

Section: Ruminant Nutrition

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T239

Microbial community shifts during anaerobic digestion of finishing cattle manure with and without distillers grains in the diet.

S. C. Fernando¹, A. K. Watson¹, Y. A. Wanniarachchi¹, T. J. Klopfenstein¹, G. E. Erickson¹, J. L. Harding¹, A. L. Shreck^{*1}, C. J. Johnson¹, M. M. Klosterman¹, ¹*University of Nebraska, Lincoln.*

Two diets were fed to finishing cattle and the manure was used to monitor methane production and microbial communities associated with anaerobic digestion of feedlot manure. Diet 1 contained 82.5% dry rolled corn (CONT) and diet 2 contained 40% wet distillers grains plus solubles (DM basis) replacing dry rolled corn (WDGS). Manure (feces and urine) was collected and frozen until used in anaerobic digesters. Continuously stirred anaerobic digesters (n = 7, 1 L capacity) were maintained for 5 mo to reach steady-state. Upon reaching steady-state, 50 mL of effluent was removed and replaced with 50 mL of manure/water slurry (9% DM) collected from CONT (n = 4) or WDGS (n = 3) fed animals on a daily basis. After a 35 d adaptation, samples were collected at 3-d intervals for microbial community analysis. The concentration of methane was measured under constant flow of N₂ gas and was 0.116 and 0.137 L/g OM fed into the digester ($P = 0.05$) from CONT and WDGS respectively. The microbial communities (Eubacterial and Archaeal) were identified using 454-pyrosequencing. An average of 10,000 and 3,000 sequences were generated from each sample to evaluate the Eubacteria and Archaea communities respectively. Community level analysis revealed structuring of microbial communities based on diet ($P < 0.001$). Bacteria belonging to the phylum *Chloroflexi* (65.7%) and *Bacteroidetes* (19.2%) dominated the microbial community in digesters receiving WDGS manure. Within phylum *Chloroflexi*, genus *Longilinea* (35.7%) and unclassified *Anaerolineaceae* (64.3%) accounted for most the sequences. In contrast, digesters receiving CONT manure was dominated by phylum *Bacteroidetes* (68.2%) and *Chloroflexi* (24.5%). Within phylum *Bacteroidetes*, genus *Proteniphilum* (50.6%) and unclassified *Porphyromonadaceae* (45.5%) accounted for a most of the sequences. These results suggest the microbial food chain that contributes toward methane production is greatly influenced by the diet fed to cattle, suggesting that dietary manipulation may provide opportunities to reduce (or increase if desirable) methane production from cattle manure.

Key Words: anaerobic digester, methane, microbial

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