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A Transformation From Methane Concentration From Sniffers to Methane Production for Implementation in Breeding Programs and Comparison With Tier 2 Equation

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ABSTRACT

Reducing methane emissions from dairy cattle has gained considerable attention due to its dual benefits of improving feed efficiency and mitigating climate change. Consequently, phenotyping methane emissions in dairy populations has become increasingly important to enable direct genomic selection for lower methane emissions in breeding programs. Sniffer devices are receiving growing attention and are currently being deployed on commercial farms. However, these devices do not measure airflow and therefore provide methane concentration measurements rather than direct estimates of methane production. In this study, a new method is proposed to estimate individual cow methane production from sniffer device data that does not rely on regression on production traits and can therefore be classified as a Tier 3 approach. This novel methane production trait was derived using sniffer measurements collected in two dairy cattle populations: Spain ($n = 1576$) and The Netherlands ($n = 2470$). The proposed trait was compared with two alternative methane production estimates derived from production traits, representing a Tier 2 and an existing Tier 3 method. Phenotypic correlations between the Tier 3 traits were high ($R > 0.90$), whereas correlations between the Tier 2 and Tier 3 methods were substantially lower, ranging from 0.04 to 0.44. Strong agreement was observed between herd-level averages of the Tier 3 traits, while discrepancies between Tier 2 and Tier 3 estimates were more pronounced. Overall, the Tier 2 equation yielded higher methane production estimates than those obtained from sniffer-based Tier 3 traits. Heritability estimates for the Tier 3 traits ranged from 0.06 to 0.13, whereas a higher heritability (0.18–0.22) was observed for the Tier 2 trait, with standard errors between 0.02 and 0.03. Repeatability estimates were greater for the Tier 3 traits, with values ranging from 0.54 to 0.58 in Spain and from 0.25 to 0.29 in The Netherlands. The Tier 2 trait also exhibited a high repeatability (0.55–0.80). We propose this new sniffer-based Tier 3 trait as an alternative methane production phenotype that is not derived from individual production traits, thereby reducing the risk of spurious associations between methane emissions and yield-related traits. The proposed phenotype showed strong agreement with previously used Tier 3 traits and exhibited comparable heritability estimates. Nevertheless, several limitations must be acknowledged. In particular, this trait provides an estimate of methane production rather than a direct measurement, as current sniffer devices cannot capture the complete expiration or eructation plume. Despite these limitations, the trait enables the estimation of genetic trends and the prediction of breeding values expressed in biologically meaningful units. As such, it represents a valuable tool for supporting mitigation strategies and informing breeding policies aimed at reducing methane emissions from dairy cattle.

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1 | Introduction

Reducing methane emissions in dairy cattle is becoming an additional breeding goal in many cattle populations. It is essential to obtain individual methane records in commercial cattle populations to implement genomic evaluation that can provide genomic EBVs for genomic selection. However, measuring methane in commercial conditions poses some challenges. Lately, devices called sniffers are being used in a larger number of commercial farms to measure individual methane records because they have higher throughput than other popular devices such as GreenFeed (C-Lock Inc.) or respiration chambers. A common characteristic of sniffers is that they rely on sensors measuring in the near infrared spectra, and they only measure gases in ppm (Garnsworthy et al. 2019). There are many different sniffer-kind devices that are used in different countries with different specificities. For instance, Spain and Denmark use different built devices based on the Guardian detector, The Netherlands uses WD-WUR v2.0, from Caritech BV. All of them vary in several aspects such as the range of the detectors, technical characteristics or the lag of the records. Canada, Italy, Switzerland are using a new integrated model called MooLogger, designed by TecnoSens S.p.A. (Brescia, Italy). Also, ICAR is covering the development and standardization of measuring individual methane emissions using sniffers (https://wiki.icar.org/index.php/Sniffer_SOP). Previous studies have shown high genetic correlation between GreenFeed and sniffers (van Breukelen et al. 2022). Concordance with hand-held laser devices was also reported to be large (Rey et al. 2019). Sniffers have been used in large dairy populations, mainly coupled with Automated Milking Systems, and provide records with large repeatability and moderate heritability (Lassen and Lovendahl 2016; Pszczola et al. 2019; López-Paredes et al. 2020; van Breukelen et al. 2022). They also allow to estimate genetic correlations with other traits or predict estimated breeding values (Pszczola et al. 2019; López-Paredes et al. 2020). Nonetheless, there is still not enough studies comparing the reliability of different sniffer measurements with other devices.

