

Test

Max Brubaker

12/16/2021

Introduction Paragraph

Current unknowns and controversies in the literature among old growth forests demand a more collective understanding of the fate and function of these systems. A recent example of such controversy is shown (Luyssaert et al. (2008), Gundersen (2021), and Luyssaert (2021)) in the debate over the functionality of old growth systems in terms of their carbon sequestration capabilities. We believe that the misrepresentation of the below ground community is a significant contributor to not only contrasting findings such as these, but also to the lack clarity in soil science and ecosystem functionality as a whole. This study aims to determine how soil fungal communities differ among forest sucssional stages (SS's) in community structure and carbon functionality. Emerging research suggests that increase in forest SS may be associated with a number of below-ground processes. For example, it is evident that microbial community composition responds to forest SS development. As forest age increases we see a shift from a r-strategic dominated community (variable environment dominated by bacteria) to a k-strategic dominated community ("stable" environment dominated by fungi) Zhou, Wang, and Luo (2017). Additionally, this increase in SS has been accompanied by an increase in microbial biomass (Zhong (2018) and Yan (2020)). Contrarily, we see reductions in both microbial biomass and diversity when forests are reverted to *stand initiation* stages (Rodriguez-Ramos et al. (2020), Zhong (2018)), with variation depending on disturbance type. It is clear in the literature that both physical and chemical disturbance can lead to substantial changes in the microbial community. Fungi have been chosen as our model organism to analyze soil microbial community and functionality. A number of studies have analyzed fungal community composition in search of "who is there," but far less have looked into soil functionality through fungal community analysis in terms of "what are they doing." There is evidence suggesting a positive correlation between soil microbial diversity and soil ecosystem functionality (Delgado-Baquerizo et al. 2016). Understanding the link between microbial community composition and forest functionality is crucial for future forest management and preservation. It will be a part of this project to test the ability of different genomic community analysis methods to provide information regarding a soil microbial community. We are aware that a experiment such as this could easily take up the entirety of a Ph.D. and that environmental sample are notoriously difficult to accurately measure in terms of genomics. We will analyze inoculated soils with known microbial communities and test the ability of certain methods (whole genome sequencing, metagenomics, and metatranscriptomics) to provide accurate representations of the community. The results from this experiment will dictate our future community analysis methods. We hope that this project will provide insight in whether or not old growth forests are functionally different from managed systems as that this understanding may shape future forest ecosystem analysis and the resulting management practices.

Paragraph 3:

intro sentence :Understanding how shifts in microbial community impact ecosystem functionality with forest succession, and how the resulting soil characteristics respond, can greatly improve our ability to infer how ecosystems are influenced by environmental change. The findings of Delgado-Baquerizo et al. (2016) suggest ecosystem functionality is dependent on specific microbial diversity and that any shift in said diversity is likely to change the functionality and resulting ecosystem previsions/services. It is apparent that as forest systems transition into later successional stages, we see a major change in microbial ecosystem diversity

(Yan (2020) and Zhou (2017)). These, among other studies (Sun (2021) and Zhou, Wang, and Luo (2017)), show that as forests age we see a shift from a r-dominated (bacteria) microbial community strategy to a K-dominated strategy (fungi). This is important because not only it shows us that as forests age we shift into a fungal dominated soil ecosystem but it also suggests that fungi are associated with forest ecosystem stability. Furthermore, it has been shown (Jiang (2021)) that the relative abundance of certain fungal communities significantly increase with succession. Conversely, in this study, it was noted that bacterial groups remained relatively unchanged. This suggests that fungi may become more involved in nutrient cycling as forest ages increase, or that bacteria are able to maintain functionality in different soil and environmental conditions. Understanding what organisms are present in soil systems is extremely important and there is a substantial amount of research present in the literature eluding to how microbial community composition changes among kingdoms (bacteria, fungi, etc). Digging deeper, a majority of fungal community analysis revolves around genomic sequencing in search of the presence or absence within specific hierarchical classifications (i.e. phylum, class, genus, etc). This however leaves us with massive oversight as to how these changes in community impact the corresponding ecosystem functionality.

- Delgado-Baquerizo, Manuel, Fernando T. Maestre, Peter B. Reich, Thomas C. Jeffries, Juan J. Gaitan, Daniel Encinar, Miguel Berdugo, Colin D. Campbell, and Brajesh K. Singh. 2016. "Microbial Diversity Drives Multifunctionality in Terrestrial Ecosystems." *Nature Communications* 7 (1). <https://doi.org/10.1038/ncomms10541>.
- Gundersen, Per. 2021. "Old-Growth Forests as Global Carbon Sinks Overestimated." *Nature* 591 (7851): E21–23.
- Jiang, Shuai. 2021. "Changes in Soil Bacterial and Fungal Community Composition and Functional Groups During the Succession of Boreal Forests." *Soil Biology and Biochemistry* 161.
- Luyssaert, Sebastiaan. 2021. "Reply to: Old-Growth Forests as Global Carbon Sinks Overestimated." *Nature* 591 (7851): E24–25.
- Luyssaert, Sebastiaan, E. -Detlef Schulze, Annett Börner, Alexander Knohl, Dominik Hessenmöller, Beverly E. Law, Philippe Ciais, and John Grace. 2008. "Old-Growth Forests as Global Carbon Sinks." *Nature* 455 (7210): 213–15. <https://doi.org/10.1038/nature07276>.
- McGee, Katie. 2019. "Determinants of Soil Bacterial and Fungal Community Composition Toward Carbon-Use Efficiency Across Primary and Secondary Forests in a Costa Rican Conservation Area." *Microbial Ecology* 77 (1): 148–67.
- Rodriguez-Ramos, Jean C., Jonathan A. Cale, James F. Cahill, Suzanne W. Simard, Justine Karst, and Nadir Erbilgin. 2020. "Changes in Soil Fungal Community Composition Depend on Functional Group and Forest Disturbance Type." *New Phytologist* 229 (2): 1105–17. <https://doi.org/10.1111/nph.16749>.
- Sun, Yuan. 2021. "Elevated Co2 Shifts Soil Microbial Communities from k- to r-Strategists." *Global Ecology and Biogeography* 30 (5): 961–72.
- Yan, Benshuai. 2020. "Change in Composition and Potential Functional Genes of Soil Bacterial and Fungal Communities with Secondary Succession in Quercus Liaotungensis Forests of the Loess Plateau, Western China." *Geoderma* 364.
- Zhong, Yangquanwei. 2018. "Decreased Occurrence of Carbon Cycle Functions in Microbial Communities Along with Long-Term Secondary Succession." *Soil Biology and Biochemistry* 123: 207–17.
- Zhou, Zhenghu. 2017. "Trends in Soil Microbial Communities During Secondary Succession." *Soil Biology and Biochemistry* 114: 92–99.
- Zhou, Zhenghu, Chuankuan Wang, and Yiqi Luo. 2017. "Effects of Forest Degradation on Microbial Communities and Soil Carbon Cycling: A Global Meta-Analysis." *Global Ecology and Biogeography* 27 (1): 110–24. <https://doi.org/10.1111/geb.12663>.