Draft 1

Max Brubaker

12/10/2021

\_\_BIG QUESTIONS–:

What if, as a part of my thesis or even just as a lab… why don’t we aim to standardize soil measurement strategies, definitions,, protocols.. we need to be doing these things on equal levels in order to be able to properly compare/contrast/understand. - could seek through SES and just discuss with individuals.

* how can we ensure that we are measuring as universal as possible? *steming from the SES discussion. We need to be making measurements and definitions* ***common use***.

# Introduction

*questions*: Why do we care about knowing soil fungal carbon functionality?

* fungal communities are primary decomposers
* fungal communities are some of the only decomposers that can break down lignin and cellulose.
* fungal communities are dominant in old growth forest systems
  + need support in old growth systems functionality.. are they are more productive or biodense?
* regardless of support or rejection of old growth forest logging we are drastically reduce a (more or less) finite resource. This resource contains *information*.

overall goal / message to display is that we do not know how these forest soil microbial communities differ in terms of functionality. This is a huge issue as we are making major decisions (such as logging old growth forests) without fully understanding the below-ground processes. We are running under this assumption that old growth forest soils are the same (or at least operate the same) as younger/managed soil systems.

I think the overall message or story I want to tell is that these systems are dynamic and that AGE MAY INFLUENCE FUNCTIONALITY. I retain an unbiased nature as to whether or not these older systems are more “functional” than younger systems but I can without a doubt say that we need to understand them more fully before we continue to decimate and eradicate them.

#### What points will support my thoughts on this?

* We know that forest communities change over time
* We *know* that microbial community influences functionality (NEED MORE RESEARCH ON THIS)
  + microbial communities influence soil chemistry, plant community, above-ground and below-ground biodiversity
  + these are all dynamic attributes… each are linked and as one changes resulting changes will follow…
* I need to have a better understanding of HOW current forest soils are being assessed… (NEED MORE RESEARCH ON THIS)
* Need more information on how microbial communities change over time.
* Need specific examples showing that we are only looking at WHO is there rather than WHAT the are doing\*.
  + eukaryotic transcriptomics.
* Need some information showing functionality of different forest succession stages.

#First Paragraph:

***intro sentence*** : (needs mad work)

Current unknowns and controversies in the literature among old growth forests demand a more comprehensive and collective understanding of the fate and function of these systems.

***body*** : (MISSING SOMETHING ABOUT FOREST DISTURBANCE AND HOW THIS CAN INFLUENCE MICROBIAL COMMUNITY)

This study aims to determine how soil fungal communities differ among forest sucessional stages in community structure and carbon **functionality**. Emerging research suggests that increase in forest succesional stage may be associated with a number of below-ground processes(CITATIONS?). For example, it is evident that microbial community composition responds to forest successional stage development. As forest age increases we see a shift from a r-strategic dominated community (bacteria) to a k-strategic dominated community (fungi) Zhou (2017). On the other hand, we see drastic reductions in both microbial diversity biomasss when forests are “reverted” to *stand initiation* stages.

A number of studies have analyzed fungal community composition in search of “who is there,” but few have looked into fungal soil functionality based on ***ribosomal metagenomics*** in search 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 this link between microbial community composition and forest functionality may greatly change what we know about forest functionality and will certainly impact forest management and preservation strategies. (needs work)

…

#Second Paragraph: (needs to build off a main point from the intro and needs to have a strong lead sentence)

Is it imoprtant to discuss how fungi are involved in ecosystem function? Even just a brief paragraph to support why we are looking at fungi as opposed to another group of microbes?

#Third Paragraph:

***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.

#Fourth Paragraph: (need more literature review)

***intro sentence*** : Understanding how functionality and microbial community change over time is crucial however, natural undisturbed succession is becoming increasingly rare by the day. Ecosystem disturbance is happening more frequently via both natural (extreame weather) and anthropogenic (logging/management) means….info on how disturbance influences microbial community…….. It is also important to understand that the type of disturbance may impact how the microbial community changes.

#Fith Paragraph:

***intro sentence*** ….. maybe talk about parameters that have been shown to change as successional stages increase???

Jiang (2021): Bacterial and *Fungal* community composition and functional changes with forest succession:

# - The results showed that forest succession significantly changed the community composition of bacteria and fungi, among which the fungal community was more sensitive to the changes with successional stage.

# - \*\*\* In this study, the soil total carbon and total nitrogen were the dominating factors affecting the soil microbial community and the structure of fungal functional groups..

Yan (2020): Fungi and beacteria functional genes ~ chronosequence - Soil microbial biomass (C, N and P) increased significantly in topsoil (0-20 cm) with vegitation succession. - Fungal abundances annd the Fungal:Bacterial was detected along a successional gradient (???)

- C and N cycle-related (potential) functional genes increased significantly and then stabbilized (\*)  
 - recalcitrant C degredation, N reduction, and denitrification-related genes increased and labile versions decreased  
 - \_\_fungal communitie were most correlated with ammonium N contents and root biomass\_\_

It is our belief that a significant portion of controversy/uncertainty in old growth forests (see Luyssaert (2021) for example) can be contributed to the lack of understanding in below-ground processes (CITATION?).

Above-ground forest processes have been studied for over a century (CITATION) and with this knowledge many regulations have been set in place. It has been noted (CITATION ~ somewhere in ogf book?) that many of these regulations have been set in place based almost soley on above-ground processes. Additionally, if in fact below-ground processes are considered, we are using “blanket understandings” of these systems as if they are all the same.

While controversy is ever present and results are variable potential trends may be emerging with the increased study of old forest chronosequences (CITATIONS?) stretching into the ***standardized old growth forest ranges***. A number of soil characteristics are appearing correlated with forest successional stage.

# Expiremental Design:

\_\_\*\*We are going to be analyzing soil fungal communities (meta - genomics,transcriptomics) of forest successional stages\*\_\_:

What parameters would also be interesting to know wth forest age (successional stage)? -**Q**: how are we defining forest “age” or successional stage. What range of area does this account for? What area do we sample over? How many areas will we measure to consider that forest covered? this leads back into how are we classifying forest stage (stand age only? how was stand age measured (check ogf book on that one)) -**Q**: are we accounting for type of disturbance? Because im pretty sure I have seen that type of disturbance may result in different forest response (Natural vs. athropogenic)

Parameters: - climate: temp, humidity, etc. - topsoil (%, depth, ratio, whatever) - lat,long, and elevation (analysis within systems?) - soil moisture - Field pH? - - % fungal biomass - % rna expression

Samples: how are we sampling? Is it possible to gps every sample? In theory gps samples could allow us to account for auto correlation between sample and are we breaking sampling methods down likey Tony or different? We need to make sure that we we are doing can remain constant across forests/sampling locations. - I feel like I tossed a grid idea around… what if you took

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>.

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.

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>.