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Selective breeding as a mitigation tool for methane emissions from dairy cattle

Y. de Haas [a,*], R.F. Veerkamp [a], G. de Jong [b], M.N. Aldridge [a]

[a] Animal Breeding and Genomics, Wageningen University & Research, 6700 AH Wageningen, the Netherlands
[b] CRV, 6800 AL Arnhem, the Netherlands

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ABSTRACT

The global livestock sector, particularly ruminants, contributes substantially to the total anthropogenic greenhouse gases. Management and dietary solutions to reduce enteric methane (**CH_4**) emissions are extensively researched. Animal breeding that exploits natural variation in CH_4 emissions is an additional mitigation solution that is cost-effective, permanent, and cumulative. We quantified the effect of including CH_4 production in the Dutch breeding goal using selection index theory. The current Dutch national index contains 15 traits, related to milk yield, longevity, health, fertility, conformation and feed efficiency. From the literature, we obtained a heritability of 0.21 for enteric CH_4 production, and genetic correlations of 0.4 with milk lactose, protein, fat and DM intake. Correlations between enteric CH_4 production and other traits in the breeding goal were set to zero. When including CH_4 production in the current breeding goal with a zero economic value, CH_4 production increases each year by 1.5 g/d as a correlated response. When extrapolating this, the average daily CH_4 production of 392 g/d in 2018 will increase to 442 g/d in 2050 (+13%). However, expressing the CH_4 production as CH_4 intensity in the same period shows a reduction of 13%. By putting economic weight on CH_4 production in the breeding goal, selective breeding can reduce the CH_4 intensity even by 24% in 2050. This shows that breeding is a valuable contribution to the whole set of mitigation strategies that could be applied in order to achieve the goals for 2050 set by the EU. If the decision is made to implement animal breeding strategies to reduce enteric CH_4 production, and to achieve the expected breeding impact, there needs to be a sufficient reliability of prediction. The only way to achieve that is to have enough animals phenotyped and genotyped. The power calculations offer insights into the difficulties that will be faced in trying to record enough data. Recording CH_4 data on 100 farms (with on average 150 cows each) for at least 2 years is required to achieve the desired reliability of 0.40 for the genomic prediction.
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Implications

The global livestock sector, particularly ruminants, contributes substantially to the total anthropogenic greenhouse gases. Management and dietary solutions to reduce enteric methane emissions are extensively researched. Animal breeding that exploits natural variation in methane emissions is an additional mitigation solution that is cost-effective, permanent, and cumulative. By adding methane production to the Dutch breeding goal, selective breeding can reduce the methane intensity by 24% in 2050. This shows that breeding is a valuable contribution to the whole set of mitigation strategies that could be applied in order to achieve the goals for 2050 set by the EU.

Introduction

Livestock production is a significant contributor to greenhouse gas emissions globally at 5.6–7.5 Gigatonne of carbon dioxide equivalent (**$GtCO_2e$**) (Herrero et al., 2016). Methane (**CH_4**) produced via enteric fermentation by ruminants is the largest contributor to agricultural greenhouse gases at 1.6–2.7 $GtCO_2e$ (Herrero et al., 2016). In the Netherlands, dairy cattle are the largest contributor to enteric CH_4 with 49% of the total (Van der Maas et al., 2009).

Genetic selection of low CH_4 emitting cows is a potential method to reduce the contribution of the dairy sector (Knapp et al., 2014). Unlike management and diet strategies which have been extensively researched (Beauchemin et al., 2008), genetics has the benefit that the effects of selection are additive and permanent. Selection experiments in other ruminants, including beef cattle (Bird-Gardiner et al., 2015), and sheep (Pinares-Patiño et al.,

* Corresponding author.
E-mail address: yvette.dehaas@wur.nl (Y. de Haas).

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2013; Jonker et al., 2017), have shown a decrease in CH_4 production when selecting for low CH_4 lines.

Breeding programmes use selection index theory to ensure maximum gains and that trait changes are in the desired direction. The current selection indexes for the Dutch national breeding goal include 15 traits from the following categories; milk production, milk components, feed efficiency, health, reproduction, longevity, calving, and conformation (CRV, 2018). It is possible to add CH_4 as another category of traits to such selection indexes. Before a CH_4 trait can be added to a selection index, it needs to be: clearly defined, recordable, affordable, have phenotypic variation, be heritable, and the genetic correlations between other traits in the index need to be known (Hazel, 1943).

Methane intensity is a promising CH_4 trait to be included in a selection index (Lassen and Løvendahl, 2016; Kandel et al., 2018). The definition of CH_4 intensity is the amount of CH_4 produced per unit of milk produced (g CH_4/kg milk). It is more advantageous to have fewer cows that produce more milk per g of CH_4 (possible with selection for reduced CH_4 intensity), than to have more cows that produce less CH_4 but less milk, which could occur if selecting on CH_4 production alone (g CH_4/day). It has already been shown that, when assuming a fixed total milk production, selection for CH_4 intensity or increased productivity will increase an individual's total CH_4 but the overall CH_4 of the farming system is reduced (Van der Maas et al., 2009; Kandel et al., 2018).

Methane from cow's breath, recorded with non-dispersive infrared units or 'sniffers', have been investigated in small studies as an accurate method of recording CH_4 intensity (Lassen et al., 2012; Lassen and Løvendahl, 2016; Difford et al., 2018; Van Engelen et al., 2018). The sniffer method is more affordable, can be scaled up, and easily incorporated with current milking technologies, compared to other methods of recording CH_4 (Lassen and Løvendahl, 2016). Methane concentration recorded with sniffers has a phenotypic SD of between 65 and 137 ppm (Difford et al., 2018; González-Recio et al., 2020; López-Paredes et al., 2020; Olijhoek et al., 2020), and heritability ranges between 0.10 and 0.26 (Difford et al., 2020; López-Paredes et al., 2020; Olijhoek et al., 2020). Some genetic correlations have been published for CH_4 production and intensity, and traits already included in the Dutch national breeding goal selection index (Lassen and Løvendahl, 2016; Breider et al., 2019; Difford et al., 2020).

