Genetic correlations between methane production and fertility, health, and body type traits in Danish Holstein cows

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ABSTRACT

Our aim was to investigate the genetic correlations between CH_4 production and body conformation, fertility, and health traits in dairy cows. Data were collected from 10 commercial Holstein herds in Denmark, including 5,758 cows with records for body conformation traits, 7,390 for fertility traits, 7,439 for health traits, and 1,397 with individual CH_4 measurements. Methane production was measured during milking in automatic milking systems, using a sniffer approach. Correlations between CH_4 and several different traits were estimated. These traits were interval between calving and first insemination, interval between first and last insemination, number of inseminations, udder diseases, other diseases, height, body depth, chest width, dairy character, top line, and body condition score. Bivariate linear models were used to estimate the genetic parameters within and between CH_4 and the other traits. In general, the genetic correlations between CH_4 and the traits investigated were low. The heritability of CH_4 was 0.25, and ranged from 0.02 to 0.07 for fertility and health traits, and from 0.17 to 0.74 for body conformation traits. Further research with a larger data set should be performed to more accurately establish how CH_4 relates to fertility, health, and body conformation traits in dairy cattle. This will be useful in the design of future breeding goals that consider the production of CH_4.
Key words: methane, functional trait, body conformation

INTRODUCTION

Farming has had a major effect on CH_4 emissions, with the ruminant population being accountable for 2 billion metric tonnes of CO_2-equivalents per year. This makes cattle the largest contributors to the increase in global greenhouse gasses (O'Mara, 2011). Ruminants produce CH_4 during digesting high-fiber feeds, and 95% of the CH_4 produced is eructed through cows' breath (Murray et al., 1976). Several animal factors are assumed to cause differences in individual CH_4 production, such as the passage rate of digesta, microbial activity, fermentation conditions, anatomical and physiological differences in the gastrointestinal tract, and grazing behavior (Iqbal et al., 2008; Hegarty et al., 2010). Also, the genetic make-up of the animal affects its rumen microbe population (Guan et al., 2008), digestive function (Hegarty, 2004), feed intake, and feed efficiency (Arthur et al., 1996, 2001; Herd et al., 1997). Therefore, some of the factors assumed responsible for differences in CH_4 production among animals have been found. However, little is known about the role genetics has in explaining those differences, or how to select for lower emitting cows.

Breeding has been practiced through the use of selection indices, with breeding goals focusing mainly on production traits, without much consideration given to the effects of it in the overall production system. However, decades of intensive selection for productive traits only has been shown to compromise cows' health and fertility status (Veerkamp et al., 2001; Walsh et al., 2011). Over the last 15 yr, national selection indices across the globe have been putting more emphasis on health and fertility traits, to try and minimize the negative effects of intensive selection on production traits only (Miglior et al., 2005). Therefore, it is of great importance to understand the direct and indirect consequences of selection for the traits included in dairy cattle breeding programs, and what potential effects, if any, mitigation strategies could have in future breeding goals.

The last decade has brought an increasing interest in understanding the relationship between CH_4 production and traits of economic interest in dairy cattle, such as milk yield (**MY**) and DMI. However, little is

known about its relationships to functional traits and body conformation. Garnsworthy (2004) showed that restoring dairy cows' fertility status to 1995 levels would cause a reduction of 10% in CH_4 production over their productive lifetime, due to a decrease in involuntary culling due to reproductive issues. Sick, unfertile cows have their productive levels, such as MY or estrus expression, compromised while generating extra costs. Fertility issues are one of the major causes for involuntary culling, which leads to animal waste and a higher number of replacements heifers needed to maintain production levels (Hegarty and McEwan, 2010). An improvement in a herd's reproductive status could help by decreasing involuntary culling and improving fertility traits, such as calving intervals, shortening unproductive periods and, therefore, lowering unnecessary costs along with CH_4 production. However, the way CH_4 production correlates to fertility, health, and body conformation traits is unknown. This information is important to know the effects of incorporating CH_4 into selection indexes. Hence, the objective of this study was to estimate genetic parameters for CH_4 production, measured by a sniffer approach in commercial Danish Holstein herds, and the genetic correlations between CH_4 and a group of health, fertility, and body conformation traits.