An important limitation of sniffers lies in the lack of airflow measurements. This technical characteristic precludes the transformation from methane concentration in ppm to methane production in grams per day. Expressing cow methane emissions in grams per day provides a mass-based measure of total emissions and enables more accurate comparisons across animals, diets, and studies. It is also more directly relevant for greenhouse gas inventories, mitigation assessment, and life-cycle analyses than concentration-based metrics. Therefore, some methods have been suggested to convert ppm to g/d through regression equations (Chagunda et al. 2009; Madsen et al. 2010). These equations rely on milk production or body weight traits, leading to spurious phenotypic and genetic correlations between methane production and yield or weight traits. As sniffers are increasingly adopted to quantify enteric methane emissions for breeding applications, there is interest in converting methane concentration measurements into estimates of methane production. This aligns with the recommendation to develop Tier 3 equations as suggested by the Intergovernmental Panel on Climate Change and the Food and Agriculture Organization of the United Nations (FAO 2020). Tier 3 methods provide animal- and system-specific estimates that better reflect real management,

diet, and genetic differences, improving the accuracy of greenhouse gas inventories and enabling the evaluation of mitigation strategies and breeding programs beyond the assumptions of generalized emission factors. Tier 3 equations that are not derived from production estimates are of special interest to avoid artefact correlations with yield traits that are themselves subject to selection within breeding programs.

Hence, the objective of this study is (1) to develop a method to convert methane concentration (ppm) measurement from sniffers to methane production (g/d) that is independent of individual's milk yield and body weight, and (2) to test it in different real data sets obtained in different environmental settings and devices.

2 | Material and Methods

2.1 | Conversion of Methane Concentration to Methane Production

Methane production was estimated from sniffer concentration measurements using a new method that relies on a theoretical phenotypic distribution of CO₂ production in each comparison group (i.e., herd-pen-year-week). This distribution can be estimated using any of the available methodologies to calculate CO₂ production (e.g., Pedersen et al. 2008; Lee et al. 2022). In this study, the method proposed by Pedersen et al. (2008) to estimate CO₂ production was used. This is also consistent with the equation in Madsen et al. (2010), which has been widely used to convert ppm from sniffers to g/d in dairy cattle and uses Pedersen et al. (2008) equation. Here, CO₂ (L/d) produced per cow was calculated based on the animal Heat Producing Units (HPU):

$$CO_2 \left(\frac{L}{d} \right) = HPU \times 180(L) \times 24$$

$$HPU = 10^{-3} \left[(5.6 \times BW^{0.75}) + (22 \times ECM) + (1.6 \times 10^{-5} \times DIP^3) \right]$$

Where BW is body weight in kg, ECM is energy corrected milk as: milk (kg/d) $\times$ (0.25 + 0.122 $\times$ fat (%) + 0.077 $\times$ protein (%)), and DIP is days in pregnancy (0 if non pregnancy was confirmed), calculated from the conception date based on known artificial insemination events and subsequent parity events.

Then, for each comparison group (herd-week-robot during the measurement period), the expected mean (CG_{expected} μ_{CO_2}) and standard deviation (CG_{expected} σ_{CO_2}) of CO₂ production was calculated using the CO₂ (L/d) from Pedersen et al. (2008) equation described above. Note that this distribution is used to determine expected levels for CO₂ production in the overall comparison group, and individual CO₂ estimations from yield or bodyweight are not further used in the method.

Records registered by the sniffer were first corrected by background concentrations. For each cow visit to the AMS, background correction was implemented by subtracting the average of the 5 lowest records per visit for CH₄ or CO₂ respectively. Then, CO₂ concentration records from each visit measured with sniffers are converted to volume. Most sniffers suck air at a flow rate of 1 L per minute. Assuming this constant flow for cow *i*

and visit j , the partial CO_{2ij} (in L/s) that was sucked by the sniffer can be calculated as CO_{2ij} (ppm) $\times 10^{-6}$. The CO_{2ij} (ppm) here refers to mean CO_2 concentration during the visit j for cow i (after background correction). Assuming a constant respiration breath, daily CO_2 production for cow i captured by the sniffer during visit j is:

$$\text{sniffer CO}_{2ij} \text{ (in L/d)} = 86,400 \text{ (s/d)} \times \text{partialCO}_{2ij} \text{ (in L/s)}$$

Using these individual calculations per visit, we can obtain the mean and standard deviation of measured CO_2 production in L/d in the comparison group: $\text{CGsniffer}_{\mu\text{CO}_2}$ and $\text{CGsniffer}_{\sigma\text{CO}_2}$, respectively. The individual measurements are then re-scaled to the expected CO_2 distribution mentioned above as:

$$\text{CO}_{2ij} \text{ (L/d)} = \text{CGexpected}_{\sigma\text{CO}_2} \times (\text{sniffer CO}_{2ij} \text{ (in L/d)} - \text{CGsniffer}_{\mu\text{CO}_2}) / \text{CGsniffer}_{\sigma\text{CO}_2} + \text{CGexpected}_{\mu\text{CO}_2}$$

This standardization also removes heterogeneity between sniffers due to tube position, feed-bin shape and potential clogs in the sniffer filters. This represents a sample of CO_2 production for each cow, not the total CO_2 production from air breath, as the flow rate captured by sniffers are limited.

