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GENETIC INSIGHTS INTO METHANE EMISSION TRAITS IN INDOOR-FED GROWING CATTLE

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SUMMARY

The present study aimed to examine the genetic variability of various methane production traits in growing beef cattle and quantify the proportion of genetic variance in daily methane production independent of performance traits such as feed intake, growth rate and body size. Methane emissions were measured using GreenFeed systems from 1,700 crossbred cattle from a commercial feedlot. Performance traits including feed intake, average daily gain, liveweight and carcass weight data were also available. Genetic parameters were estimated using animal linear mixed models. Daily methane production was moderately heritable (0.42 ± 0.09), with a genetic standard deviation of 23.43 g/d. Daily methane production exhibited moderate genetic correlations with feed intake (0.51), ADG (0.39), metabolic liveweight (0.27) and carcass weight (0.42). Genetic adjustment of daily methane production for these traits resulted in a 25% reduction in the genetic standard deviation (from 23.43 g/d to 17.55 g/d), with only 56% of daily methane productions genetic variance remaining independent of the performance traits.

INTRODUCTION

Genetic improvement provides cumulative and permanent benefits in agriculture, making it a powerful tool for sustainable advancements. Methane-related traits, such as daily methane production and residual methane production (RMP), have shown moderate heritability (0.09 to 0.43) and genetic variability (Donoghue *et al*. 2020; Ryan *et al*. 2024), making methane a potentially suitable trait for breeding programs. However, methane is often genetically correlated with key performance traits like feed intake and liveweight (Donoghue *et al.* 2020) which are already part of most national breeding objectives. These correlations raise questions about the additional benefit of directly selecting for methane if these other traits are already under selection. The primary objective of the present study was to quantify the genetic variability in methane related traits, especially those independent of traits already directly considered in most cattle breeding goals.

MATERIALS AND METHODS

Methane and carbon dioxide flux data were collected from 1,700 growing beef cattle at the Irish Cattle Breeding Federation Progeny Test Centre in Tully, Co. Kildare, Ireland, between the years 2018 and 2024. Animals included 170 bulls, 576 heifers, and 954 steers, sourced from commercial farms and representing crossbreeds of 13 breeds: Aberdeen Angus, Aubrac, Belgian Blue, Charolais, Hereford, Holstein Friesian, Jersey, Limousin, Montbéliarde, Norwegian Red, Salers, Shorthorn, and Simmental. Animals were grouped into unisex pens based on sex, breed, and liveweight, with an average pen size of 36 animals.

Pens were equipped with 10 Greenfeed emission monitoring systems (C-Lock Inc., Rapid City, SD) for methane and carbon dioxide flux measurements and 10 Insentec feed stations (Hokofarm Group BV, Marknesse, The Netherlands) for feed intake monitoring. Methane and carbon dioxide emissions were recorded as flux measurements (g/day) using the Greenfeed system. To ensure data

accuracy, only animals with at least 30 emission measures, each greater than 3 minutes in duration and at least one emission measure within 10 days of the test end were included. Methane production was calculated as the average daily methane flux across all valid measures.

Animals were fed *ad libitum* total mixed rations (TMR) comprising 13.95% hay, 40.70% water, and 45.35% concentrates, with a dry matter (DM) content of 51% and metabolisable energy (ME) value of 12.1 MJ/kg DM. Feed intake was monitored by the Insentec system, with feed disappearance assumed equal to intake. Energy intake was calculated as the sum of energy consumed from TMR and Greenfeed supplements.

Liveweight was recorded every three weeks. Average daily gain during the test period for each animal was calculated by fitting a linear regression through all liveweight observations of the animal; the same approach was also fitted through serial measures of metabolic liveweight. Animals were slaughtered at a commercial abattoir approximately 148 days after entering the test centre and carcass weight was recorded. Carcass records were available for an additional 671,100 paternal half-siblings of animals with methane measurements. Any animal born to a dam in parity >10 was omitted. Only animals with recorded parentage were included.

