

Genetic correlation between methane emission and nitrogen use efficiency proxies in Walloon dairy cows

H. Atashi^{1,2}, Y. Chen¹, C. Grelet³, A. Vanlierde³, F. Dehareng³, S. Vanderick¹,
H. Soyeurt¹ and N. Gengler¹

¹Gembloux Agro-Bio Tech, University of Liège, 5030 Gembloux, Belgium
Corresponding Author: nicolas.gengler@uliege.be

²Shiraz University, Shiraz, Iran

³Walloon Agricultural Research Center, 5030 Gembloux, Belgium

Livestock production contributes to global human-induced greenhouse gases (GHG) emissions in the form of CH₄, N₂O and CO₂. Beyond climate change, direct CH₄ emissions are also linked with efficiency in dairy cows. The aim of this study was to estimate genetic correlations between methane emissions and nitrogen use efficiency (NUE) in Walloon dairy cows. Milk mid-infrared (MIR) spectra were used to predict CH₄ emissions (PME, g/d) using existing equations. The trait log-transformed CH₄ intensity (LMI) was defined as the log-transformed ratio of PME divided by the daily milk yield (MY, kg/d) recorded on the same test-day achieving a more normal distribution. The values of predicted NUE (PNUE) and N losses (PNL) as proxies of the NUE and N loss were obtained using the combined MIR spectra, parity, and milk yield-based prediction equations on test-day MIR records with days in milk (DIM) between 5 and 50 d. The used data were restricted to the first-parity cows. Random regression test day models were used to estimate genetic parameters with the Bayesian Gibbs sampling method using a single chain of 100,000 iterates with a burn-in period of 20,000 iterates. Mean (SD) daily h² estimated for PME and LMI were 0.14 (0.05) and 0.24 (0.05), respectively. Mean (SD) daily genetic correlation estimated between PME and LMI was 0.55 (0.03). At a level of reliability of more than 0.30 for all examined traits, breeding values of 420 bulls born after 1995 were used to estimate the approximate genetic correlations (AGC) between PME and LMI and PUNE and PNL. The AGC estimated between PME and PUNE was -0.33 (0.07) and that found between LMI and PUNE was -0.60 (0.07). The AGC estimated between PME and PNL was 0.43 (0.08) and that found between LMI and PNL was 0.32 (0.08). The results showed that CH₄ emission, as an indicator of energy loss, is positively correlated with predicted nitrogen loss and negatively correlated with N use efficiency. It can be concluded that genetic selection for decreasing CH₄ emission will also decrease N loss and increase N use efficiency in dairy cows.

Abstract

Keywords: greenhouse gas emission, mid-infrared spectrum, genetic relationship

Efficiency traits in dairy production have received increasing attention as affect not only farm profitability but also losses to the environment (Phuong *et al.*, 2013). Therefore, the dairy industry is under constant pressure for further improvement of efficiency traits (Connor, 2015). If the nutrients consumed are not converted to milk, meat, body reserves, or new born calf, they are excreted into the environment, resulting in emissions such as urea (nitrogen (N) loss) and methane (energy loss) (Phuong *et al.*,

Introduction

2013). Proposed CH₄ emissions traits include CH₄ production, defined as the daily production (g/d); CH₄ yield, defined as the amount of CH₄ produced per unit of dry matter intake; CH₄ intensity, defined as CH₄ produced per unit of product (milk or meat), and residual CH₄. An increasing number of studies showed that N use efficiency (NUE), N loss (urinary urea, milk urea, and faecal urea), and CH₄ emissions are heritable traits and are correlated with milk yield and composition in dairy cows (Pickering *et al.*, 2015; Chen *et al.*, 2021a; Chen *et al.*, 2021b; Richardson *et al.*, 2021). However, both types of traits (NUE and CH₄ emissions) are challenging to record and to analyse on phenotypic and genetic level. Moreover, there is no report on the genetic correlation between proxies for N efficiency traits and methane emissions. Therefore, the aim of this study was to estimate approximate genetic correlations between CH₄ emission and the N use efficiency in Walloon dairy cows.

