

19 July 2026

Editor-in-Chief
Soil (Copernicus)

Dear editor and reviewers,

We would like to express our sincere gratitude for the time and effort dedicated to reviewing our manuscript. We kindly thank the reviewers for their insightful and constructive comments, which have significantly improved the quality and clarity of our work.

We have carefully considered all the suggestions and revised the manuscript accordingly. Below, please find our point-by-point responses to each of the comments raised.

Our responses (in red font) to the comments are provided below.

We look forward to your response.

Sincerely, Manuel Paneque (mpaneque@uchile.cl);

Reviewer #1 comments:

Fertilizer regimes reshape microbial interaction networks without altering sugarcane rhizosphere diversity

Comments:

Appreciate the author's thorough response and it was well done. A few minor things left to address after reading through the edits.

Major: Comments:

Major:

Only remaining more significant comment is just about the language when interpreting the network analyses. Network analyses are mathematical calculations by nature so first rule is that these calculations do not determine that co-occurrence results equal important/critical interactions (i.e., cooperate or compete etc) or central hubs are the absolute keystone species (it's limited by the sequencing and how analyses are performed—gives an idea for sure that needs more experimental validation). It could mean the conditions support certain microbes more than others which could lead to some of the potential interactions or vice versa or could be something else all together. The experimental structure does help to suggest that it is influenced by Ag management thus the environmental conditions in the soil or the interactions or a combination of both is what is leading to the microbiome structure but hard to delineate all of this based on sequencing even with multiple analyses on the sequencing performed. The key here is that these calculations can suggest or indicate how the conditions and potential interactions create the structure and composition so would focus on introducing that language (potential, indicative, etc.) throughout results and discussion when talking about the network analyses. Most of the minor points below will also point to specific areas.

Minor:

-Line 487—significant is used to describe difference between bacterial and fungal nodes—is this the correct word to use? Are there any statistics to reinforce?

R// Thank you for pointing this out. There are no statistical tests that support this claim, so the text was modified to “clear numerical predominance” instead of “significant”. Additionally, the text in the same paragraph was modified to suggest tendencies instead of claiming behaviors.

- Line 490-492 and some sentences below figure 5, some of this phrasing should be restructured. Network analyses/co-occurrence networks are mathematical in nature even with topological information so it is an assumption to say the fungal are the structure and bacteria provide the extensive function. That might be true but unclear without more characterization to validate that in my opinion.
- Much to my comments above—lines 570-575 is better language as interpretation with line 571 needing to be modified—not sure one can say from this that anything is ecologically significant to systems stability (could just say is a large portion of community structure which is still interesting). Ecologically significant to systems stability could be true or might not be—might be able to remove some of these individuals and others would fill in to maintain stability—would need to prove this. Key is highlighting how the analyses are indicative not absolute. Would keep following this pattern throughout.
- Similar comments to above, would tone down some language in 580 to 590—very interesting results but can’t say it is the ultimate structural backbone for example. Sequencing depth etc could be limiting on seeing the full picture. This could be a representation of the general or dominant core rhizosphere microbiome sure but need to be careful in this section about overreaching. Would need deep metagenomics to full disentangle further for the conclusions.
- Lines 923-1050—most of this language is good but would still be careful about some of the more definitive statements related back to the results noted above
- Authors have done well to strengthen the paper—just need to adapt some of the wording

R// We sincerely thank the reviewer for their valuable input and insightful comments on our work, as well as for their encouraging words regarding the improvements made to the latest version. In line with the reviewer’s suggestion, we have thoroughly revised the manuscript to improve wording, including the Abstract, Results, Discussion, and Conclusion sections. We have also carefully toned down our claims to ensure that our findings are presented as predictive trends rather than definitive ecological certainties, as further experimental validation is required. Regarding the specific line references, we encountered discrepancies between the reviewer's report and our manuscript's layout, making it challenging to map our responses point-by-point. We have made our best effort to address all concerns thoroughly; however, we kindly invite the reviewer to examine the revised sections throughout the full manuscript to ensure that all issues have been appropriately resolved.