The effect of including CH_4 intensity in the selection index of the Dutch national breeding goal is not known. Recent literature suggests that if current selection indexes are used with no selection on CH_4 traits, then CH_4 production will increase and CH_4 intensity will decrease (González-Recio et al., 2020). With active selection for CH_4 intensity, CH_4 production will continue to increase but the rate of genetic improvement will be faster in reducing CH_4 intensity (Kandel et al., 2018; Flay et al., 2019). This would reduce the total contribution of dairy cattle to global greenhouse gas production (Van der Maas et al., 2009).

So far, sniffer devices have measured CH_4 for short periods of time, under experimental conditions, or with a limited number of animals or farms. Before a trait can be included in a selection index, there needs to be reasonable confidence in the accuracy of estimated breeding values (**EBVs**) (Mrode, 2014). With an increasing rate of genotyping and the difficulty in recording CH_4 at an individual cow level, it is probable that any future CH_4 trait will rely on genomic prediction. Genomic prediction will facilitate a shorter time until adoption, assuming there is sufficient accuracy. There is a gap in the literature in regards to how many animals and farms, sniffer recorded CH_4 would need to be measured on, before an acceptable accuracy for genomic prediction is reached, and for the trait to be included in a selection index.

Our objective for this study was to determine the potential effects of including CH_4 production as a trait in the selection index of the Dutch national breeding objective. Preliminary results of this objective have been published in an abstract form (de Haas et al., 2019). Furthermore, determine how many cows and sniffer devices would be needed to achieve an accuracy suitable to include CH_4 as a trait in such an index.

Material and methods

Dutch national breeding goal

Breeding programmes use selection index theory to ensure maximum gains and that trait changes are in the desired direction. The current selection indexes for the Dutch national breeding goal include 15 traits from the following categories; milk production, milk components, feed efficiency, health, reproduction, longevity, calving, and conformation (CRV, 2018). Table 1 shows the correlations between the traits in the Dutch breeding goal, as well as the heritabilities and the number of daughters with records for that trait.

Genetic parameters for methane production

There are not many papers that have published correlations between CH_4 production and other traits in the breeding goal, but from the literature we obtained a heritability of 0.21 for enteric CH_4 production (Lassen and Løvendahl, 2016), and genetic correlations of 0.4 with milk lactose, fat, protein and DM intake (**DMI**) (Lassen and Løvendahl, 2016; González-Recio et al., 2020). Correlations between enteric CH_4 production and other traits in the breeding goal were set to zero. Phenotypic SD for CH_4 production was set to 50 g/d.

The Dutch population means were 392 g/d for enteric CH_4 production (Niu et al., 2018), and 9 000 kg milk in 305 days (CRV, 2019). This corresponds to a CH_4 intensity of 15.9 g/d per kg of milk.

Selection index calculations

The spreadsheet with desired gains of Van der Werf (2020) was used to add enteric CH_4 production to the Dutch breeding goal, with six scenarios:

1) Adding CH_4 production to the breeding goal with no weight and no records on daughters of sires (=current trend);
2) Adding CH_4 production to the breeding goal with no economic weight and increasing number of records on daughters of sires;
3) Adding CH_4 production to the breeding goal with an economic weight based on the carbon price and increasing number of records on daughters of sires;
4) Adding CH_4 production to the breeding goal with the restriction of no genetic gain in the CH_4 produced per cow;
5) Adding CH_4 production to the breeding goal with an active selection on reducing the CH_4 production per cow;
6) Simulating a breeding goal that only focusses on reducing the enteric CH_4 production per cow, using a maximum amount of available information.

Scenarios 4 and 5 were achieved by adjusting the economic weights that were put on CH_4 production per cow.

Genetic trend

From the spreadsheet with desired gains of van der Werf (2020), genetic gains for all traits, including the enteric CH_4 production, were obtained. Based on the annual overviews that are

Table 1
Heritabilities of (on diagonal) and genetic correlations (below diagonal) between the traits in the Dutch national breeding goal for dairy cattle and number of daughters (#daughs) with records for that trait (adapted from: https://www.crv4all-international.com/wp-content/uploads/2018/06/E_20-NVI_apr2018_en.pdf).

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	#daughs
1. Lactose	**0.43**															125
2. Fat	0.38	**0.58**														125
3. Protein	0.88	0.58	**0.50**													125
4. Longevity	0.36	0.35	0.42	**0.12**												125
5. Udder Health	−0.03	−0.02	−0.06	0.36	**0.09**											125
6. Int-first-last[1]	−0.34	−0.24	−0.29	0.25	0.27	**0.08**										125
7. Calving Interval	−0.44	−0.33	−0.37	0.11	0.21	0.85	**0.15**									100
8. Udder conformation	−0.08	−0.04	−0.10	0.11	0.27	−0.05	0.00	**0.34**								75
9. Feet_Leg	0.02	0.04	0.05	0.25	0.21	0.00	0.00	0.35	**0.17**							75
10. direct_calving_ease	0.07	0.15	0.11	0.24	0.15	0.20	0.24	0.00	0.00	**0.07**						200
11. maternal_calving_ease	0.00	0.00	0.00	0.16	0.09	0.25	0.24	0.10	0.10	0.19	**0.05**					75
12. direct_vitality	0.05	0.09	0.02	0.14	0.05	0.10	0.14	0.00	0.00	0.60	0.14	**0.04**				400
13. maternal_vitality	−0.04	−0.07	0.03	0.16	0.07	0.32	0.24	0.00	0.00	0.11	0.34	−0.16	**0.09**			140
14. Claw health	0.00	0.15	0.07	0.33	0.09	0.10	0.14	0.15	0.65	0.16	0.06	0.03	0.10	**0.18**		15
15. saved feed costs	0.20	0.35	0.30	0.50	−0.03	−0.10	−0.30	−0.09	−0.29	0.41	−0.20	0.17	−0.05	0.11	**0.25**	20

[1] Int-first-last: interval between first and last insemination.

provided by the national herdbook CRV, Arnhem, the Netherlands (CRV, 2020), the achieved gains per year are known, and based on the obtained and achieved gain for kg fat production, we scaled the obtained gain for the enteric CH_4 production back to yearly genetic trend.

