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ABSTRACT:

The objective of the study was to assess the ranking of dairy cows using individual level correlations for methane (CH_4) emission phenotypes on-farm using sniffers and in respiration chambers. In total 20 lactating dairy cows, ten Danish Holstein and ten Danish Jerseys were recorded using sniffers installed in milking robots for three weeks of lactation prior to relocation and acclimation at the respiration chamber (RC) facility where they were each recorded on three occasions within the RC. Pairwise bivariate linear mixed models were used to determine the individual level correlations (r_I) between sniffer phenotypes and RC phenotypes as proxies for genetic correlations. Despite differences in feeding and management, the predicted CH_4 production on farm from sniffers correlated well with CH_4 production in the RC (CH4_RC) $r_I = 0.77 \pm 0.18$ and the direct CH_4 breath concentration (CH4_C) correlated nearly as well with CH4_RC $r_I = 0.75 \pm 0.20$. The correlations between CH_4 emission phenotypes on-farm from sniffers and CH4_RC exceeded that of energy corrected milk yield, live weight and dry matter intake demonstrating the potential of sniffers measurements as large-scale indicator traits for CH_4 emissions in dairy cattle.

Keywords: Methane, sniffers, breath concentration, respiration chambers

Introduction

Methane (CH_4) is a potent greenhouse gas produced by dairy cattle and other ruminants as a natural by-product of fermentation. Research on mitigation strategies such as nutritional additives, vaccines, and genetic improvement, has gained impetus in recent years (Hill et al., 2016). Whilst a reliable and accurate measure of CH_4 emission forms the basis of evaluating all of the aforementioned strategies, they differ in requirements of accuracy and precision as well as the number, frequency and duration of measurement (Hammond et al., 2016). For instance, genetic evaluations require measurements on large numbers of animals under the environmental conditions

42 they are expected to perform in order to obtain accurate estimated breeding values (EBV) (Falconer
43 and Mackay, 1996). The accuracy of EBV is in part conditional on the accuracy and precision of the
44 phenotypes recorded. However, the accuracy of EBVs can be increased through increasing the
45 number of records per animal and/or increasing the sample size of related animals recorded (Mrode,
46 2003), i.e. increasing throughput of less precise phenotypes can still result in accurate EBVs.

47 Indirect calorimetry respiration chambers (RC) are the 'gold standard' for CH_4 emission, meaning
48 RC are regarded as the most accurate and precise measurement from which different instruments or
49 techniques are benchmarked (Grainger et al., 2007; Hill et al., 2016). The high accuracy and
50 precision of RC have the benefit of detecting relatively small effects of diets and treatments on CH_4
51 production with small numbers of animals (Patra, 2016). However, the capital investment cost for
52 RC are high and the method is labour intensive, proving to be prohibitive to obtaining
53 measurements on large numbers of animals (Grainger et al., 2007; Madsen et al., 2010).
54 Furthermore, the effects of confinement within the chamber may alter animal behaviour and are not
55 necessarily representative of all production systems like extensive grazing systems (Storm et al.,
56 2012), although promising developments have led to reductions in costs and reduced stress due to
57 confinement (Hellwing et al., 2012). Thus the merit of genetic selection under RC conditions and
58 the expectation of reduced CH_4 emissions under environmental conditions in which animals are
59 expected to perform, have been called into question (Lassen and Løvendahl, 2016).

60 A method that has proven well suited to obtaining large numbers of records on individual animals
61 under commercial conditions is the high-throughput, cost effective, and non-invasive 'sniffers'
62 installed in the feed bin of automated milking stations (AMS) or concentrate feeders (Garnsworthy
63 et al., 2012; Lassen et al., 2012; Negussie et al., 2016). The non-invasiveness is achieved by
64 limiting the animal-to-instrument interface, so that the animal is not aware it is being measured and
65 measurement does not disrupt farm activities. The disadvantages of this are a loss of precision due

66 to variable barn gas dynamics and added noise if head movement of the cow and background barn
67 gas levels are not accounted for (Huhtanen et al., 2015; Difford et al., 2016; Wu et al., 2018).
68 Furthermore, sniffer methods record the concentration of gases in the captured breath of the cow
69 during milking and are thus a spot measure of gas concentrations and not a full 24 hour mass flux
70 measure (Huhtanen et al., 2015). Rather they utilise the ratio of measures CH_4 to carbon dioxide
71 (CO_2) and predicted CO_2 as a tracer gas to approximate CH_4 production (Madsen et al., 2010).