Statistical analysis. A series of residual methane traits were estimated using animal linear mixed models in ASReml (Gilmour *et al.* 2009) to reflect methane production adjusted for performance traits of ADG, metabolic liveweight, carcass weight and energy intake. The modelling of daily methane production was progressively built up with different combinations of the performance traits as independent variables. The base model used was:

$Y = Parity_j + Het + Rec + CG_k + age_i + age*sex + sex*variable_l + sex*variable_m + a_i + e_{ijklm}$

where Y was methane production; Parity was the fixed effect of dam parity j (1, 2, 3, 4, ≥5); Het was the heterosis covariate and Rec was the recombination loss covariate for animal I; CG was the fixed effect of the contemporary group k; age_i was the fixed effect of age in months at the end of test for animal j; age*sex was the interaction effect of age in months and animal sex (bull, heifer or steer); $variable_l$ was one of liveweight, energy intake, average daily gain, carcass weight; $variable_m$ was of the subset null, metabolic liveweight, energy intake, average daily gain or carcass weight where $variable_m \neq variable_n$; a_i was the additive random effect of the animal j; and e representing the residual variance. The same animal linear mixed model structure was used to estimate variance components for the additional traits (i.e., energy intake, liveweight, ADG, and carcass weight), excluding the sex*variable interaction terms, as these were only applicable when modelling methane production with performance traits as covariates.

RESULTS AND DISCUSSION

The coefficient of genetic variation (CVg) for daily methane production in the present study was 9.27%, comparable to key performance traits such as average daily gain (CVg = 7.23%) and carcass weight (CVg = 9.61%), for which genetic gain has been consistently achieved in beef breeding programs. This similarity suggests that, with adequate selection pressure and accurate genetic evaluations, methane production can also respond to selection.

While direct selection to reduce methane emissions is feasible, beef breeding objectives are multi-trait by design, designed for balanced progress across economically and biologically important traits. The key determinant of the potential additional rate of genetic progress within a breeding program is how much of genetic variability is genetically independent of other traits already being considered in the breeding programme (Rendel and Robertson 1950). The extent of genetic correlations among the goal traits impacts the response to selection. The genetic correlation between energy intake and daily methane production (0.51) indicates that only 75% of the genetic variance in daily methane production is genetically independent of energy intake. Traits like growth rate and carcass weight also make up breeding objectives, all of which were antagonistically correlated with

methane production in the present study (Table 2), suggesting that, heavier, faster growing animals with heavier carcasses are, on average, genetically predisposed to produce more methane per day.

The presence of such (genetic) correlations between methane production and performance traits was the motivation in the present study to explore the genetic variability in residual-type traits. Residual traits, when derived via least squares regression, are independent of included regressors for the population in which they were derived. Residual traits have been traditionally calculated at the phenotypic level as a variable in themselves with the variance components of this new trait then calculated. In the present study, phenotypic adjustment of methane production had negligible impact on its heritability (Table 1). This process was undertaken in a single step, with the regressor traits included as covariates in the same model used to simultaneously estimate the variance components. Although all residual methane traits were phenotypically independent of their respective regressor traits by design, this adjustment did not eliminate underlying genetic correlations (Table 2). The three RMP traits adjusted for differences in metabolic liveweight (i.e. RMP_{lw}, RMP_{la}, RMP_{el}) were all negatively genetically correlated with metabolic liveweight (-0.41 to -0.38), highlighting that phenotypic adjustment alone was insufficient to fully remove shared genetic signal. Nonetheless, all RMP traits were strongly genetically correlated with each other ($r > 0.88$) and with unadjusted methane production ($r > 0.83$), indicating substantial shared genetic architecture.

Table 1. Mean, genetic standard deviation (σ_g), environmental standard deviation (σ_e), and heritability (h^2; standard error in parentheses) for the methane related traits (N=1700), feed intake (N=1700), performance traits (N=1700), and carcass weight (N=45,779)

Trait	Mean	σ_g	σ_e	h^2 (SE)
Methane, g/day	252.70	23.43	27.69	0.42(0.09)
Energy intake, MJ/day	152.60	11.41	8.61	0.63(0.10)
Liveweight, kg	575.70	34.24	25.64	0.74(0.10)
Metabolic liveweight, kg	117.30	5.62	3.65	0.70(0.09)
ADG, kg/day	1.56	0.15	0.18	0.42(0.09)
Carcass weight, kg	321.60	23.26	24.97	0.46(0.03)
RMP_{adg}[1]		21.59	27.70	0.38(0.09)
RMP_{energy}[1]		20.34	25.70	0.38(0.09)
RMP_{cw}[1]		23.28	25.45	0.46(0.09)
RMP_{lw}[1]		23.48	25.69	0.46(0.09)
RMP_{ca}[1]		22.40	25.75	0.43(0.09)
RMP_{la}[1]		22.71	25.99	0.43(0.10)
RPM_{el}[1]		20.76	25.30	0.40(0.10)

