

The Fecal Microbiome as a Predictor of CH₄ Emissions

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Methane production in ruminant livestock needs to be reduced as is harmful to the environment and increases feed costs. These reductions need tools that estimate how changes in diet composition and management reduced these emissions. The goal of the experiment was, therefore, to determine the relationship between the fecal microbiome and methane production. Six mature non-lactating Holstein dairy cows received one of three diets with forage to grain ratios (DM basis) of 100:0 (G0), 75:25 (G25), and 50:50 (G50). The forage of the diet consisted of 80% grass hay and 20% alfalfa hay (DM basis). The concentrate was a barley and corn based (DM=893 g/kg, CP=198 g/kg DM, NDF = 213 g/kg DM). Feed was offered three times daily at 0900, 1300, and 1700. The experiment was set up as a 3 × 3 Latin square design consisting of 5 wk experimental periods and 6 non-lactating Holstein dairy cows. Sample collection and enteric methane output measurement were conducted on two separate days during the fifth wk of each period. Rumen fluid was collected using a stomach tube and a fecal grab sample was taken at 0830 and 1500 on the day preceding enteric methane measurement. An open-circuit hood calorimetric system determined methane output over a 24 h period.

The production of methane per cow increased ($P = <0.01$) with increased grain inclusion, and were 354.5, 423.3, and 445.0 ± 10.2 Lxday⁻¹ of methane for the G0, G25, and G50 diets respectively. When methane production was adjusted based on DMI, they were 32.4, 31.5, and 29.2 ± 1.8 Lxkg DMI⁻¹ the G0, G25, and G50 diets respectively, and not affected by diet. Methane emissions exhibited a diurnal pattern, which coincided with feeding events ($P = < 0.01$). Upon microbial analysis of the samples, in the fecal samples there were 16 bacteria with correlation to diet G0 ($P < 0.05$), 8 were negatively correlated, while 7 were positively correlated. There were 23 bacteria correlated with diet G25 ($P < 0.05$), with 12 being negative, and 11 being positive. Finally, there were 11 bacteria correlating to diet G50 ($P < 0.05$), with 9 being negatively correlated and 2 being positively correlated.

Implications: The development of a methane production estimator using biomarkers in a fecal sample will help to develop strategies that cut down on feed costs, while simultaneously benefiting the environment and overall image of the dairy industry.