

Using milk mid-infrared spectra from dairy cows to predict methane measured by sniffers and GreenFeed

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Milk mid-infrared (MIR) spectra are of interest to predict enteric methane (CH₄) emissions to be used as a widely available phenotype for genetic selection on lower emissions. However, the accuracy of MIR predictions can vary greatly depending on the sample type and the calibration model used. To date, prediction models for CH₄ have successfully been created using CH₄ measurements from GreenFeed, respiration chambers and SF6. However, increasingly large numbers of individual cows are recorded with cost-effective but less accurate “sniffers”, which are used to measure CH₄ concentrations in the cow’s breath in the feed bin of milking robots. Therefore, our aim was to test the effectiveness of a MIR prediction model tested on CH₄ recorded by either GreenFeed or sniffer in Holstein cows in the Netherlands.

In total, 3,015 GreenFeed records (g CH₄/day; C-Lock Inc., Rapid city, USA) were available from 1,209 animals on 13 farms, and 40,184 sniffer records (as concentration in ppm) from 9,311 animals on 73 farms. The GreenFeed and sniffer recorded CH₄ were analysed as two separate datasets. The CH₄ records represented a 13-day average centred on the day of MIR spectrum measurement. In preliminary analyses, a partial least squares analysis was used to model the relationship between the CH₄ phenotypes and MIR spectra, by splitting the datasets into calibration and validation sets. Prediction accuracy was assessed via Monte Carlo cross-validation with 100 iterations, using a random animal-level data split (80% calibration, 20% validation). Separate models were fitted including only the GreenFeed data or the sniffer data.

The coefficients of determination of validation (R²) were 0.27 for GreenFeed recorded CH₄ (RMSE = 97), and 0.09 for sniffer recorded CH₄ (RMSE = 227). The first results suggest that CH₄ phenotypes can be predicted from MIR spectra with low to moderate accuracy. Next steps will focus on improving the prediction models by incorporating information on parity and days in milk, and performing leave-one-farm-out cross validation to investigate the usefulness for practical application.