Statistical Indicators

E-48

Breeding value methane

▪ Introduction

Methane is a potent greenhouse gas that contributes to global warming. The warming effect of methane is about 34 times more powerful than carbon dioxide, so reducing methane emissions can contribute significantly to reducing global warming. In both the Netherlands and Flanders, agriculture is tasked with reducing methane emissions.

About three-quarters of methane emissions from agriculture come from ruminants, with cows accounting for the majority. 85% of a cow's methane emissions comes from enteric rumen fermentation, where the cow will burp out the methane formed. The remaining 15% methane emissions from a cow comes from manure. Good manure management can provide a reduction in methane emissions here.

Methane emissions from cows can be measured with so-called 'sniffers' and GreenFeeds (van Breukelen et al., 2021). Since 2019, 'sniffers' have been used to measure methane emissions from cows on about 100 dairy farms in the Netherlands. Since 2022, measurements have also been made with GreenFeeds.

In addition to the measured feed intake, information can also be used from an animal's milk production, fat production, feed intake and body weight. In fact, these four characteristics provide a prediction of a cow's methane emissions.

The data from these two sources (measured methane emissions and predicted methane emissions) are used in the breeding value estimate for methane emissions. This E-chapter explains the breeding value estimation for methane emissions in more detail.

▪ Data

Methane measurements

1. **Sniffer**

Sniffers are installed in milking robots, and measure the air composition of the air collected in the feeding trough of the milking robot. The sniffer measures the concentration of methane in the air during the day. By linking to AMS (automatic milking system) data based on date and time, it is possible to identify which measurements of methane concentration in the air belong to which cow.

The sniffer measures the concentration of methane in the air in parts per million (ppm); it also measures the carbon dioxide concentration in parts per million. There is already a background concentration of methane in a dairy barn, this is caused by methane from manure and from all the air the cows exhale. The sniffer is not able to distinguish between methane from background concentrations and methane exhaled by the cow currently in the milking robot. Also, the measured methane concentration will be greater when the cow's head is closer to the sniffer at the time of exhalation. All of this means that a sniffer cannot measure a cow's methane emissions very precisely. Nevertheless, previous research has shown that sniffers do have a good ability to rank animals by methane emissions. This is also basically what breeding is all about, ranking animals on a trait to make the right selection.

All measurements in one week are combined into a weekly average. This requires a minimum of four measurements in one week. Since the time of day of measurement can have a considerable influence on methane emissions (emissions increase after a cow has eaten), this is also corrected for in the individual measurements. The formula to correct for diurnal variation is (van Breukelen et al, 2023):

$$y_{ij} = \mu + farm_i \cdot \sum_{j=1}^{1}(\sin j\theta 2\pi + \cos j\theta 2\pi) + e_i,$$

where y_{ij} is the measurement of methane emission, *farm* is the fixed effect for the *i*th farm, *j* is the order of regression, and in this analysis is chosen for an order of 1, θ is a decimal fraction of the time of measurement during the day following a 24-h diurnal cycle, and *e* is the residual error.

By working with weekly averages, the inaccuracy in the measurements by the sniffer is averaged out as much as possible. The final observation used in the breeding value estimation is the average methane emission in a week represented in parts per million.

2. GreenFeed

The GreenFeed is a type of concentrate feeding station that also measures air concentration. However, the difference with the sniffer is that the GreenFeed actively sucks in all the air, analyzing all the cow's exhaled air. This allows the GreenFeed to display the cow's methane output in grams per day.

Again, to reduce inaccuracy in the observations, a weekly average is calculated if at least three measurements were taken on an animal during that week. Also with the GreenFeed, before entering the weekly average, individual measurements are corrected for time of measurement (diurnal variation). Because it is possible that there are multiple GreenFeeds within an herd, there is also a correction for GreenFeed box within an herd. De effects for diurnal variation and GreenFeed-box are estimated in the same model which also takes into account other effects like lactation stadium, variation between animals and parity number. The estimated effects are used to correct the measured methane emission. The model to correct for diurnal variation and GreenFeed box is:

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

where $y_{ijklmnop}$ is the measurement of methane 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 *k*th animal, dim_l is days in lactation *l*, par_m is the *m*th 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.

Data in the breeding value estimation

The breeding value estimation uses both the sniffer and GreenFeed data. Most of the information is extracted from the sniffer data since this data set is many times larger than the

GreenFeed data, but this does mean that all animals get a breeding value that can be expressed in grams per day by using the genetic correlation between parts per million and grams per day.

