ESTIMATION OF GENETIC PARAMETERS FOR METHANE INDICATOR TRAITS BASED ON MILK FATTY ACIDS IN DUAL PURPOSE BELGIAN BLUE CATTLE

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INTRODUCTION

Livestock production is one of the key sources of Greenhouse gas (GHG) emissions such as methane (CH_4). Since CH_4 is 21 times more potent to carbon dioxide in greenhouse effect, reduction of CH_4 would play an important contribution to abate greenhouse emissions (IPCC, 2007).

Accurate measurement of CH_4 emission can be obtained using respiration chamber calorimetry method but the cost and the analysis time limit the number of evaluated animals (Kebreab, et al., 2006). The sulfur hexafluoride gas (SF_6) measurement is an alternative (Johnson et al., 1994) because of its relatively lower price but accurate measurement of CH_4 is complex and recording of such data is unfeasible at a large scale. Therefore, some studies have focused on the use of traits indirectly related to the CH_4 emission and easily recorded at large scale, as fatty acids (FA).

CH_4 output from ruminants is linked to microbial digestion in the rumen. The fermentation process of feed carbohydrates leads to the production of hydrogen (H_2) and the methanogenesis is the essential pathway to evacuate this generated H_2 (Moss et al., 2000). The synthesis of acetate (C2) and beta-hydroxybutyrate (C4) produces H_2 then converted to CH_4, while propionate (C3) synthesis consumes H_2 (Demeyer et al., 1975). The *de novo* synthesis of milk FA in mammary gland uses mostly C2 but also C4, and C3 (but it is almost not used for this synthesis) to make short chain FA and nearly all medium chain FA (Chilliard et al., 2000). Based on this indirect link between FA and CH_4, equations were developed to predict indicators of the CH_4 emission from FA profile (Chilliard et. al., 2009; Dijkstra et al., 2011). As the mid-infrared spectroscopy (MIR) can be used to predict the milk FA contents (Soyeurt et al., 2011), the MIR could also predict directly their CH_4 indicator traits allowing the analysis of many milk samples.

Boadi et al. (2002) suggested that 27% of the variation of CH_4 in Canadian dairy and beef heifer was related to animal variation. Haas et al. (2011) supposed also the existence of a genetic variation of CH_4. Therefore, the emission of CH_4 could be optimized through an adapted breeding program. The aim of this study was to estimate the genetic parameters of CH_4 through the use of MIR predicted CH_4 indicator traits in dual purpose Belgian blue cattle.

MATERIAL AND METHODS

Milk samples

Samples collected between 5 and 365 days in milk (DIM) from 2007 to 2011 of Dual Purpose Belgian Blue cows in their first three lactations (5,622; 3,851 and 2,526 records respectively) were obtained during the Walloon regular milk recording. The samples were analysed using a Milkoscan FT6000 to quantify the contents of protein and fat and MIR spectra.

CH_4 indicator traits

The calibration set contained 600 Walloon samples analysed by gas chromatography. CH_4 indicator traits (called CH_4_1 to 5) considered as reference value were computed from 5 published equations (Table 1) using the gas chromatography contents of FA in bovine milk fat. A t-outlier test was used to delete potential outliers. The robustness of these equations was assessed using a cross-validation and the cross-validation coefficient of determination (R^2cv) was computed (Table 2).

Table 1. Published CH_4 equations

Indicator trait	Equation (FA in g/100g of fat)	R^2	Reference
CH_4_1 (g/day)	9.97 x (C8:0 to C16:0) – 80	0.88	Chilliard et al., 2009
CH_4_2 (g/day)	-8.72 x C18:0 + 729	0.88	
CH_4_3 (g/day)	282 x C8:0 +11	0.81	
CH_4_4(g/day)	16.8 x C16:0 – 77	0.82	
CH_4_5 (g/kg DM, 17.7 kg DM/day)	24.6 + 8.74 x C17:0 anteiso – 1.97 x trans-10+11 C18 :1 – 9.09 x C18 :1 cis-11 + 5.07 x C18 :1 cis-13	0.73	Dijkstra et al., 2011

R^2 represents the relationship between the SF6 CH_4 data and the developed predictors as found in the original research.