MATERIALS AND METHODS

CH_4 Data

Data were collected in 10 commercial Holstein herds from all over Denmark, from December 2011 until July 2013. A total of 1,397 individual CH_4 measurements were recorded, by using a portable FTIR gas analyzer (GASMET 4300; Gasmet Technologies Oy, Helsinki, Finland). The FTIR technique uses an infrared transmission spectrum of an air sample, and it measures the concentration of CH_4 and CO_2 in the cows' breath, through an air inlet placed inside automatic milking systems (**AMS**). The air inlet was placed in the frontal part of the AMS, close to the animals' heads, and it recorded every 5 s, for 7 d in each farm. Cows in all herds were fed ad libitum mixed rations, and concentrate supplement was offered inside the AMS as a way to attract the cows to milking. All herds had Lely A3 AMS (Lely International N. V., Maassluis, the Netherlands), equipped with scales to collect individual live weight (**LW**) measurements. Records on LW and MY for each milking were collected within the same period, and they were merged with the CH_4 measurements for each cow. The CH_4 phenotype was obtained by using information on LW, fat- and protein-corrected milk (**FPCM**), and days carried calf (**DCC**) to predict CO_2 production

(Madsen et al., 2010), based on heat-producing units (**HPU**):

$$HPU = 5.6 \times LW^{0.75} + 22 \times FPCM$$
$$+ 1.6 \times 10^{-5} \times DCC.$$

The ratio between CH_4 and CO_2 is measured, in ppm, by the FTIR unit, and combined with the HPU estimated for each cow. The final CH_4 phenotype is expressed in liters per day. Pedersen et al. (2008) recommend a CO_2 production of 180 l per HPU per hour for individual dairy cows; therefore,

$$CH_4 \ (L/d) = CH_4/CO_2 \times 180 \times 24 \times HPU.$$

Milk yield records were available for all cows, and average daily milk production from the week the CH_4 records were collected was used to estimate FPCM, which was calculated as

$$FPCM = MY \times (0.25 + 0.122 \times fat \ \%$$
$$+ 0.077 \times protein \ \%).$$

Fat and protein percentage were provided by the Danish Cattle Database (SEGES, Skejby, Denmark), from milk recordings that were the closest to when CH_4 production was recorded in each farm, meaning maximum of 30-d interval before or after CH_4 recording. The traits LW, FPCM, and CH_4 were based on weekly averages. Cows which were above 500 DIM and cows without DIM information were excluded from the analysis. To keep as many CH_4 records as possible, no animals were discarded due to a high lactation number. However, 35% of the CH_4 records were from first lactation cows and 89% from cows in first, second, or third lactation, with the remainder being between fourth and seventh lactation.

Body Conformation, Fertility, and Health Data

Data on conformation, fertility and health were extracted from the Danish Cattle Database (SEGES). For body conformation, the traits analyzed were BCS, body depth, back line (**BL**), chest width, height, and dairy character (**DC**). Fertility traits analyzed were interval between calving and first insemination (**CF**), interval between first and last insemination (**FL**), and number of inseminations. Health traits were udder health (**UH**) and other diseases (**OD**). Information on all lactations available was considered for cows with both CH_4 and fertility, or health, or conformation traits. For the herd mates without CH_4 measurements, only cows with se-

Table 1. Definitions for conformation, fertility, and health traits

Trait	Trait definition
Conformation	
BCS	The covering of fat over the tail, head, and rump
Body depth	Distance between the top of the spine and the bottom of the body, at the start of the last rib
Back line	Assessment of the animal's withers, back, and loin
Chest width	Distance between the top of the front legs and the width of the ribs and shoulder
Height	Measured from the top of the animal's spine to the ground, between the hips, in centimeters
Dairy character	Overall evaluation of the animal's potential milking ability, considering a group of factors, such as ribs, thighs, withers, neck, and skin
Fertility	
Interval between calving and first insemination	Number of days between calving and the first insemination for the next reproductive cycle
Interval between first and last insemination	Number of days between the first and last attempts at successfully inseminating a cow
Number of inseminations	Number of times the cow had to be inseminated to get pregnant
Health	
Udder health	Mastitis incidences between d 0 to 50 of lactation
Other diseases	Covers reproductive, digestive, and foot and leg diseases that have occurred between d 0 and 50 of lactation

quential information from first to third lactations were kept in the data set; therefore, 1,720 cows in total were excluded from the body conformation, fertility, and health data sets.

Conformation traits were recorded in accordance with the World Holstein-Friesian Federation guidelines. Individual type measurements were used to obtain a linear classification of each animal. With the exception of height, all traits were scored by classifying each animal with a value from 1 to 9. All conformation traits in the present study are approved standard traits, except for BL, which is a novel trait used in the Nordic Cattle Genetic Evaluation. Trait definitions can be seen in Table 1.