With this method, all available information is used, and all animals do get a breeding value that can be expressed in grams per day or kilograms per year. This makes the translation between genotypic and phenotypic progress possible and thus it is also possible to demonstrate that methane reduction is or can actually be achieved through breeding.

Data selection

Cows and observations entering the breeding value estimation must meet a number of requirements. The requirements are outlined below:

1. an animal with observations is female, pedigree registered and the sire is known;
2. an animal with observations has less than 50% BBL blood lining;
3. calving age of heifers is no younger than 1.08 years or older than 3.00 years;
4. calving date of first time calving is known;
5. cow is no longer than 350 days in lactation;
6. an individual methane measurement does not deviate from the average methane emission in parts per million (for sniffer measurements) by more than four standard deviations
7. an individual methane measurement is between 150 and 1200 parts per million, with measured carbon dioxide being between 1000 and 10000 parts per million;
8. a weekly observation (weekly average) includes for sniffer at least four measurements and for GreenFeed at least 3 measurements;
9. cow has been in the GreenFeed for at least two minutes for an individual GreenFeed measurement.

In April 2025, the analysis was conducted on about 12,000 cows with sniffer data and about 400 cows with GreenFeed data.

Statistical model

The statistical model used in the animal model for methane emissions is split into a model for lactation 1 and 2 and a model for lactation 3+. The statistical model for lactation 1 and 2 is as follows:

$$Y1_{ijklmnopr} = HYS_i + DIM_j + AAC_k + HET_m + REC_n + INB_o + A_p + PME_l + Rest_{ijklmnopr}$$

And the model for lactation three and higher is:

$$Y2_{ijklmnopr} = HYS_i + DIM_j + PAR_k + HET_m + REC_n + INB_o + A_p + PME_l + Rest_{ijklmnopr}$$

Where:

$Y1_{ijklmnopr}$: observation on farm*year*season *i* (for sniffer data) or farm*year*month *i* (for GreenFeed data), with days in lactation *j*, age at calving *k*, heterosis effect *m*, recombination effect *n*, inbreeding effect

o, permanent environment effect *l*, to animal *p* in lactation 1 or lactation 2;
$Y2_{ijklmnopr}$: observation at farm *year *season *i* (for sniffer data) or farm *year *month *i* (for GreenFeed data), with days in lactation *j*, lactation number *k*, heterosis effect *m*, recombination effect *n*, inbreeding effect *o*, permanent environmental effect *l*, to animal *p* in lactation 3 or higher;
HYS_i : farm * year * season *i* (for sniffer data) or farm * year * month * *i* (for GreenFeed data);
DIM_j : days in lactation *j*;
AAC_k : age at calving *k*;
PAR_k : parity number *k*;
HET_m : heterosis effect *m*;
REC_n : recombination effect *n*;
INB_o : inbreeding effect *o*;
A_p : additive genetic effect of animal *p*;
PME_q : permanent environmental effect *l*;
$Rest_r$: residual term *r* of that which is not explained by $Y1_{ijklmnop}$ and $Y2_{ijklmnop}$.

The effects A, PME and Rest are random, the effects HET, REC and INB are covariables, the remaining effects are fixed.

Management effects between and within farms are corrected by farm x year x season of calving. Differences in rations, for example, are thereby corrected as much as possible, since rations explain a significant portion of methane emissions. Differences in measurement level of the sniffers are also corrected by this. Therefore, for the GreenFeed observations, there is also a precorrection by GreenFeed station, since there are multiple GreenFeeds on the same farm.

Dry matter intake largely determines methane emissions from cows. However, lactation stage, lactation number and physical development of cows largely determine the dry matter intake of cows. Therefore, these effects are corrected for in the model for methane emissions.

Figures 1 through 3 show the effects of lactation stage, age at calving and parity number on methane emissions. The effects result from the model solutions.

For lactation stage, there is a difference of about 30 grams per day between the top of the graph in mid-lactation and the bottom of the graph in early and late lactation stage. A higher methane emission in the middle of lactation can be explained because milk production and feed intake will also be highest here. The effects per week are compared here with respect to week 10. The effect at week 10 is zero in the graph.

Animals calving at an older age have higher methane emissions. This is explained by the fact that animals calving older are on average also more developed, leading to higher body weight and feed intake. The effect of age at calving is about 15 grams per day difference between animals calving young and those calving old. The effects are expressed relative to a calving age of 27 months. The effect at 27 months is zero in the graph. The effects are divided into one-month classes ranging from 19 months to 36 months. For lactation two, the classes are classified from a calving age of 28 months to 48 months. The same pattern is visible for lactation two as for lactation one.

