Incorporating genetic information about methane into the Dutch Annual Nutrient Cycling Assessment

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Abstract

Since 2016, using the Annual Nutrient Cycling Assessment (ANCA, Kringloopwijzer) tool has been mandatory for all Dutch Dairy farmers. ANCA determines the farm-specific environmental performance. This includes:

- Efficiency of feeding (conversion of N and P from feed into milk and meat).
- Crop yields for N, P, C, energy (kVEM).
- Efficiency of fertilisation (conversion form fertiliser and manure into crop yields).
- Production of manure, excretion of N and P.
- Surpluses of N, P on farm balance and soil balance.
- Carbon sequestration.
- Ammonia emissions.
- Green House Gas emissions (CH_4, N_2O, CO_2).

Therefore, one of the primary objectives of the Kringloopwijzer is to evaluate the methane (CH_4) and carbon dioxide (CO_2) emissions associated with milk and meat production. Approximately 75-80% of methane emissions on dairy farms stem from fermentation in the gastrointestinal tract, with the remainder originating from manure storage. The CH_4 emissions from rumen enteric fermentation in dairy cattle are derived from methane emission factors (EF) for different feedstuff, which is a linear application of the Dutch Tier 3 method (IPCC). While this approach is robust, it does not include genetic variation among cows with on different farms, assigning the same emission value to all cows on all farms based solely on their dietary composition and feed intake. Genetic selection is considered one promising way to reduce methane emission, given that its effects are cumulative and permanent. Consequently, there has been growing interest in incorporating genetic information into the calculation of CH_4 emissions for the entire dairy herd. In this project we evaluated the differences in average breeding value for CH_4 between farms, thus without any selection practised yet. The results demonstrate that differences between farms represents up to 3.7 to 5.1% of the CH_4 and adding the breeding value has potential in refining the existing

ANCA tool. The ambition is to use breeding value (EBV) for CH_4 emissions for Dutch cows in the coming years.

Keywords: methane emissions, farm-level, life cycle analysis.
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Introduction

Since 2016, the Dutch dairy sector has utilized the Annual Nutrient Cycling Assessment (ANCA) tool to evaluate farm-specific environmental performance indicators. These indicators encompass feeding efficiency, crop yields, fertilization efficiency, manure production, nutrient surpluses, ammonia emissions, and greenhouse gas emissions. The primary goal of the ANCA tool is to quantify methane (CH_4) and carbon dioxide (CO_2) emissions associated with milk and meat production, adhering to IPCC guidelines while integrating national emission factors. This initiative is funded by the Ministry of Agriculture, Nature and Food Quality and ZuivelNL.

Methane emissions from dairy cattle are calculated based on estimated feed intake and diet composition. Each feedstuff has 3 emission factors (EF) for methane (g/kg dry matter) for when that feedstuff is fed in diets with 3 levels of maize silage (vs grass silage) in the roughage part of the diet: EF0, EF40 and EF80, where the number indicated the percentage of maize silage. These EF factors have been derived by using the IPCC Tier 3 method (Van Dijk *et al*., 2022).This method employs a dynamic mechanistic simulation model to determine emission factors based on the chemical composition and digestion characteristics of specific feed ingredients. The ANCA tool interpolates methane emissions based on the proportion of maize silage in the diet and adjusts for variations in feed intake and emissions from young stock. While this approach allows for accurate assessment and potential mitigation of methane emissions in dairy farming, it overlooks genetic variations among cows within a single farm, assigning the same emission value to all cows based solely on their diet.

Genetic selection is considered a promising method to reduce methane emissions, as its effects are cumulative and permanent. Consequently, there is growing interest in incorporating genetic information into the calculation of CH_4 emissions for the entire dairy herd. The ambition is to utilize the breeding value (EBV) for CH_4 emissions in Dutch cows in the coming years. The initial proposal involves integrating data on the average EBV of a farm's cows to identify potential differences among farms. Therefore, the objective is to investigate how to incorporate individual genetic information into the calculation of CH_4 emissions for the entire dairy herd.

Material and methods

Data descriptions

The data included 8,858 Dutch Holstein cows with 152,172 records of CH_4 concentration (CH_4c in parts per million, ppm). These records were collected in primiparous and multiparous cows during 2019 to 2023 in 72 commercial farms in the Netherlands. Parities were grouped into categories of 1, 2, 3, and 4+, and records up to lactation week 59 were included (406 DIM).

Statistical model

Variance components and EBV were estimated with an univariate repeatability (animal) model in ASReml 4.0 software. The general model used to estimate the variance components for CH_4c was:

$$y = Xb + Z_1a + e \qquad (1)$$

where y is the vector of phenotypes (CH_4c); b represent the vector of fixed effects (herd, year-season interaction, week of lactation and the interaction of lactation number with age of cow at calving). X is the incidence matrix relating observations with fixed effects; a is the vector of direct additive genetic effects; Z_1 is the incidence matrix relating observations with random genetic effects; and e is the vector of residual effects. Distributions of the random effects are var(a) = $A\sigma^2$,where A is the pedigree relationship matrix and σ^2 is the additive genetic variance, and var(pe) = $I\sigma^2pe$, where I is an identity matrix of an order equal to the number of observations and σ^2pe is the permanent environmental variance., and var(e) = $I\sigma^2e$, where I is an identity matrix of an order equal to the number of observations and σ^2e is the residual variance. The pedigree included 98,324 individuals, with maximum 14 generations.

