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

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Pasture Grazing Systems

- Staple of Western Canadian economy
- Produce greenhouse gases (GHGs):
  - methane (CH_4), nitrous oxide (N_2O)
- Management can reduce net GHG emissions
  - **Non-bloat legumes**

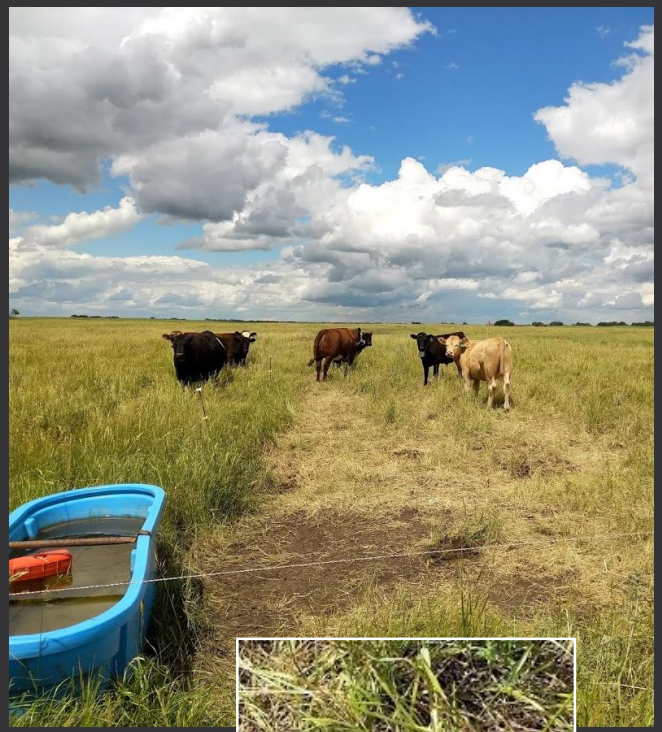
Non-Bloat Legumes in Forage

- ↑ 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
- N_2O fluxes are fleeting, event-driven

→ Difficult to understand system processes at field scale

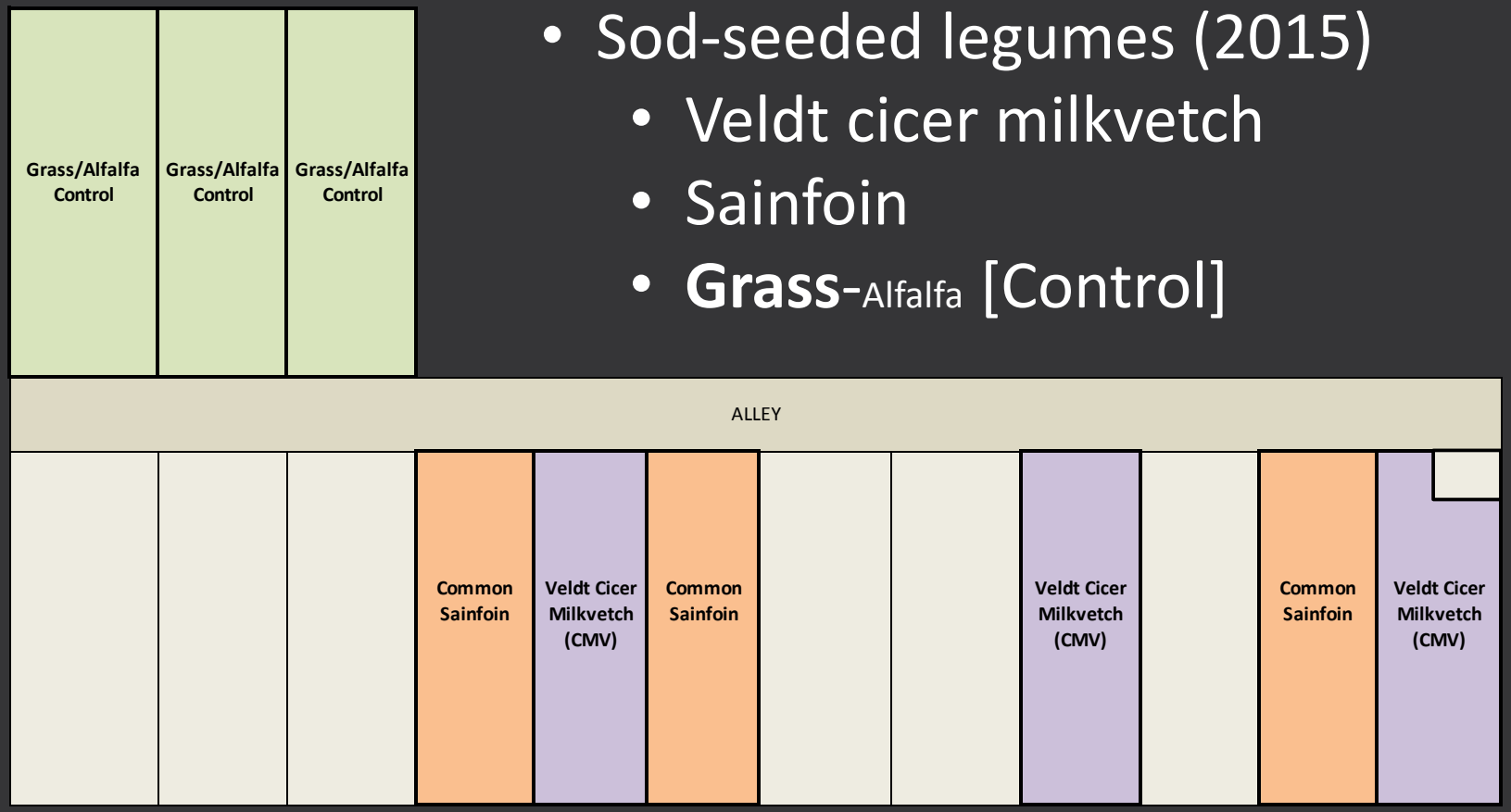
- **Knowledge of how local sampling point environmental conditions interact with microbes is key to understanding GHGs at field scale.**