72 New methods which are cheaper, faster or less invasive are continually under development and are
73 of value when the gold standard proves expensive or prohibitive to largescale recording. For genetic
74 evaluations, a new method can replace a gold standard method if the new method is heritable and
75 their genetic correlation (r_G) exceeds 0.80 (Robertson, 1959). If the r_G is moderate and the new
76 method is heritable, it can be an indicator trait (Negussie et al., 2017). However, the number of
77 related animals with simultaneous measurements from both methods required to accurately estimate
78 r_G with meaningful standard errors, is around 10^3-10^4 of animals (Visscher, 1998). If measurements
79 with both methods are taken on different animals or the same animals at different time points, the
80 required numbers for accurate estimation of r_G will be even higher (Bijma and Bastiaansen, 2014).
81 For CH_4 emission, the RC constitutes a separate environment, as other methods cannot be recorded
82 simultaneously within the RC. It is of interest to determine the ranking of animals prior to the
83 investment in thousands of records using both methods, particularly when the gold standard is
84 expensive. To this end, estimating the repeatability of each method and the individual level
85 correlations (r_I) between methods is of value. The repeatability of a method serves as the upper
86 threshold for heritability estimates and r_I serve as proxies for r_G, respectively (Falconer and
87 Mackay, 1996; Wolak et al., 2012). The objective of this study was to assess the consistency in
88 ranking of dairy cows for CH_4 emission using sniffers and respiration chambers.

89 **Materials and Methods:**

Design and Animals

This experiment was designed to compare CH_4 measurements from the non-invasive sniffer method during AMS milking with the open circuit RC, which is the intensive and traditional method. The link between the two methods was obtained by having 20 cows (ten Holstein and ten Jersey) measured first by the sniffer in a commercial setting and then transferred to the RC facility. All handling of animals was conducted according to a protocol approved by The Animal Experiments Inspectorate, Ministry of Environment and Food of Denmark (Approval number 2016-15-0201-00959).

Sniffer AMS measurement

Data on CH_4 and CO_2 gas concentrations from the breath of individual Holstein and Jersey cows recorded during milking at Danish Cattle Research Centre (DCRC, Foulum, Denmark), where sniffer sensors were installed in each of the three AMS (DeLaval International AB, Tumba, Sweden). The sniffer instrumentation comprises two sensors, the CH_4 sensor (Guardian NG, Edinburgh Instruments Ltd, Livingston, UK) and the CO_2 sensor (Gascard, Edinburgh Instruments Ltd, Livingston, UK).The equipment installation, and calibration procedures for the sensors are described elsewhere (Difford et al., 2016). The DCRC barn is a free-stall housing system with individual cubicles and cows were offered TMR with an approximate forage to concentrate ratio of (70:30) ad libitum in individualized feeding troughs (RIC-system, Insentec, Marknesse, The Netherlands). Cows were provided up to 3 kg of concentrate per day within the feed bin of the AMS, based on levels of production and thus differences in the forage:concentrate ratio between cows is expected. Cows had free access to AMS and presented on average 2.4 ± 0.86 visits/d (mean ± SD) during the measurement period. Data on live weight is recorded 10 times every second during AMS milking and processed as described in (Bossen et al., 2009). Milk production from the

AMS and fat, protein and lactose percentage estimated from 48 hour periods each week (Løvendahl and Bjerring, 2006). The estimated milk components were used to correct milk production for fat, protein, and lactose content (ECM) (Sjaunja et al., 1991).

