Internship Project: Successional Changes in Soil Microbial Communities in a Northeastern US Hardwood Forest

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Motivation

Soil microbial communities are important components of terrestrial ecosystems driving many key processes such as nitrogen (N) fixation and carbon (C) sequestration. Despite the importance of soil microbial communities, little is known about how they respond to disturbance and change with succession. Understanding soil microbial community succession is vital to understanding ecosystem functioning. The National Ecological Observatory Network (NEON) monitors causes and responses of changing ecosystems on a continental scale and provides a platform to address these concerns.

Soil microbial community samples were collected at three successional stages (disturbed, successional, mature) from a mixed northern hardwood site at Harvard Forest. Microbial community data was compared to determine if succession impacted community structure and function. Statistical and trend analyses provided insight into how soil microbial communities respond to disturbance, and ultimately how these responses influence the ecosystem processes they drive.

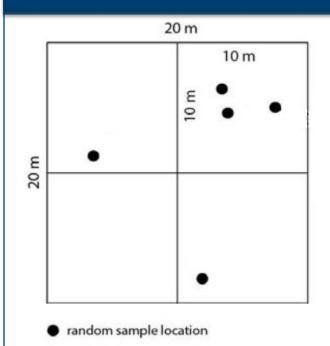


Site Description

Soil microbial community samples were collected from ten plots at three successional stages from Harvard Forest and Quabbin Reservoir research area in July 2012. Mean site temperatures range from -7°C to 20°C with a mean annual precipitation of 110cm. Successional stages: disturbed grassland 2. successional shrubland 3. mature forest: red oak (Quercus *rubra*), red maple (*Acer rubrum*), black birch (*Betula lenta*), white pine (*Pinus strobus*) and eastern hemlock

Methods

(Tsuga Canadensis).

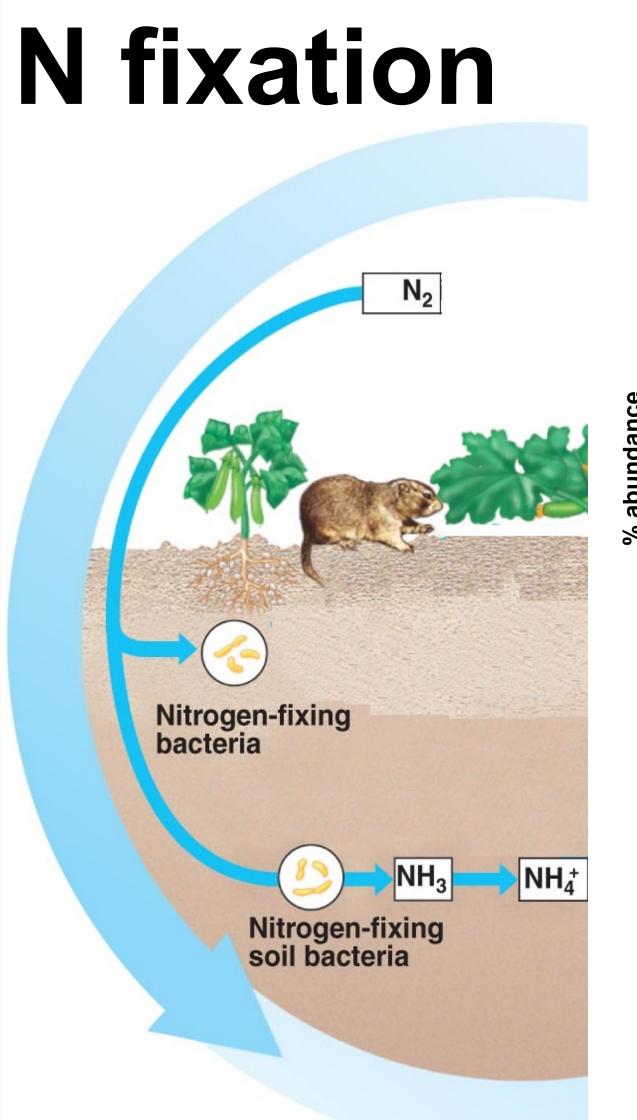


Soil samples were taken from ten of twenty randomly located 20m x 20m plots containing four 10m x 10m subplots at three successional stages (disturbed, successional, mature). Microbial DNA/ RNA was extracted from soil samples, purified, amplified and sequenced.