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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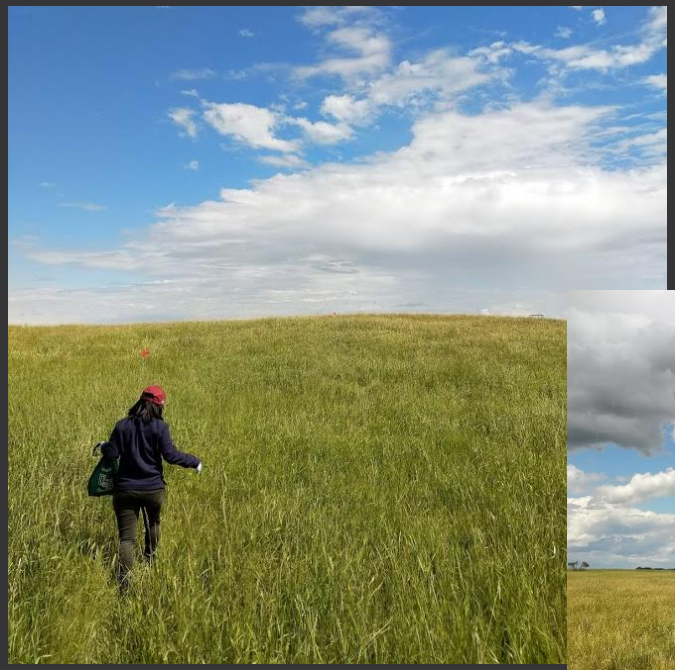
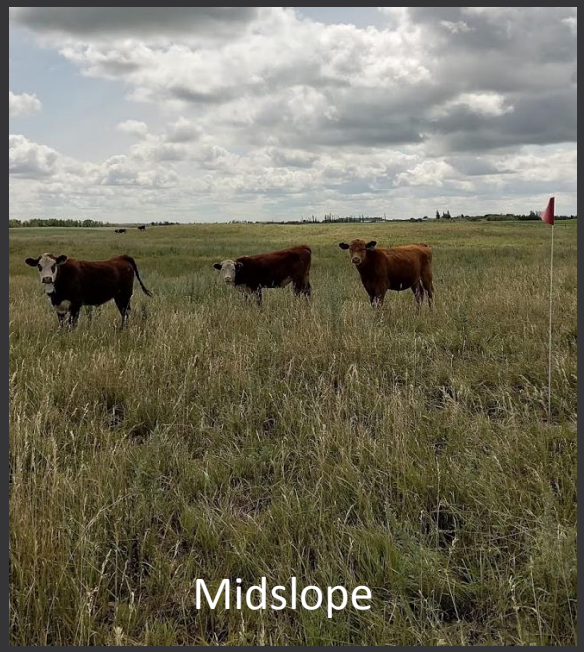