Gas concentrations from the AMS was aligned and merged with the entrance and exit time for each cow visit to the AMS. Data was omitted when the cow's head was predicted to be outside the feed bin using the algorithm described in Difford et al. (2016). The CH_4 and CO_2 gas concentrations for the morning cleaning cycle, when the AMS is empty of any cow, were taken as the ambient barn concentrations for each day, and deducted from the means of each cow visit. The starting time for each visit in the AMS was converted to 24 hour angular radians for modelling of diurnal variation (Lassen et al., 2012). The following model was used on all available DCRC data, within AMS to obtain daily visits corrected for sensor drift, daily variation, and time of day:

$$y_{ijklm} = \mu + d_i + b_j + \sum 3k=1(f_{1k}\sin\theta + f_{2k}\cos\theta) + C_l + e_{ijklm} \quad (1)$$

where y_{ijklm} is the natural logarithm of background corrected AMS visit means of CH_4 and CO_2; d_i is the effect of test day i (i = 23 d); b_j is the effect of the first day after each calibration j (j = 3); f_{1k} and f_{2k} are regression coefficients of Fourier series linear covariates of the time of day of measurement, modelled as harmonic pairs. The time of day of visit expressed as 24 hour angular radians is denoted by θ. Term C_l is the random effect parameter for each cow $C_l \sim$ ND (0, $I\sigma^2c$), and e_{ijklm} is the residual ~ ND (0, $I\sigma^2e$). In order to correct daily AMS visit means, the residuals for each visit are combined with random cow solutions, intercept, calibration day, and the regression coefficients f_{1k} and f_{2k} multiplied by the angular radian corresponding to 12:00:00 a.m. Further, the CH_4 and CO_2 concentration in ppm was averaged per week of lactation, using an average of visits weighted by the duration of visits. The average weekly CH_4 and CO_2 concentrations were natural log transformed, here after defined as CH4_C and CO2_C and combined with the weekly

136 performance data from DCRC for ECM (ECM_C), LW (LW_C), and gestation length (GL). The
137 average daily CH_4 production per week of lactation (CH4_P; L CH4/d) was calculated using the
138 ratio of CH4_C to CO2_C and the equation for CO_2 production from heat production units (HPU)
139 which utilizes ECM_C, LW_C, and GL (CIGR, 2002) and the conversion from HPU to CO_2 to
140 obtain predicted CO_2 production (CO2_P; L CO2/d) (Pedersen et al., 2008) as suggested by Madsen
141 et al. (2010). Data for the 10 Holstein and 10 Jersey cows from the last three weeks prior to
142 relocation to the facilities with the RC was retained for further analysis together with RC records.

143 ***Respiration chamber measurements***

144 The 10 lactating Holstein cows and 10 lactating Jersey cows were entered into a trial containing two
145 dietary treatments, a control and a high concentrate diet with respective forage to concentrate ratios
146 of (68:32) and (39:61) in a cross-over design with back-cross (Olijhoek et al., 2018). The trial was
147 divided into three periods with blocking consisting of four cows per block (five blocks in total per
148 period) with the same cows in each block over periods. Each cow was recorded for duration of 3 d
149 in period 1 and 2 d in periods 2 and 3. Methane and CO_2 production in the RC (CH4_RC and
150 CO2_RC) was calculated from the product of the total flow of outgoing air at standard temperature
151 and pressure, and the difference between the gas concentrations in the outgoing air and the gas
152 concentrations in the incoming air from the barn (background). Methane and CO_2 concentration
153 readings from when the chambers were opened twice daily for milking were omitted before
154 calculating the average CH_4 and CO_2 production for each cow, during each period. Live weight was
155 recorded when cows entered and left the RC and the average of these two readings taken from the
156 RC recording period (LW_RC) as per Olijhoek et al. (2018). Milk yield was recorded during
157 milking in the RC and composition determined from two subsequent milkings. The average milk
158 yield and milk composition was used to determined average energy corrected milk yield in the RC
159 (ECM_RC) during RC recording periods (Sjaunja et al., 1991; Olijhoek et al., 2018). The records

160 from these cows were retained for comparison with sniffer measures recorded at DCRC for the
161 same 20 cows.

