

INVESTIGATING THE RUMINAL METAGENOME OF GRASS AND FORAGE-FED BISON TO UNCOVER METABOLIC ACTIVITIES THAT IMPACT THE EFFICIENCY OF PLANT FIBER UTILIZATION



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Rationale. Bison have the ability to maintain better than domestic grazers on forage of poor quality. Since they are responsible for

digesting feed, rumen symbiotic microorganisms in bison may be capable of extracting more out of plant fibers. Consistent with this hypothesis, the Institute has determined that rumen bacterial species from bison are very different from their counterparts in domestic grazers, suggesting that they may be more metabolically efficient. In this context, this research primarily aims to use a metagenomics approach (high throughput scale sequencing of rumen microbial DNA) to elucidate the metabolic functions of bison rumen bacteria that are responsible for digesting plant fibers. Gaining a deeper understanding of how rumen bacteria from bison are better at utilizing feed is a necessary first step in developing innovative strategies to improve bison production on pasture and may lead to other improvements in the nutritive quality of bison products.

Species: bison
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