Carbon price

The economic value of CH_4 production used for the selection indexes was based on the shadow price of carbon dioxide (**CO_2**). The economic value was based on the expected shadow price for CO_2 for 2025 obtained from literature (DBEIS, 2017). The shadow price for CO_2 used for the calculation of the shadow price of CH_4 production was obtained from the UK Government report on "Updated short-term traded carbon values used for modelling purposes" (DBEIS, 2017). This was €36.19/tCO_2e, current exchange rate at the time of analyses.

The following formula was then used to calculate the economic values of CH_4 production;

$$\text{Economic value} = -1 * (\text{shadow price of } CO_2 * 28/1\,000\,000) * 365$$

where the multiplication by −1 was due to the direction of selection on CH_4 production being negative, shadow price of CO_2 was as described above, 28 represents the global warming potential of CH_4 and was used to convert from CO_2 shadow price to CH_4 shadow price, division by 1 000 000 converts from grams to tonnes, and multiplication by 365 was because the index calculates gain per year and CH_4 data are in grams per day, in order to align the economic value of CH_4 production with those for the other traits in the breeding goal that are also expressed on an annual basis. This resulted in an economic value of −€0.37 g/d for a year.

Genomic prediction

For scenarios 3 to 6, where there is a desire, or financial incentive, to limit or reduce CH_4 intensity, selection with genomic prediction was tested. To include genomic selection in the index, a pseudo-trait was added. This trait had a heritability of 0.99, and a genetic correlation with CH_4 production of 0.63. This genetic correlation was used based on the requirement that for a trait to be included in the national breeding goal, the reliability of prediction should be equal to or greater than 0.40 (Koenen E., Personal communication, 2019). For selection with genomic prediction, we assumed no daughters were phenotyped for the CH_4 production trait, but genotyped cows had their own performance for enteric CH_4 emission recorded.

Power calculations for recording enteric methane

The parameters for a typical dairy cow population were used to determine the number of animals, farms, sniffer devices, and the number of measurements recorded with the sniffer devices, required for a suitable reliability of genomic prediction. The parameters included; the number of markers (60 000), effective population size (Ne, 120), average chromosome length (L, 100 cM), number of chromosomes (k, 30). The effective number of chromosome segments (Me, 7 200) was calculated as 2NeLk. The total number of individuals with CH_4 recorded in the reference population (T) ranged between 1 000 and 15 000 cows. The accuracy of genomic prediction ($r_{g\widehat{g}}$) was estimated following the first equation of Daetwyler et al. (2008):

$$r_{g\widehat{g}} = \sqrt{\frac{\lambda h_o^2}{\lambda h_o^2 + 1}}$$

where h_o^2 is the observed heritability (0.21), and λ is the ratio of the number of phenotypic observations and the number of loci associated (Me/T). Reliability of genomic prediction was then estimated as $r^2_{g\widehat{g}}$.

Different recording scenarios were considered over 3 years of recording, with 100 or 50 sniffer devices available (Table 2). For both 100 and 50 sniffer devices, the units were installed for either 3 years of repeated records on the original farm, 1 year of recording on one farm and then 2 years of recording on a second farm, or every year, the unit is moved to a new farm. Each farm was assumed to have a herd size of 150 genotyped cows with a replacement rate of 0.3. Only one automatic milking station was equipped with a sniffer device per farm, but all 150 cows would have access to the sniffer.

Depending on the manufacturer, sniffer devices provide a CH_4 measurement approximately every 10 s. It was assumed that the measurements during one visit to the milking robot would be used to calculate a CH_4 record for that visit. Due to the lower accuracy of sniffers compared to other devices, it is unlikely that fitting CH_4 for each visit or even daily would be useful. A trait could be calculated from the available recorded visits, the simplest would be a mean of these visit records over some period of time. As the sniffer devices are installed inside milking robots, the longest period for one phenotypic observation would be one full lactation period. This would provide one phenotypic observation per year. There are biological differences during lactation stages which affect CH_4 production (Van Engelen et al., 2018), therefore, calculating one phenotypic

Table 2
Summary of scenarios tested and the predicted reliability of an individual's genotype based on the mean number of repeated records per cow.

Sniffer installation	Repeated records	Number of						Reliability of GEBV[1]
		Unique farms	Unique cows per farm	Mean records per farm	Cows on all farms	Total records on all farms	Records per cow	
Three years of repeated records per farm								
100 sniffer devices								
Year 1	No	100	150	150	15 000	15 000	1.0	0.20
Year 2	Yes	100	195	300	19 500	30 000	1.5	0.26
Year 3	Yes	100	240	450	24 000	45 000	1.9	0.29
50 sniffer devices								
Year 1	No	50	150	150	7 500	7 500	1.0	0.20
Year 2	Yes	50	195	300	9 750	15 000	1.5	0.26
Year 3	Yes	50	240	450	12 000	22 500	1.9	0.29
Device moved once after first year								
100 sniffer devices								
Year 1	No	100	150	150	15 000	15 000	1.0	0.20
Year 2	No	200	150	150	30 000	30 000	1.0	0.20
Year 3	Yes	200	195	225	34 500	45 000	1.3	0.24
50 sniffer devices								
Year 1	No	50	150	150	7 500	7 500	1.0	0.20
Year 2	No	100	150	150	15 000	15 000	1.0	0.20
Year 3	Yes	100	195	225	17 500	22 500	1.3	0.24
Device move to a new farm every year								
100 sniffer devices								
Year 1	No	100	150	150	15 000	15 000	1.0	0.20
Year 2	No	200	150	150	30 000	30 000	1.0	0.20
Year 3	No	300	150	150	45 000	45 000	1.0	0.20
50 sniffer devices								
Year 1	No	50	150	150	7 500	7 500	1.0	0.20
Year 2	No	100	150	150	15 000	15 000	1.0	0.20
Year 3	No	150	150	150	22 500	22 500	1.0	0.20