Material and methods

Data

Milk samples were collected on first parity cows from 2006 to 2021 by the Walloon Breeding Association (Ciney, Belgium). All milk samples were analysed using Milkoscan FT4000, FT6000, and FT+ (Foss-Electric A/S, Hillerød, Denmark) by the milk laboratory Comité du Lait (Battice, Belgium) to generate the MIR spectral data. Methane emissions (PME, g/d) were predicted from the recorded spectra using the equations developed by Vanlierde *et al.* (2021). To eliminate potential abnormal records, the PME values below the 0.1 percentile and above the 99.9 percentile were deleted (Kandel *et al.*, 2017). Methane emission intensity (PMI, g/ kg of milk) was defined as the ratio of PME divided by the daily milk yield (kg/d) recorded on the same test-day. The PMI was then log-transformed to be normally distributed and called log-transformed CH₄ intensity (LMI). Records from days in milk (DIM) lower than 5 d and greater than 365 d were eliminated. Age at the first calving (AFC) was restricted to the range of 540 to 1200 d. The final dataset consisted of 1,529,282 test-day records on 229,465 first-parity cows distributed in 1,530 herds collected from 2006 to 2021. The EBV and reliability of predicted NUE (PNUE) and N losses (PNL) were obtained from (Chen *et al.*, 2021b).

Variance component estimation and estimated breeding values

The (co)variance components for PME and LMI were estimated using the following random regression test-day model (RR-TDM).

$$y_{ijklm} = \mu + \text{HTD}_i + \sum_{b=0}^4 \text{AS}_j \sigma_b(t) + \sum_{b=0}^2 \text{HY}_k \sigma_b(t) + \sum_{b=0}^2 \text{pe}_1 \sigma_b(t) + \sum_{b=0}^2 \text{a}_1 \sigma_b(t) + e_{ijklm} \quad (1)$$

where y_{ijklm} is the test-day record (PME or LMI) on DIM m of cow l , belonging to i^{th} class of HTD, j^{th} class of AS, and k^{th} class of HY, HTD is the fixed effect of herd-test-day, AS is the fixed effect of age-season of calving defined as following: age at calving class (10 classes) \times season of calving (four seasons),

$$\sum_{b=0}^4 \text{AS}_j \sigma_b(t)$$

is the fixed regression coefficients of the age-season at calving modelled using Legendre polynomials of order 4,

$$\sum_{b=0}^2 HY_k \sigma_b(t), \sum_{b=0}^2 PE_1 \sigma_b(t) \text{ and } \sum_{b=0}^2 a_1 \sigma_b(t)$$

are, respectively, the random regression coefficients of herd-year at calving (HY), permanent environment, and additive effects modelled using Legendre polynomials of order 2, and e_{ijklm} is the residual effect.

The (co)variance components were estimated by Bayesian inference using the GIBBS3F90 software (Aguilar *et al.*, 2018). Gibbs sampling was used to obtain marginal posterior distributions for the various parameters using a single chain of 100,000 iterates. The first 20,000 iterates of the chain were regarded as a burn-in period to allow sampling from the proper marginal distributions. Genetic (co)variances on each test day were calculated using the equation described by Jamrozik and Schaeffer (1997). Daily heritability was defined as the ratio of genetic variance to the sum of genetic, permanent environmental, herd-year calving, and residual variances at a given DIM. The vector of estimated breeding values of each animal l (EBV_l), which included daily EBV from all DIM (5 to 365) as estimated by multiplying the vector of predicted additive genetic random regression coefficients by the matrix of Legendre orthogonal polynomial covariates; that is $EBV_l = T\hat{a}_l$, where \hat{a}_l is the vector of predicted additive genetic coefficients for animal l , and T is a matrix of orthogonal covariates associated with the Legendre orthogonal polynomial functions. In addition, the total EBV of animal l was obtained by averaging the EBVs from day 5 to 365 as following:

$$EBV_l = \sum_{i=5}^{365} EBV_i.$$

The approximate genetic correlations (AGC) between PMI, LMI, and PNUE, PNL were estimated using the strategy presented by Blanchard *et al.* (1983). Bulls born after 1995 (included) with more than 0.30 in reliability for EBV of all traits were selected. The method of calculating standard errors of the AGC was the same as Chen *et al.* (2021b). The total EBV and reliability of PMI and LMI were used in this part.

