Genetic parameters of mid-infrared methane predictions and their relationships with milk production traits in Holstein cattle

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ABSTRACT

Many countries have pledged to reduce greenhouse gases. In this context, the dairy sector is one of the identified sectors to adapt production circumstances to address socio-environmental constraints due to its large carbon footprint related to CH_4 emission. This study aimed mainly to estimate (1) the genetic parameters of 2 milk mid-infrared-based CH_4 proxies [predicted daily CH_4 emission (PME, g/d), and log-transformed predicted CH_4 intensity (LMI)] and (2) their genetic correlations with milk production traits [milk (MY), fat (FY), and protein (PY) yields] from first- and second-parity Holstein cows. A total of 336,126 and 231,400 mid-infrared CH_4 phenotypes were collected from 56,957 and 34,992 first- and second-parity cows, respectively. The PME increased from the first to the second lactation (433 vs. 453 g/d) and the LMI decreased (2.93 vs. 2.86). We used 20 bivariate random regression test-day models to estimate the variance components. Moderate heritability values were observed for both CH_4 traits, and those values decreased slightly from the first to the second lactation (0.25 ± 0.01 and 0.22 ± 0.01 for PME; 0.18 ± 0.01 and 0.17 ± 0.02 for LMI). Lactation phenotypic and genetic correlations were negative between PME and MY in both first and second lactations (-0.07 vs. -0.07 and -0.19 vs. -0.24, respectively). More close scrutiny revealed that relative increase of PME was lower with high MY levels even reverting to decrease, and therefore explaining the negative correlations, indicating that higher producing cows could be a mitigation option for CH_4 emission. The PME phenotypic correlations were almost equal to 0 with FY and PY for both lactations. However, the genetic correlations between PME and FY were slightly positive (0.11 and 0.12), whereas with PY the correlations were slightly negative (-0.05 and -0.04). Both phenotypic and genetic correlations between LMI and MY or PY or FY were always relatively highly negative (from -0.21 to -0.88). As the genetic correlations between PME and LMI were strong (0.71 and 0.72 in first and second lactation), the selection of one trait would also strongly influence the other trait. However, in animal breeding context, PME, as a direct quantity CH_4 proxy, would be preferred to LMI, which is a ratio trait of PME with a trait already in the index. The range of PME sire estimated breeding values were 22.1 and 29.41 kg per lactation in first and second parity, respectively. Further studies must be conducted to evaluate the effect of the introduction of PME in a selection index on the other traits already included in this index, such as, for instance, fertility or longevity.

Key words: dairy cow, methane, heritability, mid-infrared, genetic correlation

INTRODUCTION

Due to its large carbon footprint, the dairy sector must to adapt its production circumstances to address the current socio-environmental constraints (Wollenberg et al., 2016). This environmental effect is mainly related to the emission of enteric CH_4 by dairy cows occurring during the microbial fermentation of feed in rumen. Changes in feeding or adapted animal genetics are 2 relevant solutions to mitigate CH_4 emission. Compared with feeding, genetic selection has a slower response on the field, but its effect is permanent and cumulative. To conduct successful genetic mitigation of CH_4, 3 prerequisites are needed. First, CH_4 traits must be sufficiently heritable from generation to generation to allow a relatively fast significant improvement. Second, a sufficient genetic variability of this studied trait must exist in the considered dairy cow population. Third, genetic correlations of CH_4 with other traits of interest need to be known. To verify these 3 prerequisites, genetic analysis must be performed.

Currently, more and more research focuses on the genetic variability of CH_4 emitted by dairy cows. Heritability of CH_4 emission quantified using respiration chambers, considered as the gold standard for CH_4 measurements, is not available due to the technical and financial difficulties of obtaining sufficient phenotypes. However, few studies report heritability values using the gas analyzer technique. Pickering et al. (2015) found a heritability of 0.05 for the daily CH_4 emission. For the same trait, Lassen and Løvendahl (2016) reported higher values (0.25). All of these results came from relatively low-scale studies (i.e., low number of cows and herds). To increase the number of phenotypes, the use of CH_4 correlated traits that are more easily collected in the field and in many herds is relevant. Due to the high relationship between the quantity of CH_4 eructed by dairy cows and feed intake, some authors estimated the heritability of CH_4 from feed-intake-based CH_4 predictions. So, Pickering et al. (2015) found a higher heritability compared with the one obtained from a gas analyzer (0.13). Cassandro et al. (2010) reported a similar heritability value (0.10). However, de Haas et al. (2011) estimated a higher heritability value (0.35). Even if this methodology allows the collection of a higher number of phenotypes, the acquisition of feed intake and composition records is not largely generalized on a routine basis.

