



Changes throughout lactation in phenotypic and genetic correlations between methane emissions and milk fatty acid contents predicted from milk mid-infrared spectra

M.-L. Vanrobays,*¹ C. Bastin,* J. Vandenplas,*^{†2} H. Hammami,* H. Soyeurt,* A. Vanlierde,‡ F. Dehareng,‡ E. Froidmont,§ and N. Gengler*

*Agriculture, Bio-engineering and Chemistry Department, Gembloux Agro-Bio Tech, University of Liège, B-5030 Gembloux, Belgium

†National Fund for Scientific Research, B-1000 Brussels, Belgium

‡Walloon Agricultural Research Centre, Valorization of Agricultural Products, B-5030 Gembloux, Belgium

§Walloon Agricultural Research Centre, Production and Sectors Department, B-5030 Gembloux, Belgium

ABSTRACT

The aim of this study was to estimate phenotypic and genetic correlations between methane production (Mp) and milk fatty acid contents of first-parity Walloon Holstein cows throughout lactation. Calibration equations predicting daily Mp (g/d) and milk fatty acid contents (g/100 dL of milk) were applied on milk mid-infrared spectra related to Walloon milk recording. A total of 241,236 predictions of Mp and milk fatty acids were used. These data were collected between 5 and 305 d in milk in 33,555 first-parity Holstein cows from 626 herds. Pedigree data included 109,975 animals. Bivariate (i.e., Mp and a fatty acid trait) random regression test-day models were developed to estimate phenotypic and genetic parameters of Mp and milk fatty acids. Individual short-chain fatty acids (SCFA) and groups of saturated fatty acids, SCFA, and medium-chain fatty acids showed positive phenotypic and genetic correlations with Mp (from 0.10 to 0.16 and from 0.23 to 0.30 for phenotypic and genetic correlations, respectively), whereas individual long-chain fatty acids (LCFA), and groups of LCFA, monounsaturated fatty acids, and unsaturated fatty acids showed null to positive phenotypic and genetic correlations with Mp (from –0.03 to 0.13 and from –0.02 to 0.32 for phenotypic and genetic correlations, respectively). However, these correlations changed throughout lactation. First, de novo individual and group fatty acids (i.e., C4:0, C6:0, C8:0, C10:0, C12:0, C14:0, SCFA group) showed low phenotypic or

genetic correlations (or both) in early lactation and higher at the end of lactation. In contrast, phenotypic and genetic correlations between Mp and C16:0, which could be de novo synthesized or derived from blood lipids, were more stable during lactation. This fatty acid is the most abundant fatty acid of the saturated fatty acid and medium-chain fatty acid groups of which correlations with Mp showed the same pattern across lactation. Phenotypic and genetic correlations between Mp and C17:0 and C18:0 were low in early lactation and increased afterward. Phenotypic and genetic correlations between Mp and C18:1 *cis*-9 originating from the blood lipids were negative in early lactation and increased afterward to become null from 18 wk until the end of lactation. Correlations between Mp and groups of LCFA, monounsaturated fatty acids, and unsaturated fatty acids showed a similar or intermediate pattern across lactation compared with fatty acids that compose them. Finally, these results indicate that correlations between Mp and milk fatty acids vary following lactation stage of the cow, a fact still often ignored when trying to predict Mp from milk fatty acid profile. **Key words:** fatty acid, methane, dairy cattle, mid-infrared

INTRODUCTION

Greenhouse gases are large contributors to climate change (e.g., IPCC, 2006). Methane from gastro-enteric fermentation is the major greenhouse gases produced by dairy cattle (Gerber et al., 2013). Moreover, methane production (Mp; i.e., in g/d) implies loss of gross energy intake (from 2 to 12% of gross energy intake; Johnson and Johnson, 1995). Therefore, efforts to mitigate methane emissions are needed to improve the environmental sustainability and economic profitability of dairy production.

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¹Corresponding author: mlvanrobays@student.ulg.ac.be

²Current address: Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, 6700 AH Wageningen, the Netherlands.

In cattle, gastro-enteric fermentation of glucose equivalents from starch or plant cell wall polymers occurs in the rumen under anaerobic conditions and results in production of VFA (mainly acetate, propionate, and butyrate). The production of acetate and butyrate releases H_2 , whereas the production of propionate requires H_2 . Released H_2 is used by methanogenic archaea to reduce carbon dioxide into methane to avoid hydrogen accumulation in the rumen and methane is eliminated mainly through eructation (Demeyer and Fievez, 2000; Moss et al., 2000; Martin et al., 2010). Therefore, Mp is promoted by production of acetate and butyrate, whereas the propionate and methane synthesis pathways compete for the use of H_2 (Moss et al., 2000; Martin et al., 2010). Besides, acetate and butyrate are precursors of de novo synthesis of milk fatty acids (Bernard et al., 2008). Consequently, Chilliard et al. (2009) suggested a direct relationship between Mp and milk fat composition. Therefore, some previous studies were conducted to investigate raw correlations between milk fatty acids and ruminal methane and to develop equations to predict methane output based on milk fatty acid content (Chilliard et al., 2009; Dijkstra et al., 2011; Mohammed et al., 2011; van Lingen et al., 2014; Williams et al., 2014; Rico et al., 2016).

