

SOIL Discuss., referee comment RC1
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Comment on soil-2021-98

J. Aaron Hogan (Referee)

Referee comment on "Network complexity of rubber plantations is lower than tropical forests for soil bacteria but not for fungi" by Guoyu Lan et al., SOIL Discuss., <https://doi.org/10.5194/soil-2021-98-RC1>, 2021

REVIEW of EGU SOIL Discussions -- Guoyu Lan et al – Network complexity of rubber plantations is lower than tropical forests for soil bacteria but not fungi.

Main comments:

I found the introduction of network analysis lacking in explanation. The reason we write is to explain. For those who are not familiar with network analyses (and even for those who are), you should introduce key concepts – like network complexity – in an explanatory fashion. What is it? why is it important? how does it apply in the context of the study as a tool for hypotheses testing?

I found the hypotheses to be somewhat superficial in their scope. Simply testing for differences in the composition of fungi and bacteria among sites is a poor way to frame investigations that use soil sequencing data. Indeed, I think the study had more refined aims, and clearly articulating the specific hypotheses (in terms of fungal and bacterial guilds which may be selected for, or how compositional network complexity, etc. may change under certain soil environments and why) should be considered. Having specific, testable hypotheses not only strengthens the science but also increases the interest of readers. Similarly, the discussion of the potential abiotic soil drivers and of these differences should be expounded upon, in my opinion (see comments below).

The methods used for (abiotic) soil analyses need to be included (see comments below).

Some justification must be given here for “only focusing in the top 300 most abundance OTUs” (L170). I can understand why this was done – because it simplifies analyses, however, there is much evidence that suggests that abundances of OTU reads are not

indicative of naturally occurring abundance of fungi or bacteria, because for example, primer specificity, amplification preferences during PCR and host of other sources of selection variability/error that can occur in these types of dataset. I think those should at least be acknowledged. Has the analysis been explored using different subsets of the data (say the 300 most common OTUs, or the entire dataset)? did results differ? This comment also applies to other subsets of the data used in the statistical analyses (e.g., L189: "the top 50 most abundant species" etc.)

Line comments / technical corrections:

ABSTRACT

L28: you might define/ explain briefly what network structure means in the context of the main result, here.

L37: I found this sentence to seemingly jump out of the abstract without previous reference. This does not seem like a logically flowing conclusion from the previous eight sentences of the abstract. Nothing about soils was mentioned. If the main conclusion about how available K and total N drive the community/ network structure, you should mention how they vary across rubber vs. natural forests.

INTRODUCTION

L54: needs space after comma

L55: Hainan Island, China

L56: at the northern edge of Asia's rainforest distribution

L59: you might want to define soil microbiome, just to be clear about what you mean

L67-73: see studies by Song HK et al. FEMS <https://doi.org/10.1093/femsec/fiz092> and Ma H et al Forests 2019 <https://doi.org/10.3390/f10110978>

L76: "may represent system behavior" – what does this phrase mean? you might give an example or further explain/define this.

L80: "standard suite of analytical approaches" – such as?

L93: "alters microbial community composition" This is a vague hypothesis. One major criticism of these types of sequencing papers is that they test the hypothesis of difference among sites. Indeed with thousand of taxa/ OTUs, you will likely find differences. This is not a very ecologically meaningful or interesting hypothesis. Surely, with all the work that has been done on how rubber plantations affect soils, you had a more refined hypothesis? what bacterial or fungal taxa/ guilds did you think might be driving differences?

L98: "clarify the drivers" This is the more-novel / more-important part of the paper in my opinion. Identifying the drivers of why soil fungal and bacterial communities are affected by forest conversion to rubber plantation and plantation management has implications for real-world ecology. However, there is no discussion of the potential drivers in the introduction. Soil chemistry, moisture, etc are key considerations, which is influenced by litter quality and alterations to biogeochemical cycling as a result of the conversion of forest to rubber plantations. A brief overview of this might be helpful in setting up this hypothesis better.

METHODS

L88-120: Ling translates to mountain from Chinese to English, but you should still use the full Chinese names of the places (in English). Bangwangling, Jianfengling etc. These are the names of the places,

L121: on your map (Figure S1) you should label the sites, so people know, where each of the named study sites is. for example, where Bawangling vs. Jianfengling

L122: What was the depth of the soil sampling? What type of soil instrument was used (Give details on diameter etc). how was sterility maintained between soil sample collections? these are important missing details

L126: were soils sieved?

L130: being as this is a soils discussion journal, you should describe briefly what methods and instruments were used to measure soil nutrients. It may be okay to refer to the Lan

et al 2020 reference for some of the finer details, but you should give enough information to not leave readers guessing. No details are given, which is suspect.

L132-168: sequencing methods read well & were easily followed/ understood.

L183: you might define what a "keystone OTU" is (briefly and generally), before explaining how they were selected.

RESULTS

The results generally seemed solid and well presented. I like the use of the correlation analysis – relating positively and negatively correlated OTUs to one another within the framework of the network analysis. I think certain figure legends could be elaborated. For example, from the figure legend for Fig. 3, it is unclear what is being shown in the graphic.

L249 (and elsewhere) Chloroflexi (with an i at the end).

Also, throughout the results, species are referred to as "members" of certain taxonomic groups. I think could use the word species, although this is a matter of personal preference. members sounded a bit odd to me, personally.

DISCUSSION

the two papers I have linked to above (Song et al., and Ma et al.) should be incorporated into the discussion (e.g., L318 and elsewhere).

The discussion seemed adequate for the most part. I found it a bit superficial. The authors might try to weigh in more on the actual ecological significance of some of the changes they found. what does it mean for soil biogeochemical cycling or ecosystem functioning? For example, does losing some Actinobacteria from soils from natural forests to rubber plantations actually matter? There is a lot of functional redundancy among soil bacteria and fungi, especially in the tropics, so what are the potential actual consequences for such changes in the soil microbiome? I know this may seem speculative, but it's interesting to discuss this, in my opinion, even if briefly. Also, what future research directions might be informed by the findings of this study.