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Dairy system, parity, and lactation stage affect enteric methane production, yield, and intensity per kilogram of milk and cheese predicted from gas chromatography fatty acids

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ABSTRACT

Ruminants (and milk production) contribute to global climate change through enteric methane emissions (EME), and any attempt to reduce them is complicated by the fact that they are difficult and expensive to measure directly. In the case of dairy cows, a promising indirect method of estimating EME is to use the milk fatty acid profile as a proxy, as a relationship exists between microbial activity in the rumen and the molecules available for milk synthesis in the mammary gland. In the present study, we analyzed the detailed fatty acid profiles (through gas chromatography) of a large number of milk samples from 1,158 Brown Swiss cows reared on 85 farms with the aim of testing in the field 2 equations for estimating EME taken from a published meta-analysis. The average estimated methane yield (CH_4 emission per kg of dry matter intake, 21.34 ± 1.60 g/kg) and methane intensity (per kg of corrected milk, 14.17 ± 1.78 g/kg), and the derived methane production (CH_4 emissions per day per cow, 357 ± 109 g/d) were similar to those previously published. Using data from model cheese makings from individual cows, we also calculated estimated methane intensity per kilogram of fresh cheese (99.7 ± 16.4 g/kg) and cheese solids (207.5 ± 30.9 g/kg). Dairy system affected all EME estimates. Traditional dairy farms, and modern farms including corn silage in the TMR exhibited greater estimated methane intensities. We found very wide variability in estimated EME traits among different farms within dairy system (0.33 to 0.61 of total variance), suggesting the need to modify the farms' feeding regimens and management practices to mitigate emissions. Among the individual factors, parity order affected all estimated EME traits excepted methane yield, with an increase from first lactation

to the following ones. Lactation stage exhibited more favorable estimated EME traits during early lactation, concomitant with the availability of nutrients from body tissue mobilization for mammary synthesis of milk. Our results showed a coherence between the EME traits estimated from the analysis of milk fatty acids and the expectations according to current knowledge. Further research is needed to validate the results obtained in this study in other breeds and populations, to assess the magnitude of the genetic variation and the potential of these phenotypes to be exploited in breeding programs with the aim to mitigate emissions. **Key words:** dairy system, ecological footprint, greenhouse gas, global warming, cheese effect

INTRODUCTION

Ruminants are thought to be responsible for between 3 and 18% of global greenhouse gas (GHG) emissions (Pitesky et al., 2009; Knapp et al., 2014), a significant contribution to which is made by dairy cows. Feeding regimen, productivity, and manure management, and therefore dairy system, are considered the main sources of variation in the emission of enteric methane (EME), the most important GHG emitted by the dairy sector. Genetic variations among and within breeds also play a role in the amount of EME emitted by dairy cows (de Haas et al., 2011).

Direct quantification of GHG requires the facilities, tools, and knowledge normally available only in few research centers (Knapp et al., 2014), making it very difficult to directly test GHG emissions in the field with a large number of farms and cows. It is therefore essential to develop indirect methods of quantifying EME to compare different dairy systems at a practical level, and to acquire data from a wide range of individual cows as a basis for estimating breeding value for EME traits for the genetic improvement of dairy populations for these traits.

As recently reviewed by Negussie et al. (2017), many proxies have been proposed for large-scale indirect

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measurements of EME in dairy cattle for use in making management and breeding decisions. Of these, the analysis of milk fatty acid (FA) profiles and the use of proper combinations of FA are methods more easily used in the field, needing only the collection of milk samples and their analysis in the laboratory.

