

# COMPARISON OF CONVENTIONAL GRAIN-FED AND GRASS-FED FEEDING SYSTEM EFFECTS ON THE MICROBIOTA OF FECES FROM CALIFORNIA BEEF CATTLE

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## I. OBJECTIVES

Cattle feeding systems are a major factor influencing cattle gut microbiota, which can have potential impact on public health if unfavorable shifts in the microbiota are followed by fecal contamination of food production systems. The objective of this study was to compare the effects of grain-based and grass-based feeding systems on the microbial communities of feces from beef cattle.

## II. MATERIALS AND METHODS

Postweaning cattle were blocked by weight and randomly assigned to 4 treatment groups by feeding system: (1) conventional feedlot (CON,  $n=22$ ) harvested in April, (2) 20-mo grass-fed (20GF,  $n=17$ ) harvested in June, (3) grass-fed then fed grain 45 d (GR45,  $n=13$ ) harvested in July, and (4) 26-mo grass-fed (26GF,  $n=16$ ) harvested in October. Rectal fecal samples from the cattle were collected at 14 mo of age as baseline prior to treatment group assignment, and collected again 1 wk before each treatment group's harvest. Microbial DNA was extracted from samples, amplified targeting the V4 region of 16S ribosomal RNA, and sequenced via Illumina MiSeq. Raw sequences were demultiplexed and imported into QIIME2 for processing. Analysis of differences in microbiota between treatments and sampling points was conducted in R version 3.6.2. Alpha diversity was assessed by Chao1 and Shannon indices, beta diversity was assessed using PCoA via Bray-Curtis dissimilarity, and differences in relative abundances between treatments were assessed using Kruskal-Wallis and Mann-Whitney-Wilcoxon tests.

## III. RESULTS

At baseline, there were no differences ( $P>0.05$ ) in alpha diversity among treatment groups. As cattle grew older, alpha diversity of microbiome for 20GF and GR45 cattle increased ( $P<0.05$ ) at the time of harvest. At harvest, the alpha diversity of microbiome of fecal samples from 20GF and GR45 cattle was larger ( $P<0.05$ ) than from CON cattle. Beta diversity analysis of sample OTU showed samples from GR45 cattle formed distinct clusters when mapped via PCoA, indicating a different bacterial composition from other groups. Organizing OTU by phyla showed that Bacteroidetes and Firmicutes were the most dominant phyla for all treatments and sampling points. The CON cattle had larger ( $P<0.05$ ) Bacteroidetes abundances compared to GR45 cattle, supporting prior studies showing Bacteroidetes members' role in the digestion of complex carbohydrates such as undigested starch, which can be found in higher proportions in the rumen of grain-fed cattle than in grass-fed cattle. No differences ( $P>0.05$ ) in Firmicutes abundance were detected. Proteobacteria abundances of GR45 and 25GF cattle increased ( $P<0.05$ ) from baseline to harvest and were larger ( $P<0.05$ ) than CON Proteobacteria abundances.

#### IV. CONCLUSION

The results suggest that use of grain in cattle feeding systems had an impact on bacterial communities. Fecal bacterial communities from grain-fed cattle had lower bacterial diversity than grass-fed cattle. The results support the idea that Bacteroidetes play an important role in complex carbohydrate digestion. Differences in Proteobacteria abundance in the cattle primarily on grass-based systems may suggest an association between grass-fed systems and increased risk of presence of common foodborne Proteobacteria pathogens of concern. Increased alpha diversity from cattle harvested in summer months may warrant further study of seasonal effects on cattle fecal microbiota.

Keywords: beef, feces, grain-fed, grass-fed, microbiota