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Genetic correlations between Sniffer and GreenFeed methane measurements enable genomic selection in dairy cattle

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Introduction

Climate change mitigation has placed increasing emphasis on decarbonizing the livestock sector, with a primary focus on reducing greenhouse gas emissions from livestock systems, particularly enteric methane (CH_4) emitted by dairy cattle. Amongst climate change mitigation strategies, decarbonizing livestock systems strongly relies on reducing enteric methane emissions from dairy cattle. Selective breeding is a potentially efficient, permanent, and cumulative strategy to this aim. Incorporating enteric CH_4 traits into dairy cattle breeding goals could substantially reduce methane emissions, with projected reductions of up to 24% in CH_4 intensity by 2050 (de Haas et al., 2021) and 2–5% in total emissions over ten years under Spanish production conditions (González-Recio et al., 2020).

Breeding for reduced CH_4 emissions faces substantial challenges. First, potential antagonisms or favourable correlations with economically important traits such as milk yield and quality, fertility, or feed efficiency must be thoroughly characterized to prevent unintended consequences of selection (López-Paredes *et al*., 2020). Second, routine recording of CH_4 phenotypes on commercial farms remains scarce due to logistical constraints and high costs associated with traditional measurement technologies, such as respiration chambers or GreenFeed systems (GF). This scarcity limits the size of reference populations necessary for reliable estimation of breeding values and genomic prediction accuracy. Third, associated recording costs constrain the scale at which CH_4 phenotypes can be collected, particularly in extensive systems where infrastructure is less appropriated for emission measurements.

Portable sniffer systems (SF) that measure CH_4 concentration in exhaled air are becoming increasingly popular on commercial farms because they allow high-throughput, low-cost data collection under practical production conditions, such as extensive, organic or traditional farms. Establishing reliable genetic correlations between CH_4 measurements with SF vs. established methods as GF is essential for their integration into breeding programs. Few studies in dairy populations have reported moderate phenotypic correlations between SF and GF measurements, and to our knowledge, only van Breukelen *et al.,* (2023) have reported a genetic correlation of between 0.71 and 0.76.

The present study aimed to estimate the genetic correlations between CH_4 emissions measured using SF and GF units in a commercial dairy cattle population. GF records were obtained under a balance design between conventional and organic systems, and a second objective was to report and compare emissions between both.

Materials & Methods

Animals, Phenotypes, and Pedigree Information. CH_4 emission data were collected from different commercial populations of dairy cattle consisting exclusively of females reared across multiple regions of Spain. Phenotypes were recorded using SF units (Non-Dispersive Infrared (NDIR) CH_4 sensor: Guardian NG infrared gas monitor; Edinburgh Instruments Ltd., Livingston, UK and an NDIR CO_2 detector: Gascard NG; Edinburgh Instruments Ltd., Livingston, UK) in 46 farms operating under conventional production systems, and GF units (C-Lock Inc., Rapid City, SD, USA) in five farms, three managed organically and two conventionally.

After quality control, SF data comprised 22,967 weekly mean CH_4 records from to 4,325 cows, s, and GF data comprised weekly average GreenFeed CH_4 records (GF) from 138 cows (73 conventional and 65 organic farms). In total, the data base had 4,463 animals with phenotypes of CH_4 and dairy milk production. All animals were included in a pedigree of 60,520 animals. This pedigree was truncated to three generations beyond the last phenotyped individual to reduce computational demands in subsequent genetic analysis keeping 23,987 animals.

Genotypes and Quality Control. From the 4,325 animals, 3,699 were genotyped (23 with GF records and 3676 with SF records) using 45,605 SNPs from the EuroGMD beadchip. Quality control was carried out using PLINK version 1.9.0-b.8. SNPs was removed from if they met any of these criteria: call rates less than 95%, or minor allele frequency less than 0.05. Animals showing genotypes with a call rate lower than 90% were also removed. After filtering, all 3,699 animals and 42,086 effective SNPs retained for downstream analyses.

Statistical Models. Variance components and genetic parameters were estimated using two approaches: ssGBLUP and pedigree- BLUP (PBLUP), implemented in the blupf90+ software (Misztal *et al.*, 2014). Variance components were calculated with separate univariate models for GF and SF and also with bivariate model including both traits.