For animals with 2 conformation scores occurring in the same lactation, the one closest to the calving date was kept. After editing, a total of 5,758 animals were in the conformation data set, with 7,345 records. Information on number of cows, records, lactation number, and DIM per herd can be found in Table 2. For lactation number, the information shown is for all cows used in this study; for DIM, however, the information is for cows with CH_4 records only.

Fertility data were composed of 7,390 animals, with 15,821 records. Editing for traits was done following the Nordic Cattle Genetic Evaluation standards, which means only animals with CF between 20 and 230; FL between 0 and 365; and number of inseminations up to 8 were considered.

Health data were composed of 7,439 animals, with 16,169 records. Traits were measured as binary, with 0 indicating no incidence of diseases, and 1 indicating

Table 2. Number of animals, records per trait, and averages, and minimum (Min) and maximum (Max) values for lactation number and DIM, within herds[1]

Herd	No. of animals	CH_4	Conf	Fert	Heal	Lactation[2]			DIM[3]		
						Mean	Min	Max	Mean	Min	Max
1	341	110	671	751	791	2.04	1	9	144.60	0	494
2	633	237	602	1,333	1,387	1.96	1	7	120.94	3	500
3	631	186	169	1,294	1,328	1.92	1	6	112.94	1	463
4	449	69	927	1,038	1,046	1.97	1	7	99.52	1	477
5	763	125	758	1,705	1,741	1.94	1	8	94.14	1	452
6	503	91	761	926	959	1.81	1	6	134.72	0	404
7	1,444	152	1,242	2,958	2,992	1.84	1	8	110.43	0	245
8	1,487	40	998	3,149	3,151	1.86	1	7	106.70	3	338
9	388	181	53	920	977	2.17	1	8	197.22	5	500
10	800	257	1,164	1,747	1,797	1.97	1	7	191.85	0	499

[1]CH_4 = number of CH_4 records per herd; Conf = number of conformation records per herd; Fert = number of fertility records per herd; Heal = number of health records per herd.

[2]Lactation number information for all cows, across traits.

[3]DIM information for cows with CH_4 records only.

incidence of at least one disease in the period from calving until 50 d after calving. For the trait OD, the diseases considered were uterine prolapse, retained placenta, milk fever, and other reproductive diseases; soars, foot abscess, sole bruising, heel root, interdigital lesion, laminitis, and arthritis for feet and legs; and diarrhea, ketosis, displaced abomasum, enteritis, toxic abomasum, rumen acidosis, and other digestive diseases.

The pedigree was traced as far back in time as possible, and consisted of 49,643 animals. There was no limitation on the number of generations. Data for conformation, fertility, and health used in this study were collected over a period of 10 yr, from January 2005 to January 2015.

Statistical Models

For estimation of CH_4 parameters, the following linear model was used:

$$y_{ij} = \mu + \text{herd} + lact_j + \text{year} \times \text{month} + \beta_1 \times \text{DIM}$$
$$+ \beta_2 \times \text{DIM}^2 + a_i + e_i,$$

where y is the dependent phenotype CH_4, μ is the overall intercept, herd is the herd ID for each one of the 10 herds, $lact$ represents lactation number at recording, year $\times$ month indicates the year-month of calving, and DIM represents the DIM at recording. The DIM was modeled as a linear regression, and the squared DIM was included to account for changes in early lactation. The β terms represent the fixed regression coefficients for DIM and DIM^2, a is the random animal effect, and e is the residual effect.

For the body type traits, the linear model used was as follows:

$$y_{ij} = \mu + \text{herd} + \text{year} \times \text{month} + insp + \beta_1 \times \text{DIM}_c$$
$$+ \beta_2 \times \text{DIM}_c^2 + \beta_3 \times CA_{(lact)} + \beta_4 \times CA_{(lact)}^2 + a_i + pe_i + e_i,$$

where y represents the dependent phenotypes for all the body type traits analyzed, and the effects μ, herd, and year $\times$ month are the same as previously described. The $insp$ variable represents the ID of the inspector who performed the scoring, DIM_c represents the days in milk when the body type traits were scored, $CA_{(lact)}$ is the animals' age of calving nested per lactation, and both CA and DIM were modeled as linear regressions. Squared DIM and CA were included to account for changes in early lactation, β terms represent the fixed regression coefficients, a is the random animal effect, pe

is the permanent environment effect and e, the residual effect.

