Variance components estimation for methane emission in smallholders' dairy farms

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Abstract

Enteric methane (CH_4) emissions from cattle account for 70% of livestock GHG emissions in Sub-Saharan Africa. Also, climate change has impact on smallholder livestock-based food systems in terms of feed resources and emergence of new diseases. Direct selection for CH_4 is one of the approaches to mitigate the effects of climate change and this requires estimation of genetic parameters. Moreover, the amount of CH_4 emitted is influenced by the activity status (ACTs) of the cow such as feeding, ruminating, sleeping, and standing idle during time of measurement. The aim of this study was to evaluate CH_4 emissions under different activities, estimate variance components and compare accuracies of predicting CH_4 emissions using MIR information. The data consistent of over 14500 point-measurement of methane emissions measured by laser methane detectors with minimum duration of 3 minutes from 940 cows in 29 small-holders dairy farms in Ethiopia under various cow activities from July 2023 to March 2025. Records obtained under different ACTs for feeding, ruminating, sleeping, and standing idle were 2382, 7885, 660, and 3494 respectively. Pedigree information was also available for 435 cows with observation for CH_4 and the remaining 459 cows were genotyped using a 90k SNP chip. Overall average CH_4 production was 341 g/day. CH_4 production in feeding status was highest with 517 g/day on average. Pedigree BLUP (PBLUP), and single step combining both pedigree and genomic information (HBLUP) were applied to estimate variance components (VCs) using different modelling approaches. A repeatability animal model (full model (FM)) was fitted with ACTs, year-season, and average farm milk yield as fixed factors and permanent environmental effects a random effect in addition to animal. Also, records averaged within year-season subclasses (average model) were also analyzed with fixed effects of year-season and average farm milk yield and random effects of animal and permanent environmental effects. Heritability estimates for the FM were 0.09 (0.03), and 0.10(0.02) for PBLUP and HBLUP, respectively. The corresponding estimates for the average model were 0.14 (0.06), and 0.19 (0.04). For the indirect prediction of CH_4, a partial least square modelling approach was applied using milk mid-infrared data obtained in one-week period around the CH_4 measurements. The model with data restricted only to cows feeding gave higher prediction accuracy of 0.41 compared to 0.28 when using all data. In summary, heritabilities were low and consistent with published estimates, indirect predictions accuracy of CH_4 were moderate. In general, feeding status not only had the highest production average but also highest prediction accuracy and has influence on genetic parameters.

Key words: methane emission, animal activity, variance components

Introduction

Enteric methane (CH_4) emissions from cattle account for 70% of livestock GHG emissions in Sub-Saharan Africa years (GLEAM 2023), and it is of critical climate concern due to methane's short atmospheric lifespan of 12 years. Therefore, strategies to reduce enteric methane are vital for the 1.5°C global warming target and to mitigate the impact of climate change on the smallholder agri-food systems and livestock-based food systems in most developing countries in terms of feed resources, emergence of new diseases, increased levels of heat and humidity and related stresses. Studies have shown that methane emission is heritable and selective breeding for low emitting individuals through genetic selection is feasible (De Haas et al. 2021). Therefore, direct selection for methane is one of the approaches to mitigate the effects of climate change and this requires estimation of genetic parameters and variance components for methane and the capture of methane measurements. These recordings should be accurate and reflect overall methane production of individuals to maximize the accuracy of selection. The amount of the Methane (CH_4) emitted by cattle is not constant but varies with different activities because each activity changes the animal's rumen function, respiration rate, and gas release pathways (eructation, respiration).

Highest CH_4 production may occur during and after feeding. Rumen microbes ferment carbohydrates into volatile fatty acids and hydrogen which then methanogens convert hydrogen into methane. Methane peaks happen typically post-feeding especially after forage-rich diets (Rooke et al. 2014). Factors such as feed type (forage vs. concentrate), intake level, and feeding frequency strongly influence methane emission (Jiao et al. 2014).

