Effect of Diet on the Rumen Microbial Community Composition of Finishing Cattle and the Role it Plays in Methane Emissions

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Summary

To understand the relationships between diet, microbial community, and methane production cattle were esophageally tubed when fed a common diet and again during feeding of six treatment diets. Microbial community analysis via 16S tag sequencing, displayed structuring of microbial communities (Bacteria and Archaea) by diet. This study demonstrates that the diets tested altered the microbial community from the common diet but had no effect ($P > 0.05$) between dietary treatments used in the study. While the microbial community changed from the common diet to the treatments was observed, an alteration in microbial community or methane production was not observed due to fat source.

Introduction

Rumen microbes ferment low quality, cellulose rich feeds and provide the ruminant animal with energy. Products of the fermentation process consist of volatile fatty acids, which are used for energy by the animal, and methane, an unusable form of energy that is expired by the ruminant animal.

Methane is produced by a group of organisms that inhabit the rumen known as methanogens that belong to the kingdom Archaea. Little is known about this group of microorganisms but their end-product of fermentation (i.e., methane) does contribute to atmospheric greenhouse gas emissions.

The microbial community within the rumen is dictated by the composition of the diet and changes in dietary factors lead to changes in the microbial community. Thus, dietary intervention can be used to reduce methane from cattle by changing the rumen microbial community composition. Dietary intervention strategies for mitigation of methane are being explored (*2015 Nebraska Beef Cattle Report*, pp. 105–107). Understanding the relationship between diet, methane, and microbial community will help identify microbial species associated with methane and to develop new intervention strategies for methane mitigation. The purpose of this study was to identify the effect of fat source on microbial community composition, and to understand how fat source affects methane emissions in finishing cattle.

Procedure

A 125-d finishing study was conducted during the summer of 2013 to identify the effect of fat source on methane production and microbial community composition. Rumen samples were collected by esophageal tubing from 60 steers on a common diet containing 50% alfalfa and 50% Sweet Bran®. The cattle were then assigned randomly to one of six treatments diets (10 steers/treatment). Treatments consisted of a corn-based control with no added fat, 50% modified distillers grains plus solubles (MDGS), and two additional corn-based diets with either 3% corn oil or 3% tallow. These four diets all contained monensin (Rumensin, Elanco Animal Health) at 30 g/ton (DM basis). Two additional treatments that include a corn control and 50% MDGS without monensin (*2015 Beef Cattle Report*, pp. 105–107) were included to test for the effect of monensin. The animals were esophageally tubed to evaluate microbial community composition. The rumen samples were collected and placed in liquid Nitrogen to snap freeze the rumen sample instantly and inhibit continued microbial growth. Microbial DNA was extracted and purified from all rumen samples utilizing the MoBio PowerMag Soil DNA Isolation Kit (Carlsbad, California). The V3 hypervariable region of the 16S rRNA gene from the rumen eubacterial community and the V6 region of the 16S rRNA gene from the rumen archaea communities were amplified using the polymerase chain reaction (PCR). Following PCR, the resulting amplicons were sequenced using the Ion Torrent Personal Genome Machine (PGM). The sequence reads generated were analyzed using published Bioinformatic pipelines UPARSE (http://drive5.com/uparse/, Edgar, 2013) and QIIME (qiime.org/). Statistical analysis was performed using the phantom package within Matlab.

Results

The common diet was used as a baseline for comparison of methane and microbial community composition on the treatment diets. When animals are shifted from the common diet to treatment diets, microbial communities changed displaying that diet influences rumen microbial community composition. However there was no shift in the bacterial and archaeal community due to fat source. (Figure 1 and 2).

The diets utilized in this study displayed no change in microbial community structure due to oil and fat additions. These diets did not provide an opportunity to control the microbial community composition to reduce methane emissions in cattle. However, continued research is needed to find other dietary factors that may impact methane production negatively in the finishing phase and aid in developing management based mitigation strategies without impacting animal performance.