[1] GEBV: genomic estimated breeding value.

observation per lactation period (i.e., early, mid, late) could be useful, this would provide three repeated records per year (assuming lactation stage was fitted as a fixed effect and not a separate trait). It was assumed that at least 100 days per period would be used in the calculation of one observation, allowing for: errors, days where the sniffer device needs maintenance, potential that the cow does not visit the robot with the device installed, and reproductive management. Shorter periods could be more useful and provide more repeated records, with two observations per lactation period, six trait observations per year would be available with at least 50 days included in the calculation of each observation. Finally using observations of just 10 days, which is in line with the previous sniffer studies (Lassen and Løvendahl, 2016; López-Paredes et al., 2020), would provide at least 30 observations per year.

Recording on the same farm for multiple years, or using shorter recording periods per phenotypic observation, has the potential to improve the reliability of prediction. With repeated records, the reliability of prediction for an individual's genotype was estimated following the method of Van Vleck (1993), as implemented by Tenghe et al. (2018):

$$\text{Reliability of individual's phenotype} = \frac{mh^2}{(m-1)t+1}$$

where m is the number of records per cow, h^2 is the heritability (0.21) used in the selection index calculations, and t is the repeatability (0.35, 0.50, or 0.65). Reliability of genomic prediction was then estimated as previously with the Daetwyler et al. (2008) equation with h_o^2 replaced with the reliability of the individual's phenotype.

Results

Selection index theory

Selection index calculations show how much the traits are predicted to change per year. This is plotted in Fig. 1 for both CH_4 production (g/d) and CH_4 intensity (CH_4 production expressed per kg of milk). It shows that average annual CH_4 production per cow will

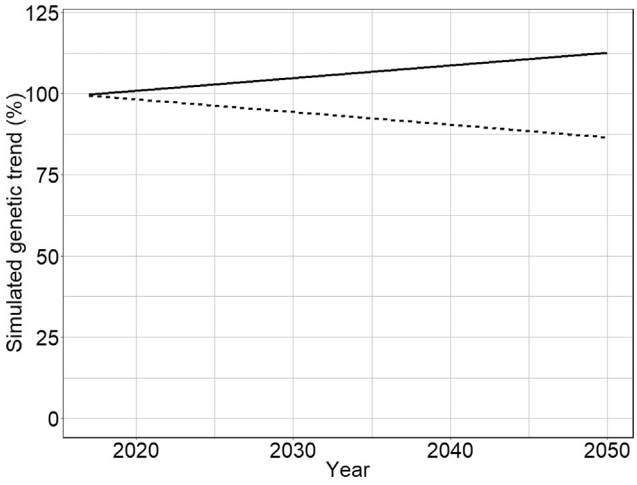

Fig. 1. Simulated genetic trends in enteric methane production (solid line) and methane emission intensities (methane emission per kg milk; dashed line) with the current breeding goal for dairy cattle.

steadily increase by 1.5 g/d as a correlated response to selection for the current breeding goal. However, the CH_4 intensity drops. When extrapolating these, the average daily CH_4 production of 392 g/d will increase to 442 g/d in 2050 (+13%). However, in the same period, the CH_4 intensity will reduce by 13%.

Further reductions can be achieved when actively selecting lower methane-emitting cows, by adding more weight on CH_4 in the national breeding goal (Fig. 2). By putting economic weight on CH_4 production in the breeding goal, selective breeding can reduce the CH_4 intensity by 24% in 2050. This shows that breeding is a valuable contribution to the whole set of mitigation strategies that could be applied in order to achieve the goals for 2050 set by the EU. Selecting actively against CH_4 would result in healthy, fertile, long-living cows that emit less CH_4. Actively selecting against CH_4 emission, however, requires large-scale recording of individual CH_4 emissions.

Comparison of the scenarios (Table 3) shows that when no economic weight is put on CH_4 production, adding 10, 20, 50 or 100 daughters with CH_4 records does not have a large impact on the genetic trend. Any small impact on the genetic trend in this scenario (no economic weight) is probably due to small changes in selection pressure caused by the traits that do have an economic value and are correlated with CH_4, and the small amount of extra information the daughters provide. For the proceeding scenarios where there is an incentive for selecting CH_4, genomic prediction provided similar results as sires with 20 progeny. Adding an economic weight on CH_4 production based on the carbon price does slow down the increase in CH_4 production as a correlated response with ~1 g/d (i.e., difference scenario 1 (5.79 g/d) and scenario 2 (4.72 g/d) in Table 3) in 3.75 years, but still, the CH_4 production will increase per year, and the CH_4 intensity will decrease. With a breeding goal aiming for no gain in CH_4, the genetic trend for milk production drops by 70–130 kg, depending on the number of daughters with records for CH_4 production per sire. Achieving no gain in CH_4 can only be realized with high economic values of −1 to −1.8, which corresponds to carbon prices between 100 and 175€/tCO_2e. With a breeding goal aiming for a reduction in CH_4 production, but still taking into account the other breeding goal traits; i.e., selecting for healthy, fertile, long-living cows that emit less CH_4, the genetic trend for milk production drops by 170–280 kg, depending on the number of daughters with records for CH_4 production per sire. The economic values will have to be −2 to −3.6, which corresponds to carbon prices between 195 and 350€/tCO_2e. Finally, an unrealistic breeding goal was assumed with only a focus on CH_4 reduction, to show what breeding could potentially achieve. This maximal reduction in CH_4 production was determined based on a scenario with no negative genetic trend in milk production when sires had at least 100 daughters with records. A genetic trend of −12.75 g/d CH_4 production in 3.75 years can then be achieved, resulting in a 29% reduction in 2050 (Fig. 2).