For fertility traits, the linear model used was

$$y_{ij} = \mu + \text{herd} + \text{year} \times \text{month} + insmonth$$
$$+ \beta_1 \times insage_{(lact)} + \beta_2 \times insage_{(lact)}^2 + a_i + pe_i + e_i,$$

where y is the dependent phenotypes for the fertility traits, herd and year $\times$ month have been previously described, and $insmonth$ represents the effect of insemination month, nested per lactation. The $insage_{(lact)}$ is the animals' age at insemination, nested per lactation, and it was modeled as a linear regression, in which the β terms represent the fixed regression coefficients, a is the random animal effect, pe is the permanent environment effect, and e is the residual effect.

Lastly, the linear model used for OD and UH was

$$y_{ij} = \mu + \text{herd} + \text{year} \times \text{month} + \beta_1 \times CA_{(lact)} + \beta_2 \times CA_{(lact)}^2$$
$$+ a_i + pe_i + e_i,$$

where y represents the dependent phenotypes UH and other diseases, and all the other effects have been previously described.

The random effects for the models were assumed to be independent and normally distributed, with means of zero. The (co)variance structure used was

$$\text{Var}\begin{bmatrix} \mathbf{a} \\ \mathbf{pe} \\ \mathbf{e} \end{bmatrix} \sim N \left(0, \begin{bmatrix} \mathbf{G}_0 \otimes \mathbf{A} & 0 & 0 \\ 0 & \mathbf{Pe}_0 \otimes \mathbf{I} & 0 \\ 0 & 0 & \mathbf{R}_0 \otimes \mathbf{I} \end{bmatrix} \right),$$

where $\mathbf{G}_0$ is the additive genetic (co)variance matrix; $\mathbf{A}$ is the additive genetic relationship between animals matrix; $\mathbf{Pe}_0$ is the permanent environmental variance matrix, for the body type, fertility, and health traits; $\mathbf{R}_0$ is the residual variance matrix; and $\mathbf{I}$ is the identity matrix containing as many rows and columns as records for each one of the traits analyzed.

Variance and covariance components estimation was performed by DMU (Madsen and Jensen, 2014), using the (AI)REML procedure. The correlations between CH_4 and each of the traits studied were estimated by bivariate analysis, and a Taylor series approximation was used to estimate the standard errors.

Because CH_4 records were generally not recorded on the same day as the other traits analyzed in this study, a model where residual covariances between the traits analyzed were fixed to zero was also tested. For heritabilities estimation, all data available was used,

Table 3. Descriptive statistics of the data set, with number of cows per trait, number of observations, mean, SD, minimum and maximum values for CH_4 production, BCS, body depth (BD), back line (BL), chest width (CW), height (H), dairy character (DC), calving to first insemination interval (CF), first to last insemination interval (FL), number of inseminations (NI), other diseases (OD), and udder health (UH)

Trait	Unit	No. of cows	No. of records	Mean	SD	Minimum	Maximum
CH_4	L/d	1,397	1,397	380	60	247	714
BCS	1–9	5,758	7,345	4.14	1.01	1.00	9.00
BD	1–9	5,758	7,345	6.09	0.91	2.00	1.00
BL	1–9	5,758	7,345	6.53	0.90	3.00	9.00
CW	1–9	5,758	7,345	5.05	0.89	1.00	8.00
H	cm	5,758	7,345	147	6	119	166
DC	1–9	5,758	7,345	5.23	0.92	1.00	8.00
CF	d	7,390	15,821	76	36	20	360
FL	d	7,390	15,821	45	61	0	341
NI	—	7,390	15,821	2.2	1.5	1	8
OD	—	7,439	16,169	0.26	0.44	0.00	1.00
UH	—	7,439	16,169	0.11	0.32	0.00	1.00

whereas for the correlations estimated in this study, only records from cows with both CH_4 and the other traits we analyzed were included.

RESULTS

The descriptive statistics of the data set used are shown in Table 3. There were 1,397 individual CH_4 records available, whereas the number of records for the other traits varied from 7,345 (for body traits) to 16,169 (for health traits). For all traits except CH_4, observations were available for at least the first and second lactations.

Heritability estimates and variance components for the traits analyzed are presented in Table 4. Permanent environment variance was not estimated for CH_4, because there were no repeated measures for this trait. Heritability estimates for CH_4 and for all body conformation traits were moderate and significant, and ranged from 0.17 (for chest width) to 0.74 (for height). However, health and fertility traits show, as expected,

low heritabilities, showing values from 0.02 (for FL and UH) to 0.07 (for CF). Standard errors were low for all heritability estimates.

