Investigation of Land Management Histories and Fertilizer Treatments on Diversity of Rhizobial *nifH* Gene in the Cover Crop *Vicia villosa* (Vetch)

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Background

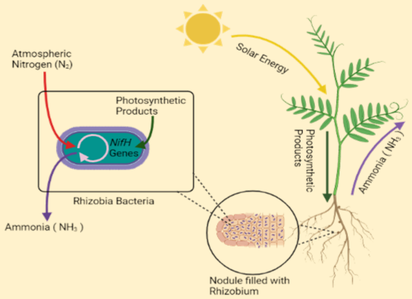


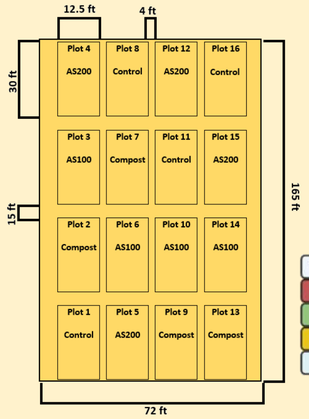
Figure 1: Hairy vetch is Nitrogen Fixing due to its symbiotic relationship with Rhizobium bacteria that converts N_2 to NH_3

The objectives of our investigation were to assess how land management history and fertilizer treatments affected Rhizobium *nifH,* diversity and soil abundance to help expand our knowledge of soil health

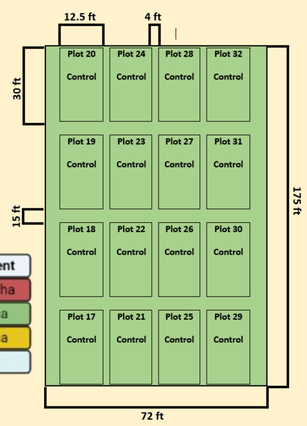
Methods

Field Design

Field 1 (2012)
Corn Land History



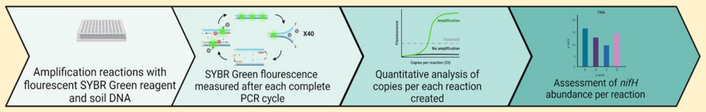
Field 2 (2020)
Grain Land History



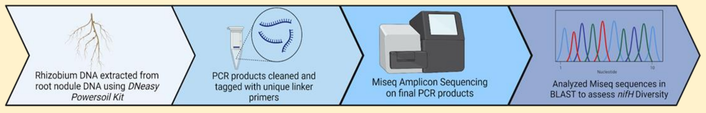
Treatment	Nitrogen Content
Compost	224 kg total N/ha
AS200	AS224 kg N/ha
AS100	AS112 kg N/ha
Control	No Nitrogen

- Two adjacent fields In Logan Utah were planted with a hairy vetch cover crop in fall 2020.