The underlying biological phenomenon is the production of CH₄ in the rumen and other fore-stomachs of ruminants by rumen microbes from the H₂ generated from carbohydrate fermentation to produce acetate and butyrate (Demeyer and van Nevel, 1975; Morvay et al., 2011). These 2 VFA are the main substrate of de novo synthesis of the even short- and mid-chain FA by the mammary gland of dairy cows (Chilliard et al., 2000) and consequently a direct relationship is present between EME and the de novo synthesis in the udder. Also, other milk FA are related to the rumen environment and microbiota activity, such as odd- and branched-chain FA, which are mainly produced by microbial activity (Castro Montoya et al., 2011), and long-chain UFA, which tend to depress microbial fermentation and EME in the rumen (Doreau and Ferlay, 1993).

Some interesting studies have been carried out in recent years using the gold standard for EME measurements, respiration chambers, and for FA profile analysis, GC (see the extensive review of van Gastelen and Dijkstra, 2016). These studies have focused on different sources of forage in feeds (Dehareng et al., 2012; Dijkstra et al., 2016; Rico et al., 2016), different oil-seeds (Chilliard et al., 2009; Mohammed et al., 2011), and rumen-active supplements (Dijkstra et al., 2011). Being based on EME measurements in the respiration chambers, each one of these studies was carried out with small numbers of cows and few diets in strictly experimental conditions, so the results cannot be easily generalized to field conditions (Williams et al., 2014). On the other hand, van Lingen et al. (2014) undertook a meta-analysis of the relationships between EME and milk FA profiles by combining the data from 4 experiments carried out at the University of Reading (United Kingdom; Crompton et al., 2010, 2011; Reynolds et al., 2010, 2012), and 4 experiments carried out at Wageningen University (the Netherlands; van Zijderveld et al., 2011a,b; van Gastelen et al., 2014), covering 30 different diets. They devised 2 equations for predicting EME traits, one for methane yield (CH₄ per kg of DMI) and one for methane intensity (CH₄ per kg of fat- and protein-corrected milk, CM). Both have a good level of accuracy, considering that the data were obtained from different experiments, and with different diets and environmental conditions, even though lower than equations obtained from single studies in one location

and few diets (Chilliard et al., 2009; Mohammed et al., 2011; Rico et al., 2016).

Few, if any, studies have applied these equations obtained from meta-analysis of large-scale data sets from field surveys to predict EME, and little information is available on the cheese-making ability of different cows as a basis for calculating EME per kilogram of cheese produced.

In this study, we applied the van Lingen et al. (2014) equations to a set of data from a large-scale field survey to quantify the EME traits predicted by selected milk FA and to assess their main sources of variation. The specific aims were (1) to estimate methane yield (per kg of DMI), methane intensity (per kg of milk and per kg of cheese), and daily methane production of individual cows; (2) to compare different dairy systems; (3) to quantify the variations in the estimated EME traits among different herds reared in the same dairy system; and (4) to analyze the effect of parity and lactation stage of individual cows on the estimated EME traits.

MATERIALS AND METHODS

Dairy Farming Systems and Herds

This study is part of the Cowability-Cowplus projects. Briefly, we carried out the study on 85 herds located in Trento Province (northeastern Italian Alps) and registered with the milk-recording program of the local Provincial Breeders' Federation (Federazione Provinciale Allevatori, Trento, Italy). The herds were selected from 610 farms to represent different environments and dairy farming systems (Sturaro et al., 2013).

Briefly, 29 of the herds were from farms designated as "traditional" dairy systems. These were small (average 18.6 ha of cultivated land) with a small number of cows (average 28) kept tied all year round in old facilities, and fed mainly meadow hay and small amount of compound feeds (about 18% of DMI). Milking was mechanically carried out at individual stalls. The 56 farms designated as "modern" dairy systems were larger, with more cows (average 45) kept in free stalls and milked in milking parlors. The feeding regimen of 30 of these modern farms did not use TMR, and was often similar to traditional farms but with more compound feed per cow (about 30% DMI). Of the 26 dairy farms using TMR (concentrates accounting for about 50% of DMI), 9 included corn silage in the diet and 17 added water to moisten the TMR. The farms were sampled once in a calendar year to ensure that the various dairy systems were evenly distributed throughout the year, except in August.

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