Sensitivity aanalysis

As part of the proposal to include genetics in the annual nutrient cycle assessment, mean EBV for CH_4c per farm were calculated, divided in quantiles and plotted to detect differences among farms. Differences among quantiles were calculated to determine the maximum difference in CH_4c between them. The data was divided into four equal groups (called quantiles) based on the values of the mean EBV per farm. Then, the dataset was split into 4 quantiles which assigns each observation to one of four equally sized groups according to the distribution of the mean EBV per farm. Subsequently, a mean of each quantile group was calculated, to allow us to see how the average value in each group compared to the overall average. Finally, we measured how much this group's average differed from the overall average.

Results and discussion

Descriptive statistics

The daily average for CH_4c was 552 parts per million (ppm), whereas, the standard deviation was 272. Genetic variance was 5,434, phenotypic variance was 14643, and the heritability was 0.12 (SE=0.01), whereas, the permanent environmental ratio was 0.33 (SE=0.01). Number of cows per farm (n=72) varied between 38 and 245. This average is consistent with values previously reported for Holstein cows (Difford *et al*., 2020; Manzanilla-Pech *et al*., 2022; van Breukelen *et al*., 2022).

Average breeding values per farm and quantiles

Average breeding values per farm varied between +41 to -5 for the 72 farms (Figure 1). Standard errors ranged between 1 to 8. However, when EBV were grouped per quantile (Figure 2) the difference between quantile 1 and quantile 4 is 20.6 points. This showed a difference between farms present in the first quantile compared to the farms in the fourth quantile. By increasing the number of quantiles this difference will increase too (e.g. 10 quantiles will lead to a difference of 28 points between farms.

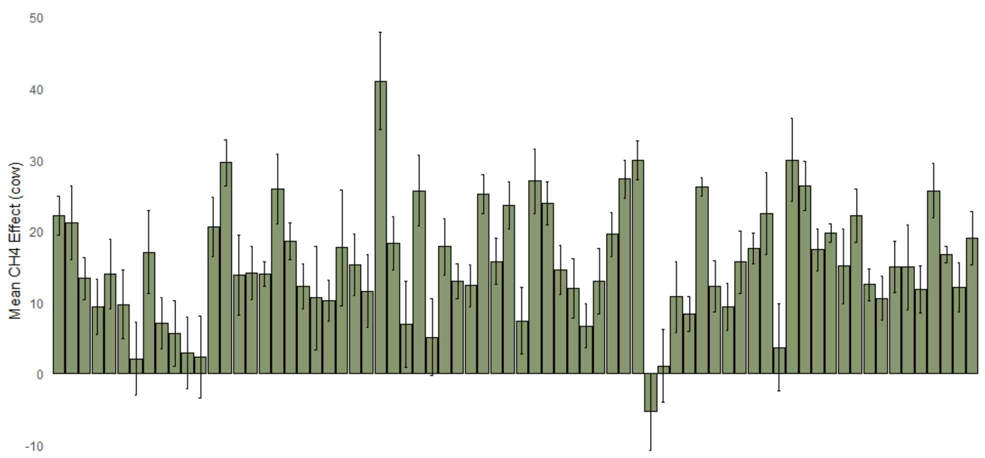

Figure 1. Average EBV for CH4c (ppm) per farm (n=72) with SE.

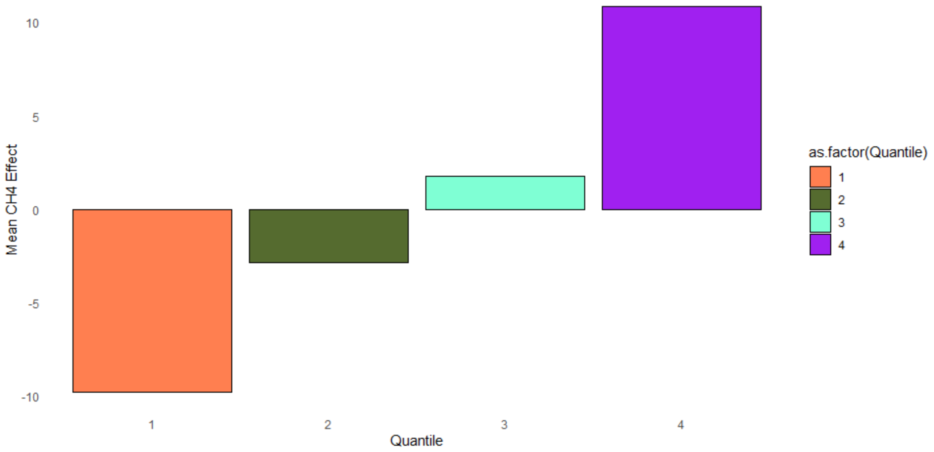

Figure 2. Quantile differences (25%) between farms for average EBV for CH_4 ppm.

Applications

The results of this study demonstrate that differences between farms can be detected by averaging their breeding values. This method has potential applications in refining the existing ANCA tool by incorporating a correction factor. Although still in development, the final correction factor will be based on CH4 g/d. The EBV for CH_4 g/d will utilize the genetic correlation (0.76; van Breukelen *et al*., 2023) between CH_4 concentration in ppm measured by sniffers and CH4 g/d determined by the GreenFeed system. Finally, the correction factor would adjust for the average genetic merit of the animals present on each farm, leading to more accurate evaluations and comparisons.

Conclusion

This pilot study aimed to assess the feasibility of incorporating genetic information into the calculation of CH_4 emissions from ANCA for the entire dairy herd. This study showed that it is feasible to detect differences among farms when averaging the CH_4 breeding values of the cows per farm. The difference between extreme farms was 20 points between the top and bottom 25% and up to 28 points (CH_4c ppm) between the top and bottom 10%, which represents up to 3.7 to 5.1% of the enteric CH_4c per farm. These results are promising and will be used as first step to build the new additions around the ANCA formulation that will involve genetic information.

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