The daily methane production (L/d) estimated from each visit can then be calculated from measured CH_{4ij} and CO_{2ij} concentrations (mean values after background correction), and the estimated CO_{2ij} (L/d) production calculated above using CO_2 concentration as a tracer:

$$\text{CH}_{4ij} \left(\frac{\text{L}}{\text{d}} \right) = \text{CO}_{2ij} \left(\frac{\text{L}}{\text{d}} \right) * \frac{\text{CH}_{4ij} \text{ (ppm)}}{\text{CO}_{2ij} \text{ (ppm)}}$$

Finally, the density of methane (0.714 g/L) was used in order to convert to grams per day (this value may be fine-tuned based on real farm atmospheric pressure and temperature if available) and obtain estimated methane production (METP). Note that this procedure does not rely on individual body weight or milk yield. It rather relies on the expected CO_2 production from the comparison group, which is anyway adjusted for in the statistical models used for genetic evaluations, and the individual methane to CO_2 ratio ($\text{CH}_4:\text{CO}_2$). Hence, METP is suitable for genetic evaluation and EBV are expressed in terms of methane production with respect to the genetic base, without depending on animals' weight or milk yield. This method also solves the problem of the heterogeneity of measurements between AMS due to different feed-bin shapes or nose placement in the feed-bin. The ratio $\text{CH}_4:\text{CO}_2$ is expected to be constant regardless of the shape of the feed-bin and the amount of breath or eructated gas that is sucked by the sniffer. Furthermore, the measurements are standardized to the expected distribution of CO_2 in the comparison group, which is much more homogeneous between herds and comparison groups, and does not depend on technical limitations from sniffer installations.

It must be pointed out that the method assumes that the amount of breath captured by the sniffer is a good representation of the overall breath plume exhaled by the animal, and this is a limitation of the method. Nonetheless, it is known that gas concentration and production in the feed bin are highly correlated

(Garnsworthy et al. 2019). Furthermore, it is worth noticing again that CO_2 production per cow is re-scaled to expected CO_2 production from the comparison group. Another limitation of the method is that it extrapolates a sample of CO_2 sucked by the sniffer during the milking to total CO_2 production. This limitation is alleviated when several visits are averaged per day or (preferably) week. van Breukelen et al. (2023) showed that weekly averages are more repeatable and also preferred for variance component estimation.

2.2 | Benchmark Equations

To evaluate the robustness of the proposed methane production phenotype, it was compared with two widely used reference equations that estimate methane production in grams per day: (i) A Tier3-like equation proposed by Madsen et al. 2010 (METPm) and (ii) the Tier 2 equation (TIER2) for enteric methane emissions outlined by the Intergovernmental Panel on Climate Change (IPCC 2006). In a nutshell, METPm is calculated from CO_2 production derived from heat-producing units, which in turn are predicted from energy-corrected milk, live weight, and days in pregnancy. In contrast, TIER2 relies on estimates of energy intake, feed characteristics, and methane conversion factors to predict emissions at the population level. By benchmarking the proposed method against these approaches, we aimed to assess whether the novel phenotype provides comparable estimates while minimizing potential biases introduced by productive traits. A brief description of the calculation of each trait is shown next:

- i. **METPm.** Here, methane production is estimated indirectly based on CO_2 production predicted from heat-producing units (HPU):

$$\text{CH}_4 \text{ (L/d)} = \frac{[\text{CH}_4]}{[\text{CO}_2]} \times \text{CO}_2 \text{ production (L/d)}$$

$$\text{CO}_2 \left(\frac{\text{L}}{\text{d}} \right) = \text{HPU} \times 180 \text{ (L)} \times 24$$

$$\text{HPU} = 10^{-3} \left[(5.6 \times \text{BW}^{0.75}) + (22 \times \text{ECM}) + (1.6 \times 10^{-5} \times \text{DIP}^3) \right]$$

where ECM is energy-corrected milk, BW is body weight, and pregnancy is days in gestation. This formulation directly incorporates productive traits, potentially inflating correlations with yield traits. Then, the density of methane (0.714 g/L) was used to convert to grams per day (Madsen et al. 2010).

- ii. **TIER2.** The IPCC Tier 2 method (IPCC 2006) was used to estimate daily methane production, based on energy intake from body weight and milk yield related traits, and on the methane conversion factor:

$$\text{CH}_4 \text{ (g/d)} = \frac{\text{GEI} * Y_m}{55.65}$$

where GEI is gross energy intake (MJ/day), Y_m is the fraction of gross energy lost as methane (default 6.5% for dairy cattle), and 55.65 MJ/kg is the energy content of methane. This method is widely used for inventories at the population level but does not rely on animal-level gas measurements.

2.3 | Data From Spain

Gas concentrations measurements from 1576 dairy cows of 23 Spanish commercial farms of different regions of Spain were collected during two to four consecutive weeks in the period from February 2021 to June 2023. Methane and CO₂ concentrations (ppm) were measured every second using a nondispersive infrared methane detection device (Guardian NG infrared gas monitor; Edinburgh Instruments Ltd., Livingston, UK). Visits with mean CO₂ < 2500 ppm were removed. Also, only visits with mean CH₄ and CO₂ (ppm) within the interval of $\pm 3SD$ in the corresponding comparison group were kept. For estimating variance components, weekly averages were used. Cows with < 5 or > 35 records per week were removed. Weeks with less than 5 records and cows with records in only 1 week were also excluded.

