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Genetic background of methane emission by Dutch Holstein Friesian cows measured with infrared sensors in automatic milking systems

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ABSTRACT

International environmental agreements have led to the need to reduce methane emission by dairy cows. Reduction could be achieved through selective breeding. The aim of this study was to quantify the genetic variation of methane emission by Dutch Holstein Friesian cows measured using infrared sensors installed in automatic milking systems (AMS). Measurements of CH_4 and CO_2 on 1508 Dutch Holstein Friesian cows located on 11 commercial dairy farms were available. Phenotypes per AMS visit were the mean of CH_4 , mean of CO_2 , mean of CH_4 divided by mean of CO_2 , and their \log_{10} -transformations. The repeatabilities of the \log_{10} -transformated methane phenotypes were 0.27 for CH_4 , 0.31 for CO_2 , and 0.14 for the ratio. The log_{10} transformated heritabilities of these phenotypes were 0.11 for CH₄, 0.12 for CO₂, and 0.03 for the ratio. These results indicate that measurements taken using infrared sensors in AMS are repeatable and heritable and, thus, could be used for selection for lower CH₄ emission. Furthermore, it is important to account for farm, AMS, day of measurement, time of day, and lactation stage when estimating genetic parameters for methane phenotypes. Selection based on log₁₀-transformated CH₄ instead of the ratio would be expected to give a greater reduction of CH_4 emission by dairy cows.

Key words: methane emission, dairy cow, AMS, nondispersive infrared sensor

INTRODUCTION

Agriculture contributes 24% of the total global greenhouse gas emissions (IPCC, 2014). The single largest pollution source within agriculture is enteric fermentation (i.e., the breakdown of feed in the rumen that results in the production of CH₄; Gerber et al., 2013). Approximately 8% of the worldwide agricultural greenhouse gas emissions originate from enteric CH_4 emissions by dairy cows (FAOSTAT, 2012; FAO, 2014), showing the impact of dairy production on global warming. In December 2015, agreements were made in Paris between 195 countries to tackle climate change and keep global warming firmly below 2°C (UNCCC, 2015). These agreements have further emphasized the importance of the reduction of CH_4 emission by dairy cows.

Reduction of CH_4 emission by dairy cows can be achieved through a combination of mitigation strategies comprising dietary, microbial, management, and breeding strategies (Cottle et al., 2011; Hristov et al., 2013). Selective breeding has the advantage of giving a cumulative, permanent, and long-term reduction of CH_4 emission. An example of breeding for reduced CH_4 is the reduction of 13% of CH_4/kg of milk in Dutch dairy cattle that has been realized from 1990 to 2010 by selection for higher milk production (Vellinga et al., 2011). A further reduction of CH_4 emission through selective breeding is wanted and requires quantification of possible genetic variation in CH₄ emission.

To quantify possible genetic variation in CH_4 emission, CH_4 emission needs to be measured on large numbers of individual cows. One of the measurement methods could be infrared sensors installed in automatic milking systems (AMS). The infrared sensor samples the breath of the cows present in the AMS and measures CH_4 and CO_2 concentration continuously. An advantage of this system is that cows visit the AMS several times per day, and these repeated visits ensure repeated measurements of the same cow over the day and over time (Garnsworthy et al., 2012a). Furthermore, sensors can easily be moved from one AMS to another and, thus, provide the opportunity to measure individual CH₄ emission on large numbers of cows.

Previous studies have shown that CH₄ measurements based on infrared sensors in AMS are repeatable. Lassen et al. (2012) summarized CH₄ measurements per AMS visit by taking the mean of CH_4 , the mean of CO_2 , and the mean of the ratio between CH_4 and CO_2 ;

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repeatabilities ranged between 0.22 and 0.46 for 50 Holstein cows and 43 Jersey cows. Bell et al. (2014b) found a repeatability of 0.74 for mean of CH_4 per AMS visit for 36 Holstein-Friesian cows. These repeatabilities illustrate that infrared sensors in AMS could provide the repeatable measurements on individual cows that are needed to quantify possible genetic variation in CH_4 emission.