Additive genetic and residual correlations were estimated for CH_4 and all the other traits (Table 5). The genetic correlations were moderate to low and mostly not significant, except for the correlations between CH_4 and BCS, BL, and DC. The highest absolute r_g was between CH_4 and BL. Cows with a low genetic merit for BL will score the lowest for BL, and our results indicate that low genetic merit for BL could influence CH_4 production. For BCS and CH_4, r_g was moderate negative, implying that a change in genetic merit for BCS could affect CH_4 production. For CH_4 and DC, r_g was moderate positive, so a high genetic merit for DC could also mean high genetic merit for CH_4 production. For CH_4 and OD, r_g was almost significant, in a favorable direction, implying that cows with a genetic merit for low emissions could also be less susceptible to diseases.

As CH_4 records were generally collected at large intervals from when health, reproduction, and body scor-

Table 4. Heritability (h^2) estimates with respective SE, additive genetic variances $\left(\sigma_a^2\right)$, permanent environment variance $\left(\sigma_{pe}^2\right)$, residual variance $\left(\sigma_e^2\right)$, and phenotypic variance $\left(\sigma_p^2\right)$ for CH_4 production, BCS, body depth (BD), back line (BL), chest width (CW), height (H), dairy character (DC), calving to first insemination interval (CF), first to last insemination interval (FL), number of inseminations (NI), other diseases (OD), and udder health (UH)

Trait	h^2 (SE)	σ_a^2	σ_{pe}^2	σ_e^2	σ_p^2
CH_4	0.25 (0.07)	850.22	—	2,504.71	3,354.94
BCS	0.26 (0.03)	0.23	0.09	0.56	0.88
BD	0.28 (0.03)	0.15	0.09	0.31	0.56
BL	0.18 (0.02)	0.14	0.11	0.50	0.76
CW	0.17 (0.02)	0.12	0.12	0.45	0.70
H	0.74 (0.02)	9.91	0.04	3.40	13.36
DC	0.25 (0.02)	0.14	0.0000013	0.43	0.57
CF	0.07 (0.01)	85.70	76.30	972.07	1,134.07
FL	0.02 (0.008)	83.41	159.65	3,375.95	3,619.01
NI	0.04 (0.009)	0.08	0.05	2.12	2.26
OD	0.04 (0.008)	0.007	0.0000003	0.18	0.18
UH	0.02 (0.007)	0.002	0.0000001	0.09	0.09

ing traits were recorded, we also tested models where the residual covariances were set to zero. However, the results were very similar to models where the residual covariances were estimated; accordingly, very low residual correlations were observed between traits using the proposed model.

The Wilmink term (Wilmink, 1987) was used to compare results to models where quadratic regressions were fitted. The results when using the quadratic regressions did not differ from the ones we got when using the Wilmink term; therefore, we believe that the data used in this study support the level of regression when applying quadratic terms.

DISCUSSION

To our knowledge, no previous studies have reported genetic correlations between CH_4 production and body conformation, fertility, and health traits, and information related to CH_4 production is still scarce in the literature. This is due to several factors, such as the challenges to establish an accurate CH_4 phenotype and the lack of inexpensive methods that accurately provide individual CH_4 records for a large number of animals. To be able to use information on CH_4 production in animal breeding programs, accurate and inexpensive phenotypes are needed and methods to quantify CH_4 production in a proper way should be improved (de Haas et al., 2017). The inclusion of CH_4 production in breeding goals will only be effective when the heritability and correlations with other important traits in dairy cattle are known (Wall et al., 2010). It also needs to be considered that health and fertility traits are not routinely recorded in many countries; therefore, fitness

traits still are not well-established part of a TMI across the globe.

A few studies have investigated heritability estimates for CH_4 production, in general with a limited number of records. In beef cattle, a heritability of 0.40 was found (Donoghue et al., 2013), and an estimate of 0.29 was found in sheep (Pinares-Patiño et al., 2013). In dairy cattle, Lassen and Løvendahl (2016) investigated 3 different phenotypes reflecting CH_4 production, namely CH_4-to-CO_2 ratio, the ratio of CH_4 per kilogram of output, and the one used in the current study (weekly CH_4 average in liters). Their results showed that, regardless of the phenotype used, CH_4 production seems to be moderately heritable, with estimates varying from 0.16 (for the CH_4-to-CO_2 ratio) to 0.21 (for the other 2 phenotypes). Also in dairy cows, Pszczola et al. (2017) found heritability estimates for CH_4 production ranging from 0.23 to 0.30 over lactation. Our results seem to be similar to the literature, which suggest that variation exists among animals. Thus, there are opportunities to select for lower CH_4 emitting cattle.