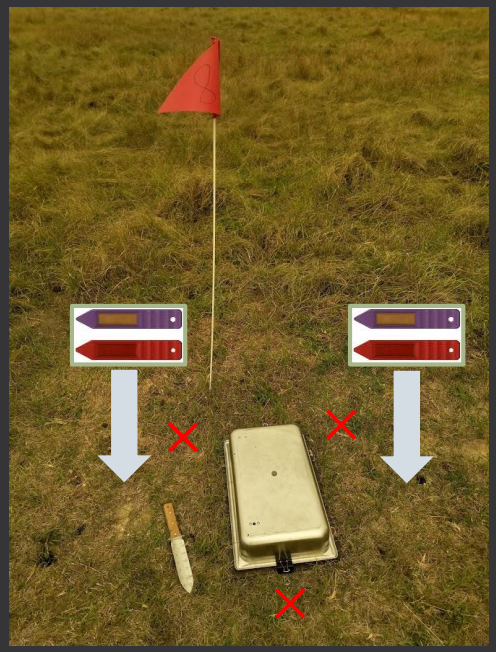
June

July-August

September

Field Study Methodology



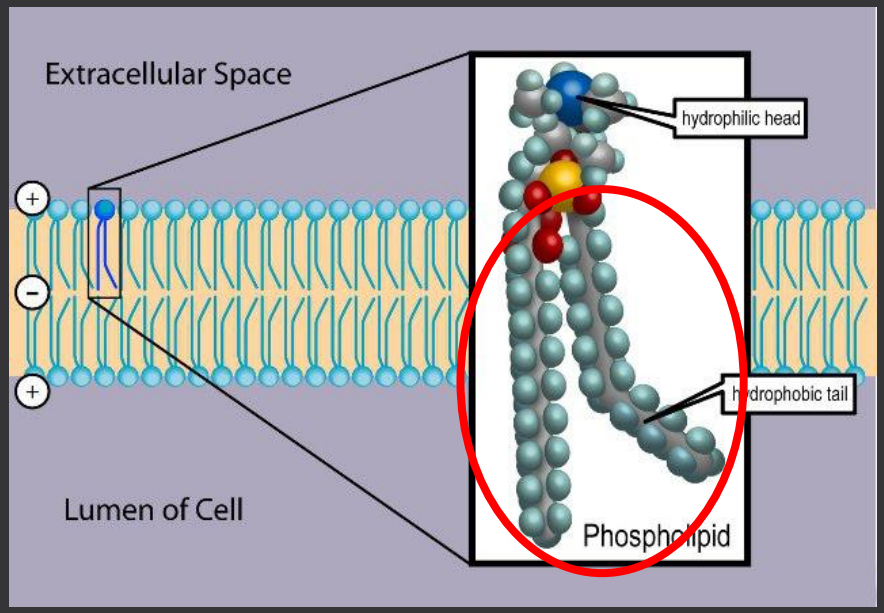


- pH
- Soil Moisture
- WEOC
- Inorganic N