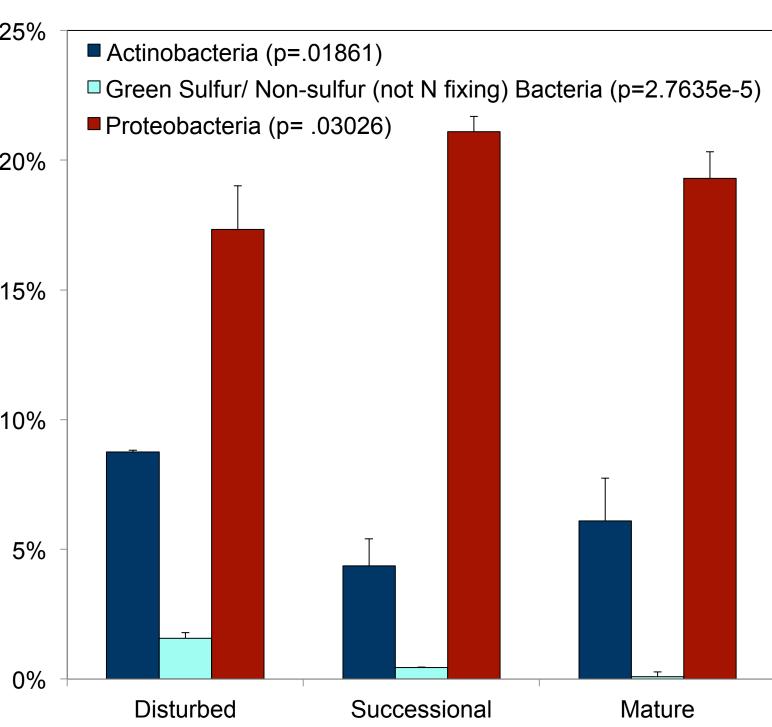
Organism abundance analysis used 16S rRNA data and MG-RAST (mRNA) best hit classification. Community information from the different stages was compared to determine if succession had a significant impact on soil microbial community structure and function. Statistical (ANOVA, cluster based analyses) and trend analyses were used to provide insight into how soil microbial communities respond to disturbance and change with succession.



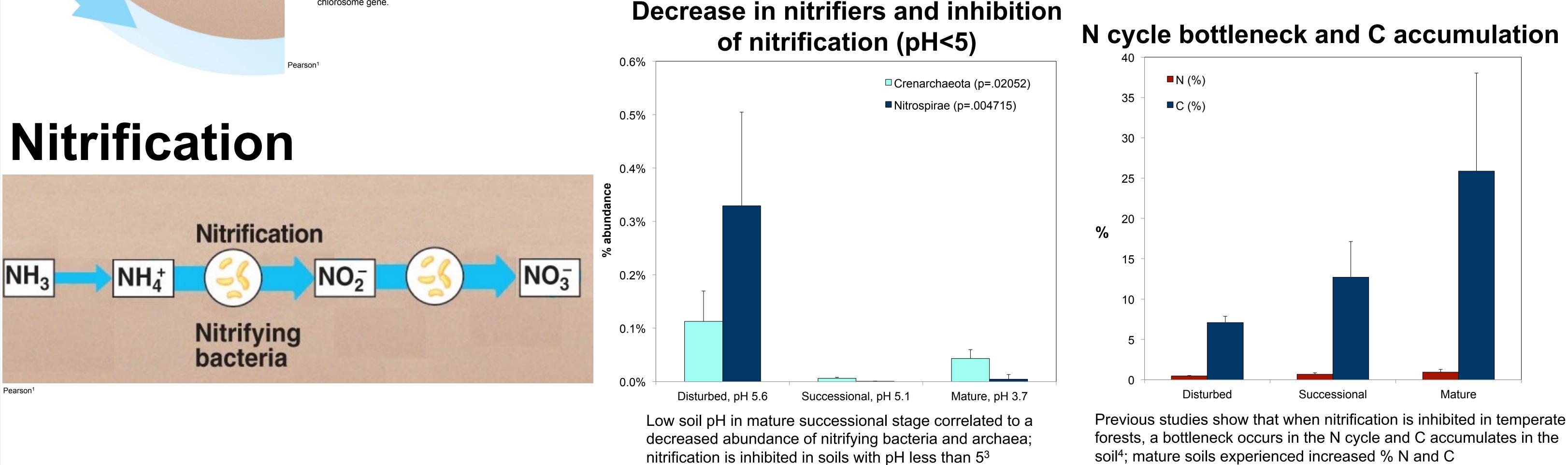
The Nitrogen Cycle is Altered by Succession