162 ***Statistical Analysis***

163 Pairwise bivariate animal repeatability models were used to estimate variance components
164 controlling for fixed effects. All analyses were performed using DMU version 6 (Madsen and
165 Jensen, 2014). The model for the RC traits was as follows:

166 $y_{ijklmn} = \mu + B_i + P_j + L_k + D_l + C_m + e_{ijklmn}$ (2)

167 Where y_{ijklmn} is the trait of interest (CH4_RC, CO2_RC, LW_RC and ECM_RC), μ is the intercept,
168 B is the i'th breed (I = 2 levels), P is the j'th effect of block nested in period (j = 12 levels), L is the
169 k'th lactation number (k = 3 levels), D is the l'th effect of diet (l = 2 levels), C_m is the random effect
170 of the m'th cow $C_m \sim$ ND (0, $I\sigma^2c$), and e is the residual ~ ND (0,$I\sigma^2e$).

171 The model for the on-farm traits was as follows:

172 $y_{ijklm} = \mu + W_i + BR_j + L_k + C_l + e_{ijklm}$ (3)

173 Where y_{ijklm} is the trait of interest (CH4_P, CO2_P,CH4_C,CO2_C, LW_C and ECM_C), μ is the
174 intercept, W is the i'th week of lactation (I = 2 levels), BR is the j'th breed nested within AMS (j = 3
175 levels), L is the k'th lactation number effect (k = 3 levels), Cl is the random effect of the l'th cow C_l
176 ~ ND (0, $I\sigma^2c$), and e is the residual ~ ND (0,$I\sigma^2e$).

177 For all pairwise comparisons between RC and on-farm traits it was necessary to restrict residual
178 covariance to zero as cows were recorded in different environments. Repeatability estimates (*t*)
179 were obtained from the variance components by using the equation:

180 $$t = \frac{\sigma_c^2}{(\sigma_c^2 + \sigma_e^2)}$$

Individual level correlations (*rI*), were computed as the correlation between random cow effects using variance components as show in equation 4: (4)

$$rI = \frac{\sigma^2_{c1,c2}}{\sqrt{\sigma^2_{c1}} \cdot \sqrt{\sigma^2_{c2}}} \quad (5)$$

The standard errors of the individual level correlations and repeatability estimates where derived using Taylor series approximations.

Results and Discussion

The descriptive statistics for sniffer and RC phenotypes can be found in Table 1. The sniffer predicted mass flux CH4_P and CO2_P were closer to that of RC mass flux phenotypes CH4_RC and CO2_RC albeit with lower means, higher variability and consequently higher coefficients of variation (CV). The sniffer breath concentration phenotypes (CH4_C and CO2_C) were more different from predicted and measured mass flux phenotypes, with lower means, higher variability and CV. All CH_4 and CO_2 phenotypes where moderately to highly repeatable ranging from t = 0.53 for CH4_C to t = 0.87 for CO2_P. Live weight and ECM were retained as control variables to ensure that the RC environment was not considerably different from that of the on-farm environment for these production traits. The means, SD and CV for LW and ECM were compared across environments with similar descriptive statistics and repeatability estimates for example LW_C and LW_RC had similar means 568.2 vs 564.5 kg and repeatability t=0.93 and t=0.98, respectively. Recognizing that in the case of the sniffer phenotypes, they are an average of many measurements from the AMS over a full week of lactation whereas RC phenotypes are the average of measurements over a 2 – 3 d period in the RC.

The individual level correlations between sniffer and RC phenotypes are reported in Table 2. For ECM and LW the individual level correlations (r_I) between on-farm AMS and RC were close to

unity 0.86 ± 0.15 and 0.92 ± 0.04, respectively. These rI indicate very similar ranking of cows across environments, suggesting confinement within the RC had limited effects on ranking for these traits. Many studies have reported that confinement within RC alters behavior and can induce stress resulting in a drop in feed intake (Beauchemin and McGinn, 2006; Llonch et al., 2016). However, the RC in the present study were constructed from transparent polycarbonate to reduce costs and increase cow welfare, as supported by a study describing that these RC provoked no drop in DMI, (Hellwing et al., 2012).