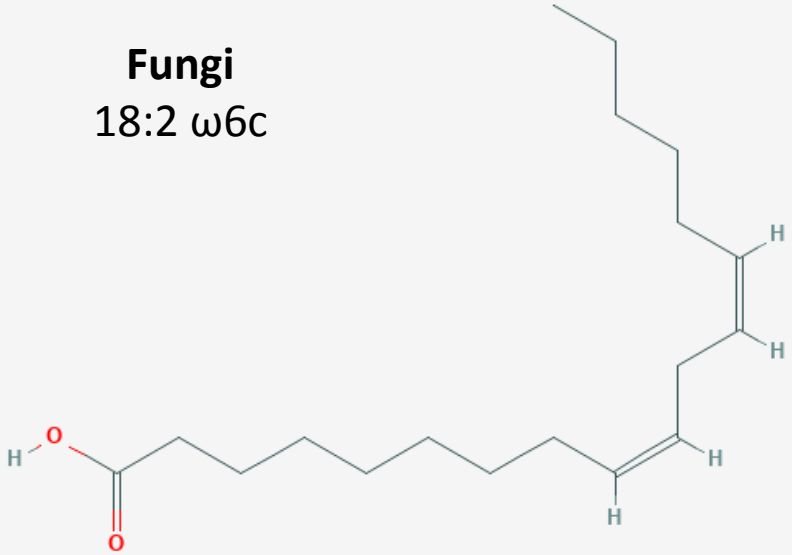
Enzyme Analysis

PLFA Analysis

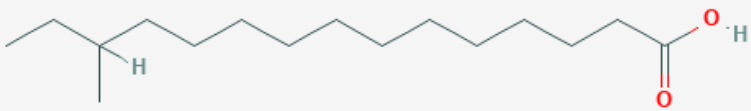
PLFA Biomarkers



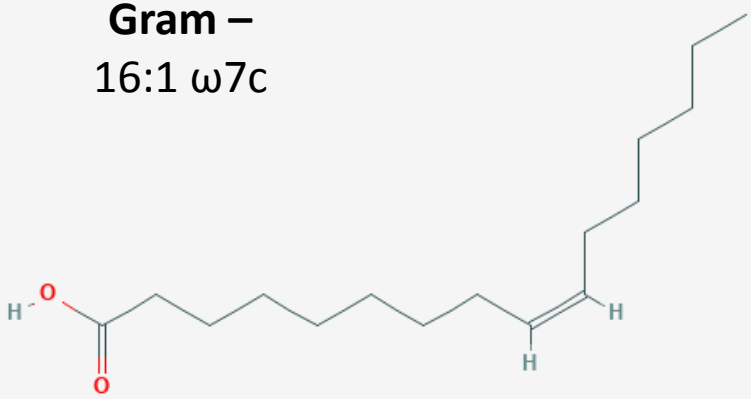
Fungi
18:2 ω6c



Gram +