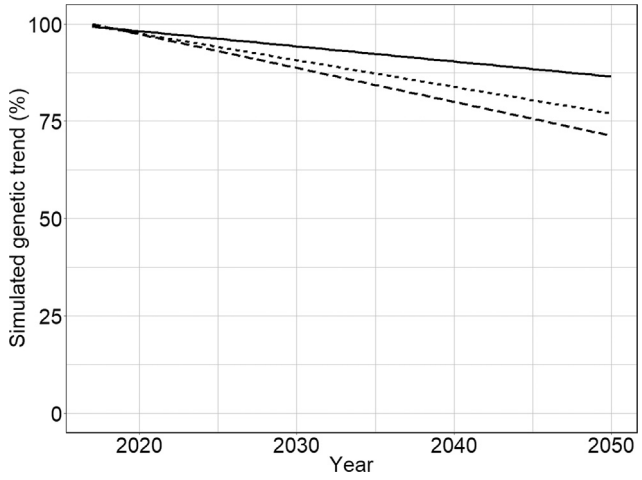

Fig. 2. Simulated genetic trends in methane emission intensities (methane emission per kg milk) of dairy cattle in three situations: current trend (solid), combined selection for methane and other relevant breeding goal traits (small dash), theoretical maximum when exclusively focussing on methane (large dash).

Power calculations

To achieve a reliability of genomic prediction above 0.40 (Fig. 3) would require approximately 25 000 genotyped cows to have a CH_4 record. When considering using sniffer devices over multiple years, the same number of measurements is recorded regardless of the strategy (22 500 records for 50 sniffer devices and 45 000 records for 100 sniffer devices), but the number of cows recorded is different. Capturing repeated records by leaving 50 sniffer devices on the same 50 farms for 3 years limits the number of cows recorded (12 000 cows), and extends the time until the required threshold would be reached. Only if the 50 sniffer devices were moved to new farms each year (150 total), would there be close to enough cows with a CH_4 record (22 500), even with a high trait repeatability of 0.65, the reliability of prediction (0.39) is still only approaching the required 0.40. With 100 sniffer devices, a reliability of 0.40 is achieved in the second year regardless of whether sniffer devices are moved or not. Having repeated records on 100 farms is the only scenario where the number of cows recorded (19 500) is fewer than 25 000 but still offers sufficient reliability (0.41).

So far only one observation per cow per lactation was considered. Reducing the observation period increases the number of repeated records per cow, thereby increasing the reliability of genomic prediction (Fig. 3). With a trait repeatability of 0.35 or 0.50, the scenarios with 100 sniffer devices achieved the threshold in the first year when using observations from three lactation periods, 50 days, or 10 days (3, 6, and 30 observations in a year, respectively). At the higher trait repeatability of 0.65, only three lactation periods required an additional year of recording before reaching a reliability of 0.40. When considering the 50 farms and a trait repeatability of 0.35, both observation periods of 50 and 10 days achieved the 0.40 reliability threshold after 2 years of recording, and three observations approached the threshold (0.37) but did not achieve it until the third year. However, this is a considerable improvement compared to the scenario with only one observation a year. Similar results were observed with the higher trait repeatabilities.

Discussion

In this study, we showed that with the current Dutch breeding goal, the genetic trend in CH_4 production is increasing, but the genetic trend in CH_4 intensity is decreasing. Actively selecting on lower emitting dairy cows will decrease this trend even further. In order to actively select on lowering the enteric CH_4 emission of dairy cattle by breeding, data on 100 farms (with on average 150 cows each) need to be collected for at least 2 years, in order to achieve the desired reliability of the genomic prediction.

Impact of breeding

Technical solutions to reduce enteric CH_4 emissions have been, and continue to be, extensively researched. Animal breeding exploits natural animal variation in CH_4 emissions, and we have shown that it is an additional mitigation strategy that is cost-effective, permanent, and cumulative. A continuous reduction in CH_4 intensity through breeding for low(er) emitting cows will help

Table 3
Genetic trends per generation interval of 3.75 years in enteric methane (CH_4) production (g/d) and in milk production (kg), of dairy cattle with the implicit economic value of CH_4 and the maximal reduction in methane intensity (g CH_4/kg milk) that could be achieved in 2050 compared to 2017 with this scenario.