These CH_4 phenotypes can be influenced by farm conditions (Bell et al., 2014a), hour of the day (Garnsworthy et al., 2012b), and week of lactation (Lassen et al., 2016); therefore, these effects were studied. Farm conditions can affect CH_4 emission via the differences in feed regimens between farms (Bell et al., 2014a; Hammond et al., 2016). Hour of the day can influence CH_4 emission, as cow behavior, time after feeding, and ambient conditions change throughout the day (Garnsworthy et al., 2012b; Lassen et al., 2012; Bell et al., 2014b). Week of lactation can affect CH_4 emission, as the amount and composition of feed varies throughout lactation (Garnsworthy et al., 2012b; Bell et al., 2014a; Lassen and Løvendahl, 2016).

Repeated measurements obtained from infrared sensors can be used to estimate the variation in CH_4 emission between cows. Lassen and Løvendahl (2016) found genetic variation in CH_4 emission that was summarized in several phenotypes. The heritabilities ranged between 0.16 and 0.21, providing support for the use of CH_4 concentrations measured using infrared sensors in AMS to decrease CH_4 emission through selective breeding.

The aim of our study was to quantify the genetic variation of CH_4 emission by Dutch dairy cows measured using infrared sensors installed in AMS. The data set comprised CH_4 and CO_2 measurements taken with infrared sensors on Dutch Holstein Friesian cows located on commercial dairy farms. Measurements were summarized into different CH_4 phenotypes per AMS visit and repeatability and heritability were calculated for these phenotypes.

MATERIALS AND METHODS

Ethical Statement

This research was accredited by the animal experimentation committee of Wageningen University and Research and the central committee animal trials under application number 2013085 and trial code 2013097.

Methane Sensor

Methane phenotypes were measured using sensors. These sensors were tested in climate respiration chambers (**CRC**) before they were installed on commercial farms. In this test, CH_4 emissions of 20 individual Holstein Friesian cows were recorded in CRC for 3 consecutive days and, simultaneously, by the sensor. In the CRC, CH_4 and CO_2 were measured every 12.5 min as described by Heetkamp et al. (2015). The sensors were gas analyzers (SenseAir LPL CH_4/CO_2 , Rise Acreo, Stockholm, Sweden) that were installed in line with the cow's nostrils when standing and facing forward. Air was drawn through the instrument at 1 L/min; CH_4 and CO_2 concentrations were measured continuously using a nondispersive infrared (**NDIR**) technique and logged twice per second. Phenotypes were defined as CH_4 production (L/d) from CRC; CH_4 concentration (ppm) from sensor; and $CH_4:CO_2$ ratio from sensor.

Data

Methane and CO_2 concentrations (ppm) were measured on 1,508 primiparous and multiparous dairy cows from 11 commercial farms in the Netherlands. On 9 of these farms, cows were fed in the morning, whereas on 1 farm cows were fed in the evening. In addition, some farms had automatic feed pushers that compiled the feed continuously during the day, and 1 farm had an automatic feeder that fed the cows freshly mixed feed up to 30 times a day. Furthermore, cows on some farms could graze during the day whereas cows on other farms were kept indoors. More than 85% of the cows were at least 7/8 Holstein Friesian. Measurements were taken during milking in AMS (Lely Astronaut A4, Lely Industries NV, Maassluis, the Netherlands) using NDIR sensors. A total of 4 sensors were used to collect all data by installing them consecutively in different AMS. Measurements were taken in a total of 23 AMS, 1 to 4 AMS per farm, between November 2013 and March 2016. The data from these sensors were linked to the data from the AMS to obtain the identification numbers (**ID**) of the cows and, subsequently, additional animal information, such as week of lactation. The data of the sensors were aligned to the AMS visits as both were recorded on different devices. The alignment between these devices was based on the pattern of AMS visits (i.e., duration and order of AMS visits and the time between the AMS visits). This pattern was aligned in such a way that CH_4 and CO_2 concentrations were highest during AMS visits and lowest in between AMS visits. After alignment, the ID of the cows were used to link sensor data to data from the cooperative cattle improvement organization CRV (Arnhem, the Netherlands) to obtain the pedigree. The pedigree was traced back 2 generations, resulting in 4,214 animals in the pedigree.

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