16:0 Anteiso

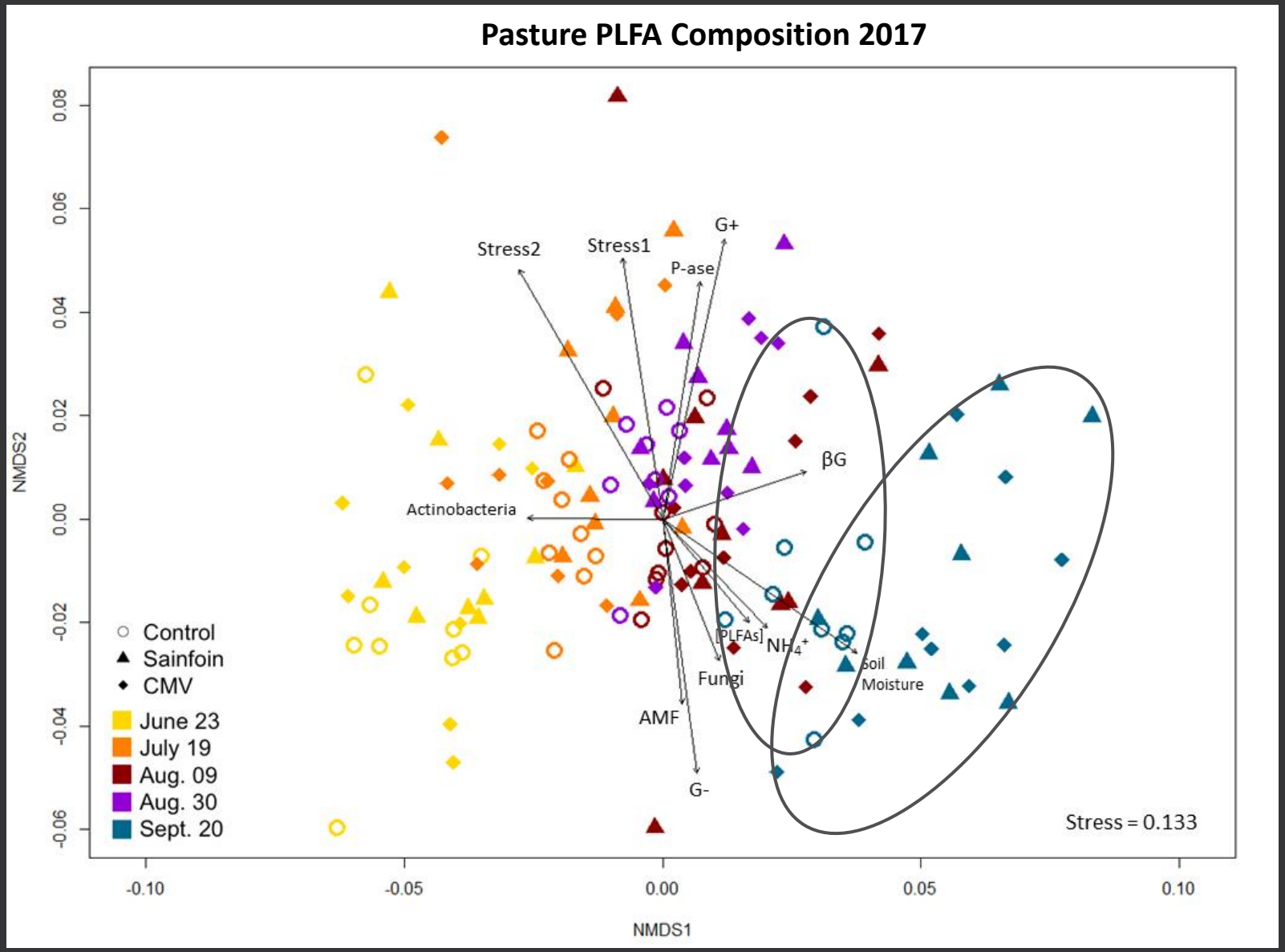


Gram –
16:1 ω7c

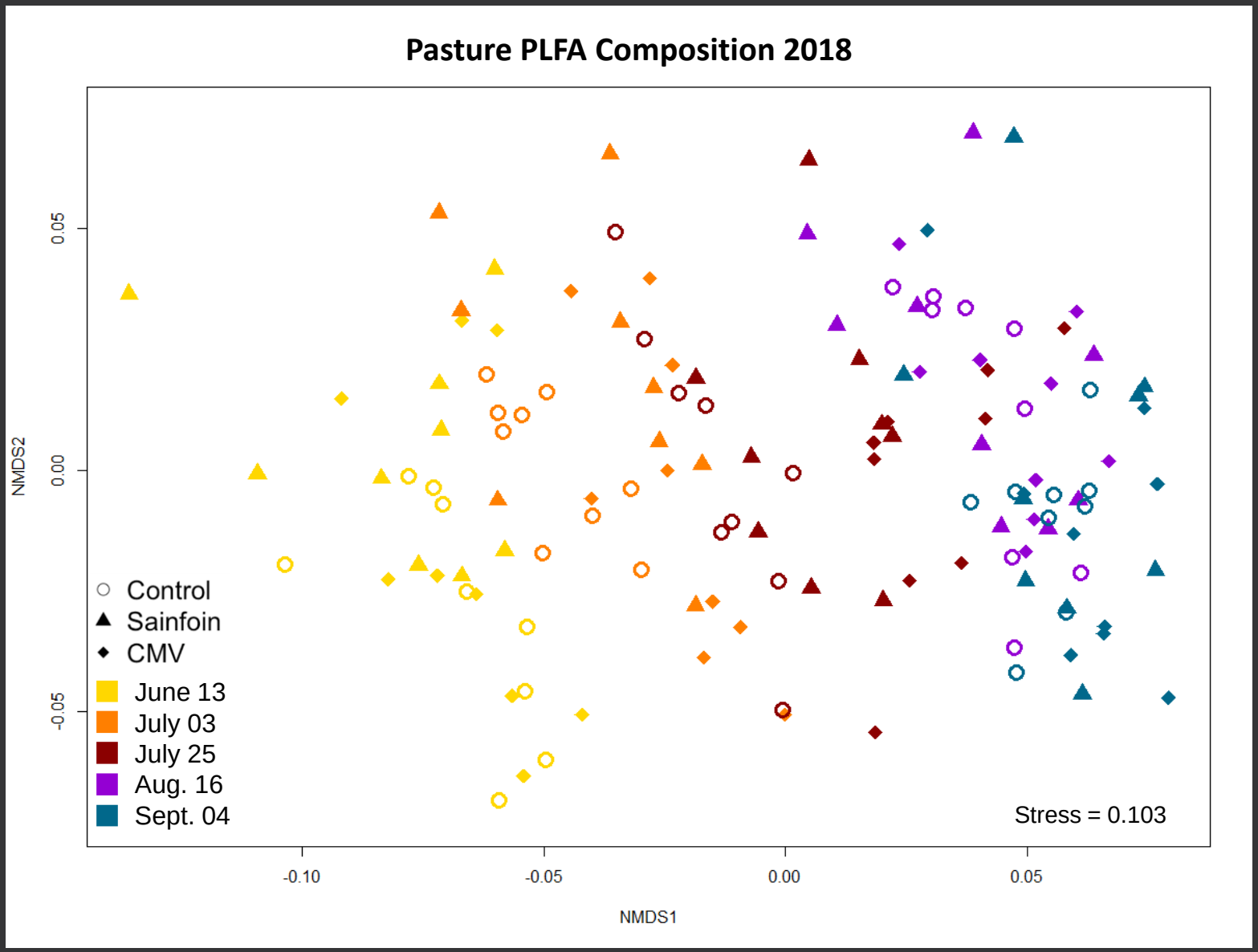


…& AMF, actinobacteria, and stress indices.
Some groups have multiple biomarkers.