Generally, positive correlations between ruminal methane on the one hand, and SFA, short-chain fatty acids (**SCFA**), medium-chain fatty acids (**MCFA**), or de novo fatty acids on the other hand were reported (Chilliard et al., 2009; Dijkstra et al., 2011; Mohammed et al., 2011; van Lingen et al., 2014; Rico et al., 2016). From experiments using a maize-silage-based diet complemented or not by 3 different physical forms of linseed (crude, extruded, or oil), Chilliard et al. (2009) found high positive correlations between Mp and individual SFA from C6:0 to C16:0 (in % of total fatty acids; between 0.88 and 0.91). Based on 3 experiments focusing on fat supplementation through 10 dietary treatments, positive correlations between methane yield (i.e., expressed in g/kg of DMI) and C8:0, C10:0, C11:0, C14:0 iso, C15:0 iso, C16:0, and C17:0 anteiso (in % of total fatty acids) were in the range of 0.30 to 0.47 (Dijkstra et al., 2011). Mohammed et al. (2011) supplemented diets of cows with different types of oils (palm, sunflower seed, linseed, or canola seed) and obtained a positive correlation of 0.39 between Mp and sum of SFA (in % total FAME). van Lingen et al. (2014) performed a meta-analysis (8 experiments and 30 different dietary treatments) to calculate correlations between methane yield (i.e., expressed in g/kg of DMI) or methane intensity (i.e., expressed in g/kg of fat- and protein-corrected milk) and milk fatty acid profile (in g/100 g of fatty acids) from data based on cows fed with various diets. Correlations between

methane yield and almost all de novo fatty acids were positive. Positive correlations for methane intensity with all SCFA and MCFA were also found, except with C4:0 (-0.28 for C4:0 and between 0.02 and 0.36 for other fatty acids). From experiments using different forage sources (i.e., corn silage, alfalfa silage, barley silage, timothy silage, corn and alfalfa silage, barley and corn silage, or timothy and alfalfa silage), Rico et al. (2016) found positive correlations between Mp and de novo fatty acids (in % of total fatty acids; 0.34). On the contrary, correlations between methane and UFA (Chilliard et al., 2009; Mohammed et al., 2011; van Lingen et al., 2014) or long-chain fatty acids (**LCFA**; Dijkstra et al., 2011; van Lingen et al., 2014; Rico et al., 2016) were generally negative (from -0.01 to -0.42). However, based on data from 8 experiments with forage-based diets supplemented with a large variety of complements, Williams et al. (2014) found, for some of their experiments, correlations between Mp and C8:0 and sum of C18 that were not consistent with other studies. Finally, Mohammed et al. (2011) and Williams et al. (2014) concluded from their study that milk fatty acid profile only was not appropriate to predict methane reliably.

Overall, these studies used a restricted number of records, even with meta-analyses (less than 300 records). Indeed, obtaining measurements of methane on a large scale remains difficult and expensive, thereby preventing estimations of correlations between methane and milk fatty acids on large data sets and across lactation. Hence, indicator traits or indirect measurements of methane, hereafter called proxies of methane output, that could be measured at a large scale, could be useful to study these correlations (Ellis et al., 2007). Over the last years, in addition to attempting to use fatty acids, other proxies of methane were developed. For example, such proxies can be derived from feed intake and diet composition (e.g., Ellis et al., 2007; de Haas et al., 2011). Another proxy of Mp based on milk mid-infrared (**MIR**) spectra and lactation stage was developed by Vanlierde et al. (2015). Given that milk MIR spectra are collected routinely through milk-recording schemes, MIR prediction of Mp could be very useful to conduct phenotypic and genetic studies on Mp at large scale.

In addition, previous studies investigating the relationships between milk fatty acids and methane did not consider that these relationships may vary throughout lactation. However, it is known that both milk fatty acid profile and Mp change over lactation, and that the patterns of milk fatty acid content and of Mp over DIM are different (Bastin et al., 2011; Garnsworthy et al., 2012). Milk fatty acid profile changes both phenotypically and genetically during lactation especially according to the metabolic status of cows (Bastin et

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