Can genomics cope with a 30% reduction of methane emission from livestock in 10 years?

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Abstract

Livestock will face an important challenge within the next decade to cope with the objective of cut by 30% methane emissions, as agreed in the COP26. This study summarises the latest genetic parameter estimates between methane, dry matter intake, microbiota composition, and production and body traits in Spanish dairy cattle. We evaluated the expected genetic progress after including methane into the breeding goal under different scenarios. Under the current trend in the cow population size, it is only possible to achieve the objective if methane is included with a large weight in the selection index and it is accompanied of other strategies. This may generate conflict with dairy producers and balanced strategies must be considered.

Introduction

As many as 104 countries have promised to cut their methane emissions by at least 30 percent by 2030 at the 26th session of the Conference of the Parties (CoP26) to the United Nations Framework Convention on Climate Change (UNFCCC) summit in Glasgow, United Kingdom. In 2019, methane in the atmosphere reached record levels, around two-and-a-half times above what they were in the pre-industrial era. Methane has a warming potential between 28-34 times that of CO_2 over a 100-year period. Over a 20-year period it is around 84 times as powerful as carbon dioxide per unit of mass. Ruminants are considered one of the most important sources of global methane (CH_4) emissions, producing around 4,623 Mt of CO_2 equivalents (CO_2e) per year, with dairy cattle being responsible for 2,128 Mt of CO2e per year. Around 40% of total CH_4 comes from enteric fermentation in ruminants (Moss *et al*., 2000). Eructated CH4 is not only an important contributor to global warming, but also represents a loss of dietary energy because it is equivalent to between 2 and 12% of net energy intake (de Haas *et al*. 2011, Johnson and Johnson 1995). Levels of methane emissions are linked to the intake capacity of the animal. Consequently, reducing enteric CH_4 emissions in ruminants has become an important area of research, aligned with the commitment to reduce its greenhouse gases emissions by 2030. The short methane lifetime in the atmosphere (10yrs) offers an interesting opportunity to reduce the global warming contribution from this gas in a shorter period. Decreasing enteric CH_4 from ruminants without altering animal production is desirable both as a strategy to decarbonize the livestock economy and to improve feed conversion efficiency. Selective breeding is an interesting strategy to tackle CH_4 emissions from ruminants. There is great potential in adopting genetic and genomic selection strategies, given that several studies have reported that enteric CH_4 is a heritable trait (Lassen and Løvendahl, 2016; Pszczola *et al*., 2019). Enteric methane is mainly produced by microorganisms in the rumen during the feed fermentation. Investigating the ruminal microbiota and understanding their role during the methanogenesis will help to develop better breeding strategies. Besides, microbiota composition has also been reported to be heritable (Saborío-Montero *et al.*, 2020).

The objective of this study is to evaluate the (co)variance parameter estimates between traits related to methane emissions, intake, conformation and production. Then, the genetic changes to reduce methane emissions in the next decade under 3 different selective breeding scenarios were evaluated.

Material and Methods

Data consisted of 11,042 weekly averaged records for dry matter intake (DMI) obtained from 551 dairy cows in 5 farms, as well as 4,624 methane emission measurements using a non-dispersive infrared methane detector installed within the feed bin of the automatic milking system during 14 to 21 days period from 1,501 cows in 14 farms. In addition, ruminal content was extracted from 437 cows with methane phenotypes. Data for milk yield, protein yield, fat yield, fertility, body depth, rump width, chest width and predicted live weight from 11,228 cows were included in the analysis. Heritability and genetic correlations were estimated from bivariate models within a single step framework using AIREML (Misztal *et al.*, 2002).

The large complexity of the ruminal microbiota was aggregated through principal component analysis (PCA), into few principal components (PC) that were used as proxies of the core metagenome. Bivariate animal models were applied using these PC and methane production as phenotypes.

The selection responses under the different scenarios was assessed using selection index theory, including methane production as an additional trait in the breeding goal. We assumed the current selection index (ICO) in the Spanish Holstein population as the benchmark. The other two scenarios included methane with either an economic weight (based on carbon tax) or desired genetic gains (20% reduction in ten years while maintaining positive genetic trends of protein and benefits per cow).

Results

Genetic parameters. Table 1 shows the genetic parameter estimates obtained in this study. The heritability estimates for methane production (0.17±0.05) and methane concentration (0.18±0.04) were moderate, and their genetic correlations with milk yield traits ranged between (-0.05±0.11 and 0.50±0.11). In general, higher genetic correlations were estimated with body capacity traits, ranging from 0.14 to 0.31. The estimated heritability for DMI was moderate (0.16±0.03), with a genetic correlation with milk yield of 0.41 (0.11), and with capacity index of 0.20±0.09. Genetic correlations between methane traits and DMI were positive and ranged from 0.20±0.48 to 0.27±0.43. The heritability estimates for the first PC was >0.30 at all taxonomic levels. The microbiome aggregated variables showed strong genetic correlation with methane traits (0.42±0.19 and 0.83±0.19), and dry matter intake (0.32±0.36).

Table 1. Heritability (diagonal) and genetic correlations (above diagonal) estimates[1] of traits of interest.