For parity number, animals in lactation 3, 4, 5 and 6 have higher methane emission than animals in higher lactations. This is explained by the fact that older animals will also absorb less feed and also have lower milk production compared to mature cows in lactation 3, 4, 5 and 6. The is difference is about 10 grams per day. The effects in the figure are relative to lactation 3. The effect of lactation 3 in the figure is zero.

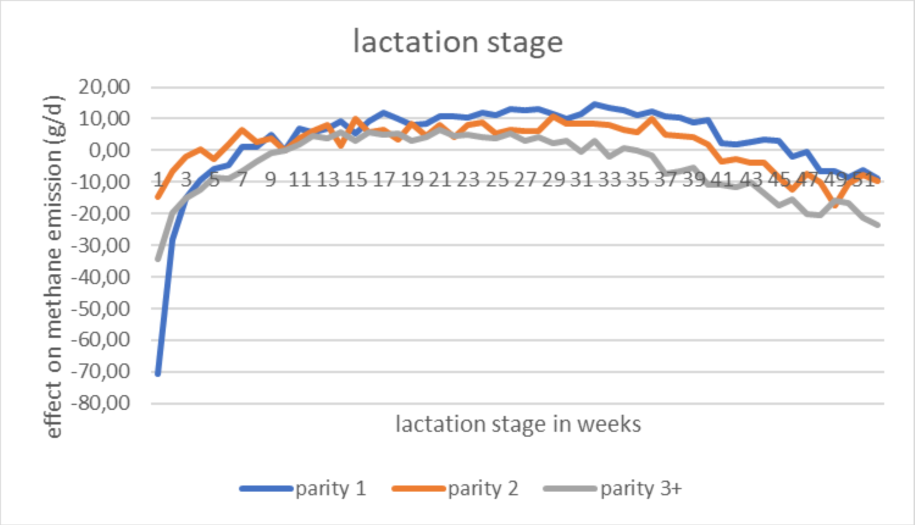

Figure 1. Effect of lactation stage in weeks on methane emissions in grams per day.

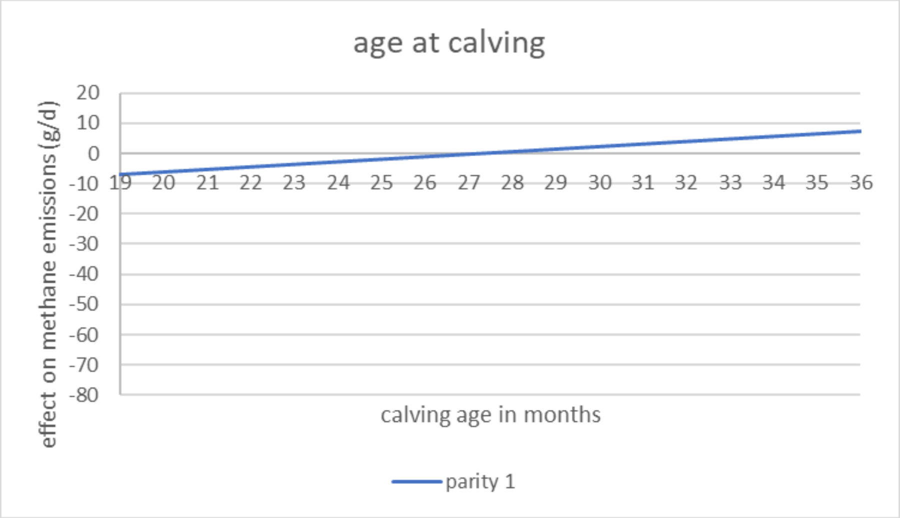

Figure 2. Effect of calving age in months on methane emissions in grams per day for cows in parity 1.

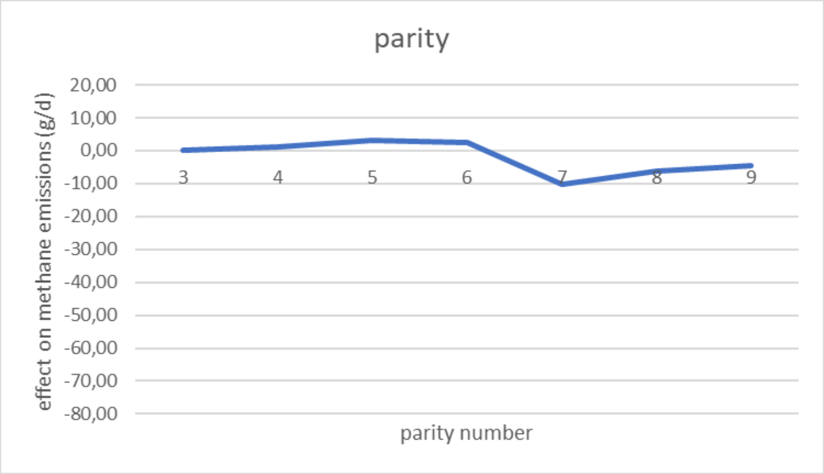

Figure 3. Effect of parity number on methane emissions in grams per day.

