

Comment on soil-2021-95

Anonymous Referee #2

Referee comment on "Soil bacterial communities triggered by organic matter inputs associates with a high-yielding pear production" by Li Wang et al., SOIL Discuss., <https://doi.org/10.5194/soil-2021-95-RC2>, 2022

The authors of the manuscript soil-2021-95 "Soil microbial community triggered by organic matter inputs supports a high-yielding pear production" present a dataset based on 6 sites, each with a high-yield and low-yield treatment, named "yield-invigorating" and "yield-debilitating". Four composite samples (composite of nine individual samples) were taken per treatment. According to the introduction, the authors assume the higher yield at "yield-invigorating" pear orchards to be associated to a unique microbial community, which in turn is affected by abiotic factors. The objectives of this study were to i) identify differences in taxonomic diversity and composition of the bacterial community between the treatments, and ii) determine abiotic factors shaping the bacterial community composition. The broader implication stated would be the targeted manipulation of soil bacterial composition in order to support higher pear production. I want to highlight the impressive variety of statistical methods and results. I also appreciate the data provided in the supplemental material, which provides additional transparency. However, this variety of methods causes a lengthy results part, which sometimes loses the focus on the research question. While at the same time, important information is missing in the M&M section (i.e. a literature based metamodel explaining the rationales behind each pathway, how the model was fitted).

I have three major concerns:

One major concern is the lack of a clear definition of the treatments "yield-invigorating" and "yield-debilitating", thus both terms remain vague from abstract to conclusions. In M&M it is stated, that yield-debilitating orchards received more chemical fertilizer under intensive management (unclear what intensive management refers to), while yield-invigorating orchards were "usually" amended with more organic fertilizer under integrated nutrient management. How did the NPK and OM inputs differ between the treatments. And how consistent were the treatments across the six sites? Is the fertilisation regime the only difference between the two treatments? The terms "yield-invigorating" and "yield-debilitating" indicate a trend in increased or reduced yield over

time, however, Table S1 does only provide yield data for 2019, and yield is only given as average yield per plot and not given for each individual replicate, which results in a limited observation of 12 yields.

Furthermore, the conclusions drawn are very speculative, and correlation between distinct bacterial communities between treatments with yield (the main factor defining treatment) are interpreted as causal for higher yields. However, yield varies largely between the different sites, as do the bacterial communities. An increase in key taxa might be linked to treatment, thus fertilisation (which was indicated to vary between treatments), but does not necessarily cause higher yields. There is a lack on discussion on the direct effect of higher SOM on yield, plant growth and root exudation (which might also affect microbial community composition).

Third, statistical analyses miss to investigate important effects of SOM on yield, and of pH on microbial community composition. The structural equation model approach could promote valuable insights and help to disentangle direct and indirect effects of SOM on yield. However, this would need an inclusion of a direct path from SOM to yield. Furthermore, the authors assume that soil pH (major factor influencing bacterial community) is not of importance in the study cited. However, including pH into the model would allow to prove this assumption. In general, the SEM is lacking the information how much of variation in yield is explained. From Fig. 5A it looks like yield explained ~8% of variation in bacterial community. Vice versa, this questions the conclusion that the bacterial community structure affects growth.

Unfortunately, I cannot recommend publication in its current form and therefore propose a rejection.

I hope the authors still take the time to consider my recommendations regarding the revision of this manuscript.

title The shown data does not allow to assume causality between distinct bacterial community upon organic fertiliser inputs and high yield. Therefore, the title should be revised.

abstract

e.g. L33 Try to write the abstract in a way that it is understandable to a broader audience, without using too many very terms specific to a certain method (meta-modules).

L37 I don't agree on conclusion that the factors presented are causal for higher yields.

introduction

L52 Consider adding a sentence on the role of fungi in perennial agroecosystems (e.g. orchards).

L59 Which monoculture system does Lu et al. 2013 refer to? Be more precise.

L64 I miss the logical link to LLs 62-63. Why is it desirable to identify indicators of bacterial community composition in response to high-yielding crop production?

L70 What does "forms" mean?

L75 Delete therefore. Is not logically linked to the sentence in LLs 73-75.

L75-L77 Be more precise. Do you mean, that it depends on the scale which chemical properties are related to bacterial community composition? Does this refer to your assumed absence of pH as relevant factor in your soils? (L378-L379)

L80-L87 Reduce paragraph on pear to one sentence.

L88-L89 What do you mean by that? It is unclear. Revise. Plus Zorz et al. 2019 refer to lake microbiomes. Consider choosing a reference related to agroecosystems.