Work Flow for Assessing *nifH* Abundance



Work Flow for Assessing *nifH* Diversity



Results

Real Time Quantitative PCR Results

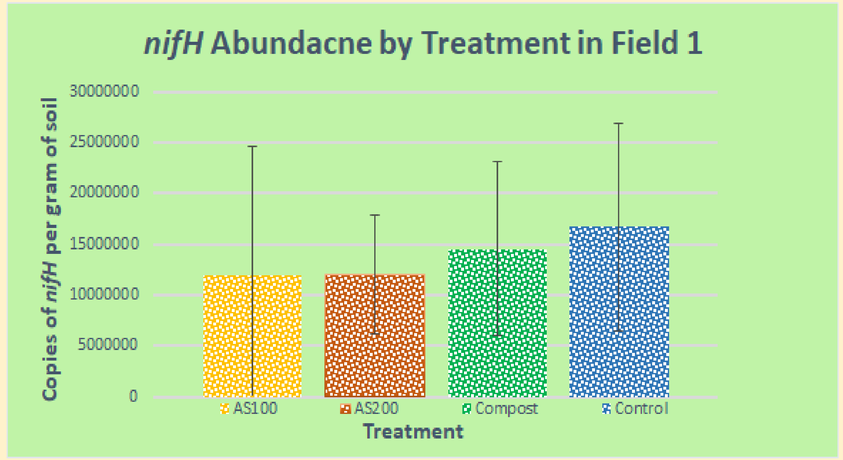


Figure 3 Mean n*ifH* soil abundance (± SD) in field 1 separated by fertilizer treatment. The four treatment groups where: control (no-nitrogen), low-ammonium sulfate (AS112 kg N/ha), high-ammonium sulfate (AS224 kg N/ha), and steer-manure compost (224 kg total N/ha). Treatment group did not have a significant effect on nifh soil abundance (alpha = 0.050 P = 0.506).

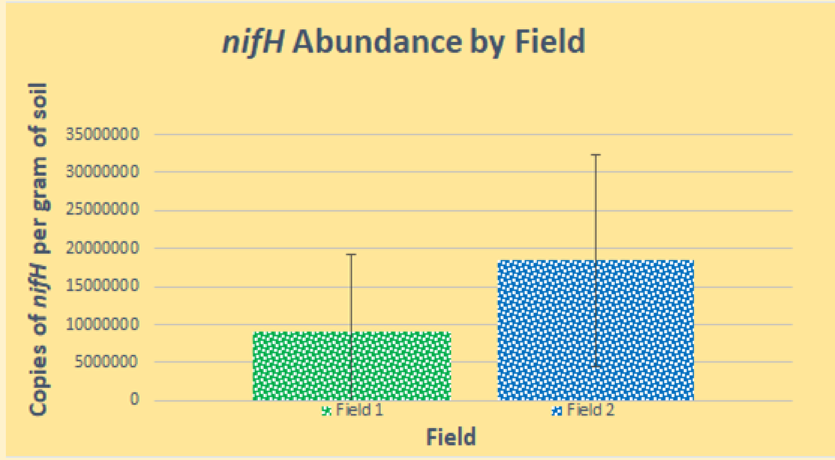


Figure 2 Mean n*ifH* soil abundance (± SD) in fields with different land management historys. Field one had been receiving a randomized block design of fertilizer treatments for 9 years pier to sampling and plants mostly with corn. Field 2 was planted in small grain and did not receive the same fertilizer treatments. Field land management had a significant effect on nifh soil abundance (alpha = 0.050 p = 0.003).

Discussion and Conclusions

- Field 2 (grain history) had a higher *nifH* soil abundance than field 1 (corn history)
- Within field 1, there was not significant difference in *nifH* soil abundance between treatment types. However, AS100 had the highest average *nifH* soil abundance, followed by the control, AS200 and compost.
- Field 2 may have had a higher *nifH* abundance due to the nitrogen limiting environment from lack of fertilizer treatment.
- The nitrogen limiting environment may have resulted from the fact that small grains like wheat (field 2) remove ~1.2 pounds of nitrogen from soil per bushel. Compared to corn (field 1) which removes ~0.9 pounds of nitrogen from soil per bushel.[3]
- Nitrogen limiting environments can facilitate a need for more rhizobial symbiosis to produce more nitrogen for the plant.
- Future work includes analyzing genomes from Miseq Amplicon sequencing to access diversity in *nifh*.

References

[1] Jones, Kathryn M, et al. “How Rhizobial Symbionts Invade Plants: the Sinorhizobium-Medicago Model.” *Nature Reviews. Microbiology*, U.S. National Library of Medicine, Aug. 2007, www.ncbi.nlm.nih.gov/pmc/articles/PMC2766523/.
[2] BioRender.” *BioRender App*, app.biorender.com/.
[3] George Silva, Michigan State University Extension. “Nutrient Removal Rates by Grain Crops.” *MSU Extension*, Michigan State University Extension, 29 July 2021, www.canr.msu.edu/news/nutrient_removal_rates_by_grain_crops.
[4] Special thanks to the Norton Laboratory
[5] Thank you in part to the National Science Foundation OK-LSAMP Program Grant No. HRD-1911370 OK-LSAMP