Trait	Kg Protein	Kg Fat	Kg Milk	ICAP	DMI	Methane (ppm)	Methane (g/d)	Microbiome (PC1)
Kg Protein	**0.33**	0.64	0.78	0.29	0.53	0.07	0.13	-0.02
Kg Fat	0.05	**0.28**	0.87	0.32	0.50	0.30	0.32	0.18
Kg Milk	0.07	0.08	**0.40**	0.30	0.41	-0.05	0.04	0.04
ICAP	0.01	0.02	0.01	**-**	0.20	0.31	0.14	0.12
DMI	0.19	0.11	0.11	0.09	**0.16**	0.20	0.27	0.32
Methane (ppm)	0.13	0.14	0.11	0.04	0.48	**0.17**	0.97	0.42
Methane (g/d)	0.12	0.13	0.11	0.07	0.43	0.03	**0.18**	0.83
Microbiome (PC1)	0.31	0.72	0.28	0.04	0.36	0.21	0.13	**0.42**

[1] Standard errors are shown below diagonal

Expected genetic gain after including methane in the breeding objective. The inclusion of methane in the current ICO would slightly modify the genetic responses, with no relevant change in methane response, which would still increase per cow in future generations. A partial reduction of 20% would only be possible by applying ad-hoc weights for methane in the selection index to achieve such a desired genetic gain (Figure 1). This would come at an expense of a slower genetic progress in milk yield and its components (2kg of protein per cow), and thus the economic response (5€/cow/year).

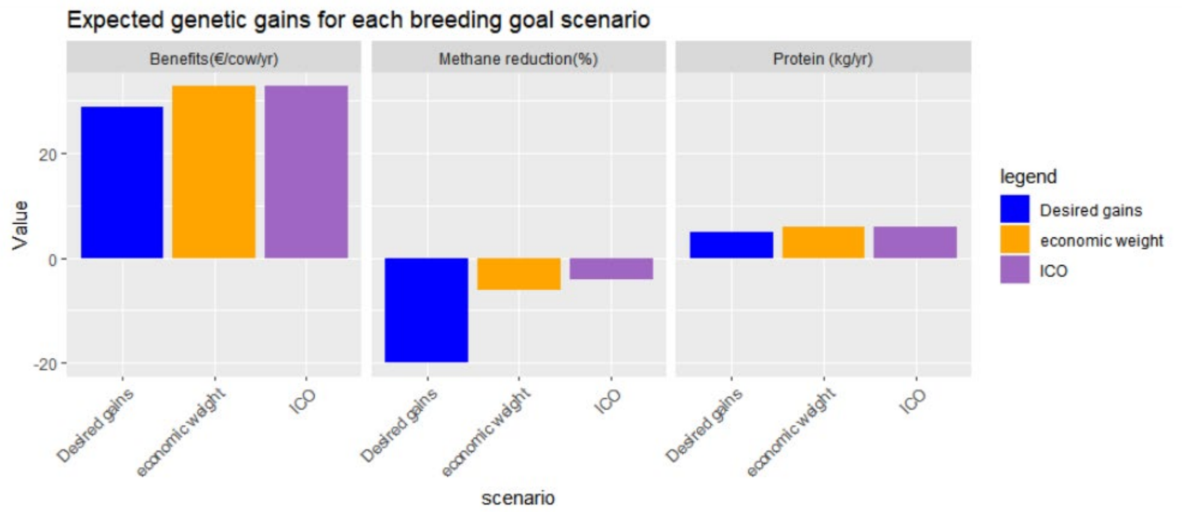

Figure 1. Expected genetic response on benefits, methane emissions, and protein yield according to each selection index scenario (current total merit (ICO) index, economic weight on methane, desired genetic gains) based on the current productive circumstances of Spanish dairy cattle.

Discussion

The results from our study suggest a correlated response in methane emissions when selecting for more ravenous animals, although these estimates showed large standard errors. These results highlight an important interrelationship between methane production and dry matter intake, with a significant role of the microbiome composition. The core microbiome composition condensed in aggregated PC variables was controlled by the cow genome. The PCA allowed us to condense the huge and fuzzy taxonomical and functional information from the metagenome into a few PC. We selected the PC1 (h^2=0.42±0.05) because it showed the largest association with methane, and separates bacteria from eukaryotes (protozoa and fungi) in the rumen. Protozoa and Fungi provides substrate to methanogenic archaea and their relative abundances represent an important driver of methane emissions (López-Garcia *et al.*, 2022).

Our results suggest that selecting cows that make a more efficient utilization of energy intake is feasible through selection on correlated type traits such as body capacity, stature, and body depth, without compromising high productive performance. Selection for lower methane emissions is expected to have similar results. The inclusion of the microbiome composition may assist on a more efficient selection on lower emissions and higher feed efficiency.

Conclusions

The recent Global Methane Pledge aims to limit methane emissions by 30% in 10 years compared with 2020 levels. Selective breeding can contribute to reducing methane emissions from ruminants. Current selection trends will not contribute enough to achieve this goal. Selection indices will need to include methane related traits with weights calculated based on desired genetic gains. This would slow down the genetic gain of other important traits. Even with a slower genetic progress on milk yield traits, selective breeding could achieve a 20% reduction of methane emissions while increasing profitability of dairy cattle.

This study may serve as an example on how selective breeding may be applied to reduce methane emissions in other cattle and small ruminants populations. Selective breeding would contribute in a permanent and cumulative manner to such a reduction. However, other nutritional and technological measurements should be applied complementary to achieve the 30% reduction goal.

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