Parameters

The heritabilities, repeatabilities, and genetic standard deviations of the methane traits are presented in table 1.

Table 1. Heritability (h^2), repeatability (r^2) and genetic standard deviation of the methane traits in parity 1 (p.1), parity 2 (p.2) and parity 3+ (p.3+).

trait	unit	h^2	r^2	genetic standard deviation
sniffer p. 1	parts per million	0.14	0.49	20.0
sniffer p. 2	parts per million	0.14	0.55	21.4
sniffer p. 3+	parts per million	0.19	0.55	28.0
GreenFeed p. 1	grams per day	0.34	0.60	42.4
GreenFeed p. 2	grams per day	0.37	0.60	51.9
GreenFeed p. 3+	grams per day	0.37	0.60	51.9

The heritability of methane emissions in parts per million (sniffer) is 0.14 for lactation 1, 0.14 for lactation 2 and 0.19 for lactation 3+. The heritability of methane emission in grams per day (GreenFeed) is 0.34 for lactation 1 and 0.37 for both lactation 2 and lactation 3+.

The genetic correlation between parts per million and grams per day is 0.76 and was estimated by Wageningen Livestock Research (WLR) (van Breukelen et al., 2023).

Breeding values

Nine breeding values are estimated, the first eight of which are shown below. The ninth breeding value follows in section *Selection index*.

Based on both parts per million and grams per day, a breeding value is estimated for parity 1, 2 and 3+ (2 traits x 3 parities = 6 breeding values), with a total breeding value also determined for both traits based on the three lactation breeding values. This makes eight breeding values in total.
The weightings in the total breeding value are 0.423, 0.288 and 0.227 for parity 1, parity 2 and parity 3+, respectively.

Using the genetic correlation between parts per million and grams per day, all animals with phenotypic data for parts per million also get a breeding value in grams per day, and vice versa, the same applies: animals with phenotypic data in grams per day also get a breeding value in parts per million.

Selection index

The total breeding value in grams per day will be inserted into the selection index. The breeding values for milk production, fat production, feed intake and body weight will also be inserted into the selection index. From literature, and WLR has the same findings, it is known that these are the traits that in absolute terms have the highest genetic correlation with methane emissions.
Through the genetic correlations, information from the breeding values for milk production, fat production, feed intake and body weight can be used to increase the reliability of the breeding value for methane in grams per day. In addition, for animals without phenotypic data, a breeding value for methane emissions can still be estimated based on these predictors.

In the breeding value estimation, correlations of 0.39, 0.19, 0.20 and 0.09 are used between methane emissions and milk production, fat production, feed intake and body weight, respectively. Thus, higher milk production, higher fat production, higher feed intake and higher body weight correspond to higher methane emissions, which is actually undesirable because attempts are made to reduce methane emissions.

The result of the selection index is a breeding value of methane in grams per day including predictors.
Using the selection index increases the reliability of the breeding value for methane in grams per day by about 7 to 8% for bulls without daughter information.

Publication

The trait that will be published is methane emissions in grams per day including predictors. A breeding value above 100 will mean more genetic predisposition to lower methane emissions, while a breeding value below 100 means lower genetic predisposition to lower methane emissions. Breeding values above 100 are therefore desirable, as this gives lower methane emissions. A breeding value of 100 will correspond to methane emissions of 435 grams per day, with four point breeding values corresponding to 36 grams per day.

Breeding values will only be estimated for Holstein cattle.

Base

See chapter ‘Bases for breeding values and base differences’.

Literature

Van Breukelen, A.E. , Aldridge, M.N. , Veerkamp, R.F. , Koning, L. , Sebek, L.B. , de Haas, Y. (2021). Measurements of enteric CH4 from two noninvasive sensors for genetic evaluations. *WIAS Annual Conference 2022*.

Van Breukelen, A. E., Aldridge, M. N., Veerkamp, R. F., Koning, L., Sebek, L. B., & de Haas, Y. (2023). Heritability and genetic correlations between enteric methane production and concentration recorded by GreenFeed and sniffers on dairy cows. *Journal of Dairy Science*, *106*(6), 4121-4132.