

Selecting for reduced methane emissions using ruminal metagenomics from two dairy cattle populations

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Ruminant digestion produces methane, a major greenhouse gas impacting global warming and animal feed efficiency. Reducing emissions through the selection of low-emission parents is ideal but currently challenging and costly due to the need for extensive cow emission measurements. Additionally, different methane emission traits could be genetically weakly correlated, complicating the combination of reference populations. Indirect selection on core ruminal microbiome features present in most animals, that is heritable with high phenotypic variance and genetically correlated with emissions could be a feasible alternative and could connect populations with different traits. This study incorporated long-read ruminal microbiome sequences of 402 Australian and 432 Spanish dairy cows, with distinct methane emissions traits, to identify a core 1,292 KEGG identifiers (KOs) present in all animals that predicted up to 86% of methane variance in Australia and 63% in Spain. From these, 115, including two involved in methane metabolism (K01689 and K21071), showed a high coefficient of variation; a heritability of 0.25 ± 0.05 in Australia and 0.40 ± 0.09 in Spain; and a genetic correlation with emissions of up to $|0.60|$ in Australia and $|0.34|$ in Spain. Interestingly, the breeding values for methane emissions of unphenotyped animals were correlated with the breeding values for 13 KOs present in at least 70% of animals (up to $|0.22|$). Our findings suggest potential to reduce enteric methane emissions through a targeted ruminal metagenome core of KOs, predict emissions in unphenotyped commercial cattle populations using their rumen metagenome, and utilise the microbiome for predicting emissions across varying emission traits and feeding and management systems. If validated, our results could impact global ruminant emission reduction efforts.

Additional keywords: Enteric methane emissions, ruminal metagenome, genomic selection.