

Abstract Submission Form

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Preferred presentation

Oral

Preferred session

Session 8: Global challenges in measuring methane in ruminants

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Title of your paper

Reducing dairy cattle enteric methane emissions using rumen metagenome

Insert ABSTRACT text

Ruminant digestion produces methane, a potent greenhouse gas impacting global warming and animal feed efficiency. Reducing these enteric methane emissions (EME) through farming and breeding decisions

is ideal. However, recording these emissions in commercial farms is currently challenging and costly. Additionally, EME traits could be weakly correlated, complicating the combination of reference populations. However, all these traits have the same underlying biology – methane is mainly produced by the rumen microbiota. Here we show that rumen metagenome could potentially be used for farming and breeding decisions aimed at reducing EME in cattle. We studied long-read ruminal metagenome sequences of 834 dairy cows, from which 402 were located on a research farm in Australia and 432 on commercial farms in Spain. The Australian population was phenotyped for enteric methane production (MeP_Australia; g/d) and the Spanish one for enteric methane concentration (MeC_Spain; ppm). The relative abundance (RA) of 1,292 KEGG ontology (KO) features, identified in the metagenome sequence, present in all animals was used to construct a microbial relationship matrix. When included in a linear mixed model, adjusted by environmental effects, the matrix explained 86% of the variance of MeP_Australia and 63% of MeC_Spain, with prediction accuracies of ~ 0.40 and ~ 0.10 , respectively. The RA of these KO were also included as the response variable in univariate GBLUP models to estimate their heritability, and their breeding values were correlated with those of MeP_Australia and MeC_Spain to estimate the genetic correlations between KO and emissions. The KO's heritability was 0.25 ± 0.05 in Australia and 0.40 ± 0.09 in Spain, and the genetic correlations with emissions up to $|0.60|$ in Australia and $|0.34|$ in Spain. Then, we estimated the response to selection on MeP_Australia and MeC_Spain per generation using a selection intensity of 2.665 (top 1%) in three scenarios: direct selection, indirect selection on ruminal microbial KO cores using a selection index and combining direct and indirect selection in another index. Three cores were used for this purpose. Two of them included the 30 KO with highest genetic correlation with emissions in Australia and Spain, respectively. The third core included 24 KO previously reported as genetically correlated with EME in beef cattle. As the maximum KO heritability in our research farm (Australia) was 0.6, this value was used as the maximum heritability allowed in Spain to reduce possible unknown environmental effects from commercial farms. We estimated a reduction in MeP_Australia of approximately 6% with direct selection, between 4 and 6% with indirect selection on the cores, and up to 8% by combining direct and indirect selection (a 25% extra reduction). For MeC_Spain, larger reductions were estimated with indirect selection on the cores compared with direct selection, agreeing with a previous study. MeC_Spain was estimated to be reduced by approximately 8% with direct selection, between 11 and 13% with indirect selection on the cores, and between 13 and 14% by combining direct and indirect selection. The large variance of EME explained by the 1,292 KO suggest that ruminal metagenome could be used to reduce methane emissions, for example, identifying and removing high-emitter animals based on their ruminal microbiome profile. Our estimated selection responses on EME along with ruminal microbial KO suggest potential larger reductions of these emissions compared to only direct selection and could allow the selection of parents that lack emissions records, as is the case for most commercial cows. The estimated reduction in one population's EME by selecting on another's ruminal metagenome core indicates the potential for combining reference populations in breeding programs through their ruminal metagenome, irrespective of each population's EME trait. If validated, our results could impact global ruminant emission reduction efforts.

Enter keywords

Rumen microorganisms, metagenomics, methane production, phenotypic variation, genomic selection