[1] RMP_{adg}, methane adjusted for ADG; RMP_{energy}, methane adjusted for energy intake; RMP_{cw} methane adjusted for carcass weight; RMP_{lw}, methane adjusted for liveweight; RMP_{ca}, methane adjusted for carcass weight and ADG; RMP_{la} methane adjusted for liveweight and ADG; RMP_{el} methane adjusted for energy intake and liveweight

Using the genetic correlations estimated in the present study (Table 2 and 3), the genetic variability in daily enteric methane production genetically independent of a combination of other traits was also calculated as

$$\sigma_A^2(1 - R^2) = \sigma_A^2(1 - \boldsymbol{C'V^{-1}C})$$

where σ_A^2 is the additive genetic variance for daily methane production, R^2 is the proportion of variation in daily methane production explained by the performance traits, **C** is the vector of genetic correlations between the daily methane production and the performance traits, and **V** is the matrix of genetic correlations among the performance variables.

When daily methane production was adjusted for the same covariate(s) either phenotypically or genetically, the resulting traits were strongly genetically correlated (>0.97), indicating that both adjustment methods captured nearly identical genetic signals. When daily methane production was genetically adjusted for energy intake, metabolic liveweight, ADG, and carcass weight simultaneously, only 56% of the genetic variance of daily methane production remained independent of these traits. This adjustment reduced the genetic standard deviation by 25%, from 23.43 g/d to 17.55 g/d, with the CVg reducing from 9.27% to 6.94%.

Table 2. Genetic correlations between methane production and the residual traits with energy intake, ADG, metabolic liveweight and carcass weight (SE in parenthesis)

	Energy	ADG	MWT	Carcass
Methane	0.51 (0.09)	0.39 (0.11)	0.27 (0.11)	0.42 (0.09)
RMP_{adg}[1]	0.43 (0.11)	0.06 (0.13)	0.07 (0.13)	0.15 (0.14)
RMP_{lw}[1]	0.26 (0.12)	0.06 (0.14)	-0.38 (0.11)	-0.21 (0.13)
RMP_{cw}[1]	-0.13 (0.15)	0.06 (0.14)	-0.25 (0.12)	-0.16 (0.14)
RMP_{energy}[1]	-0.11 (0.14)	-0.11 (0.14)	-0.07 (0.14)	-0.13 (0.15)
RMP_{ca}[1]	0.42 (0.11)	0.13 (0.14)	-0.28 (0.12)	-0.17 (0.14)
RMP_{la}[1]	0.25 (0.12)	-0.05 (0.15)	-0.38 (0.12)	-0.22 (0.13)
RMP_{el}[1]	-0.12 (0.13)	-0.08 (0.15)	-0.41 (0.12)	-0.21 (0.12)

[1] RMP_{adg}, methane adjusted for ADG; RMP_{energy}, methane adjusted for energy intake; RMP_{cw} methane adjusted for carcass weight; RMP_{lw}, methane adjusted for liveweight; RMP_{ca}, methane adjusted for carcass weight and ADG; RMP_{la} methane adjusted for liveweight and ADG; RMP_{el} methane adjusted for energy intake and liveweight

Table 3. Genetic correlations among energy intake, average daily gain (ADG), metabolic liveweight (MWT), and carcass weight (SE in parenthesis)

Trait	ADG	MWT	Carcass weight
Energy intake	0.63 (0.08)	0.71 (0.06)	0.76 (0.05)
ADG		0.51(0.10)	0.55(0.09)
MWT			0.95(0.01)

CONCLUSION

Genetic adjustment showed that only 56% of the genetic variance in methane production was independent of intake, growth, and carcass traits. This suggests a significant overlap in genetic control, highlighting the importance of evaluating which traits are already under selection. To justify including a methane trait in a breeding program, it is essential to ensure it captures unique genetic variation beyond existing performance traits.

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