Approximated genetic correlation

Means (SD) for PME, PMI and LMI were 326.8 (67.65) g/d, 14.97 (5.70) g CH₄/kg of milk yield, and 2.64 (0.35), respectively. The mean PME found (326.8 g/d) was in the range reported by previous studies (Pickering *et al.*, 2015; Kandel *et al.*, 2017). Heritability estimates for PME and LMI were relatively stable across lactation, with a mean h^2 of 0.14 and 0.24, and peak h^2 of 0.21 and 0.30, respectively. Moderate h^2 were estimated for PME and LMI in agreement with the literature (De Haas *et al.*, 2011; Kandel *et al.*, 2017; Sypniewski *et al.*, 2021). A total of 420 bulls were used to estimate AGC between the proxies for N efficiency traits and methane emissions. Most of them belong to the US (137), the Netherlands (111), and Canada (52). The average reliabilities (SD) of EBV for PME, LMI, PNUE, and PNL were 0.84 (0.16), 0.84 (0.16), 0.48 (0.15), 0.49 (0.15), respectively. Estimated AGC (SE) between PME and PNUE was -0.33 (0.07) and between LMI and PNUE was -0.60 (0.07). The AGC (SE) estimated between PME and PNL was 0.43 (0.08) and between LMI and PNL was 0.32-(0.08). Methane emissions, as an indicator of energy lose, are positively correlated with PNL and negatively correlated with PNUE. These results seem to suggest that selection of NUE and CH₄ simultaneously is possible.

Results and discussion

Conclusion

This study suggests that genetic selection for decreasing CH₄ emissions could also decrease N loss and increase NUE in dairy cows. The AGC estimates found in this study could be helpful to setup future breeding goals. Furthermore, we only start to apprehend the complexity of holistic breeding goals accounting not only for feed and production efficiencies, and GHG emissions but also resilience and productivity.

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References

- Aguilar, I., S. Tsuruta, Y. Masuda, D. Lourenco, A. Legarra and I. Misztal.** 2018. BLUPF90 suite of programs for animal breeding with focus on genomics. Proceedings of the world congress on genetics applied to livestock production, p 11-16.
- Blanchard, P., R. Everett and S. Searle.** 1983. Estimation of genetic trends and correlations for Jersey cattle. *J. Dairy Sci.* 66: 1947-1954.
- Chen, Y., H. Atashi, S. Vanderick, R. Mota, H. Soyeurt, H. Hammami and N. Gengler.** 2021a. Genetic analysis of milk urea concentration and its genetic relationship with selected traits of interest in dairy cows. *J. Dairy Sci.* 104: 12741-12755.
- Chen, Y., S. Vanderick, R. Mota, C. Grelet and N. Gengler.** 2021b. Estimation of genetic parameters for predicted nitrogen use efficiency and losses in early lactation of Holstein cows. *J. Dairy Sci.* 104: 4413-4423.
- Connor, E.** 2015. Invited review: Improving feed efficiency in dairy production: Challenges and possibilities. *Animal* 9: 395-408.
- De Haas, Y., J. Windig, M. Calus, J. Dijkstra, M. De Haan, A. Bannink and R. Veerkamp.** 2011. Genetic parameters for predicted methane production and potential for reducing enteric emissions through genomic selection. *J. Dairy Sci.* 94: 6122-6134.
- Jamrozik, J and L. Schaeffer.** 1997. Estimates of genetic parameters for a test day model with random regressions for yield traits of first lactation Holsteins. *J. Dairy Sci.* 80: 762-770.

Kandel, P., M.-L. Vanrobays, A. Vanlierde, F. Dehareng, E. Froidmont, N. Gengler and H. Soyeurt. 2017. Genetic parameters of mid-infrared methane predictions and their relationships with milk production traits in Holstein cattle. *J. Dairy Sci.*100: 5578-5591.

Phuong, H., N. Friggens, I. De Boer and P. Schmidely. 2013. Factors affecting energy and nitrogen efficiency of dairy cows: A meta-analysis. *J. Dairy Sci.* 96: 7245-7259.

Pickering, N. K., M. G. Chagunda, G. Banos, R. Mrode, J. McEwan and E. Wall. 2015. Genetic parameters for predicted methane production and laser methane detector measurements. *J. Anim Sci.* 93: 11-20.

Richardson, C., T. Nguyen, M. Abdelsayed, P. Moate, S. Williams, T. Chud, F. Schenkel, M. Goddard, I. van den Berg and B. Cocks. 2021. Genetic parameters for methane emission traits in Australian dairy cows. *J. Dairy Sci.*104: 539-549.

Sypniewski, M., T. Strabel and M. Pszczola. 2021. Genetic Variability of Methane Production and Concentration Measured in the Breath of Polish Holstein-Friesian Cattle. *Animals* 11: 3175.

Vanlierde, A., F. Dehareng, N. Gengler, E. Froidmont, S. McParland, M. Kreuzer, M. Bell, P. Lund, C. Martin and B. Kuhla. 2021. Improving robustness and accuracy of predicted daily methane emissions of dairy cows using milk mid infrared spectra. *J. Sci. Food Agric.*101: 3394-3403.