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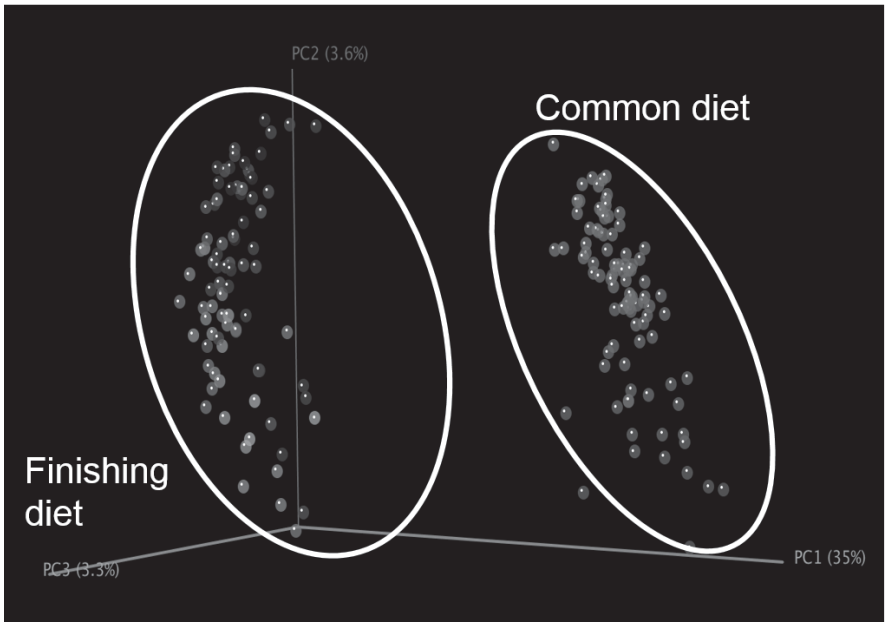

Figure 1. Bacterial community composition—shift from common to treatment diets but no dietary shift due to fat source with finishing treatment diets.

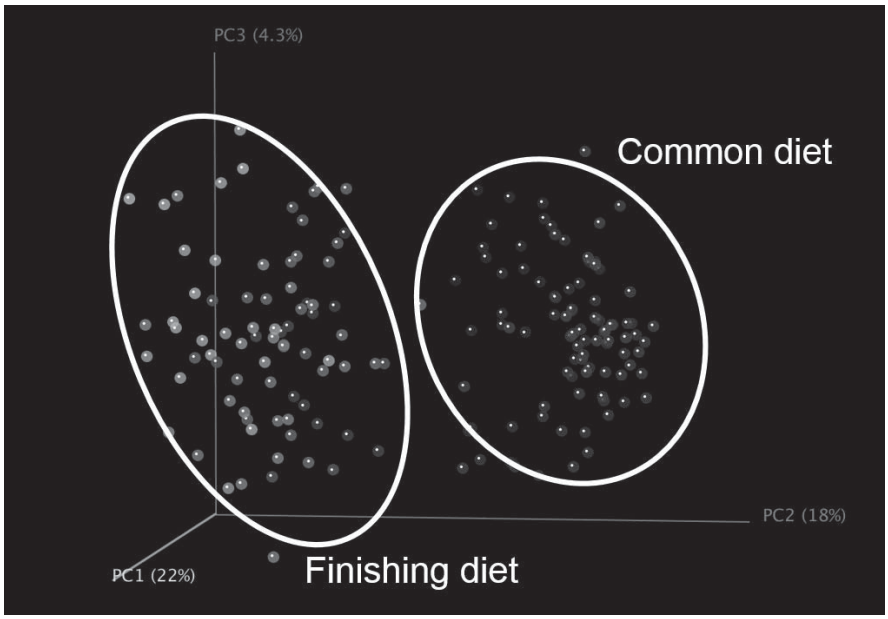

Figure 2. Archaeal community composition—shift from common to treatment diets but no dietary shift due to fat source with finishing treatment diets.