GreenFeed observations. The total number of cows was 7,175. The distribution over the parities was 38,934, 33,097 and 67,067 for sniffer observations, and was 5,450, 3,589 and 935 for GreenFeed observations, for respectively parity 1, parity 2 and parity 3+. All cows were at least 87,5% Holstein. Parameters were estimated using an animal model, including a H^{-1} pedigree-genomic augmented inverse matrix (Aguilar et al., 2010; Christensen & Lund, 2010).

Model

The statistical model used for methane emissions was split up into a model for parity 1 and parity 2 and a model for parity 3+. The model for parity 1 and parity 2 is given in formula 2:

$$Y1_{ijklmnopr} = HYS_i + DIM_j + AAC_k + HET_m + REC_n + INB_o + A_p + PME_l + Rest_{ijklmnopr} \qquad (2)$$

The model for parity 3+ is given in formula 3:

$$Y2_{ijklmnopr} = HYS_i + DIM_j + PAR_k + HET_m + REC_n + INB_o + A_p + PME_l + Rest_{ijklmnopr} \qquad (3)$$

In which:

Y1	observation on methane for cows in parity 1 and parity 2;
Y2	observation on methane for cows in parity 3+;
HYS	herd x year x season *i* (for sniffer observations) or farm x year x month *i* (for GreenFeed observations);
DIM	days in lactation *j*;
AAC	age at calving in months *k*;
PAR	parity number *k*;
HET	heterosis effect *m*;
REC	recombination effect *n*;
INB	inbreeding effect *o*;
A	additive genetic effect of animal *p*;
PME	permanent environmental effect *l*;
Rest	residual term *r* of that which is not explained by $Y1_{ijklmnop}$ and $Y2_{ijklmnop}$.

The effects A, PME and Rest were random, the effects HET, REC and INB were covariables, the other effects were fixed.

Correlations with other traits

Genetic correlations between the methane traits and traits in the Dutch/ Flemish total merit index were estimated using the MACE procedure. The MACE procedure can be used to estimate genetic correlations between deregressed sire estimated breeding values (EBVs) of different traits (Larroque and Ducrocq, 1999; Schaeffer, 1994). The initial function of the MACE procedure was to evaluate bulls for one trait across countries by Interbull (Interbull Centre, 2017).

The genetic correlations were estimated for both the overall breeding value for CH4 ppm and CH4 g/d. The breeding values for the methane traits were estimated using a single step approach, and only Holstein bulls with a reliability of at least 40% were used to estimate genetic correlations.

Results & Discussion

Model effects

Figures 2 to 4 show the effects of lactation stage, age at calving and parity number on methane emissions for gpd. These effects resulted from the model solutions.

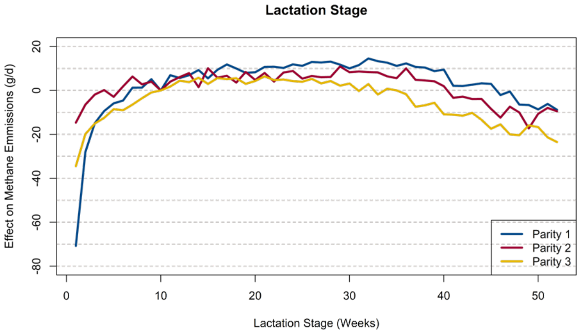

Figure 2. Effect of lactation stage in weeks on methane emissions in grams per day for parity 1, parity 2 and parity 3+. Solutions are standardized with week 10 within each lactation.

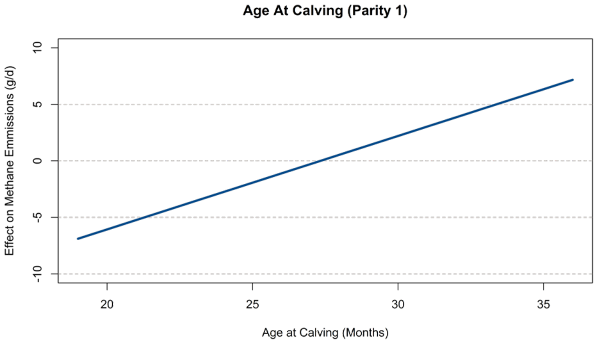

Figure 3. Trendline of solutions for effect of age at calving in months on methane emissions in grams per day for parity 1.

