Comment on soil-2021-95
Anonymous Referee #1

Referee comment on "Soil bacterial community triggered by organic matter inputs supports a high-yielding pear production" by Li Wang et al., SOIL Discuss., https://doi.org/10.5194/soil-2021-95-RC1, 2021

The authors of the study „Soil bacterial community triggered by organic matter inputs supports a high-yielding pear production“ addressed an important and interesting topic by searching for specific characteristics and members of the soil microbiome that can be linked to soil fertility, in this case expressed as the yield of pears. The authors present a well-designed study with appropriate and sophisticated methods. The overall presentation of the study is well-done. I have some minor issues and one major issue, which needs consideration before publication.

My major issue is related to the causality of the relation between the microbiome and soil fertility/pear yield. This becomes mostly obvious in the discussion, but also elsewhere in the manuscript. In this context, it is important to distinguish between direct conclusions that can be drawn from your results and speculations. It seems to me that SOM is the main driver as mentioned in L317. However, in the following discussion, the picture arises, that the microbiome is the main driver without showing clear mechanistic evidence from the data. It is therefore important to keep the right order of effects in mind, which would be, from my point of view, SOM change ==> microbiome change ==> fertility. An additional benefit of the more complex networks for soil fertility could be the resistance against stress. However, this was not tested in this study and could only be hypothesized. In such a case, there would be a direct mechanistic link between fertility and the microbiome. Overall, I suggest that the authors are more careful with what they conclude from their data. The approach to look for some general characteristics of the microbiome and its correlation with yield across different sites is interesting enough in itself.

Specific comments

L36 I suggest to write this more carefully. Factor suggests that there is a mechanistic link between e.g. beta diversity and productivity of the orchard. However, as long as there are no ideas about specific mechanisms, it might be that this is simply a non-causal correlation. For example, both might be primarily driven by SOC without direct mechanistic link. However, this is of course a valuable result and I would write it in a way that points towards the need to underpin this relation with mechanistic studies.
I suggest to strongly reduce this paragraph. The details about the importance of pears in China are not so important for this study. It is enough to know that pears are an important fruit and that improving the productivity is desirable.

"...properties of the study sites were compared...

What does "roughly according" mean? I suggest to shortly present the methodological deviations from the reference.

Fig 2B I miss a label on the y axis, something like "bacterial abundance".

I don't understand the message of this sentence. Please revise this sentence.

Please provide some reasons for filtering the ASVs. With this analysis you want to characterize the different communities, but you exclude part of the communities.

What are the Zi and Pi values and what do they mean. This needs to be explained for readers that are not familiar with the applied statistics.

VPA analysis?

Please explain the meaning of the two graphs in 5C.

You cannot say that these agroecosystems are more stable, because you did not investigate the stability, i.e. the response to stress. Please revise this sentence accordingly.

I wouldn't say "responsible". In the following sentences, you do not provide evidence from the literature, that there might be a direct mechanistic link between the abundance of these phyla and yield productivity. "To be involved in biological processes..." is by far not specific enough to provide such a mechanistic link. You also write that Chloroflexi have taxa with different ecological traits. However, since you did not evaluate, whether specific taxa with specific traits are dominating the abundance of Chloroflexi in your soils, your conclusion are based speculation and not on sound literature knowledge.

Which processes?

What does "scale-free, modular and "small world" exactly mean? Please provide some more background on this.

"...indicated stronger..."

Which study do you address with "this study"? Yours or Coyte et al. 2015?

Usually, most of the agricultural ecosystems are fertilized. It would be, therefore, interesting to know whether this was an organically fertilized soil.

Do the Chloroflexi really "manipulate" the microbiome, i.e. intending to actively change the microbiome? Or is it that they merely affect the microbiome by their degradation of polymers? Maybe, they are "only" representatives for the change in the microbiome, which was induced by organic fertilization, i.e. they are not active players but passive responders? Please elaborate more on such questions, because it seems to me important, that your nice results are properly discussed based on direct conclusions from your results and not on speculation.
What is the ecological relevance of pyrogallol?

These two paragraphs are disconnected to the line of argumentation, which was presented before. Please integrate these two paragraphs better into your discussion.

better "microbial residues"

The conclusion is more a repetition of the main results than a presentation of conclusion related to the larger challenge.