Various technologies have been proposed to measure methane emission in cattle, each with different levels of accuracy, cost, practicality, and suitability for on-farm vs. research use (Sorg 2021). Most of these technologies record CH_4 when animals are in a particular state such as feeding or milking. These short time measurements of several minutes a day over a week are then generalized to estimate the methane production per day. Since animals may be different state of activities, such as feeding, drinking, milking, lying/resting, standing, walking or ruminating, CH_4 production may vary under different activities (ACTs). Therefore, to estimate an accurate amount of CH_4 production during a day, a comprehensive recording which includes these activities is needed for accurate predictions.

Methane recording in small holders' cattle farms is challenging and extra care needs to be taken for accurate and practical recording in scale. Laser Methane Detectors (LMD) are portable devices which has comparatively low purchase and running costs and results in only low-to-moderate behavioural changes of the animals but requires relatively high labour resources and has a moderate throughput in terms of the number of records per time (Sorg 2021).

Of the various technologies proposed to measure methane emissions in dairy cattle, the most commonly used include the GreenFeed and Fourier-transformed infrared (FTIR) breath analysers (sniffers) installed in feed bins (Sorg 2021).

Unlike GreenFeed or Sniffers which are installed in feed bins for recording methane only in the feeding status of cows, LMD can record methane during any cow activity, thereby providing the potential for a better estimation of overall methane produced by a cow.

As recording methane emission is still challenging and expensive, proxy traits such as milk mid-infrared (MIR) profiles are studied to indirectly predict CH_4 as an easy and cost-effective approach to record the trait. Training models for predicting methane emissions through proxy traits, relies highly on the accurate measurements of methane emissions under various the animal activities.

The aim of this study was to evaluate methane emissions under different activities, estimate variance components and compare accuracies of predicting methane emissions using MIR information under different ACTs.

Materials and Methods

About 14500 point-measurement of methane emissions from 940 cows recorded using handheld laser methane detectors in 29 small-holders dairy farms spanning a wide range of environmental conditions in Ethiopia were used for the study.

The duration of each point measurement was 3 to 5 minutes under various cow activities. Data was recorded at random times and days once or twice a month from July 2023 to March 2025. Each animal had between 2 to 32 records from farms with different management systems. The animals were of different ages, stages of lactation and were crossbreds resulting from crossing local cattle breeds with mostly Holstein and Jersey. After quality control 14421 records were analyzed and were recorded under different ACTs. A total of 2382, 7885, 660, and 3494 measurements were taken during feeding or ruminating or sleeping or standing idle respectively. Pedigree information was available for 435 cows with observation for CH_4 and 459 cows were genotyped using a 90k SNP chip.

Initially a fixed effect model consisting of ACTs, age at recording, breed proportion, lactation number, lactation stage, year-season, and average farm milk yield as management criteria were fitted to determine the factors with significant effect on methane.

Pedigree BLUP (PBLUP) and single step combining both pedigree and genomic information (HBLUP) were applied to estimate variance components (VCs) fitting significant effects from the fixed effect model.

An initial analysis indicated that repeatability of methane measurement was low at 0.26. Given this low repeatability, two sets of models were considered for estimation of genetic parameters. One set of models used the individual records of cows as the dependent variable or methane averaged year-season subclasses. The latter represents the average of subsequent measurements methane for a cow over a season of about 3-6 months and so mimics measurements of methane from other equipment such as the GreenFeed.

The full model (FM) including ACTs, year-season, and average farm milk yield as fixed factors and permanent environmental effects a random effect in addition to animal is:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wp} + \mathbf{e}$$

where $\mathbf{y}$ is the observed CH_4 measurements, $\mathbf{b}$ is the vector of fixed effects, $\mathbf{a}$ is the random animal effect, $\mathbf{p}$ is the random permanent environmental effect, and $\mathbf{e}$ is the residual. Matrices $\mathbf{X}$, $\mathbf{Z}$, and $\mathbf{W}$ are the incidence matrices connecting fixed and random effects to the observations.

The model based on CH_4 records overaged a year-season subclasses (average model) consisted of fixed effects of year-season and average farm milk yield and random effects of animal and permanent environmental effect.