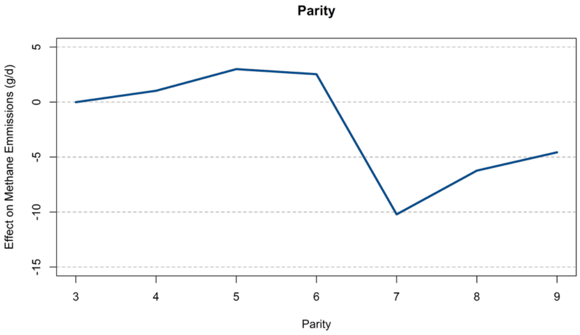

Figure 4. Effect of parity number on methane emissions in grams per day.

For lactation stage, the difference between the top of the graph in mid-lactation and the bottom of the graph in early and late lactation stage is about 30 grams per day. The estimates per week are relative to week 10.

Heifers calving at an older age have higher methane emissions. The effect of age at calving is about 15 grams per day difference between animals calving at a young and those calving at an old age. The effects are relative to a calving age of 27 months.

For parity number, animals in parity three, four, five and six have higher methane emissions compared to the older cows in later parities. The difference is about 10 grams per day. The effects in the figure are relative to parity 3.

Genetic parameters

Genetic parameters were estimated for weekly CH4 emissions in ppm measured with sniffers (CH4 ppm) and weekly CH4 emissions in grams per day measured with GreenFeeds (CH4 g/d) for parity 1, parity 2 and parity 3+. Table 1 shows the heritabilities, repeatabilities and genetic standard deviations of the methane traits. Table 2 presents the genetic correlation between parities for the methane traits.

Table 1. Heritabilities (h2), repeatabilities (r2), and genetic standard deviation (σ_a) for methane traits in parity 1 (par.1), parity 2 (par.2), and parity 3+ (par.3).

Trait	h^2	r^2	σ_a
CH4 ppm par.1	0.14	0.49	21.1
CH4 ppm par.2	0.14	0.55	23.3
CH4 ppm par.3	0.19	0.55	28.3
CH4 g/d par.1	0.34	0.60	43.2
CH4 g/d par.2	0.37	0.60	50.4
CH4 g/d par.3	0.37	0.60	50.4

The heritabilities in table 1 shows that CH4 emissions have a moderate heritability, with heritabilities between 0.14 and 0.19 for weekly measurements with sniffers and heritabilities between 0.34 and 0.37 for weekly measurements with GreenFeeds. Higher heritabilities for CH4 emissions measured with GreenFeeds are expected since measurements of GreenFeeds are of a higher quality.

The measurements for CH4 ppm are re-scaled and converted to a mean of 0, what makes that the standard deviations given in table 1 cannot directly be related to the measurements in ppm.

The genetic standard deviations of CH4 g/d in table 1 are based on the real observations. These are different from the genetic standard deviation of EBV CH4 g/d on an absolute scale, as that one is taken into account the reliability of the EBVs.

Table 2. Genetic correlations for methane traits between parity 1 and 2 (par.1-2), parity 2 and 3+ (par.2-3), and parity 1 and 3+ (par.1-3).

	genetic correlations		
trait	par.1-2	par.2-3	par.1-3
CH4 ppm	0.74	0.79	0.47
CH4 g/d	0.73	0.69	0.38

The genetic correlations in table 2 between parity 1 and parity 2 and between parity 2 and parity 3+ are considered as moderate to strong genetic correlations with values in the range 0.69 – 0.79.

Between parity 1 and parity 3+, the genetic correlations were lower and considered as moderate with a value of 0.47 for CH4 ppm and 0.38 for CH4 g/d. This lower correlation can be expected based on the estimated correlations between the other parities.

The genetic correlation between CH4 ppm and CH4 g/d was not estimated in this research, since the number of cows and observations was relatively small for CH4 g/d and there were no cows with observations on both CH4 ppm and CH4 g/d. This genetic correlation was already estimated for the Dutch population Holstein cows, based on a dataset with more CH4 g/d observations compared to this research, at 0.76 (van Breukelen et al., 2023). This genetic correlation was used in the genetic variance/covariance matrix between CH4 ppm and CH4 g/d for all combinations of parities.