Table 2. MIR prediction equations for CH4 (g/day) based on Walloon data

Indicator	N	Mean	SD	R^2cv
CH_4_1	597	446.75	68.50	0.92
CH_4_2	602	421.52	60.71	0.91
CH_4_3	595	368.53	43.23	0.72
CH_4_4	588	459.55	88.11	0.92
CH_4_5	592	368.34	51.33	0.69

Estimation of genetic parameters

Single trait random regression test-day models were used to estimate the variance components of the studied CH4 indicator traits:

$$\mathbf{y=X\beta+Q(Zp+Zu)+e}$$

Where **y** was the vector of observations for each trait, **β** was the vector of fixed effects (herd x test day, DIM (24 classes), and age at calving (3 classes)); **p** was the vector of permanent environmental random effects, **u** was the vector of additive genetic effects; **q** was coefficients of 2nd order Legendre polynomials; **e** was the vector of residuals. **X** and **Z** were incidence matrices. Variance components were estimated using restricted maximum likelihood method. Lactation heritability (h^2) values were calculated as the ratio of 305-d genetic variance to the sum of 305-d genetic variance, 305-d permanent environmental variance and 305-d residual variance. Average daily h^2 was the averaged h^2 estimated separately for each DIM between 5 and 305 DIM as the ratio of the genetic variance at that DIM to the total variance. The same mixed model and data was used to estimate breeding values (EBV) using best linear unbiased prediction.

RESULTS

Estimated CH_4 Production

The MIR CH_4 predicted content ranged from 317g to 411g/day (Fig 1). CH_4_5, which was based on other hypothesis, estimated the lowest and CH_4_1 predicted highest amount of CH_4 per day. For all studied indicator traits, larger amount of CH_4 was estimated for the second lactation compared to the first one. However, this trend is almost flat from second to third and following lactation (data not shown).

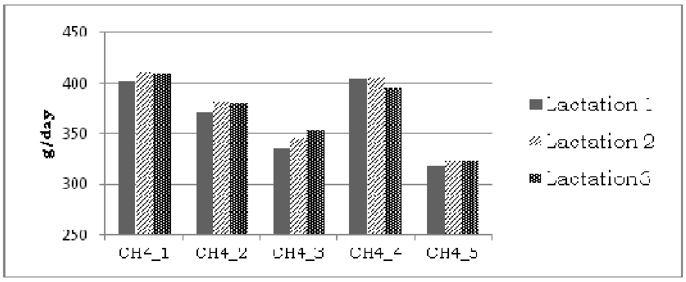

Fig 1. Predicted CH_4 content (g/day) for the first three lactations

The estimated CH_4 content varied also throughout the lactation. It was lower at the beginning of the parity increased up to 80th DIM and stayed constant.

Heritabilities

Daily h^2 ranged between 0.05 and 0.40. For CH_4_1 (highest R^2 with SF_6 data, Table 1) average daily h^2 were 0.21, 0.20 and 0.10 for the first three lactations. Lactation h^2 ranged between 0.26 and 0.66 (Table 3). CH_4_3 and CH_4_5 gave the most different values compared to the other traits.

Table 3. The average daily and lactation h^2 of the studied traits

Indicator	Average daily h^2			Lactation h^2		
	Lact 1	Lact 2	Lact 3	Lact 1	Lact 2	Lact 3
CH_4_1	0.21	0.20	0.10	0.37	0.46	0.26
CH_4_2	0.16	0.15	0.15	0.38	0.39	0.28
CH_4_3	0.23	0.36	0.21	0.54	0.66	0.37
CH_4_4	0.23	0.27	0.16	0.50	0.63	0.44
CH_4_5	0.05	0.07	0.09	0.27	0.39	0.46

Observed and genetic correlations among the traits

The observed and genetic correlations were estimated for all studied traits. Both observed and genetic correlations between CH_4_1 and CH_4_2 were close to one. Lower correlations were found among other studied traits. However, for all studied traits the correlations were positive (Table 4).