Indirect prediction of methane using MIR data

A corresponding 7714 milk mid infrared profiles from 608 individuals were available within ±7 days of LMD records. Out of 930 spectral points, three spectral regions were considered for the calibration process (968–1 577 cm-1, 1 720–1 809 cm-1, and 2 561–2 966 cm-1), resulting in the selection of 289 data points.

Savitzky-Golay filtering approach with 3rd order polynomial and a window size of 5 data points was used to improve the spectra resolution by eliminating constant baseline, and to obtain robust prediction models by restricting the insertion of bias into the model. We used Sgolay function implemented in R Signal package for this calibration process.

A partial least square modelling approach using 10 principal components to predict the methane emission using MIR information using R PLS package was used for prediction.

The full model to predict CH_4 by MIR information was as below:

CH_4 ~ MIR + milk fat% + milk protein% + body weight + milk yield.

The reduced model included only MIR information performed as below:

CH_4 ~ MIR.

A 5-fold cross validation approach was used so that one fifth of data was sampled randomly as validation set and the rest was used to train the model for prediction of methane emission by MIR data. One hundred sampling and prediction were performed and the average correlation value between predicted and actual measurements were calculated as accuracy of prediction.

Results & Discussion

Overall average methane production was 341 g/day. Methane production in feeding status was highest with 517 g/day on average. Average methane production under other activities were 296, 303, and 332 g/day for ruminating, sleeping, and standing idle, respectively.

Table 1: Summary statistics of data used in this study

trait	No. of animals	No. of records	mean	SD
CH4	940	14427	341	122
Milk yield	608	6423	12.5	4.7
Fat %	608	7714	2.97	1.44
Protein %	608	7714	3.36	0.6
MIR*	608	7714	-	-
genotypes	459	-	-	-

*Milk mid-infrared profiles.

The fixed effect model indicated that animal activity significantly influenced the methane production followed by age at recording.

Heritability estimates for the full model were 0.09 (0.03) for PBLUP and 0.10(0.02) for HBLUP models. Genotypic data increased the heritability estimates by only 0.01 which may be due to low genetic connectivity between animals in the pedigree. The corresponding estimates for the average model were 0.14 (0.06), and 0.19(0.04), which are higher than those from the full model, showing a significant difference in variance components in the two models with and without ACTs fitted. The heritability estimates are in the range of estimates from other publications for methane emission in cattle (Van Breukelen et al. 2023; Lassen and Løvendahl 2016; Ghavi Hossein-Zadeh 2022; Pszczoła et al. 2017). Moreover averaging over several point measurements as is common in other studies may increase the heritability estimates (Van Breukelen et al. 2023; 2022).

The partial least square modeling approach to predict methane emission by proxy traits using data restricted to only feeding activity had a higher accuracy of 0.41 compared to when using all data with accuracy of 0.28. studies show prediction of methane emission using MIR data in the range of 0.25 to 0.7 (McParland et al. 2024; Shadpour et al. 2022; Shetty et al. 2017). No study was found to compare prediction on methane emission recorded across various ACTs in cattle. Interestingly feeding status not only had the highest production average but also the highest prediction accuracy and a substantial influence on variance components estimation.

The accuracy of prediction using repeated records were studies to find the optimum number of records using LMD device. We examined animals with 1 to 12 records for the prediction. The results showed that 6 records per individual is the optimum number of records as show the highest accuracy while is value of accuracy is comparable to individuals having more records (Table 2).

Table 2: Changes in accuracy of predicting methane emission using milk mid infrared data in different number of records.

Average records	Accuracy	RMSE
1	0.24	168
2	0.28	149
3	0.29	133
4	0.37	124
5	0.39	122
6	0.45	116
7	0.47	116
8	0.45	109
9	0.45	107
10	0.45	106
11	0.46	105
12	0.45	106

*Residual mean square error.

Conclusions

The results indicate that heritability estimates for CH_4 using LMD were low at 0.09 to 0.14 but consistent with estimates reported using other more expensive equipment. The indirect prediction accuracies using MIR data were moderate and are encouraging. Furthermore, animal activities play an important role not only in terms of correctly measuring methane production but also influences estimation of genetic parameters and accuracy of prediction of CH_4 from MIR data.

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