To introduce CH_4 into the breeding goal, it is important to know how CH_4 production relates to, and thereby affects, the other traits we have been selecting for in dairy cattle (Wall et al., 2010). The estimated genetic correlations in our study show how selection for decreased CH_4 production could affect body conformation, fertility, and health traits, and even though most of the estimates were not significant, tendencies will be discussed.

To be able to sustain high yield levels without compromising their metabolic status, cows need to be able to recover relatively quickly from the negative energy balance period they go through in early lactation. Therefore, selection for cows with a higher genetic merit for BCS is desirable. Our results suggest this would be beneficial for decreasing CH_4 production as well as improving fertility. Such as BCS, DC is also used as an indicator of a cow's energy balance status (Veerkamp and Brotherstone, 1997). The genetic correlation between CH_4 production and DC was unfavorable, which agrees with the documented negative genetic correlation between BCS and DC (Lassen et al., 2003). The negative genetic correlation between BL and CH_4 production is difficult to explain from a biological point of view.

Our results suggest that implementation of CH_4 production in selection indices will not have a negative effect on cows' fertility status. If anything, our results point toward a favorable relationship between fertility traits and CH_4 production, which agrees with our results for BCS. Better BCS also contributes to better fertility status in dairy cattle, so it seems reasonable to assume that cows with fewer reproductive issues would also produce less CH_4. However, the estimated r_g be-

Table 5. Additive genetic (r_g) and residual (r_e) correlations with SE between CH_4 production and BCS, body depth (BD), back line (BL), chest width (CW), height (H), dairy character (DC), calving to first insemination interval (CF), first to last insemination interval (FL), number of inseminations (NI), other diseases (OD), and udder health (UH)

	CH_4	
Trait	r_g (SE)	r_e (SE)
BCS	−0.28 (0.10)	−0.03 (0.06)
BD	−0.03 (0.12)	0.04 (0.06)
BL	−0.30 (0.13)	−0.005 (0.06)
CW	−0.20 (0.13)	−0.05 (0.06)
H	0.01 (0.08)	−0.03 (0.07)
DC	0.28 (0.10)	−0.04 (0.06)
CF	0.17 (0.13)	−0.02 (0.03)
FL	0.28 (0.21)	−0.02 (0.03)
NI	0.07 (0.17)	0.02 (0.03)
OD	−0.32 (0.16)	0.02 (0.03)
UH	0.06 (0.19)	−0.06 (0.03)

tween CH_4 and OD was close to significant, suggesting an unfavorable relationship between traits. This might come from the use of milk in the prediction equation for methane production (Lassen and Løvendahl, 2016) and the phenotypic relationship between high yield leading to higher incidence of diseases, therefore causing compromised health (Egger-Danner et al., 2015). More data are needed to obtain reliable genetic correlations between health traits and CH_4 production. This is important when considering how health fits into the complex interactions among a cow's energy balance, BCS, and fertility. Sick cows tend to reduce their intake, resulting in a greater body reserves mobilization during early lactation, leading to a more severe negative energy balance, again resulting in cows more susceptible to infections as well as decreased immune response (Bauman and Currie, 1980; Collard et al., 2000). Therefore, it seems relevant to investigate the possible influences of CH_4 production in this complex scenario.

Better ways to quantify CH_4 production are needed. In this study a prediction method using information on milk production LW and DCC was used (Madsen et al., 2010). This could bias the results because the data that have been used to some extent reflect milk production. Some of the correlations could also indicate this, though this is not general. The CH_4 phenotype includes information by itself and reflects information that is biologically relevant for the future placement of CH_4 production in a breeding goal.

Lastly, linear models were used for all traits considered in this study, including the 2 discrete traits (UH and OD). Both traits have shown reasonable frequencies and therefore the use of a linear model is a limited violation of the nature of the traits. Moreover, only one observation is available per lactation for each animal, which makes the use of Bayesian or generalized linear mixed models inadequate, due to possibly leading to biased correlation estimates (Breslow and Clayton, 1993). Such methods might be implemented in the analysis of data where methane as well as the health traits are measured over longer periods, such as full lactations.

