Next steps towards the development of a collaborative genomic evaluation system for residual methane production in Walloon Holstein cows

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Abstract

Greenhouse gases emissions from ruminants are one of the causes of climate change. Methane (CH_4) from dairy cows is a major greenhouse gas and is also associated with the energy use efficiency in dairy cows. This study aimed to use data of CH_4 emissions (PME, g/d) predicted using the recorded milk mid-infrared (MIR) spectra to develop a genomic evaluation system for CH_4 of Holstein cows in the Walloon region of Belgium. The preliminary relationships among predicted CH_4 (PCH_4, defined as the estimated breeding value for PME), expected CH4 (ECH_4, estimated based on production traits), residual CH4 (RCH_4) [defined as PCH_4- ECH_4] and MACE traits and local indices were also investigated. The data of PME predicted between 2007 and 2023 on Walloon Holstein cows were used. The number of used test-day records (cows) was 2,129,225 (319,301), 1,675,056 (250,707), 1,184,377 (178,882) for the first, second, and third lactation, respectively. Genotypic data on 28,317 SNPs were available for 18,378 (3,887 sires) animals. The EM-REML method was employed to estimate the variance components. Mean (SD) daily PME per cow was 324 (68) g/d, 353 (71) g/d, and 367 (73) g/d for the first, second, and third lactation, respectively. Mean (SD) heritability estimates for daily PME were 0.13 (0.04), 0.13 (0.04), and 0.14 (0.04) in the first, second and third lactation, respectively. The average reliability of PCH_4 for the selected bulls was 70% and ranged from 51% to 98%. The corresponding value for RCH_4 was 71% and ranged from 50 to 98%. The ECH_4 was estimated for 1,170 selected international sires using available GEBV of milk, fat, and protein yields as: $ECH_4 = b_1GEBV_{MY} + b_2GEBV_{FY} + b_3GEBV_{PY}$. The Pearson correlation of PCH_4 and RCH_4 was 0.83. PCH_4 was correlated with production traits (from 0.16 to 0.51) while RCH_4 was independent of them. The Pearson correlation among PCH_4 with MACE traits and local indices ranged from 0.05 to 0.45, while the results of RCH_4 ranged from -0.01 to 0.14. Our results suggest that an efficiency CH_4 trait could be incorporated into our current genomic evaluation systems, but our results also showed that definitions of methane efficiency solely on production traits can be dangerous.

Key words: Methane production, mid-infrared spectroscopy, single-step genomic evaluation

Introduction

Emissions of greenhouse gases (**GHG**) such as carbon dioxide (**CO_2**), methane (**CH_4**), nitrous oxide (**N_2O**), and halocarbons are considered to have a considerable impact on climate change (Knapp et al., 2014). Dairy cattle production is a significant contributor to the global human-induced GHG emissions mainly in the form of CH_4 (De Haas et al., 2021). Each dairy cows emits between 60 and 160 kg of CH_4 per year (Hristov et al., 2013). The produced CH_4 is a part of feed energy that is not metabolized by the animal for productive, reproductive or maintenance purposes and the majority is eliminated in the atmosphere by eructation and respiration. It has been reported that between 2 and 12% of the total gross energy intake in dairy cows is lost in the form of CH_4 (Johnson and Johnson, 1995, Boadi and Wittenberg, 2002, Benchaar and Greathead, 2011). Therefore, next to the environmental impact, methane production has a negative effect on energy use efficiency and may have therefore a direct, however not yet clearly established, economic value that may be a financial incentive for dairy farmers beyond carbon taxes or similar potential future developments.

Opportunities for nutritional and microbial manipulation to reduce enteric CH_4 emissions have been extensively investigated in dairy cows (Benchaar and Greathead, 2011, Tseten et al., 2022). However, genetic selection of lower CH_4 emitting cows should be added as an effective tool to any combination of strategies, making a permanent, cumulative over generations, and long-term contribution to reduce CH_4 production from dairy cattle (González-Recio et al., 2020, Manzanilla-Pech et al., 2022). However, conducting a successful genetic selection needs to establish a method to measure the trait of interest on many animals at low costs. Milk mid-infrared (MIR) spectra, currently used to predict various milk components, has been proven to be a fast and cheap method for predicting the amount of daily CH_4 produced by individual daily cows (Vanlierde et al., 2021) providing an opportunity for genetic studies and genetic evaluations (Kandel et al., 2017). Although MIR-predicted daily CH_4 production was found to be a heritable trait (Kandel et al., 2017), it also relates to traits of milk yield and milk composition beyond links between daily CH_4 production and other traits of interest. Moreover, the assessment of the best way how CH_4 should be reported in will need the collection of new information. Therefore, the primary aim of this report is to report the next steps towards the development of a collaborative genomic evaluation system for residual methane production in Walloon Holstein cows, the final aim being the development a genomic evaluation system using MIR-predicted CH_4 and MACE traits.