N fixing bacteria community shift



Shift from free living N fixing bacteria (Actinobacteria, Green Sulfur Bacteria) in disturbed stage to rhizobium (Proteobacteria) in mature stage. Note: Green Non-sulfur bacteria do not fix N, but were included in analysis because both Green sulfur and non-sulfur bacteria have chlorosome gene

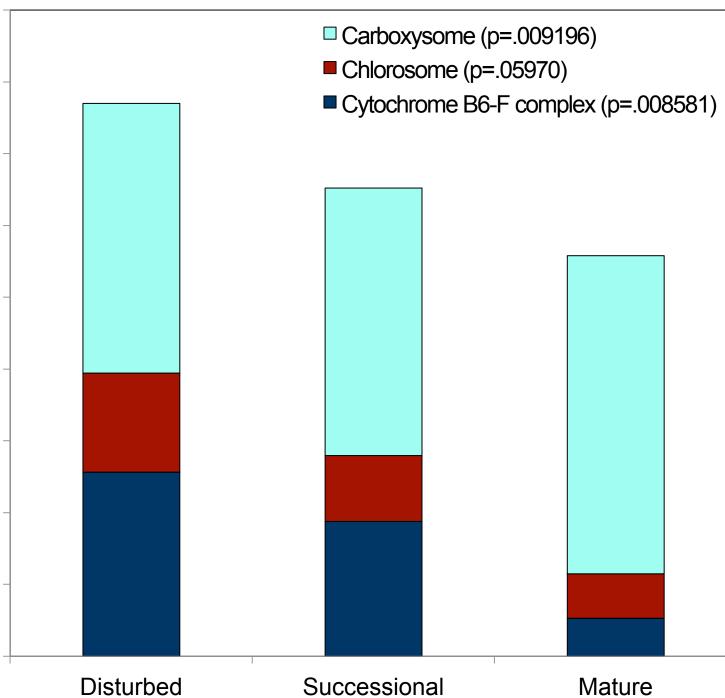


Discussion

- A bottleneck in the N cycle causes inhibition of nitrification and a buildup of C in mature soils; temperature forests act like C sinks.
- Disturbed sites act like C sources, as disturbances reset the process of succession and allow nitrification to occur.
- Mild frequent disturbance such as climate change could likely cause a feedback loop, constantly resetting the process of succession and preventing soils from accumulating C.