Data from productive traits, such as milk production, protein percentage (%), and fat percentage (%), were available in all farms in the same period of methane measurements. Cows which were above 365 days in milking were excluded from the analysis. No cow was discarded by number of lactation. Three levels of number of lactations at recording date were defined: first, second, and third and next.

The pedigree was traced back to 16 generations, with an average of six equivalent generations and 34,085 individuals. Genomic information was available for 1631 animals, 1273 cows with phenotype and 358 sires and grandsires. The animals were genotyped with the EURO12K SNP chip (Illumina) and then imputed to 54,609 SNPs, as described in Jiménez-Montero et al. (2013) using the Spanish reference population provided by the Spanish Holstein Association (CONAFE, Madrid, Spain), which contained more than 200,000 genotyped animals. Those SNPs in the reference population that had allele frequency < 0.05, minor allele frequency < 0.05, call rate < 0.90, were monomorphic or located in the sex chromosomes were filtered out, resulting in a panel with 40,132 SNPs. Moreover, the parent-progeny Mendelian conflicts were verified, excluding those animals with more than 10% of SNPs with conflict or SNP that presented conflict in more than 100 animals.

The statistical model to estimate variance components was as follows:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_h\mathbf{h} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_p\mathbf{p} + \mathbf{e},$$

where $\mathbf{y}$ is the methane phenotype (METP, METPm or TIER2), $\mathbf{b}$ denotes the vector for fixed effects estimates (lactation number and month of calving), with corresponding incidence matrix $\mathbf{X}$; $\mathbf{h}$ is the vector of the contemporary group (herd-week-year-robot) effect as random with incidence matrix $\mathbf{Z}_h$, and assumed to be distributed as $\mathbf{h} \sim N(0, \mathbf{I}\sigma_h^2)$; $\mathbf{a}$ is the vector of direct animal genetic effects with incidence matrix $\mathbf{Z}_a$, assumed to be distributed as $\mathbf{a} \sim N(0, \mathbf{H}\sigma_a^2)$, where $\mathbf{H}$ is the numerator relationship matrix based on the pedigree and genomic relationship (Legarra et al. 2009, 2014; Misztal et al. 2018) and σ_a^2 is the additive genetic variance. Then, $\mathbf{p}$ is the vector of (within-lactation) permanent effect $\mathbf{p} \sim N(0, \mathbf{I}\sigma_p^2)$, where $\mathbf{I}$ is the identity matrix, and σ_p^2 the permanent variance, with corresponding incidence matrix $\mathbf{Z}_p$, and $\mathbf{e}$ denotes the vector of residuals distributed as $N(0, \mathbf{I}\sigma_e^2)$, where $\mathbf{I}$ is the identity matrix and σ_e^2 denotes the residual variance.

The analyses were implemented with GIBBSF90+ from the BLUPF90+ suite of programs (Misztal et al. 2018), using 50,000 Gibbs sampling iterations discarding the first 5000 as burn-in.

2.4 | Data From the Netherlands

Sniffer records from 2471 dairy cows of 21 commercial farms in the Netherlands were collected continuously during the period from 2022 to 2024. Methane concentration (in parts per million; ppm) and carbon dioxide were measured using sniffers located in the automated milking systems (AMS) (WD-WUR v1.0 and v2.0, Carltech BV), sampling every 5 s. Visits with mean methane or CO₂ (ppm) within $\pm 3SD$ of the overall mean were kept. For estimating variance components, weekly averages were used. Cows with < 5 records per week were removed. Weeks with less than 5 records and cows with less than 3 records in a comparison group (herd-year-season class) were also excluded. Season was defined according to the calendar seasons.

Data from productive traits such as milk production, protein percentage, and fat percentage were available in all farms in the same period of methane measurements. Cows which were above 365 days in milking were excluded from the analysis. Three levels of the number of lactations at the recording date were defined: first, second, and third or further. No cow was discarded by number of lactation.

The model was as follows:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_p\mathbf{p} + \mathbf{e},$$

where $\mathbf{y}$ is the vector of phenotypes as above; $\mathbf{b}$ is the vector of fixed effects: herd, year-season interaction ($j = 55$), week of lactation ($k = 1-52$), age of cow at calving in months ($l = 110$) nested within parity ($m = 1, 2, \geq 3$); $\mathbf{a}$ is the vector of direct additive genetic effects; $\mathbf{p}$ the vector of random permanent environment effects; and $\mathbf{e}$ is the vector of residual effects. The matrices $\mathbf{X}$, $\mathbf{Z}_a$ and $\mathbf{Z}_p$ are the incidence matrix relating observations with the fixed effects, random genetic effects, and random permanent environment effects, respectively. The random effects were assumed to be distributed as $\text{var}(\mathbf{a}) = \mathbf{A}\sigma_a^2$ where $\mathbf{A}$ is the pedigree relationship matrix and σ_a^2 is the animal additive genetic variance, $\text{var}(\mathbf{p}) = \mathbf{I}\sigma_p^2$, where $\mathbf{I}$ is an identity matrix of an order equal to the number of animals and σ_p^2 is the permanent environmental variance., and $\text{var}(\mathbf{e}) = \mathbf{I}\sigma_e^2$, where $\mathbf{I}$ is an identity matrix of an order equal to the number of observations and σ_e^2 is the residual variance. The pedigree included 64,334 animals with an average of 14 generations. Variance components were estimated with a repeatability animal model in ASReml v. 4.2.1 (Gilmour et al. 2021).

