

The revisions have substantially improved the clarity of the manuscript. I appreciate the authors re-evaluating their analysis of treatment-specific networks given the sample size. Identifying the core community consistent across treatments is a sound approach, given that the communities are stable across treatments, and I also like the strategy of identifying unique ASVs that respond to increments of N, P, and K. However, two issues remain that the authors need to address.

1. Figure 6 is not clear and does not accurately represent the results the authors describe. In Panel 6A, which number corresponds to the 18 unique ASVs mentioned at Line 640 that appear with increments of N relative to basal N? Panel 6B shows 49 unique ASVs present in P1 and P2 compared to N1, but the text at Line 642 reports 40. Panel 6C has a similar problem: it is not clear how the 6 unique ASVs identified in response to K increment are derived. Because four treatments are involved, the circular Venn layout cannot display all intersections and is missing some regions. I recommend a different visualization, such as an UpSet plot, which would represent all overlaps completely and resolve these discrepancies.
2. The unified global network is appropriate given the number of samples, but it means the study cannot assess whether different fertilization treatments altered microbial interactions. The discussion in Section 4.3 (Lines 910–922) makes claims that the analysis does not support and should be removed. Similar statements in the Abstract (Lines 21–24), Section 4.3 (Line 1070), and the Conclusion (Line 1083) are likewise unsupported and should be revised or removed.

Minor comments:

1. The control and blank labels appear to be interchanged in Table 3