Sniffer CH4_P showed the highest r_I of any on-farm phenotype with CH4_RC 0.77 ± 0.18, which approaches the suggestive threshold of 0.80 for no significant re-ranking, however the standard errors thereof are large. This finding agrees with that of Hellwing et al (2013), who compared CH_4 production calculated from the ratio of CH_4 to CO_2 measured within the RC and predicted CO_2 production to CH4_RC and CO2_RC for 157 cow measurements in 8 feeding experiments and found an R^2 of 55% corresponding to a correlations R= 0.74. The performance of CH4_P is reliant on the accuracy of CO2_P as a predicted tracer gas, the r_I between CO2_P and actual measured CO_2 production (CO2_RC) was similarly high $r_I = 0.79 \pm 0.14$ as that of CH4_P and CH4_RC. A criticism of this CO_2 prediction equation is that the metabolizable energy (ME) efficiency and mobilization of body tissues is not taken into account, running the risk of over predicting CO_2 production of efficient cows (increased LW and ECM at a fixed level of intake) and under predicting CO_2 production of inefficient cows (Madsen et al., 2010; Huhtanen et al., 2015). It may be possible to improve the r_I between CH4_P and CH4_RC through improving the prediction accuracy of CO2_RC by taking into account ME utilization. For instance, Negussie et al (2016) compared CH4_P in the breath of 20 lactating Nordic Red cattle from concentrate feeders and CO2_P predicted from ME intake and found CH4_P to have a high concordance correlation coefficient 0.70 and phenotypic correlation 0.80 with CH4_RC.

Since all prediction equations have some level of inherent error and traits used in the prediction of CO2_P, e.g. ECM_C, are already in the breeding goal, there is interest in assessing value of directly measured traits like CH4_C and CO2_C with RC traits. In this instance CH4_C ranked animals comparatively well with CH4_RC $r_I = 0.75 \pm 0.20$ as compared to CH4_P and CH4_RC $r_I = 0.77 \pm 0.18$ and exceeded that of commercial control variables ECM_C, LW_C and DMI_C, which are routinely used to predicted CH_4 production (Ramin and Huhtanen, 2013).

A number of authors have labelled breath gas concentration measures as imprecise (Huhtanen et al., 2015; Goopy et al., 2016; Wu et al., 2018), which is congruent with our results as seen by the lower repeatability estimates of CH4_C and CO2_C and the increased CV. However, the aforementioned studies often compare mass flux CH_4 production (g/day) to CH_4 breath concentrations using the coefficient of determination (R^2) and its radicand Pearson's correlation coefficient R, with the expectation that a deviation of R^2 or R from unity (1.0) indicates imprecision. Recognizing that CH4_C is a separate, by likely correlated trait from CH4_RC, deviations in R^2 from 1.0 are to be expected regardless of imprecision. Moreover, these studies often compute R in the presence of repeated measures per subject without explicitly modelling the random effect of subject, which has the effect of biasing correlations downwards when one or both of the traits has some imprecision (i.e $t < 0.80$), known as attenuation of error (Spearman 1904; Adolph & Hardin 2007). Conversely, these studies often fail to account for non-genetic between subject variation (for instance parity, lactation stage, breed etc.) which can inflate estimates of R. When repeatability ($t > 0.80$) and precision is high in one or both phenotypes, and between subject non-genetic factors are accounted for and single measurement are taken per subject, then the phenotypic correlation (r_P) can be a good predictor of r_G (Cheverud, 1988; Roff, 1995). In the case of repeated measurements per subject when one or both traits have some imprecision r_P is still biased downwards and it is necessary to partition variation into between subject variation and within subject variation (i.e. residual error or

251 imprecision) and compute r_I which are one step closer to r_G (Adolph and Hardin, 2007; Dingemanse
252 and Dochtermann, 2013). Individual level correlations have been used as proxies for r_G in difficult
253 or expensive to measure traits in dairy cattle such as DMI (Veerkamp et al., 2013), CH_4 production
254 (Zetouni et al., 2018) and energy balance (Løvendahl et al., 2010).