For GF records, the model included fixed effects of parity (four levels), management system (conventional or organic), and lactation stage (four levels) and genetic and farm-by-season-by-measurement-station random effects. For SF records, the model included fixed effects of parity and lactation stage and genetic, farm-by-season-by-measurement-station and permanent random effects. As variance components we computed the heritability ($h^2 = \sigma^2_u/\sigma^2_y$) and Intra-herd heritability ($h^2_{IH} = \sigma^2_u/\sigma^2_{y\text{-}IH}$) with both univariate and bivariate models. The genetic correlation between GF and SF CH_4 phenotypes were obtained from bivariate analyses, and compared with an alternative genetic correlations between CH_4 traits were estimated using the Pearson correlation adjusted by reliability, following the methodology proposed by Calo et al. (1973):

$$r_g = \text{sqrt}(\sum R_1.R_2)/ (\sum R_1.R_2).\ r_p \qquad (1)$$

where R_1 and R_2 represent the individual reliabilities of the EBVs for the two traits, and r_p is the Pearson correlation between the EBVs of both traits. To calculate the genetic correlation using Eq 1., EBVs and reliabilities of animals with offspring measured by both GF and SF were used. We also estimated management system differences (conventional or organic) in CH_4 emissions measured with GF and milk production.

Results & Discussion

The daily mean for CH_4 production measured with GF was 361.33 ±82 g/day and measured with SF was 342.74±163.46 g/day. Estimates of variance components for CH_4 emissions measured by SF and GF systems using PBLUP and GBLUP models are presented in Table 1. Heritabilities for SF were low for both PBLUP (0.042 ± 0.008) and GBLUP (0.035 ± 0.005), whilst h^2_{IH} was between 0.12–0.15 similarly to those reported by (Lopez-Paredes et al., 2020)

with part of these animals. Substantially higher heritability estimates were obtained for GF measurements. Heritabilities were 0.70 ± 0.09 for BLUP and 0.73 ± 0.09 for GBLUP and h^2_{IH} was 0.88±0.09, larger estimates in comparison to other heritabilities reported for this trait in dairy (0.21-0.35, Lopes et al. 2024; Manzanilla-Pech 2021). Univariate and bivariant heritabilities estimates were equivalent in all cases.

Table 1. Variance components (± standard deviation) for CH_4 emissions measured with GreenFeed (GF) or sniffer (SF) for BLUP and GBLUP.

		PBLUP			GBLUP		
		h^2	h^2_{IH}	r_g	h^2	h^2_{IH}	r_g
Bivariant	SF	0.042±0.008	0.15±0.03	0.70±0.39	0.035±0.005	0.12±0.02	0.48±0.32
	GF	0.70±0.09	0.88±0.09		0.73±0.09	0.88±0.09	
Univariant	SF	0.042±0.008	0.15±0.03	0.69*	0.035±0.005	0.12±0.02	0.29*
	GF	0.65±0.22	0.87±0.10		0.64±0.23	0.88±0.09	

[1] h^2: heritability, h^2_{IH}: Intra-herd heritability and r_g: additive genetic correlation
*Genetic correlation estimated as in Eq. 1

The additive genetic correlation between SF and GF in the bivariate models was 0.70 ± 0.39 when estimated with PBLUP and 0.48 ± 0.32 when estimated with GBLUP. A total of 36 sires met the criterion of having offspring evaluated with both methodologies and were available to estimate the approximations of genetic correlation with EBVs from univariate models using Eq. 1. The approximated genetic correlations were 0.69 for BLUP and 0.29 for GBLUP. Limited genotyped animals with GF information may explain this lower genetic correlation.

CH_4 differences between conventional or organic systems. Cows managed under organic production systems exhibited lower absolute GF-measured CH_4 emissions in g/day (303.43 ± 62.65 g/day) than cows in conventional systems (412.89 ± 59.85 g/day), equivalent to -28%. Daily milk production was also lower in the organic system (23.15 ± 4.82 kg/day) compared with the conventional system (37.57 ± 9.97 kg/day). When expressed as CH_4 intensity (CH_4 per unit of milk), organic production showed 18% higher values (13.82 ± 4.71 gCH_4/kg of milk) than conventional production (11.67 ± 3.38 gCH_4/kg of milk). More pronunced results, but in the same direcction, were found for Brito and Silva (2020) in a Jersey population where CH_4 intensity was 71% larger in organic production compared with conventional. Organic systems might emit more enteric CH_4 per kg of milk due to more fibrous and less digestible diets (grass feed) and less productivity (Nunes et al. 2025).

Conclusions

This study shows that CH_4 emissions measured SF and GF systems are moderately to highly genetically correlated, with estimates ranging from 0.48 to 0.70, although with large standard errors due to the limited number of GF records. In addition, dairy cows managed under organic systems emitted less CH_4 per day (-28%), but 18% higher CH_4 intensity (g CH_4/kg of milk) compared with conventional systems. Genotype x Environment interaction in terms of methane production may be studied in the future.

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