3 | Results

3.1 | Summary Statistics

Estimates of daily methane production (g/d) varied by method and country (Table 1). In Spain, the METP yielded an average of 311 g/d (SD = 88), while in the Netherlands the average was 299 g/d (SD = 148). These estimates were comparable to those

obtained for METPm and TIER2, showing overlapping distributions but with different means. For example, in Spain, the TIER2 showed the highest estimate at 470 g/d (SD = 77), followed by METPm at 340 g/d (SD = 97). A similar pattern was observed in the Netherlands, where the TIER2 method estimated 355 g/d (SD = 68) and METPm 296 g/d (SD = 132). Values for Tier3 traits fell within the range of emissions per cow previously reported in the literature, although the averages were slightly lower than those reported from GreenFeed in a similar population (van Breukelen et al. 2023). This suggests that the equation to estimate carbon dioxide production may underestimate real values. However, TIER2 seemed to overestimate observed values in previous studies.

Scatter plots in Figures 1–4 illustrate the relationships among methane production estimates obtained using different methods at the individual (Figures 1 and 2) and herd levels (Figures 3 and

4). Positive correlations were observed across methods in both countries; however, the strength and linearity of these relationships varied, reflecting methodological differences. Strong agreement (Pearson's $R = 0.90$ in Spain and $= 0.82$ in The Netherlands) was observed between the Tier 3 methods (METP and METPm), with regression coefficients close to unity (Figures 1 and 2). Nevertheless, some deviations from linearity were evident between these Tier 3 approaches. These discrepancies can be attributed to differences in how individual CO₂ production was estimated. METP is based on CO₂ concentrations measured by the sniffer device and scaled to the theoretical CO₂ production of the comparison group (e.g., herd). In contrast, METPm relies on CO₂ production estimated from body weight and milk, fat, and protein yields using the heat-producing units equation described by Pedersen et al. (2008). The TIER2 method showed greater divergence from the Tier 3 traits, particularly in the Dutch population, with phenotypic correlation ranging from 0.08 to 0.44.

TABLE 1 | Number of cows with records in each country with their respective methane production (CH₄ g/d) estimated from different methods.^a

	Number of cows	Number of records	METPm	TIER2	METP
Spain	1576	6513	340 (97)	470 (77)	311 (88)
The Netherlands	2471	40,973	273 (92)	353 (67)	275 (97)

Note: SD are shown within parentheses.

^aMETPm: Conversion from Madsen et al. (2010); TIER2: Equation 10.21 from IPCC (2006); METP: method proposed in this study.

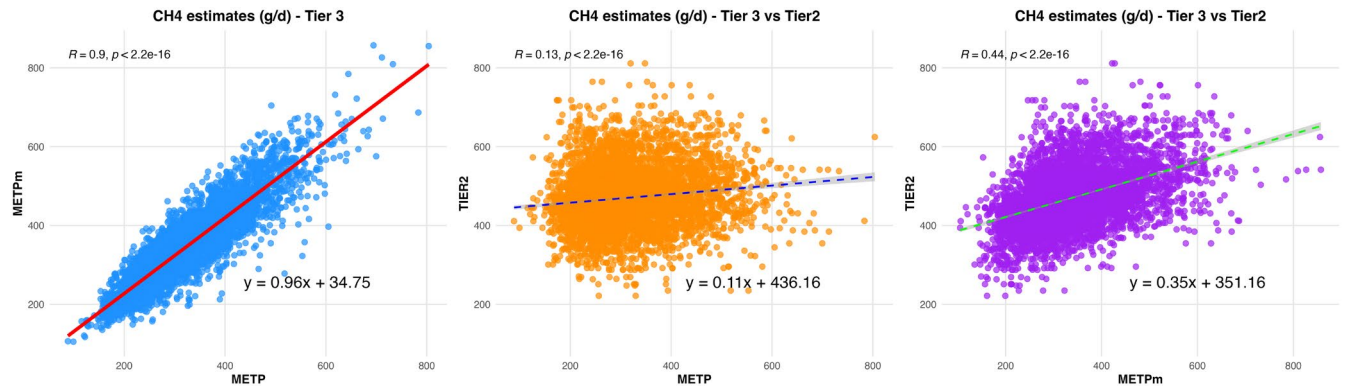


FIGURE 1 | Scatter plot between individual methane production (g/d) estimated using different approaches in the Spanish data set. [Colour figure can be viewed at [wileyonlinelibrary.com](https://onlinelibrary.wiley.com)]