Results – Soil Microbial Community Composition



Results – Soil Microbial Community Composition



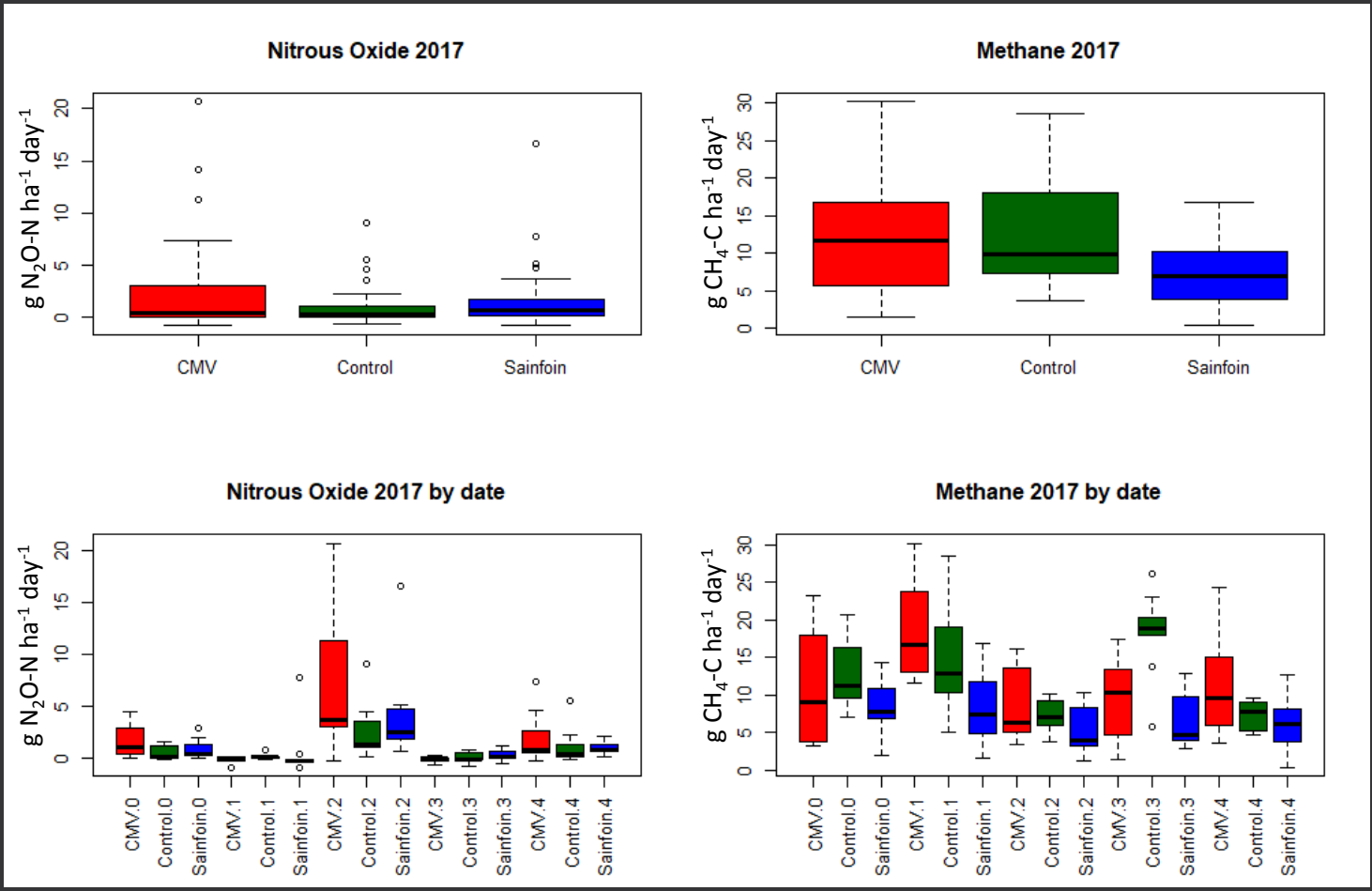
Results – Soil Microbial Community Composition

- Significant dissimilarities between both legume pastures and the control in 2017
  ($p < 0.01$; PERMANOVA)
  → within-group dissimilarity $\leq$ between-group

- Preliminary within-treatment analysis suggests dominant mechanisms driving community structure differ between treatments.