Scenario		Genetic trend CH_4 production (g/d)	Genetic trend milk production (kg)	Economic value CH_4	Max reduction in CH_4 intensity (%)
1	current breeding goal: no weight, 0 daughters	5.79	307.06	0.00	13
2a	no weight, records on 10 daughters	5.66	306.85	0.00	13
2b	no weight, records on 20 daughters	5.58	306.72	0.00	13
2c	no weight, records on 50 daughters	5.47	306.54	0.00	14
2d	no weight, records on 100 daughters	5.39	306.41	0.00	14
3	economic weight of carbon price (0 daughters)	4.72	285.25	−0.37	14
3a	economic weight of carbon price (10 daughters)	4.33	284.37	−0.37	14
3b	economic weight of carbon price (20 daughters)	4.08	283.82	−0.37	15
3c	economic weight of carbon price (50 daughters)	3.70	282.98	−0.37	15
3d	economic weight of carbon price (100 daughters)	3.43	282.39	−0.37	16
3e	economic weight of carbon price (genomic prediction)	4.29	284.99	−0.37	14
4	no genetic gain (0 daughters)	0.00	178.55	−1.82	15
4a	no genetic gain (10 daughters)	0.00	202.93	−1.47	17
4b	no genetic gain (20 daughters)	0.00	214.28	−1.30	17
4c	no genetic gain (50 daughters)	0.00	227.72	−1.10	18
4d	no genetic gain (100 daughters)	0.00	235.06	−0.99	19
4e	no genetic gain (genomic prediction)	0.00	212.83	−1.36	17
5	active selection on CH_4 reduction (0 daughters)	−5.79	26.65	−3.65	15
5a	active selection on CH_4 reduction (10 daughters)	−5.79	75.16	−2.98	19
5b	active selection on CH_4 reduction (20 daughters)	−5.79	98.22	−2.66	21
5c	active selection on CH_4 reduction (50 daughters)	−5.79	126.03	−2.27	23
5d	active selection on CH_4 reduction (100 daughters)	−5.79	141.37	−2.06	24
5e	active selection on CH_4 reduction (genomic prediction)	−5.79	97.52	−2.73	21
6	selection on maximal CH_4 reduction (0 daughters)	−12.75	−197.76	−7.85	11
6a	selection on maximal CH_4 reduction (10 daughters)	−12.75	−114.72	−5.93	20
6b	selection on maximal CH_4 reduction (20 daughters)	−12.75	−75.61	−5.15	23
6c	selection on maximal CH_4 reduction (50 daughters)	−12.75	−25.64	−4.27	27
6d	selection on maximal CH_4 reduction (100 daughters)	−12.75	1.58	−3.81	29
6e	selection on maximal CH_4 reduction (genomic prediction)	−12.75	−74.69	−5.26	23

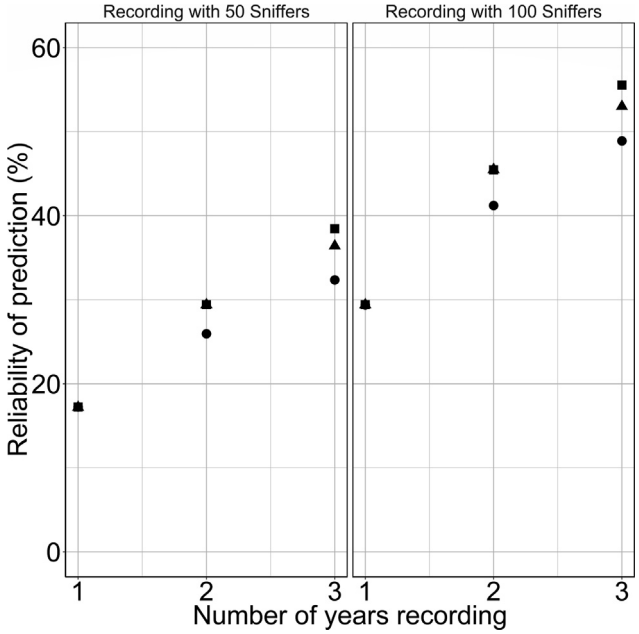

Fig. 3. Reliability of genomic prediction as a predictor of the true breeding value for methane emission of dairy cattle with 50 or 100 sniffer devices available (left or right, respectively), and different recording scenarios, estimated following Daetwyler et al. (2008). Circle; Repeated records with the same farms recorded on each year, Triangle; Repeated records with the same farms in the first and second year but sniffer devices are moved to new farms in the third year, Square; Sniffer devices are moved to a new farm every year with no repeated records.

in reaching the targets set at the Paris COP meeting in 2015 (Framework Convention on Climate Change - United Nations., 2015).

The calculated impact of breeding depends on the chosen parameters. For Dutch data, no parameter estimations exist yet, so we collated information from the literature. A heritability of 0.21 is well within the range of reported heritabilities in dairy cattle, sheep or beef cattle (Pickering et al., 2015b; Brito et al., 2018). A recent review of Lassen and Difford (2020) collated genetic correlations between CH_4 emission traits and existing selection index traits in dairy cattle. The genetic correlations with milk production traits ranged between 0.37 and 0.61, with a low sSE (0.07) on the lowest estimate large SE on the highest estimate (0.32) (Lassen and Løvendahl, 2016; Difford et al., 2018; Breider et al., 2019). Genetic correlations with feed efficiency traits were estimated by Difford et al. (2020) for two populations, and shown to be inconsistent across both countries and trait definitions for feed efficiency, ranging between −0.69 and 0.69 with large SEs up to ~0.4. Our assumed correlations on 0.4 with milk production traits and −0.4 with saved feed costs fit well within the range of published results. Lassen and Difford (2020) reviewed also the genetic correlations with other breeding goal traits, such as reproduction and health, and concluded that selection for reduced CH_4 emissions has minimal consequences on these traits, but analyses of larger datasets are needed to confirm or deny the genetic correlation structure of other traits. This is also confirmed in a Spanish study on data from 1 500 animals from 14 commercial farms (López-Paredes et al., 2020). Assuming a genetic correlation of zero, as we did, does therefore fit with the current knowledge.

When looking at a dairy system level, however, Wall et al. (2010) showed that selection for improved fitness traits (e.g., lifespan, health, fertility) will help to reduce emissions by reducing wastage of animals. Improving lifespan in dairy cows will reduce greenhouse gas emissions of the system by reducing the number of followers required to maintain the herd at a given size. Also, Van Middelaar et al. (2015) showed that improving the longevity of cows with one genetic SD is important when aiming for mini-

mizing the greenhouse gas emissions. Garnsworthy (2004) estimated, via modelling, that if cow fertility was restored to 1 995 levels from 2 003 levels, CH_4 emissions from the dairy industry would reduce by 10% to 15%. Therefore, correlated responses of national breeding goals can be expected, but the genetic correlation structure still has to be confirmed (or denied) in large studies.