Estimated Breeding values

The EBVs of sires which have daughters with traits were estimated for the first three lactations (Table 5). The maximum range was 21.28 kg for the first

Table 4. Observed (above the diagonal) and genetic (below the diagonal) correlations among the studied CH_4 indicator traits.

	CH_4_1	CH_4_2	CH_4_3	CH_4_4	CH_4_5
CH_4_1	1.00	0.99	0.51	0.88	0.61
CH_4_2	0.96	1.00	0.52	0.88	0.65
CH_4_3	0.64	0.70	1.00	0.25	0.16
CH_4_4	0.81	0.71	0.35	1.00	0.65
CH_4_5	0.62	0.61	0.24	0.66	1.00

parity for CH_4_3. The range of EBV for CH_4_1 was 11.6, 13.0 and 6.3 kg for the first three lactations and R/SD was of 6. The values of R/SD calculated for all studied traits were similar. For CH_4_1, the genetic variability was on 3.58 kg^2, 4.10 kg^2 and 1.27 kg^2 for the first three lactations.

Table 5. Descriptive statistics of EBV for sires

N	Lactation 1 (127 bulls)			Lactation 2 (112 bulls)			Lactation 3 (97 bulls)		
Indicator	SD	Range	R/SD	SD	Range	R/SD	SD	Range	R/SD
CH_4_1	1893	11603	6.13	2027	13019	6.42	1125	6259	5.56
CH_4_2	1492	9440	6.32	1535	8975	5.85	1091	5932	5.44
CH_4_3	3696	21280	5.76	3038	16322	5.37	2082	11180	5.37
CH_4_4	2701	13446	4.98	3573	18882	5.28	2174	12208	5.61
CH_4_5	566	4018	7.15	815	4779	5.88	832	4903	5.84

R/SD= Range/Standard Deviation; SD and Range in g/lactation

DISCUSSIONS

The estimated MIR based CH_4 content was similar to the CH_4 emission measured from respiration chamber *in vivo* (i.e., 371 to 453 g/day from Zijderveld et al., 2011) and from SF_6 method (311g/day from Cavanagh et al., 2010). In this study, significant changes were observed throughout the lactation which was expected because of the indirect link between milk FA and CH_4 eructed by dairy cows (Chilliard et al., 2009; Dijkstra et al., 2011).

The obtained h^2 values suggested a potential transmission from generation to generation of the capacity of the CH_4 eructation. Previously reported h^2 for the predicted CH_4 production in Holstein cow was 0.12 (Cassandro et al., 2010) and 0.35 (Haas et al., 2011). Therefore, the h^2 values obtained in this study were globally in agreement with the previously published results.

The choice of the best CH_4 indicator trait is important for further genetic studies. CH_4_1 seems to be the most relevant because it had with CH_4_2 the best correlations to SF_6 CH_4 data (Chilliard et al., 2009); and, with CH_4_4, had the highest R^2cv (0.92) for its prediction from MIR. Because of difference in definitions and as the genetic correlation with CH_4_5 was low, it could be relevant to continue to consider CH4_1 and CH4_5 for further studies.

The obtained standard deviations, range/SD ratios of EBV suggest that there is an appreciable amount of variation existing between high CH_4 producing and low CH_4 producing animals. These results and the h^2 estimates confirmed the genetic variability of CH_4 suggested previously by Haas et al. (2011) and Cassandro et al. (2010).

In conclusion, this study showed the potentiality to predict CH_4 indicator traits by MIR and suggests the existence of a phenotypic and genetic variability of the CH_4 content eructed by dairy cows.

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