Overall breeding values

Breeding values were estimated for both CH4 ppm and CH4 g/d for parity 1, parity 2, and parity 3+. An overall breeding value was calculated for both traits based on the EBV in parity 1, parity 2, and parity 3 with a weight of respectively 0.423, 0.288, and 0.227.

Correlation with other traits

The genetic correlations with the total merit index and the underlying traits of this index are presented in Table 3.

Table 3. Genetic correlations for overall methane traits with production, health, and conformation traits. (EBVs for methane traits: higher EBV is lower methane emission)

trait	CH4 ppm	CH4 g/d
NVI (total merit index)	-0.00	-0.06
milk production	-0.08	-0.39
fat production	-0.28	-0.19
protein production	-0.01	-0.18
longevity	0.12	0.03
udder conformation	-0.08	-0.01
feet & legs	0.02	0.04
fertility index	0.00	0.04
udder health index	0.05	-0.07
claw health	0.01	0.07

feed intake	-0.11	-0.20
body weight	-0.03	-0.09

Higher breeding values for methane reflect lower CH4 emissions, since lowering the CH4 emissions is desirable. Therefore, the genetic correlation with production is negative, meaning that a higher breeding value for production corresponds to a lower breeding value for methane. Animals that are more productive, will on average emit more CH4.

The correlations of CH4 g/d with the other traits are somewhat larger than the correlations of CH4 ppm with the other traits. This is expected given the fact that the GreenFeed is able to measure CH4 emissions more precisely compared to the sniffer.

All correlations are small, only the correlation between CH4 g/d and milk production can be considered as moderate. The largest genetic correlations for CH4 g/d are found with milk production (-0.39), fat production (-0.19), protein production (-0.18), feed intake (-0.20), and body weight (-0,09). The correlations with health and conformation traits are small and very close to zero, meaning that it is possible to breed for less CH4 emissions without affecting the health and conformation of the animals.

Selection index

Because the number of phenotyped animals is relatively small compared to other traits, the reliability of the EBVs is rather low. To increase this reliability, indicators traits are used in a selection index.

The methane trait used in the selection index is CH4 g/d because the unit of this trait makes it possible to calculate the genetic progress, reduction of CH4 emissions, as a quantity. This will also be the trait that is published to farmers and bull-owners. CH4 g/d does still contain information about CH4 ppm by using the genetic covariance between both traits.

Next to CH4 g/d, the other traits in the selection index are milk production, fat production, feed intake, and body weight. These traits have the largest correlations with methane, and that is also expected from a biological point of view.

Table 4 presents the genetic standard deviations and heritabilities of the traits in the selection index and the genetic correlations between them. The correlations between the traits are all estimated based on bull breeding values. The genetic standard deviations are based on the EBVs, with for relative EBVs a fixed genetic standard deviation of 4.5.

Table 4. Genetic standard deviations of EBV (σ_a) and heritabilities (diagonal) and *genetic correlations* (below diagonal) of the traits in the selection index.

trait	σ_a	CH4 g/d	milk production	fat production	feed intake	body weight
CH4 g/d (-)	4.5	0.56				
milk production (kg)	745	*-0.39*	0.58			
fat production (kg)	28	*-0.19*	*0.50*	0.57		
feed intake (kg)	1.37	*-0.20*	*0.56*	*0.67*	0.20	
body weight (-)	4.5	*-0.09*	*0.05*	*0.15*	*0.41*	0.60

The heritability for CH4 g/d, 0.56, is based on the heritability for the overall trait, which takes into account that there are multiple measurements on CH4 emissions, in multiple parities.

Daughter proven bulls will not profit much from the selection index. The reliability of their breeding value for CH4 g/d will, depending on the number of phenotyped daughters, increase with 0 to 3% by using the correlation structure with the other traits in the selection index.

Genotyped animals without progeny information on CH4 emission will increase their EBV with 5 to 10%, depending on their reliabilities for the traits in the selection index.

Publication

The breeding value that is published by CRV is overall CH4 g/d after the selection index. This is a relative breeding value with mean of 100, based on animals born in 2020, and a genetic standard deviation of 4.0 (assuming a reliability of 80%).

The mean CH4 emission for Dutch and Flemish Holstein cows is 435 grams per day (van Breukelen et al., 2023), with a genetic standard deviation of 36 grams per day. This genetic standard deviation is on the scale of relative breeding values and is standardized to 80% reliability, so 4 points breeding values is equal to 36 grams per day. The true genetic standard deviations are given in table 1.