Materials and Methods

Data

Data of CH_4 emissions (PME, g/d) predicted between 2007 and 2023 on Walloon Holstein cows using the recorded milk MIR spectra were used. Records from days in milk (**DIM**) lower than 5 d and greater than 365 d were eliminated. The number of used test-day records (cows) was 2,129,225 (319,301), 1675056 (250,707), 1,184,377 (178,882) for the first, second, and third lactation, respectively.

Genomic data

Genomic data was available for 18,378 (3,887 sires) animals. Non-mapped SNP, SNP located on sexual chromosomes, SNP with Mendelian conflicts, and those with minor allele frequency (**MAF**) less than 5% were excluded. The difference between the observed and expected heterozygosity was estimated, and if the difference was greater than 0.15, the SNP was excluded (Wiggans et al., 2009). Finally, genotypic data used consisted in 28,317 SNPs located on 29 Bos taurus autosomes (**BTA**).

Model

Variance components and estimated (genomic) breeding values (**G(EBV**)) of the animals were estimated based on the integration of the random regression test-day model (**RR-TDM**) into the single-step GBLUP procedure (**SS RR-TDM**) using a multi-trait model (PME_1, PME_2, and PME_3), considering the fixed effects HTD and random effects of –herd-calving-year (**HY**), animal additive genetic (**a**), permanent environmental (**PE**), and residual. The genomic relationship matrix (**G**) is constructed by VanRaden Method I. (VanRaden, 2008), and **G** is blended with the additive relationship matrix (**A**) assuming that

60% of the total genetic variance was explained by SNP effects.

Because of computational demands, genetic parameter estimation was performed using six different subsets each representing 10% of the herds in the dataset. On average, the subsets contained 211,325, 162,385, and 113,551 records from 30,562, 23,932, and 17,002 cows in the first, second, and third lactation, respectively.

The EM-REML method was employed to estimate the variance components in REMLF90, with each of the subsets (Misztal et al., 2014). The average GEBV of PME was calculated by summing the daily GEBV divided by number of DIM. Subsequently, the mean of the average GEBV for the first three locations was computed (**PCH$_4$**). Then, sires having at least 30 CH$_4$-phenotyped daughters, and genomic reliability (**GREL**) for PCH$_4$ ≥ 0.50 were selected for the next analyses (n = 1,170). As these sires were all also locally evaluated, Multiple Across Country Evaluation (**MACE**), respectively local (G)EBV for traditional evaluated and reported traits were also available for all these sires.

The expected CH$_4$ (**ECH$_4$**) was estimated for the selected sires using GEBV of milk, fat, and protein yields (collected from the Walloon genetic evaluations of dairy cattle (https://www.elinfo.be/indexEN.html) as: $ECH_4 = b_1GEBV_{MY} + b_2GEBV_{FY} + b_3GEBV_{PY}$ and the residual CH$_4$ (**RCH$_4$**) was defined as: $RCH_4 = PCH_4 - ECH_4$. In this study regression coefficient b_1, b_2 and b_3 were developed directly from the observed covariances between (G)EBV.

Polygenic reliability, calculated based on the Effective Daughter Contributions and computed using established procedures in routine genetic evaluations, was used as a prior to estimate GREL. Double-counting due to pedigree information was removed (Zaabza et al., 2022) and GREL computed implementing an approach based on Gao et al. (2023). The GREL of RCH$_4$ was calculated using the method (selection index) given by VanRaden et al. (2018). The Pearson correlations among the PCH$_4$ and RCH$_4$ with the selected MACE traits and local indices were calculated based on the selected sires. The MACE traits included udder health (represents the opposite SCS), longevity, fertility, direct calving ease (**DCE**), maternal calving ease (**MCE**), and local indices included production economic index (**V€L**), member economic index (**V€M**), capacity economic index (**V€C**), udder economic index (**V€P**), functional type economic index (**V€T**), functional economic index (**V€F**), global economic index (**V€G**) (https://www.elinfo.be/indexEN.html).

Results and Discussion

Mean (SD) daily PME per cow were 324 (68) g/d, 353 (71) g/d, and 367 (73) g/d for the first, second, and third lactation, respectively. Mean (SD) heritability estimates for daily PME were 0.13 (0.04), 0.13 (0.04), and 0.14 (0.04) in the first, second and third lactation, respectively.