Breeding goal

Breeding has the potential to reduce enteric CH_4 emissions from dairy cows, but how it should be placed in the context of breeding goals is still under debate. Breeding goal traits to genetically reduce CH_4 emissions in dairying are (1) CH_4 production as a mass flux rate per day (in litres or grams per day), (2) methane yield, which is CH_4 production divided by feed intake (e.g., CH_4 production per kg DMI, (3) methane intensity per unit product (e.g., CH_4 production per kg milk yield), and (4) residual methane production (e.g., CH_4 regressed on DMI, BW and milk yield) (de Haas et al., 2017). The European climate goals are to reduce the overall greenhouse gas emission, and therefore, CH_4 production is the most appropriate breeding goal trait, and not any of the ratio traits. Expressing it as a ratio, is, however, a useful metric to describe groups of animals; e.g. per breed, per herd, per country (Gerber et al., 2013), but the goal should be to lower the CH_4 emission per animal.

Current international dairy breeding goals involve the improvement of multiple traits simultaneously, usually compiled in a total merit index to ensure balanced breeding. Total merit indices consist of many traits, and enteric CH_4 might in the (near) future be one of them. Selecting based on a total merit index avoids establishing extreme divergent selection lines for e.g. low and high methane emitters. Selecting one trait can result in unforeseen, and possibly unwanted, correlated effects, like the rumen differences shown in two divergent selection lines of sheep in New Zealand (Bain et al., 2013). They showed that the rumen content, volume and surface area differed significantly between high and low emitting sheep, with low emitting sheep having a smaller rumen than high emitting sheep.

Traits in a total merit index are weighed to maximize economic gain, and those weights are either based on economic values or on desired gains. At this moment, however, no carbon-pricing scheme exists for dairy cattle farming in the Netherlands. We therefore used the expected shadow price for CO_2 for 2025 obtained from literature (DBEIS, 2017) as a proxy economic value for enteric CH_4 emissions. It was shown that this carbon price was not enough to realize a negative genetic trend for enteric CH_4 emissions of dairy cattle; in fact, the carbon price had to be 10 times higher (36€ vs 350€). It is therefore questionable whether carbon pricing alone is sufficient to mitigate climate change (Rosenbloom et al., 2020). The economic value was not only based on the expected shadow price for CO_2, but also on the global warming potential (**GWP**) of CH_4. For this, the GWP100 was used, which refers to the GWP over 100 years. However, recent studies have modified the use of GWP so that it accounts for the differences between short- and long-lived gases, which is referred to as GWP* (Cain et al., 2019; Lynch et al., 2020). Enteric CH_4 emissions of cattle are classified as short-lived gases, these gases do not build up in the atmosphere, so their warming potential is shorter lived than of long-lived gases (like fossil CO_2). This results in a much higher GWP for CH_4 than 28 CO_2-equivalents in the short term, and a lower GWP after that (Lynch et al., 2020). On average, the GWP* of CH_4 will be lower than the GWP100. When using GWP*, the calculated economic value for CH_4 production will be lower with the same expected shadow price for CO_2, which will reduce the impact of genetic selection.

Large-scale recording of enteric methane

Genomic prediction offers the shortest period of time and similar rates of gain (compared to progeny testing) before selection for lower CH_4 production can begin. If the decision is made to implement genomic breeding strategies to reduce enteric CH_4 production, and to achieve the expected breeding impact, there needs to be a sufficient reliability of prediction. The only way to achieve that is to have enough animals in a reference population phenotyped and genotyped. The power calculations offer insights into the difficulties that will be faced in trying to record enough data, but also provide optimism with potential methods of increasing the reliability of prediction and reducing the time period before selection can begin. Importantly, it is possible to obtain sufficient reliability within a relatively short period of time.

Before a trait is included in national evaluations, the reliability of prediction needs to be sufficiently high for accurate predictions and confidence in the values. In this example, we assumed a trait would not be included unless a threshold of 0.40 was achieved. By recording CH_4 on 100 farms, this threshold could be achieved in just 2 years, with phenotypic information on 19 500 cows collected in that time period. Of course, there are many factors that increase or decrease the required cows, farms, and time periods, but this is a useful indicator as no matter which parameters are used, a very large number of cows and farms will need to be measured.

There are now many methods of recording CH_4 at a cow level, but the options for recording at such a large scale are limited. Respiration chambers, while the most accurate method, have a low throughput, and a high cost (Hammond et al., 2015). The use of devices that measure CH_4 and flux, such as GreenFeed™ (Hammond et al., 2015), has been very beneficial for increasing the number of cows recorded and providing a reliable measurement. However, on such a large scale, they would not be logistically or economically viable. In most scenarios, such devices record 30 cows during a 2 week period (Hammond et al., 2015; Sorg et al., 2018). Therefore, multiple devices would be required per farm, or management strategies and infrastructure changes implemented to record on all cows. The use of handheld lasers would provide a means of increasing the number of cows recorded, however, they only offer a spot sample, require a large amount of labour, and have a lower accuracy (Pickering et al., 2015a; Sorg et al., 2018). It is unlikely that the use of reference gases such as SF_6 would be used at a large scale, due to animal welfare concerns caused by the invasive nature of the current methods (Deighton et al., 2014).

