

## ***Interactive comment on “Bacterial and fungal predator – prey interactions modulate soil aggregation” by Amandine Erktan et al.***

### **Anonymous Referee #2**

Received and published: 17 March 2020

General: In general I find this study to be well executed and of interest. Including trophic structure in our assessments of soils is an important and understudied topic.

While most of the work is well executed, the authors spend a large portion of their discussion talking about bacterial mucosal production, but this is never actually tested. If a huge portion of the work depends on understanding how trophic structure influences bacterial mucosal production, then it would be important that this is assessed. I would be hesitant to focus so intently on this interpretation, and spend more time addressing the various components you did test.

Additionally, I believe that the  $^{13}\text{C}$  portion of this analysis to determine differences in soil and litter derived C needs to be expanded on. This could be an important conclusion, but it is unclear how this work was done, and whether or not labeled litter

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was added.

Abstract: No specific comments.

Intro: In general, this is a well written introduction. The authors lay out multiple factors on how microbes and mesofauna influence soil aggregation. It is at times a bit repetitive though, consistently focusing on the lack of trophic structure assessment to soil aggregation.

Additionally, I believe that the authors focus on soil aggregation limits the scope of this study. The authors are assessing multiple components of the soil environment, and therefore, it would be ideal if they could expand their introduction of topics beyond soil aggregation. The authors explore the influence of trophic interactions on soil microbial community formation and on the incorporation of C and on CO<sub>2</sub> emissions. If the authors were more concise, they would have room to include additional dimensions to their work.

Methods:

Line 101: Can you clarify this detail a bit more? I think the point is that when you add mesofauna they introduce new microbial organisms, and to account for this you also added microbes to the control treatments, but I am not entirely clear on this detail. How did you detail the Predator associated microbiota?

I find the 13C-12C comparison protocol confusing. Could you expand your discussion of how you are able to differentiate between soil and litter sources? In particular, how are you assessing the final amount of 13C in your soils. Are you obtaining this information from GCMS work, or are you specifically measuring them using an isotopic analysis device? Additionally, I am unclear as to how you are able to ultimately differentiate whether the 13C in your sample came from litter or soil, unless you inoculated with 13C labeled litter.

Results:

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Are the control treatments truly just *E. coli*? I presume that because they were made from field soil, there is also a natural microbial community. This is not necessarily a problem, but if you are labeling these as *E. coli* only, that may be misleading.

Line 211: Awkward phrasing, maybe adjust to “Neither soil aggregate formation nor stability differed” and break this sentence up into two different sentences.

Lines 210-214: This paragraph starts with fungal results, but then also addresses other treatments. Maybe split this into two paragraphs, as it is difficult to follow the portion of the results in the second half of this paragraph.

Discussion:

While PLFA is an acceptable method, its ability to measure more fine scale changes in community composition is limited. It is possible that changes did occur, but they were not obvious with PLFA analysis.

Is it possible that your soils were water limited prior to the experiment, and that by adding water to the system, that alone was responsible for helping stabilize the soil aggregates?

Line 223: missing a )

Is the collembolan species used known to also feed on bacteria? If so, how would this influence the results?

Why are the CO<sub>2</sub> respiration amounts not mentioned throughout the study? It seems like this would be of interest considering that these metrics are often used to estimate microbial biomass.

Additional literature to consider including:

Bradford, M.A., 2016. Re-visioning soil food webs. *Soil Biology and Biochemistry* 102, 1–3.

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Bailey, V.L., Fansler, S.J., Stegen, J.C., McCue, L.A., 2013. Linking microbial community structure to  $\beta$ -glucosidic function in soil aggregates. The ISME journal 7, 2044.

Crowther, T.W., Thomas, S.M., Maynard, D.S., Baldrian, P., Covey, K., Frey, S.D., van Diepen, L.T.A., Bradford, M.A., 2015. Biotic interactions mediate soil microbial feedbacks to climate change. Proceedings of the National Academy of Sciences 112, 7033-7038.

Grandy, A.S., Wieder, W.R., Wickings, K., Kyker-Snowman, E., 2016. Beyond microbes: Are fauna the next frontier in soil biogeochemical models? Soil Biology and Biochemistry 102, 40-44.

Jiang, Y., Liu, M., Zhang, J., Chen, Y., Chen, X., Chen, L., Li, H., Zhang, X.-X., Sun, B., 2017. Nematode grazing promotes bacterial community dynamics in soil at the aggregate level. The ISME Journal 11, 2705-2717.

Lucas, J.M., McBride, S., Strickland, M.S.S., 2020. Trophic level mediates soil microbial composition and function. Soil Biology and Biochemistry.

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