

## CHARACTERIZATION OF THE RUMEN BACTERIAL COMMUNITIES OF BISON HEIFERS FED A GRASS-BASED DIET VS A GRAIN-BASED FREE-CHOICE DIET

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*Rationale.* Ruminant animals depend on a diverse microbial community (e.g., bacteria, archaea, protozoa, and fungi) in their rumen to digest the structural carbohydrates of forage diets. Ruminal microbe communities are relatively understudied in North American bison. There is also an



indication that bison may be better adapted and perform better than domestic ruminants when feeding on low-quality forages, which may be related to ruminal communities. This Institute study compared the diversity and composition of ruminal bacteria in bison heifers fed a grass-based and then grain-based diet in order to characterize the overall bacterial community and changes that occur when diet is shifted from natural forage to high energy grains. A better understanding of the bison rumen microbiome will ultimately lead to practical applications for their conservation and production.

*Outcomes.* Bacteriodes and Firmicutes were the dominate bacteria phyla across all samples collected. A total of 57,132 and 59,133 species-level operational taxonomic units (OTU's) were identified in the grass-fed heifers at two study locations, respectively, in contrast to 13,240 and 22,516 OTUs found in the same

heifers on a grain-based diet. At the first location, 28 of the most abundant OTUs were different between diets, while 17 were different at the second location. Only 74 OTUs were considered abundant (representing >1% of total sequences in at least one sample) and most of these (69) were from unknown bacterial species. For a more complete summary please see the following:

Fresno-Rueda, A. 2021. Characterization of the rumen bacterial communities of bison heifers fed a grass-based diet vs a grain-based free-choice diet. MS Thesis. South Dakota State University. <http://openprairie.sdstate.edu/etd/5744>