0.18% 0.16% 0.14% 0.12% 0.10% 0.08% 0.06% 0.04% 0.02% 0.00%

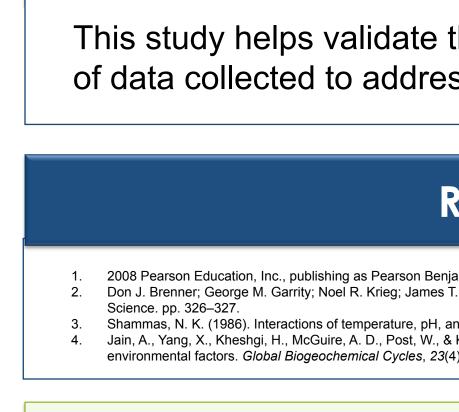


Activity of genes associated with free living N fixers high in disturbed successional stage

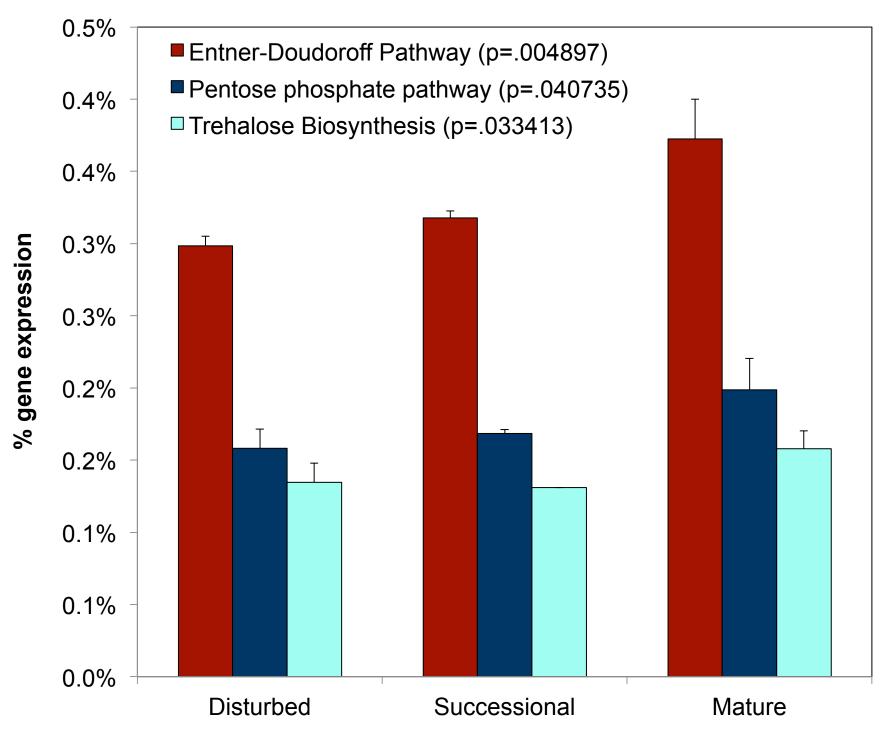
Future Research

Control:

- Measure nitrification in different successional stages • Nitrification should be inhibited in mature forest plots/ not inhibited in disturbed plots Does inhibition correspond to a decreased abundance of nitrifiers? **Experiment:**
- . Lower pH in a disturbed site
- 2. Raise pH in a mature forest site
- Is nitrification inhibited? • Does soil C increase?



Shift in activity of genes associated with N fixing bacteria



Activity of genes associated with rhizobium high in mature successional stage²

soil⁴; mature soils experienced increased % N and C

Conclusion

This study helps validate the NEON sampling design and ability of data collected to address biologically meaningful questions.

References

2008 Pearson Education, Inc., publishing as Pearson Benjamin Cummings Don J. Brenner; George M. Garrity; Noel R. Krieg; James T. Staley (2005). proteobacteria: The alpha-. Shammas, N. K. (1986). Interactions of temperature, pH, and biomass on the nitrification process. Journal (Water Pollution Control Federation), 52-59 Jain, A., Yang, X., Kheshqi, H., McGuire, A. D., Post, W., & Kicklighter, D. (2009). Nitrogen attenuation of terrestrial carbon cycle response to global

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