255 The r_G remains the most informative correlation metric for assessing how best to incorporate an
256 alternative method into a selection index. This point is illustrated in the development of the portable
257 accumulation chambers (PAC) which are a short-term total CH_4 emission flux method alternative to
258 RC used in sheep. Goopy et al. (2011) compared the two methods in 39 sheep, by measuring for 22
259 hours in the RC and then measuring 1 and 2 hours immediately after, in the PAC and found r_P =
260 0.67. In a subsequent genetic study on 3601 lambs with 4733 records in PAC and 8655 in RC,
261 Jonker et al. (2018) found $r_G = 0.67 \pm 0.11$ between the methods. In this case, r_P was a good proxy
262 for r_G but at a fraction of the cost and justified the investment in obtaining the thousands of records
263 required to accurately define r_G. Furthermore, the PAC is not genetically equivalent to the RC, but
264 has promise as a large scale, cost effective indicator trait. Importantly, Jonker et al. (2018) reported
265 $r_P = 0.27 \pm 0.02$ in the presence of repeated measurements and not r_I which was a biased predictor
266 of r_G. Given r_I for sniffer CH_4 traits ranged from 0.75-0.77 and were higher than PAC correlations
267 with RC, should these correlations be validated in a genetic evaluation, sniffers have the potential to
268 cost effectively generate the large scale recording of thousands of dairy cows for routine genetic
269 evaluation of CH_4 emissions.

270 These are the first r_I reported for any CH_4 recording method with the RC method. Method
271 comparisons to date have made inconsistent use of different correlation metrics. Garnsworthy et al.
272 (2012) recorded CH_4 production in 12 lactating Holstein cows for 10 days in the AMS using
273 sniffers and found an $R^2 = 0.78$ and $R = 0.88$ with a single record of CH_4 production from RC.
274 Similarly, Negussie et al. (2016) recorded CH4_P using sniffer senor installed in automatic

concentrate feeders on 22 Finnish Ayrshire cows with subsequent records for CH_4 production in RC and found (R = 0.80), repeated measures were not taken with the RC method nor were between subject non-genetic effects such as party or lactation stage accounted for. Conversely, (Muñoz et al., 2004, 2012) compared CH_4 production from the SF_6 technique with the RC and had repeated measures per method per cow and controlled for technical factors such as bolus release rate, recording period etc. but failed to correct for breed, parity or lactation stage or to compute r_I, instead reporting $R^2 = 0.69$ and R = 0.83. A single study comparing multiple alternative methods has reported repeated measures correlations (r_{RP}) taking into account repeated measures per cow per method (i.e. similar to r_I without accounting for non-genetic between subject effects) (Sorg et al., 2018). Sorg et al. (2018) found an r_{RP} ranging from 0.57 - 0.74 for CH_4 production between the laser measuring device, GreenFeed and two sniffer systems in lactating Holstein cows from northern Europe. Although the different correlations metrics reported maybe be biased predictors of the r_G between methods, the r_I reported herein for sniffer CH_4 phenotypes and CH_4 production in the RC are promising as indicator traits.

Conclusion

Methane emission traits derived from breath gas measurements during milking correlated the highest with CH_4 production in RC, exceeding that of LW, ECM and DMI. The individual level correlations with CH_4 production in the RC indicate that sniffer CH_4 traits have the potential to serve as large scale indicator traits of CH_4 production in the RC. Genetic correlations between RC phenotypes and breath gas phenotypes are still needed for effective use in genetic selection indices. Given the difficulties in acquiring suitably large numbers of cows in RC, the most feasible current way to obtain accurate genetic correlations between alternative methods and the RC is through international collaborations and incorporation of genomic information. Given the promising

individual level correlations between sniffer phenotypes and RC further research into genetic correlations between sniffers and RC for CH_4 emission is warranted.