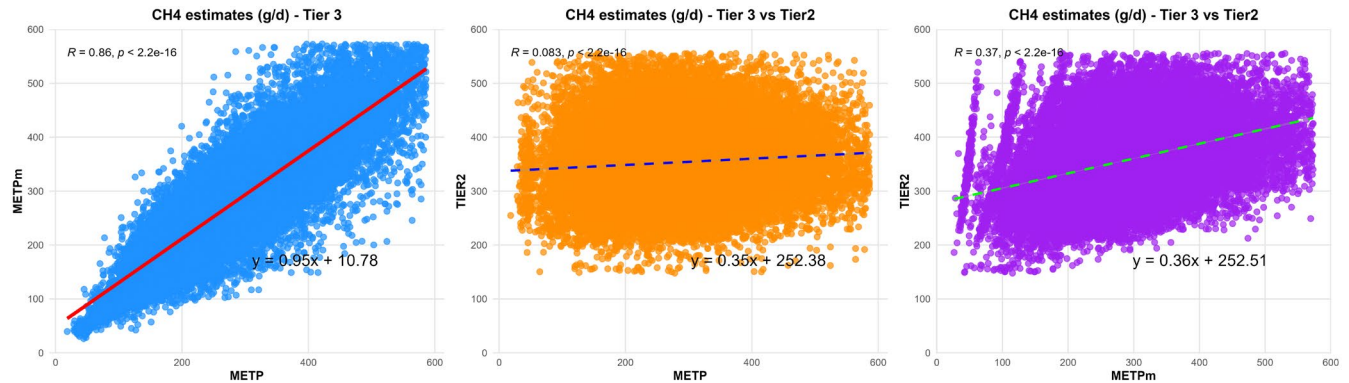


FIGURE 2 | Scatter plot between individual methane production (g/d) estimated using different approaches in the Dutch data set. [Colour figure can be viewed at [wileyonlinelibrary.com](https://onlinelibrary.wiley.com)]

When methane production estimates were aggregated at the herd level, strong agreement was observed between the two Tier 3 traits in both countries, with Pearson correlation coefficients exceeding 0.98, regression coefficients close to unity, and a low intercept (as small as 4.25 g/d) (Figures 3 and 4). In contrast, differences between the TIER2 and Tier 3 methods were more pronounced. Pearson correlations ranged from 0.52 to 0.55 in Spain, and 0.35 to 0.36 in The Netherlands, with large intercept values (approximately 370 g/d in Spain and 252 g/d in The Netherlands) and regression coefficients below 1 (Figures 3 and 4). These results indicate that the TIER2 method produces estimates with lower dispersion and higher mean values compared with the Tier 3 methods.

3.2 | Heritability and Variance Components

Heritability estimates differed across traits and populations (Table 2). In Spain, moderate heritability estimates were obtained: 0.11 (HPD: 0.04–0.17) for METP and 0.13 (HPD: 0.08–0.19) for METPm. A larger heritability was estimated for TIER2 of 0.22 (HPD: 0.13–0.29), reflecting the dependence of this trait on yield traits, which usually have larger heritabilities. In The Netherlands, METPm yielded lower heritability (0.06 ± 0.02), whereas METP resulted in $0.09 (\pm 0.02)$, and TIER2 produced higher heritability estimates at $0.18 (\pm 0.03)$, as in the case of the Spanish data set.

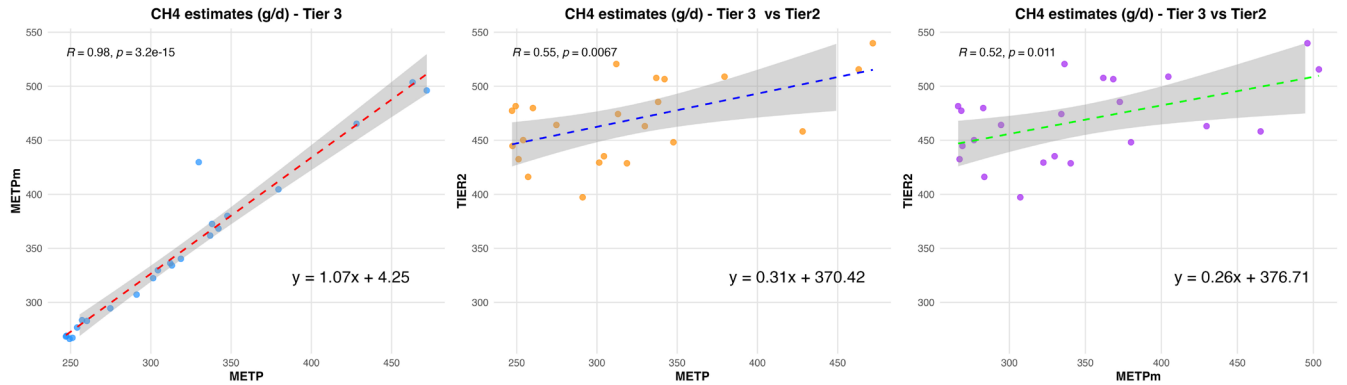


FIGURE 3 | Scatter plot between herd mean methane production (g/d) estimated using different approaches in the Spanish data set. [Colour figure can be viewed at [wileyonlinelibrary.com](https://onlinelibrary.wiley.com)]