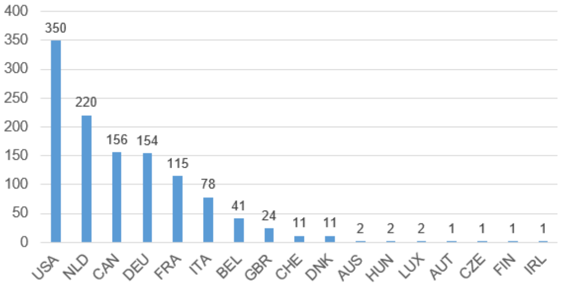

Figure 1: Distribution of 1,170 sires based on country of origin.

The distribution of the selected sires based on the country of origin is presented in Figure 1. As Wallonia is importing most of its Holstein semen and this from many countries over 100 bulls were present from major exporting countries like USA, NLD, CAN, and DEU. Sires from other exporting countries, especially including ITA and GBR were less present, still one can speculate that many internationally important sires were evaluated.

The distributions of standardized PCH$_4$ and RCH$_4$ for the selected sires are shown in Figure 2. The average GREL of PCH$_4$ for the selected bulls was 70% and ranged from 51% to 98%. The corresponding values for RCH$_4$ were 50% and ranged from 50 to 98% (Figure 3). As GEBV for RCH$_4$ was computed combing CH$_4$ with relatively reliably evaluated production traits (in ECH$_4$), GREL for RCH$_4$ did not show the loss of reliability that maybe one could expect for a residual trait.

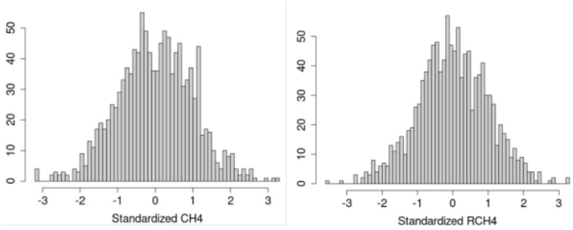

Figure 2: Distribution of standardized GEBV for PCH$_4$ and RCH$_4$ (n = 1,170 sires)

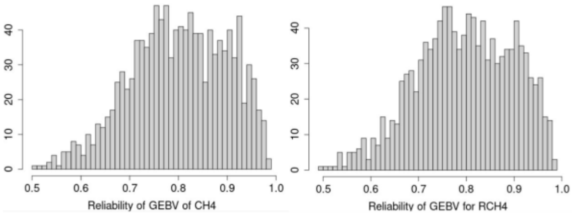

Figure 3: Distribution of reliability for PCH$_4$ and RCH$_4$ (n = 1,170 sires)

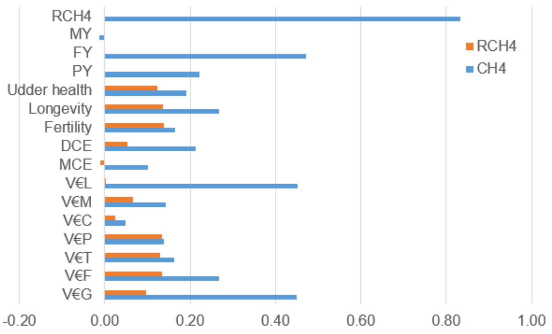

Figure 4: Pearson correlations of PCH$_4$ and RCH$_4$ with selected traits and indices (n = 1,170 sires).

The estimated Pearson correlations among PCH$_4$, RCH$_4$, MY, FY, and PY are presented in Figure 4. The correlation of PCH$_4$ and RCH$_4$ was 0.83 showing that a large part of variance of RCH$_4$ was not explained by ECH$_4$. PCH$_4$ was correlated with production traits while RCH$_4$ was independent of them as expected by its definition. These results were similar to those reported by Van Doormaal et al. (2023).

The Pearson correlations PCH$_4$ with other MACE and the local (G)EBV and indices ranged from 0.05 to 0.45, while the results of RCH$_4$ ranged from -0.01 to 0.14 (Figure 4). The correlations of PCH$_4$ with other traits and indices were bigger than those results of RCH$_4$. It is important to remind that positive correlations mean that in the case of a direct selection against PCH$_4$, but also RCH$_4$, we would lose production (because of its definition not for RCH$_4$), udder health, fertility, longevity, calving ease and all indices. Even if these results should be considered preliminary, they indicate that expression of CH$_4$ traits must be done be very carefully and the definition of methane efficiency solely on production traits (Van Doormaal et al., 2023) can be dangerous.

Conclusions

The RCH$_4$ has been defined as an efficient trait to be included into genetic selection programs for dairy cows. This trait is not associated to production levels and has the potential to decrease CH$_4$ emissions without impacting milk, fat, and protein yields. Our results showed that the Walloon genomic evaluation system can evaluate many foreign AI sires. However, our results also showed that definitions of methane efficiency solely on production traits can be dangerous.

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