Microbial Metropolis: Understanding how legume pasture systems interact with soil microbial communities, and subsequent greenhouse gas emissions

Jesse Reimer, Joel Ens, J. Diane Knight, Melissa Arcand & Bobbi Helgason

jesse.reimer@usask.ca
Pasture Grazing Systems

- Staple of Western Canadian economy
- Produce greenhouse gases (GHGs):
  - methane (CH$_4$), nitrous oxide (N$_2$O)
- Management can reduce net GHG emissions
  - Non-bloat legumes
Non-Bloat Legumes in Forage

• ↑ protein uptake
• ↓ CH$_4$ from rumination
• ↑ soil C content
• ↑ N input into system

• Effects on soil microbial communities responsible for GHG emissions?
Pastures are Highly Heterogenous

- Active, living systems
Pastures are Highly Heterogenous

- Active, living systems
- Field-scale variability is high
- $\text{N}_2\text{O}$ fluxes are fleeting, event-driven

→ Difficult to understand system processes at field scale

- Knowledge of how local sampling point environmental conditions interact with microbes is key to understanding GHGs at field scale.
Research Questions:

• How do soil microbes interact with their environment within legume-grass pastures?

• How do these interactions affect microbial GHG fluxes?
Termuende Research Ranch – near Lanigan, SK

- Randomized paddocks
- Sod-seeded legumes (2015)
  - Veldt cicer milkvetch
  - Sainfoin
  - **Grass-**Alfalfa [Control]

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Termuende Research Ranch – near Lanigan, SK

June

July-August

September
Field Study Methodology

- pH
- Soil Moisture
- WEOC
- Inorganic N

Midslope

Enzyme Analysis

PLFA Analysis
PLFA Biomarkers

...& AMF, actinobacteria, and stress indices. Some groups have multiple biomarkers.
Results – Soil Microbial Community Composition

Pasture PLFA Composition 2017
Results – Soil Microbial Community Composition

Pasture PLFA Composition 2018

Stress = 0.103

- June 13
- July 03
- July 25
- Aug. 16
- Sept. 04

Control
Sainfoin
CMV

Stress = 0.103
Results – Soil Microbial Community Composition

• Significant dissimilarities between both legume pastures and the control in 2017 \((p < 0.01; \text{PERMANOVA})\)
  \(\Rightarrow\) within-group dissimilarity \(\leq\) between-group

• Preliminary within-treatment analysis suggests dominant mechanisms driving community structure differ between treatments.
Results – Greenhouse Gases

- Treatment effects largely non-significant
Results – Greenhouse Gases

- Sainfoin total methane consumption significantly less than milkvetch, control (p < 0.02, TukeyHSD)
Results – Biological Interactions with Environment

- Soil moisture, nutrient fluxes limiting
Results – Interactions Affecting Greenhouse Gas Fluxes

- GHGs across field influenced by:
Conclusions

• Treatment effects largely outweighed by seasonal effects, field heterogeneity.

• Tight nutrient cycling and moisture levels limiting microbial activity and N$_2$O fluxes.

• Analysis of data using further statistical methods will reveal interactions in more detail.
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