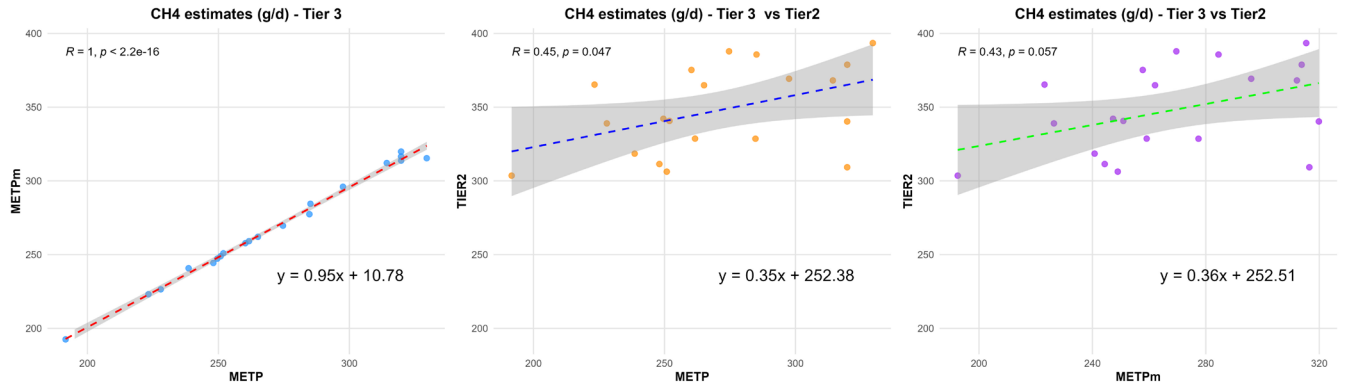


FIGURE 4 | Scatter plot between herd mean methane production (g/d) estimated using different approaches in the Dutch data set. [Colour figure can be viewed at [wileyonlinelibrary.com](https://onlinelibrary.wiley.com)]

TABLE 2 | Heritability estimates for methane production traits^a estimated using different Tier 2 (TIER2) and Tier 3 (METP and METPm) methods in each country data set.

	METPm	TIER2	METP
Spain ^b	0.13 (0.08–0.19)	0.22 (0.13–0.29)	0.11 (0.04–0.17)
The Netherlands ^c	0.06 (0.02)	0.18 (0.03)	0.09 (0.02)

^aMETPm: Conversion from Madsen et al. (2010); TIER2: Equation 10.21 from IPCC (2006); METP: method proposed in this study.

^bPosterior HPD are shown within parentheses.

^cStandard errors are shown within parentheses.

Table 3 shows repeatability estimates for each trait within country. They ranged from 0.25 to 0.80, with higher values in the Spanish dataset. Among traits, TIER2 showed the highest repeatability: 0.80 (HPD: 0.79–0.81) in Spain and 0.55 (SE = 0.03) in The Netherlands. Tier 3 traits (METP and METPm) showed similar repeatabilities within country (0.54–0.58 in Spain and 0.25–0.29 in The Netherlands), indicating moderate repeatability overall.

4 | Discussion

Sniffer devices are increasingly used to measure methane emissions at large scale in commercial dairy populations. These devices, however, only measure gas concentration in ppm, and conversion to methane production (g/d) requires equations regressed on individual information such as milk yield or body weight. Equations that convert ppm to g/d based on milk yield (e.g., Madsen et al. 2010; IPCC Tier 2 equations) disadvantage cows (and their sires) producing more milk, fat, and protein, since methane is positively regressed on milk yield. Consequently, methane production estimates may inadvertently integrate production traits, potentially biasing heritability or genetic correlation estimates. Latest studies on large data sets showed low (positive and negative) genetic correlation between methane and milk yield. For instances, low positive genetic correlation was reported in Pszczola et al. (2019), Manzanilla-Pech et al. (2022) and van Breukelen et al. (2025), while low and negative values were reported in Rojas de Oliveira et al. (2024) and Kandel et al. (2017).

Our study proposes a new method to convert methane concentration (ppm) from sniffers into methane production (g/d) independent of individual milk yield and body weight. The heritability and repeatability estimates were consistent with previous estimates from sniffer devices (de Haas et al. 2011; López-Paredes et al. 2020; Manzanilla-Pech et al. 2022; van Breukelen et al. 2023). The method still relies on the expected CO₂ production of the comparison group in which the measurements were taken (e.g., herd, pen, robot), which is calculated from milk yield records within the comparison group. This approach avoids spurious associations between methane production estimates and production traits or body weight, as the contribution of an individual to the expected CO₂ production in the comparison group is expected to be minimal, especially in groups with large size. Adjusting for the comparison group in the model is also expected to alleviate the possible small dependence between the estimated methane production and its own milk yield level. As a result, heritability and genetic correlation estimates are less likely to be confounded by traits other than the direct methane

measurement from sniffer devices. Expressing breeding values in methane production units offers several advantages for the dairy industry. Mitigation strategies require methane emissions to be expressed in production units over time (e.g., g/d or L/year). Breeding values expressed in methane units enable estimation of mitigation potential from selective breeding at the national inventory level. Genetic progress can also be quantified as a percentage reduction relative to a baseline. For example, the Global Methane Pledge, launched at COP26 in 2021, is a voluntary commitment by nearly 160 countries to reduce global methane emissions by at least 30% below 2020 levels by 2030, aiming to limit global warming to 1.5°C and improve public health (IEA 2022).