Sniffers are currently the only device that provides the convenience required for large-scale recording, at a reasonable cost point, while maintaining sufficient reliability of measurements, but there are still concerns regarding the limited validation of the method (Difford et al., 2018; Sorg et al., 2018; Garnsworthy et al., 2019). Sniffer devices could provide the largest amount of cows with CH_4 records, but there is a possibility of supplementing them with the other devices. It would be easiest to combine data sources that provide CH_4 measurements with the same units, for sniffers that would be CH_4 concentration (in ppm). The largest difficulty would be ensuring that the same trait is being measured. Sniffers offer a method of long-term recording, capturing data at all points of the lactation curve. While it would be possible to combine data sources from different methods, they do not capture the variation caused by various fixed effects, it is unknown what effect this will have on the reliability of prediction.

If other data from different devices are considered, a national breeding programme could also be supplemented with international data. This is already done with other traits, but relies on the fact that countries have a good genetic linkage, and enough

animals recorded with similar reliabilities of genomic EBVs (Dürr and Philipsson, 2012; Van Eenennaam et al., 2014). At the moment, CH_4 recording across countries is a patchwork of recording methods, data set sizes, and production systems. No country currently has enough data to meet the requirements that would be needed for sharing. This could be overcome if countries decided to collaborate in a large-scale recording programme and combining resources. At the moment, no such programme exists and countries continue to work independently. It is most likely that a small number of national breeding programmes implement some form of large-scale recording and connections are made between them at a later date.

If data sources from other methods, or countries, are not used to obtain a sufficient reliability of prediction, there are still ways that the amount of recording can be reduced. One method to achieve a 0.40 reliability of prediction is to increase the reliability of an individual's recorded breeding value. One method of doing this is adding repeated records. So far, we have only discussed a conservative one record for a full lactation period, or one potential repeated record per year. The test period could be reduced to the lactation period, to 50 days, or even shorter to 10 day periods, which would align with other recording methods and other traits.

Increasing the number of repeated measurements is the most convenient method to increase reliability of prediction, a larger increase can be achieved by recording on more cows and farms. With the conservative test period of one record per lactation, recording on new farms is beneficial if the number of sniffer devices is limited by availability. With 50 sniffer devices available and recording on a new farm each year, the threshold is almost reached within 3 years. If it is appropriate to reduce the test period, and there was an ability to record on new farms after each period, the threshold would be reached after four recording periods, or within 2 to 3 years. If the number of sniffer devices is above 100, there is no need to move the sniffers and repeated records are sufficient.

The uncertainty regarding test periods is just one limitation of the power analysis. Other assumptions were also made, such that all animals recorded were also genotyped. The rate of genotyping continues to increase, for these results to be relevant, the farms selected for measuring would need to be targeted based on if the herd is genotyped, otherwise an additional cost is required to have them genotyped. That would be achievable with the current systems; otherwise, the time to the threshold would be extended. Another assumption was farm size, 150 cows per farm were used for this analysis, more important is the total number of cows recorded. Assuming the mean herd size is at least 150, this would not be an issue and could be used as another target alongside genotyping when selecting farms to be included in recording.

There are some assumptions in the index and power calculation that could underestimate the rate of gain when using genomic prediction. With a sufficient reference population, genomic selection can begin earlier and would have shorter generation intervals without a need for daughters to mature. Importantly, we did not consider that some sires could still have progeny tested daughters with genomic selection.

The relevance of this work is a demonstration of the fact that, for an enteric CH_4 trait to be included in a national breeding goal, there needs to be a large and targeted recording scheme. The parameters used were either means or a range of values. For example, a lower or higher heritability could have been used instead of the literature mean. However, the effect of selecting other values within the range of published estimates would have a limited impact on the final outcome, a very large number of farms and cows would still need to be recorded.

Conclusions

The global livestock sector, particularly ruminants, contributes substantially to total anthropogenic greenhouse gas emissions. Management and dietary solutions to reduce enteric CH_4 emissions are extensively researched. Animal breeding that exploits natural variation in CH_4 emissions is an additional mitigation solution that is cost-effective, permanent, and cumulative. By adding CH_4 production to the Dutch breeding goal, selective breeding can reduce the CH_4 intensity by 24% in 2050. This shows that breeding is a valuable contribution to the whole set of mitigation strategies that could be applied in order to achieve the goals for 2050 set by the EU. If the decision is made to implement animal breeding strategies to reduce enteric CH_4 production, and to achieve the expected breeding impact, there needs to be a sufficient reliability of prediction. The only way to achieve that is to have enough animals phenotyped and genotyped. The power calculations offer insights into the difficulties that will be faced in trying to record enough data. Recording CH_4 data on 100 farms (with on average 150 cows each) for at least 2 years is required to achieve the desired reliability of 0.40 for the genomic prediction.

Ethics approval

This study is based on a data simulation (with input from literature), therefore, no data was collected on animals and no ethics statement is needed.

Data and model availability statement

None of the data were deposited in an official repository. Data and model are available upon request, the software used is available to reviewers.

Author ORCIDs

Y. de Haas: https://orcid.org/0000-0002-4331-4101
R.F. Veerkamp: https://orcid.org/0000-0002-5240-6534
G. de Jong: https://orcid.org/0000-0001-9365-5089
M.N. Aldridge: https://orcid.org/0000-0002-9033-3081

Author contributions

Conceptualization: **Yvette de Haas (YdH)**, **Roel F. Veerkamp (RFV)**, **Gerben de Jong (GdJ)**, **Michael N. Aldridge (MNA)**; Methodology: **YdH**, **RFV**, **GdJ**, **MNA**; Software: **MNA**; Formal analysis: **YdH**, **RFV**, **GdJ**, **MNA**; Visualization: **YdH, MNA**; Writing – original draft: **YdH, MNA**; Writing – review & editing: **YdH, RFV, GdJ, MNA**; Funding acquisition: **YdH, RFV**. All authors have read and agreed to the published version of the manuscript.

Declaration of interest

The authors declare no conflict of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

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