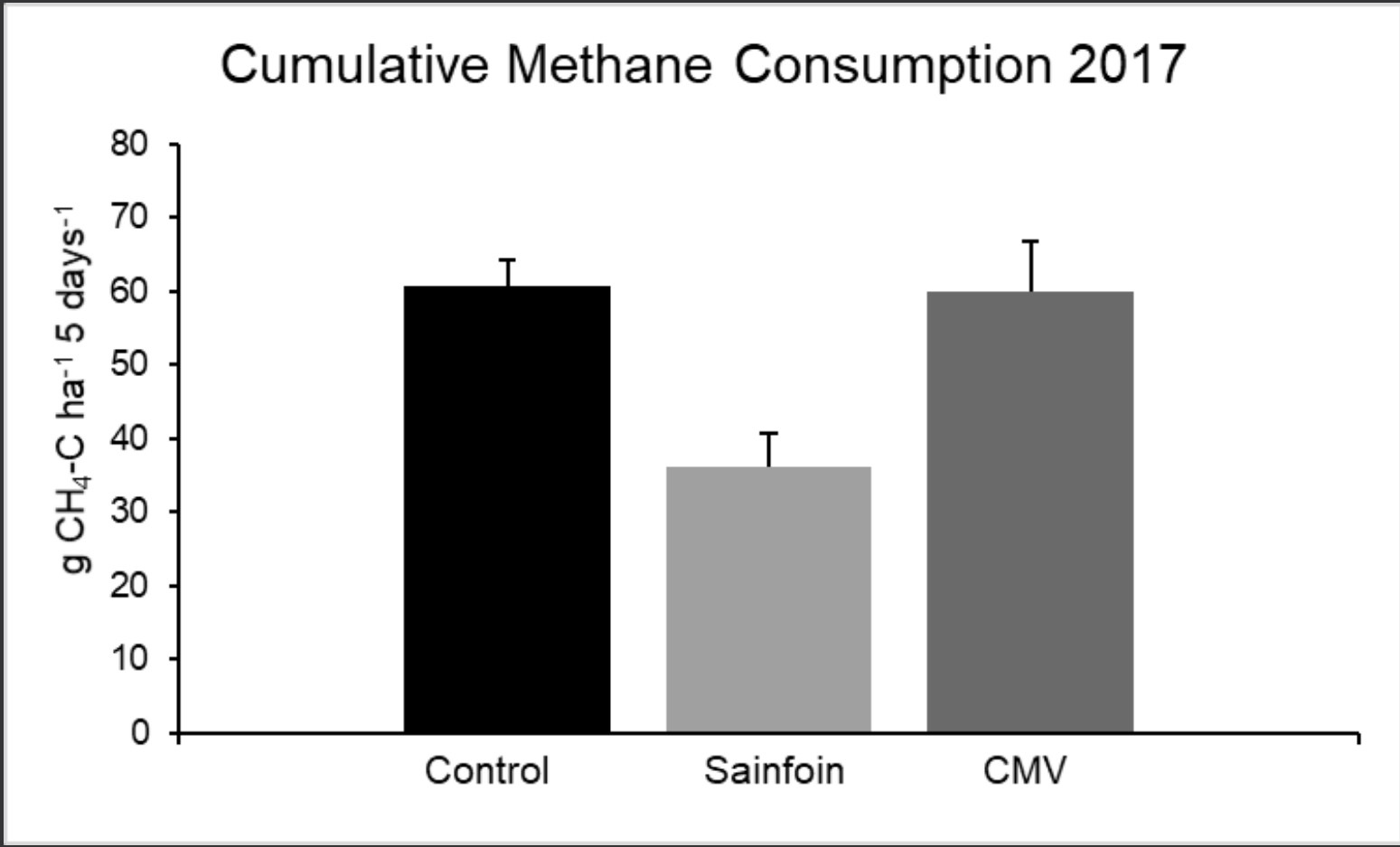
Results – Greenhouse Gases

- Treatment effects largely non-significant



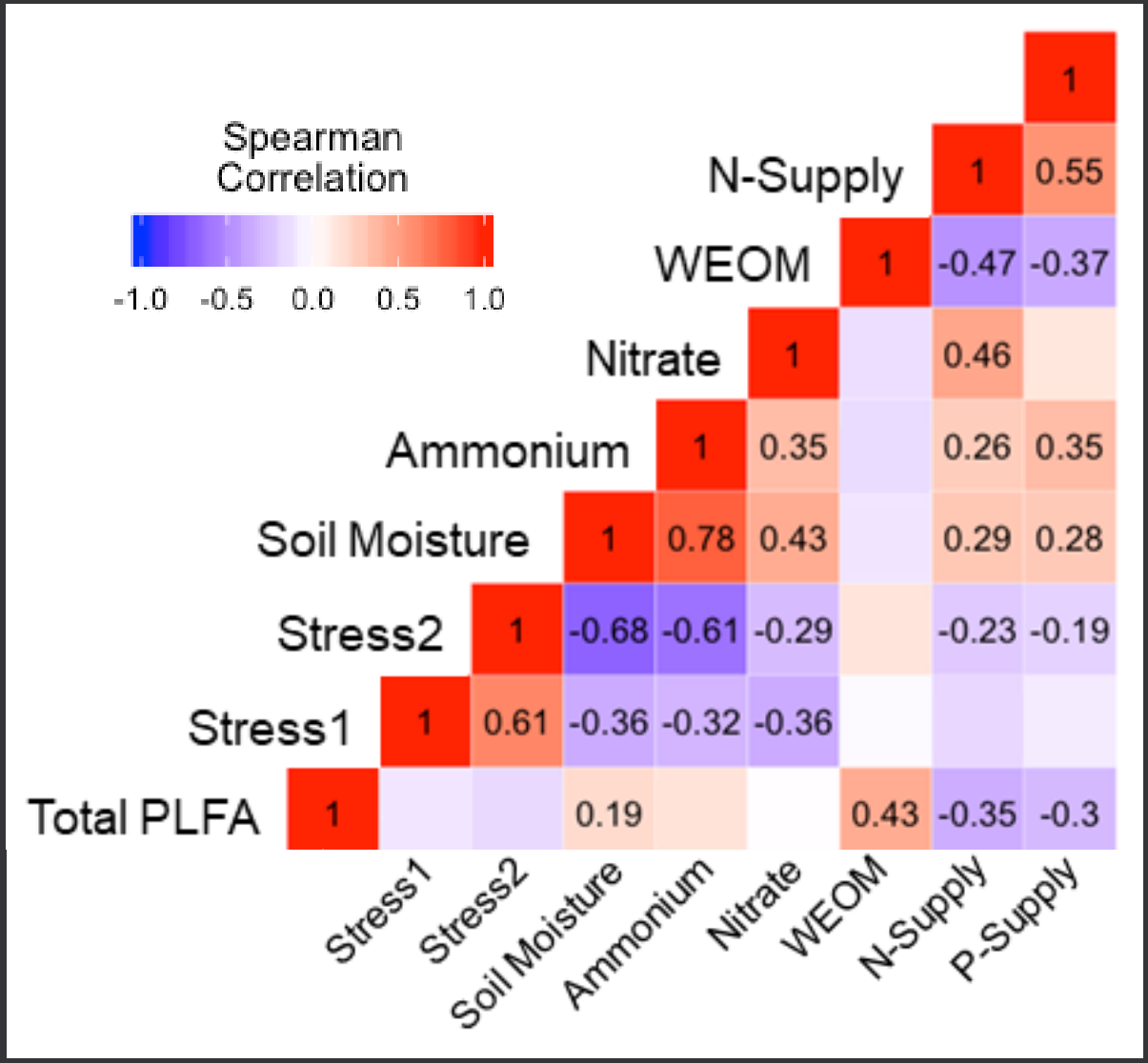
Results – Greenhouse Gases

- Sainfoin total methane consumption significantly less than milkvetch, control ($p < 0.02$, TukeyHSD)



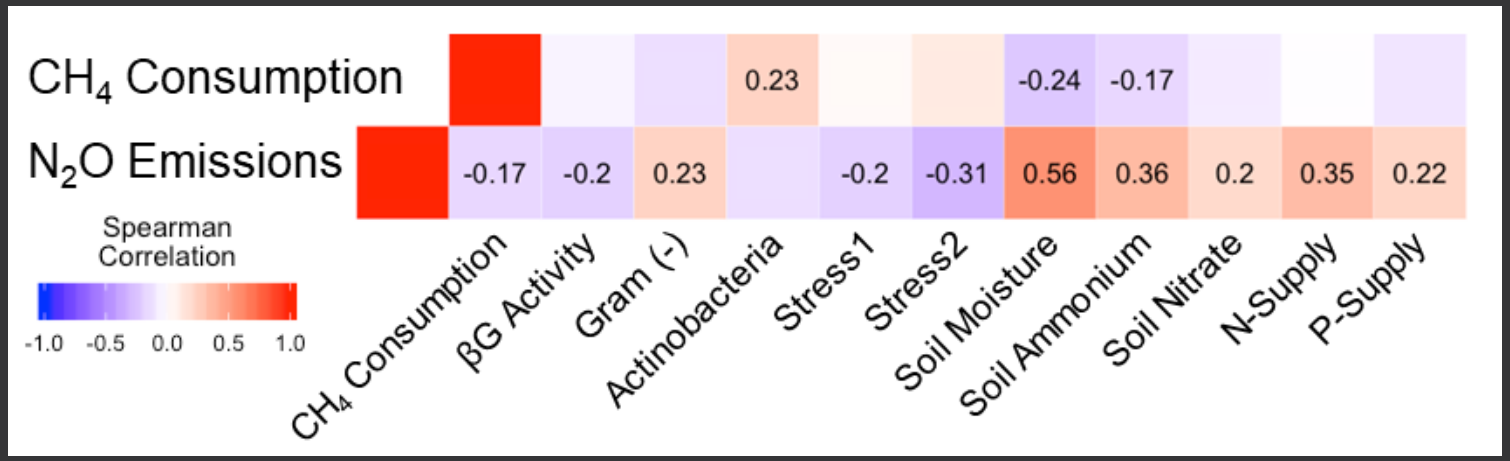
Results – Biological Interactions with Environment

- 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_2O fluxes.
- Analysis of data using further statistical methods will reveal interactions in more detail.

Acknowledgements

Supervisors: Bobbi Helgason & Melissa Arcand
Committee: Diane Knight, Jeff Schoenau

Post-doc and PhD researchers:
Joel Ens, Gazali Issah, Jiancan Liu, Tram Thai, Bree Kelln

Staff and undergrad assistants – Helgason, Arcand, and Farrell & Knight laboratories; WBDC.

Funding:
Canadian Agricultural Partnership – Agricultural Greenhouse Gases Program (AGGP)

AGGP II Project Leads: Diane Knight, Bart Lardner

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