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Table 1. Descriptive statistics for on farm measurements and respiration chamber measurements.

	Unit	Mean	SD	CV (%)	t[1]
On farm[2]					
CH4_P	L/d	573	73.9	12.9	0.58 ± 0.11
CO2_P	L/d	6771	578.7	8.5	0.87 ± 0.11
CH4_C	ppm	410	137.0	33.4	0.53 ± 0.11
CO2_C	ppm	5746	1791.7	31.2	0.56 ± 0.12
CH4/CO2_C	ppm/ppm	0.071	0.009	12.7	0.38 ± 0.13
ECM_C	Kg/d	38.1	5.93	18.1	0.71 ± 0.08
LW_C	Kg	568.2	57.3	10.1	0.93 ± 0.02
DMI_C	Kg/d	22.2	4.9	21.5	0.73 ± 0.07
Respiration Chamber[3]					

CH4_RC	L/d	521	56	10.7	0.61 ± 0.12
CO2_RC	L/d	6538	702.3	10.7	0.72 ± 0.10
CH4/CO2_RC	L/L	0.081	0.006	7.7	0.57 ± 0.14
ECM_RC	Kg/d	28.3	5.6	19.8	0.65 ± 0.12
LW_RC	Kg	564.5	62.3	11.0	0.98 ± 0.01

[1]t = repeatability intraclass correlation coefficient. [2]On farm phenotypes: CH4_P = predicted methane production; CO2_P = predicted carbon dioxide production; CH4_C = methane breath concentration; CO2_C = carbon dioxide breath concentration; CH4/CO2_C = ratio of methane to carbon dioxide breath concentration; ECM_C = Energy corrected milk yield; LW_C = live weight; DMI_C = dry matter intake. [3]Respiration chamber phenotypes: CH4_RC = methane production; CO2_RC = carbon dioxide production; CH4/CO2_RC = ratio of methane to carbon dioxide production; ECM_RC = energy corrected milk yield; LW_RC = live weight.

Table 2 Individual level correlations between on farm phenotypes and respiration chamber phenotypes

	Respiration chamber[2]				
On farm[1]	CH4_RC	CO2_RC	CH4/CO2_RC	ECM_RC	LW_RC
CH4_P	0.77 ± 0.18	0.63 ± 0.10	0.70 ± 0.24	0.68 ± 0.21	-0.09 ± 0.29
CO2_P	0.74 ± 0.13	0.79 ± 0.14	0.41 ± 0.29	0.58 ± 0.22	0.20 ± 0.27
CH4_C	0.75 ± 0.20	0.80 ± 0.16	0.03 ± 0.39	0.21 ± 0.35	0.60 ± 0.22
CO2_C	0.62 ± 0.24	0.76 ± 0.18	-0.35 ± 0.38	0.06 ± 0.40	0.69 ± 0.18
CH4/CO2_C	0.60 ± 0.27	0.29 ± 0.37	0.83 ± 0.23	0.68 ± 0.23	-0.66 ± 0.24
ECM_C	0.66 ± 0.20	0.54 ± 0.23	0.52 ± 0.26	0.86 ± 0.15	-0.14 ± 0.27
LW_C	0.54 ± 0.22	0.68 ± 0.16	-0.32 ± 0.33	-0.24 ± 0.28	0.92 ± 0.04
DMI_C	0.70 ± 0.17	0.64 ± 0.18	0.18 ± 0.33	0.33 ± 0.26	0.39 ± 0.22

[1]On farm phenotypes: CH4_P = predicted methane production; CO2_P = predicted carbon dioxide production; CH4_C = methane breath concentration; CO2_C = carbon dioxide breath concentration; CH4/CO2_C = ratio of methane to carbon dioxide breath concentration; ECM_C = Energy corrected milk yield; LW_C = live weight; DMI_C = dry matter intake. [2]Respiration chamber phenotypes: CH4_RC = methane production; CO2_RC = carbon dioxide production; CH4/CO2_RC = ratio of methane to carbon dioxide production; ECM_RC = energy corrected milk yield; LW_RC = live weight.