



Survey of cattle rumen microbiome under different natural grazing systems: linkage to grazing behaviour and productivity

## CHARACTERIZING THE RUMEN MICROBIOME DURING GRAZING

PROJECT NO.: FRG.16.19

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**Background:** The microbial community in the rumen contains bacteria, archaea, protozoa and fungi that interact with each other and the host animal in complex ways to digest feed particles and provide energy to support cattle growth and production. This rumen microbiome has impacts on feed efficiency, dry matter intake, average daily gain, and methane production.

Previous research on the rumen microbiome has generally focused on cattle receiving standardized feedlot diets, but grazing systems are often more complex and diverse. Different nutrient sources can have a substantial impact on the rumen microbes, therefore the behaviour and impacts of the rumen microbiome on cattle production under grazing conditions may be very different than in a feedlot system.

### Objectives:

1. Assess variation in the rumen microbiome in heifers and cows under three different grazing scenarios (tame pasture, deferred native grass, and stockpiled dormant native grass) over two grazing seasons
2. Determine rumen functional features and shifts in response to the different grazing scenarios and any contributions to cattle productivity
3. Identify associations between the rumen

microbiome and cattle phenotypes (growth, intake, feed efficiency, etc.).

**What they did:** 79 cows and 49 heifers were followed through two production cycles – wintering on silage in a drylot, then grazing tame pasture in the spring, followed by grazing native pasture in the summer, and finally, grazing deferred/stockpiled native pasture in the fall. Fecal samples, rumen fluid and forage clippings were collected at all time points, resulting in 548, 542, and 74 samples, respectively, for analysis. Volatile fatty acids (VFAs), an important energy source for the rumen microbial population and cattle themselves, were analyzed from the fecal and rumen fluid samples along with important metabolites. Forage samples also underwent metabolomic analysis.

**What they learned:** There were significant changes in VFA production as diets changed throughout the production cycle as well as changes between years. This is not surprising as we expect different VFAs to be produced in different amounts depending on diet. Rumen microbial composition and diversity were significantly different among the production systems. Most of the differences in bacterial populations were found between drylot and tame pasture systems, while protozoa showed the most variation in abundance between tame pasture and native grassland. Eukaryotes, like protozoa, tended to be more populous but less diverse in the rumen when lower quality feed was available, likely due to their role in degrading lignin and pectin. In addition, low quality feed contained less available crude protein, which resulted in lower amounts of available nitrogen to both the animal and the rumen microbes. The simpler protozoal community may contain more bacteria predators and enhance nitrogen cycling within the rumen.

Heifers consistently had higher rumen bacterial populations with lower numbers of archaea, protozoa, and fungi than cows; and while heifers had higher total rumen VFA production, their VFA utilization was lower than cows. This may be due to the different grazing behavior between heifers and cows. Significant variation was observed for the microbial metabolome based on grazing period. Rumen microbial metabolites differed between high residual feed (RFI, inefficient) and low RFI animals (efficient), with largest differences in metabolites among RFI divergent animals observed during grazing of stockpiled native forage.

**What it Means:** This was the first study to compare linkages between plant, rumen, and fecal samples throughout full production cycles under different types of grazed forages as well as winter-fed silage. Given the shifts in microbial populations and metabolites, VFA production, and VFA utilization under different dietary conditions, there are opportunities to better match different cattle classes with their environment for improved performance. Enhanced knowledge of microbial changes in vegetation and how those impact rumen microbial populations in different grazing systems may one day provide a method to optimize efficiency on high forage diets.

*This project was also supported by the Canadian Agricultural Partnership, and NSERC*



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