The new trait METP showed greater agreement METPm than with TIER2, both at the individual and herd levels. This was expected as both METP and METPm are based on the calculation of heat-producing units (Pedersen et al. 2008), whereas TIER2 is based on the IPCC Tier 2 equation which relies on maintenance and production requirements and conversion factors dependent on feed digestibility. Tier 2 equations therefore require stronger assumptions about feed intake and quality, which are rarely recorded in commercial dairy farms. While Tier 2 equations are widely used in national greenhouse gas inventories—where the goal is to quantify emissions from different sectors at an intermediate level of detail—they remain within an estimation framework rather than direct measurements. By contrast, methods such as those used to estimate METP and METPm are based on individual-level measurements and can capture site-specific and temporal variability, qualifying as Tier 3 methods. Tier 2 equations appear less accurate in representing methane emissions of individual cows under specific circumstances, and Tier 3 methods are therefore preferred for breeding programs. Notably, TIER2 consistently overestimated methane emissions compared with METP and METPm (considered Tier 3 methods) across all datasets, particularly in the Dutch population. Although heritability estimates were modest, they indicated a meaningful genetic component of methane emission traits. The new proposed trait showed similar heritability as two other common traits expressing methane in grams per day: METPm also derived from sniffers and TIER2 from production and body weights. The two traits derived from sniffer measurements showed similar heritability estimates across the two populations studied, consistent with previous reports using sniffers (Pszczola et al. 2017; Breider et al. 2019; López-Paredes et al. 2020; Manzanilla-Pech et al. 2022) or GreenFeed systems (van Breukelen et al. 2023). Heritability estimates for TIER2 were similar to previous studies using a similar approach (de Haas et al. 2011; Pickering et al. 2015). Importantly, TIER2 mainly captured genetic and phenotypic variability from milk yield and body weight rather than from methane emissions per

TABLE 3 | Repeatability estimates for methane production traits^a estimated using different Tier 2 (TIER2) and Tier 3 (METP and METPm) methods in each country data set.

	METPm	TIER2	METP
Spain ²	0.58 (0.55–0.60)	0.80 (0.79–0.81)	0.54 (0.51–0.56)
The Netherlands ³	0.25 (0.03)	0.55 (0.03)	0.29 (0.03)

^aMETPm: Conversion from Madsen et al. (2010); TIER2: Equation 10.21 from IPCC (2006); METP: method proposed in this study.

^bPosterior HPD are shown within parentheses.

^cStandard errors are shown within parentheses.

se. This discrepancy between Tier 2 and Tier 3 methods has important implications at inventory and policy levels. Notably, cattle and dairy cattle in particular undergo intensive genetic selection which has modified relevant complex traits with an important effect on the physiology of the animal. Hence, regression equations calculated on animals from a couple of decades ago may not represent the current animals with a significantly different metabolism and physiology. Further comparison with direct measurements that do not require conversion to g/d is needed to fully assess the implications of these approaches. It must be pointed out that this study is not intended to formally determine what equation is more accurate, as a real observation of methane production was not available in the data set. The aim was to demonstrate how the proposed method performs relative to commonly used approaches under similar conditions.

The new approach proposed in this study to estimate methane production was tested in two datasets from different countries, with consistent results supporting its robustness. The trait can be incorporated into genetic evaluations for populations using sniffer-based methane recording systems. Some fine-tuning may be necessary across devices. For example, to account for differences in sampling flow between sniffer models. Nevertheless, this method could be integrated into methane recording guidelines to harmonize methane traits across countries adopting sniffer-based systems. It should be emphasized, however, that this approach remains an estimation of methane production and does not overcome the fundamental limitation of sniffer devices, which cannot directly measure absolute methane output. Still, expressing methane in production units provides a more relevant metric for mitigation purposes and avoids dependence on individual production traits.

5 | Conclusions

Our findings reveal substantial differences among existing methods to estimate methane production, with important implications for their application in genetic evaluations and environmental impact assessments. Traits derived from Tier 3 approaches appear more suitable for breeding programs, as they are based on direct measurements and avoid biases introduced by production traits.

The new method proposed here offers a promising approach to standardizing methane traits from sniffer devices, enabling their expression in methane production units. Such units can be directly interpreted in terms of the mitigation potential of breeding programs and allow meaningful comparisons between animals. Although the method does not deliver absolute methane production values and cannot fully overcome the inherent limitations of sniffer devices, it provides estimates expressed in relevant mitigation units while remaining independent of milk yield and body weight.

Further refinements of the approach may enhance the accuracy of the estimates. In particular, incorporating proxies or direct measurements of the proportion of total exhaled and eructated gases captured by the sniffer would significantly improve the conversion. Future developments in sniffer technology are

expected to facilitate these improvements and increase the reliability of methane phenotypes for genetic evaluation.

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Ethics Statement

The authors have nothing to report.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are available from breeder associations. Restrictions apply to the availability of these data, which were used under license for this study.

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