Mating an average cow (EBV 100) with a bull with an EBV of 104 for CH4 g/d will, on average, result in offspring with EBV 102, which corresponds to 18 grams less CH4 emissions per day.

The average reliability for daughter proven bulls is 46.5%, with reliabilities up to 83%. Number of daughters is in the range of 1 – 576. The average reliability for genomic bulls is 32.2%, with reliabilities up to 43%. These reliabilities will increase as more animals are phenotyped in the coming years.

EBVs will be published for bulls with at least one phenotyped daughter, and for genotyped bulls if the bull-owners give CRV permission to do so. The EBV should have a reliability of at least 25%. If not, a parent average is calculated and published when the reliability of the overall EBV before selection index is at least 10%.

Cow EBVs are published for all cows with phenotypic information and all cows with genotypic information. If not, parent averages are calculated and published if the reliability of the EBV after selection index is at least 10%.

EBVs will only be estimated and published for Holstein Friesian (HF) cows, as there is only phenotypic data available from HF cows.

Conclusions

CH4 emissions in dairy cows can be measured large-scale. More than 14,000 dairy cows were phenotyped with sniffers in the period 2019-2025 on 89 Dutch herds, and more than 400 dairy cows were phenotyped with GreenFeeds in the period 2022-2025 on one Dutch herd.

CH4 emissions of dairy cows is a heritable trait. CH4 ppm has a heritability of respectively 0.14, 0.14 and 0.19, while CH4 g/d has a heritability of respectively 0.34, 0.37 and 0.37, for parity 1, parity 2, and parity 3+.

The EBV that is published is overall CH4 g/d. A mean EBV, 100, corresponds to a CH4 emission of 435 grams per day. The genetic standard deviation is 4 points and corresponds to 36 grams per day. Lower CH4 emissions are desirable, so EBVs above 100 reflects animals with below average daily CH4 emissions. Mating a cow with EBV 100 with a bull with EBV 104 results, on average, in offspring with EBV 102. The CH4 emission of the offspring will be, on average, 18 grams per day lower than her dam.

More productive animals tend to have a somewhat higher CH4 emission. So, animals with high EBVs for production tend to have lower EBVs for CH4 emission on average. However, genetic correlations with production are small to moderate (-0.39, -0.19, and -0.18 for respectively milk, fat, and protein), indicating that there is still enough variation between animals that makes it possible to select animals that are productive with lower CH4 emissions. Also higher feed intake and more body weight are related to somewhat higher CH4 emissions. So, animals with higher EBVs for feed intake and bodyweight tend to have lower EBVs for CH4 emission. Genetic correlations on EBVs are -0.20 and -0.09 for respectively feed intake and body weight.

Genetic correlations with health, longevity, and conformation traits are estimated to be small. So breeding on lowering CH4 emissions from dairy cows will not affect the health, longevity, and conformation of the animals.

The reliabilities for bulls are ranging from 25 to 83%, depending on their pedigree, daughter information, and genomic information. The average reliability is 46.5% for daughter proven bulls and 32.2% for genomic bulls. Reliabilities will increase when more cows are phenotyped.

Estimating breeding values for CH4 emissions made sustainable dairy breeding possible in the Netherlands and Flanders. Farmers can breed for dairy cows which emit less CH4 without compromising on production and health.

Acknowledgements

Setting up a breeding value estimation for CH4 emissions was part of the *Climate Smart Cattle Breeding* project. This project aimed at: 1. phenotyping dairy cows in the Netherlands on their CH4 emissions, 2. estimating breeding values for cows and bulls in the Netherlands, 3. developing tools to make the genetic level of CH4 emissions on a herd visible for farmers, and 4. encouraging farmers to reduce the CH4 emissions of their cows by selective breeding. The project was conducted from 2020 to 2025 and was funded by the *Dutch ministry of Agriculture, Fisheries, Food Security and Nature* (LVVN, The Hague, the Netherlands) and the project partners Wageningen University and Research (WUR, Wageningen, the Netherlands), FrieslandCampina (Royal Friesland Campina, Amersfoort, the Netherlands) and CRV (CRV u.a., Arnhem, the Netherlands).

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