Our study has shown the possible effects on body conformation, fertility, and health traits if CH_4 production gets included in a selection index. For the traits we have used, it seems the effects, if any, would be positive, due to the favorable genetic correlations between CH_4 production and the other traits of economic interest investigated in this study. Further studies and more data are needed to validate our results, and international collaborations would be very useful in evaluating how variable CH_4 production actually is, and how the residual correlations also vary among countries. This information is extremely important for the future of livestock breeding when considering climate changes.

CONCLUSIONS

Methane production seem to be a variable and moderately heritable trait, and its inclusion in breeding goals and selection indices may have a limited effect, if any, on body type, fertility, and health traits in dairy cattle based on the correlations estimated in this study. However, studies with more records and more animals are necessary to elucidate these relationships.

ACKNOWLEDGMENTS

REFERENCES

Arthur, P. F., J. A. Archer, D. J. Johnston, R. M. Herd, E. C. Richardson, and P. F. Parnell. 2001. Genetic and phenotypic variance and covariance components for feed intake, feed efficiency, and other postweaning traits in Angus cattle. J. Anim. Sci. 79:2805–2811.

Arthur, P. F., R. M. Herd, J. Wright, G. Xu, K. Dibley, and E. C. Richardson. 1996. Net feed conversion efficiency and its relationship with other traits in beef cattle. Pages 107–110 in Proc. Aust. Soc. Anim. Prod. Australian Society of Animal Production, Sydney, Australia.

Bauman, D. E., and W. B. Currie. 1980. Partitioning of nutrients during pregnancy and lactation: A review of mechanisms involving homeostasis and homeorhesis. J. Dairy Sci. 63:1514–1529.

Breslow, N. E., and D. G. Clayton. 1993. Approximate inference in Generalized Linear Mixed Models. J. Am. Stat. Assoc. 88:9–25. https://doi.org/10.1080/01621459.1993.10594284.

Collard, B. L., P. J. Boettcher, J. C. M. Dekkers, D. Petitclerc, and L. R. Schaeffer. 2000. Relationships between energy balance and health traits of dairy cattle in early lactation. J. Dairy Sci. 83:2683–2690. https://doi.org/10.3168/jds.S0022-0302(00)75162 -9.

de Haas, Y., M. Pszczola, H. Soyeurt, E. Wall, and J. Lassen. 2017. Invited review: Phenotypes to genetically reduce greenhouse gas emissions in dairying. J. Dairy Sci. 100:855–870. https://doi.org/ 10.3168/jds.2016-11246.

Donoghue, K. A., R. M. Herd, S. H. Bird, P. F. Arthur, and R. S. Hegarty. 2013. Preliminary genetic parameters for methane pro-

duction in Australian beef cattle. 20th Bienn. Conf. Assoc. Adv. Anim. Breed. Genet. Napier, New Zeal. 290–293.

Egger-Danner, C., J. B. Cole, J. E. Pryce, N. Gengler, B. Heringstad, A. Bradley, and K. F. Stock. 2015. Invited review: Overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits. Animal 9:191–207. https://doi.org/10.1017/S1751731114002614.

Garnsworthy, P. C. 2004. The environmental impact of fertility in dairy cows: A modelling approach to predict methane and ammonia emissions. Anim. Feed Sci. Technol. 112:211–223. https://doi.org/10.1016/j.anifeedsci.2003.10.011.

Guan, L. L., J. D. Nkrumah, J. A. Basarab, and S. S. Moore. 2008. Linkage of microbial ecology to phenotype: correlation of rumen microbial ecology to cattle's feed efficiency. FEMS Microbiol. Lett. 288:85–91. https://doi.org/10.1111/j.1574-6968.2008.01343.x.

Hegarty, R. S. 2004. Genotype differences and their impact on digestive tract function of ruminants: A review. Aust. J. Exp. Agric. 44:458–467. https://doi.org/10.1071/EA02148.

Hegarty, R. S., D. Alcock, D. L. Robinson, J. P. Goopy, and P. E. Vercoe. 2010. Nutritional and flock management options to reduce methane output and methane per unit product from sheep enterprises. Anim. Prod. Sci. 50:1026. https://doi.org/10.1071/AN10104.

Hegarty, R. S., and J. C. McEwan. 2010. Genetic Opportunities to Reduce Enteric Methane Emissions from Ruminant Livestock. Pages 181–186 in Proc. 9th World Congr. Genet. Appl. Livest. Prod., Leipzig, Germany.

Herd, R. M., P. F. Arthur, J. A. Archer, and E. C. Richardson. 1997. Genetic improvement in feed efficiency in beef cattle. Pages 184–191 in RAAN Conference Proceedings, Armidale, Australia.

