The authors of the manuscript soil-2021-95 "Soil microbial community triggered by organic matter inputs associates with a high-yielding pear production" carefully revised the manuscript and supplementary materials according to the reviewers' suggestions, particularly in regards to the concerns that data does not allow to draw the conclusion that distinct microbial communities directly increase pear-yields. There are still some minor concerns I recommend to consider.

Furthermore, after revisiting the structural equation model again, I recommend to undertake a major revision of the SEM or to delete it. In general, the M&M section to the SEM does not allow to reproduce and understand how the SEM was built and whether it clearly supports the research question or not. However, I am not convinced that the SEM was built in a way it allows to identify what drives the differences in pear yield between the treatments, which was what the study aimed for, as indicated in the introduction and L 341. This is due to the following reasons:

1) From the M&M it is not transparent whether the paired approach was accounted for (for example by including a random effect for site using the lavaan.survey package). If not, the model will try to explain overall yield, not the increase or difference between treatments.
2) Across site variances in SOM content and pear yield are larger than between treatment differences.
3) The SEM Figure 7 revealed that SOM has an effect on yield mediated through Beta. However, beta diversity by PCoA largely differed across sites and did not show differences between treatments (Figure 3A) as previously commented. Which support my assumption, that the model is fit to explain overall yield differences, not treatment related yield increases. (Also, I miss information in the M&M on whether beta diversity (PCoA) in the SEM refers to PCoA1 or PCoA2 or is a composite of both.)
4) Overall, the SEM explained > 70% of variance in yield. However, it might only explain differences across sites but does not allow to conclude on how differences in soil organic matter content affect yield of yield-debilitating and yield-invigorating orchards.

The SEM has to be revised or the results and discussion section adjusted to indicate that the SEM explains differences across sites. The model as it current state does not allow the conclusion in L 451 – 455: "Worth to mention, soil organic matter was not directly linked to the yield in the constructed model, indicating that soil organic matter maintain the high-yielding pear production probably via the indirect way. Therefore, we proposed that yield-invigorating soils harbour unique bacterial communities that may improve soil biological fertility, which could be driven by soil organic matter and manipulated by keystone species (Chloroflexota) through altering the bacterial interactions."

L 71   Rousk et al. 2010 did not investigate microcosms (in the cited study).

L 98 - 105   Thanks for clarifying the definition of "yield-debilitating" and "yield-invigorating"
                treatments. Please revisit this newly written part for proof-reading and grammar
                checking. I recommend adding the mean ± standard deviation increase in pear yield
                to estimate the order of magnitude. While revisiting your manuscript, I wondered

why you did not include average crop-yield orchards as a control. You might want to add a comment on that.

L 163   introduce abbreviation as follows: Amplicon Sequence Variant (ASV)

L 231   This is not the reference I was referring to and citing the indicated study here is not meaningful. Sorry, I should have specified: Grace JB (2006) Structural Equation Modeling and Natural Systems. Cambridge University Press, Cambridge. Revise!

L 232   Add criterion for goodness-of-fit index.

L 243 - 246   Would be interesting to give more details on which chemical soil properties differed between YI and YD. I assume it is only organic matter content? Please, indicate statistical results which support that OM was higher in YI than in YD.

L 401 - 406   Thanks for adding a paragraph on what you mean by "small-world". This is helpful.

L 421   Revise! "…, was recognized as a key phylum in improving pear yield" → "…, was recognized as key phylum associated with higher pear yields".

Figure 7   Also see my comment on the SEM. I apologize I had overseen the direct path from SOM to yield, which was already included in your model in your initial submission. Providing an R2 for the whole model seems not meaningful. Instead, the R2 should be indicated for each endogenous variable in your model (i.e. beta diversity, microbial biomass, key taxa, network module hubs, network connectors and yield) indicating the variance explained by your model for each parameter.

Table S2   Thanks for providing a table on fertilisation regime. However, it is a bit confusing. Did YI and YD receive the same amounts of mineral fertilisers or do N,P,K values refer to a total (including N,P,K in organic fertilisers)? Please revise the Table so it becomes clear how much mineral fertiliser was added, and how much organic fertiliser. From the text I understood that YI orchards received less mineral fertiliser. Is that correct?

Figure S6   This is not the meta-model I suggested, however it helps to understand the underlying concept or your model.