Another alternative is the use of milk composition as a proxy of CH_4 emission. The fatty acid (**FA**) profile seems to be valuable information (Chilliard et al., 2009; Dijkstra et al., 2011). So, van Engelen et al. (2015) estimated the heritability of CH_4 yield (g/kg of DMI) predicted from several groups of FA. The heritability obtained ranged from 0.12 to 0.44. As the FA profile can be predicted using mid-infrared (**MIR**) spectrometry (Soyeurt et al., 2011), this method could be used to predict directly the quantity of CH_4 eructed daily by dairy cows. So, Dehareng et al. (2012) developed the first MIR CH_4 equation, which was later improved by Vanlierde et al. (2015, 2016). As this methodology is used currently for the milk recording, which implies an individual milk sample collection from all productive cows in all participating herds every 4 or 6 wk, the MIR CH_4 phenotypes have the advantage of being fast and cheap, and allowing large-scale data recording. Moreover, as it is known that the quantity of CH_4 eructed by dairy cows varies within and between lactations (Garnsworthy et al., 2012), the first objective of this study is the estimation of the genetic parameters of MIR CH_4 emission (**PME**, g/d) and intensity (**PMI**, g/kg of milk) traits from first- and second-parity Holstein cows. Moreover, as the relationships of CH_4 emission and intensity with other economically important traits

are relatively unknown at a large scale, the second objective of this paper was to estimate the phenotypic and genetic correlations between those 2 MIR CH_4 traits with milk (**MY**), fat (**FY**), and protein (**PY**) yields.

MATERIALS AND METHODS

Data

Milk samples were collected from first- and second-parity Holstein cows between January 2010 and April 2014 as part of the routine milk recording undertaken in the Walloon region of Belgium by the Walloon Breeding Association (Ciney, Belgium). All milk samples were analyzed using Foss Milkoscan FT6000 spectrometers (Hillerød, Denmark) by the milk laboratory Comité du Lait (Battice, Belgium) to quantify the contents of fat and protein and to generate the spectral data.

The PME (g/d) was predicted from the recorded milk MIR spectra using the lactation-stage-dependent equation developed by Vanlierde et al. (2015). Briefly, this CH_4 MIR prediction equation was developed from 446 CH_4 measurements from 142 Belgian and Irish cows. Reference daily CH_4 emissions of individual cows were determined using the SF_6 tracer gas technique with a gas collection period of 24 h. The calibration data set was characterized by a mean of 416 ± 128 g of SF_6 CH_4/d with a minimum and maximum of 180 and 942 g/d. The lactation-stage-dependent equation was developed from those reference values and their corresponding daily milk MIR spectra. The standard error of calibration of this equation was 63 g/d. The calibration coefficient of determination was equal to 75%. More details about the sample collection and data treatment are reported in Vanlierde et al., (2015). The PMI (g/kg of milk) was defined as the ratio of PME divided by the daily MY (kg/d) recorded on the same test-day. This trait was then log-transformed to be normally distributed and called log-transformed CH_4 intensity (**LMI**). To eliminate potential abnormal records, the predicted MIR CH_4 trait values below the 0.1 percentile and above the 99.9 percentile were deleted.

Only cows between 5 and 365 DIM and with at least 75% Holstein genes were studied. If a cow had CH_4 records for second parity, this cow must also have records for first parity to be considered in the study. As proposed by the International Committee for Animal Recording, milk production records were retained if they were between 3 and 99 kg of MY, 1 and 7% of PY, and 1.5 and 9% of FY. Moreover, only herds having at least 100 MIR CH_4 phenotypes were kept in this study. Therefore, the final data set contained 366,126 and 231,400 test-day records collected from 56,957 and