Iqbal, M. F., Y.-F. Cheng, W.-Y. Zhu, and B. Zeshan. 2008. Mitigation of ruminant methane production: current strategies, constraints and future options. World J. Microbiol. Biotechnol. 24:2747–2755. https://doi.org/10.1007/s11274-008-9819-y.

Lassen, J., M. Hansen, M. K. Sørensen, G. P. Aamand, L. G. Christensen, and P. Madsen. 2003. Genetic Relationship between body condition score, dairy character, mastitis, and diseases other than mastitis in first-parity Danish Holstein cows. J. Dairy Sci. 86:3730–3735. https://doi.org/10.3168/jds.S0022-0302(03)73979-4.

Lassen, J., and P. Løvendahl. 2016. Heritability estimates for enteric methane emissions from Holstein cattle measured using noninvasive methods. J. Dairy Sci. 99:1959–1967. https://doi.org/10.3168/jds.2015-10012.

Madsen, J., B. S. Bjerg, T. Hvelplund, M. R. Weisbjerg, and P. Lund. 2010. Methane and carbon dioxide ratio in excreted air for quantification of the methane production from ruminants. Livest. Sci. 129:223–227. https://doi.org/10.1016/j.livsci.2010.01.001.

Madsen, P., and J. Jensen. 2014. A user's guide to DMU, version 6, release 5.0. Cent. Quant. Genet. Genomics Dept. Mol. Biol. Genet. Univ. Aarhus Res. Cent. Foulum, Tjele, Denmark.

Miglior, F., B. L. Muir, and B. J. Van Doormaal. 2005. Selection indices in Holstein cattle of various countries. J. Dairy Sci. 88:1255–1263. https://doi.org/10.3168/jds.S0022-0302(05)72792-2.

Murray, R. M., A. M. Bryant, and R. A. Leng. 1976. Rates of production of methane in the rumen and large intestine of sheep. Br. J. Nutr. 36:1–14. https://doi.org/10.1079/BJN19760053.

O'Mara, F. P. 2011. The significance of livestock as a contributor to global greenhouse gas emissions today and in the near future. Anim. Feed Sci. Technol. 166–167:7–15. https://doi.org/10.1016/j.anifeedsci.2011.04.074.

Pedersen, S., V. Blanes-Vidal, H. Joergensen, A. Chwalibog, A. Haeussermann, M. J. W. Heetkamp, and A. J. A. Aarnink. 2008. Carbon dioxide production in animal houses: A literature review. Agric. Eng. Int. Manuscript BC 08 008. Vol. X. December.

Pinares-Patiño, C. S., S. M. Hickey, E. A. Young, K. G. Dodds, S. MacLean, G. Molano, E. Sandoval, H. Kjestrup, R. Harland, C. Hunt, N. K. Pickering, and J. C. McEwan. 2013. Heritability estimates of methane emissions from sheep. Animal 7(Suppl. 2):316–321. https://doi.org/10.1017/S1751731113000864.

Pszczola, M., K. Rzewuska, S. Mucha, and T. Strabel. 2017. Heritability of methane emissions from dairy cows over a lactation measured on commercial farms. J. Anim. Sci. 95:4813–4819. https://doi.org/10.2527/jas2017.1842.

Veerkamp, R. F., and S. Brotherstone. 1997. Genetic correlations between linear type traits, food intake, live weight and condition score in Holstein Friesian dairy cattle. Anim. Sci. 64:385–392. https://doi.org/10.1017/S1357729800015976.

Veerkamp, R. F., E. P. C. Koenen, and G. De Jong. 2001. Genetic correlations among body condition score, yield, and fertility in first-parity cows estimated by random regression models. J. Dairy Sci. 84:2327–2335. https://doi.org/10.3168/jds.S0022-0302(01)74681-4.

Wall, E., G. Simm, and D. Moran. 2010. Developing breeding schemes to assist mitigation of greenhouse gas emissions. Animal 4:366. https://doi.org/10.1017/S175173110999070X.

Walsh, S. W., E. J. Williams, and A. C. O. Evans. 2011. A review of the causes of poor fertility in high milk producing dairy cows. Anim. Reprod. Sci. 123:127–138. https://doi.org/10.1016/j.anireprosci.2010.12.001.

Wilmink, J. B. M. 1987. Adjustment of test-day milk, fat and protein yield for age, season and stage of lactation. Livest. Prod. Sci. Elsevier Sci. Publ. B. 16:335–348.