L93-L94 It is unclear from introduction, why yield-invigorating bacterial communities should differ or be unique. Revise introduction so that your hypothesis has a

better fundament.

methods

L116-L121 I miss a clear definition of the treatments. What does it mean, that yield-invigorating orchards were “usually” amended with more organic fertiliser. Did yield-debilitating orchards also receive organic fertiliser sometimes? Was the fertilisation regime/ the treatments consistent over all six sites? Table S1 does not provide “detailed information”. It just provides information stated in L103. Could you provide detailed information on the amount of NPK and organic fertiliser inputs for each site?

L168 + Provide references for all statistical software and packages used.

L204-L208 When applying structural equation modelling it is good practice to provide a conceptual meta-model summarising underlying theoretical pathways, plus a table providing references to the hypothesised pathways. Please consider adding this information. Additionally, you should include a fit index, which is robust to sample size, such as the comparative fit index. Consider citing Grace (2006).

results

L222-L223 The PCoA analysis shows clustering between sites. However, the PCoA does not clearly separate the treatments (Fig 2A). Revise.

L237-L241 Long sentence. Revise.

L244 Please check <https://ncbiinsights.ncbi.nlm.nih.gov/2021/12/10/ncbi-taxonomy-prokaryote-phyla-added/> for new standards in taxonomic names.

L258-L262 Move to M&M.

L272 What are the threshold values Z_i and P_i ?

L289-L291 Why is pH not included. Not explained so far. And probably not meaningful to exclude soil pH, due to its important influence on microbial community composition.

L291 RDA1 does only explain 17.4% of variation in bacterial community composition this does not support a strong influence of OM on community composition. Revise wording.

discussion

L311 I don't agree that Fig.1C suggests a direct significant correlation between bacterial community and pear yield. Why do you assume it to be direct? Both could be correlated to SOM. The distinct bacterial community composition was not associated to yield but to treatment (as far as I understood). Yield differed across sites.

L316 Shared across six sites?

L317 Well-organized not neutral à "more interactive"?

L332 Delete "always".

L336-L338 Incomplete sentence.

L339 Define what you mean by soil "biological" fertility.

L345 See my major concern on the conclusion drawn on causality.

L354 What do you mean by "small world"?

L355 Revise conclusions.

L361 Basal shifts in network architecture linked to fertilisation regime and or OM quality?

L365 Which study does "this" refer to?

L370 How does the fertilisation regime in the cited study relate to the fertilisation regime in the presented study?

L380-L374 Too speculative. Revise.

L378 Two points on a log-scale already are a huge difference in terms of soil pH. However, more important than the range across sites would be the difference between treatments – which looks small, indeed. However, best would be to include pH in the analysis and to show, that it really plays a minor role in determining bacterial community upon treatments.

L380 Not only a question of higher SOM content, but probably also associated to quality. Discuss.

L384 Fierer 2004 does not state that diversity increases with higher C content. He states that diversity depends on SOM quantity and quality.

L385 see comments on SEM.

Fig 1 Separate A from B and C and make it an own figure. Does not belong to results.

Figure 1 C Why are there so many dots? If microbial composition distance was calculated for each replicate, it should be 48 dots. Additionally, yield data only represents orchard average per tree, thus it should be only 6 points (or lines, where the 48 dots of microbial composition distance align). Why are there more than 6 levels of yield distance?

The relationship does not look linear. Consider choosing another colour for the dots.

Fig 2 Shapes in A too small. Do not abbreviate yield-invigorating and yield-debilitating wherever the space allows to write the name (plus consider changing the treatment names).

Figure 2 A The PCoA analysis shows clustering between sites. However, the treatments does not clearly separate the treatments. Revise L222-L223.

Figure 3 B Consider moving this to supplement. Does not add much to the main story.

Fig 4 You show many results and provide a lot of valuable information. However, I am not sure how this Figure adds to the research question. Additionally, size too small. Hard to read.

Fig 5 Important figure.

Figure 5 A Implications are a bit unclear for Fig 5 A. Does this implicate if yield only explains 2% of bacterial community composition variation, only 2% of yield can be explained by the community composition?

Figure 5 B Soil pH should be included. See previous comment on that.

Figure 5 D Again, why are there so many points?

Fig 6 Structural equation model seems a good approach to address the question whether bacterial community composition improves pear yield. However, to address this question a direct path from SOM to yield must be included in the model. Additionally, soil pH as a major driver of community composition, should be included as well, even if hypothesised to play a minor role in this study. The major lack of this SEM is that no information on R^2 is provided. How much of the yield is explained by the SEM? All these points are needed to address the cited research question and to draw the conclusion drawn. Additionally, what does beta diversity PCoA mean? Unclear. The comparative fit index, which is not sensitive to sample size should be included. It remains unclear, how the model was developed and fitted.