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Interactive comment on “Metabolic tradeoffs and heterogeneity in microbial responses to temperature determine the fate of litter carbon in a warmer world” *by* Grace Pold et al.

Grace Pold et al.

apold@umass.edu

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Thank you for your helpful and insightful comments on our manuscript. Please find the reviewer comments in quotes, followed by our responses.

“Overall, the work is interesting and timely but results and conclusions were sometimes overstated. Simulations are not the same as observations and at best provide possibilities when all underlying assumptions are accepted as adequate to the goals of the project.”

Agreed. We have rephrased some of our results and conclusions to highlight the modeling nature of this study.

“Abstract: the next-to-last sentence was an important summary of the work, but it was inverted and complex to unpack. Consider rewording and maybe dividing into two sentences.”

Thank you. We modified the sentence to read “Litter C loss was exacerbated by variable and elevated CUE at higher temperature, which effectively lowered costs for extracellular enzyme production”

“The 2nd paragraph of the introduction was a good synopsis of the state-of-art for estimating CUE and logical argument for a more flexible approach.”

Thank you.

“The 3rd paragraph of the introduction makes a case for taxonomic variation in extracellular enzyme production with temperature that may affect growth efficiency, but it takes a couple of reads to understand this point. Consider revising to clarify.”

Thank you. We moved up extracellular enzyme production in the first sentence to make it clear that is what this paragraph is really about, and then re-wrote the rest of the paragraph.

“Also, the final sentence links rapid growth to more enzyme production, which seems counter-intuitive given that increased costs associated with producing more enzymes reroute resources from growth. This point needs more support.”

We see how it might be counter-intuitive because uptake is missing from this analysis. Fast-growing taxa need to take up more resources to maintain that growth. It doesn’t mean they are growing efficiently. Hopefully the revised paragraph makes this clearer.

“The rationale for the third of the selected suite of simulations isn’t clear. Is there some reason why bacteria and fungi might have opposite responses to temperature? This adds complexity to the work that needs justification.”

We have observed that there is a greater positive range of Ct values for bacterial isolates relative to fungal isolates in our laboratory study (in review); however, we have thus far been unable to determine what biological factors underlie this difference. So in the absence of a known mechanism causing differences in Ct range between bacteria and fungi, we explored the effect of potential differences in Q10 within the constraints of DEMENT.

“Did the last 5000 of 6000 iterations approximate steady-state?”

No. We have never managed to get DEMENT to consistently attain a steady state. In some instances a quasi-steady state can be attained for one or two random seeds (starting communities) out of 20. But this comes with the cost of the litter C stabilizing at a concentration so high the leaves may as well be diamonds and/or those same seeds not attaining a near-steady state once the temperature is increased in the model. So for all practical purposes, we did not find a steady state attainable with the model. This is consistent with earlier work with DEMENT (ex. Allison 2014, Frontiers in Microbiology).

“How many of the outputs were omitted due to unrealistically high litter accumulation?”

0 to 5 per scenario. We have added a row to table 2 showing how many runs were excluded from each scenario based on this criteria.

“Was there any obvious reasons why this happened, such as too little biomass or constrained enzyme production? This might be an interesting result.”

It is almost always due to taxon diversity loss. By chance, taxa capable of producing enzymes to effectively break down one of the substrate classes is lost, and the result is that litter component accumulates at or near the rate of daily litter addition.

“Line 114: what is “biomass-weighted CUE? “

‘Biomass-weighted CUE’ means that the CUE is calculated not as just the average for each taxon, but rather the contribution of each taxon to the final CUE calculation increases proportionate to the fraction of total microbial biomass that taxon contributes.

A definition has been added into the revised version.

“Why were richness and diversity calculated on different sets of data? they cannot be compared for insights to evenness, for example on line 138.”

Great catch – thank you. This was an unintentional carry over from looking at model stability. The values have been updated in Table 2 and the text.

“Line 135: I didn’t understand the statement. Was the dampening effect a result of extending the microscale model across a macroscale environment? The next line suggests not but refers to the current study instead of the citation.”

Yes – Weider et al. 2015 proposes that microscale models lead to more homogeneous predictions as they are scaled up to the macroscale because any given single parameter will lead to fluctuations, but that the variation in physiology averages out when different phenotypic populations can asynchronously respond to their environment. However, we found that introducing variability in the CUE temperature response – equivalent to sampling a greater physiological parameter space (or pulling from a macroscale-type pool of phenotypes) – increases uncertainty in the response of litter decomposition to simulated warming. We have broken up this sentence to clarify the intended meaning.

“Line 138: minor issue: MBC is listed as 0.15 in text but 0.16 in table 2.”

Thank you for catching the rounding error. The value has been corrected in the text.

“Richness and ËĞ diversity were not calculated on the same data, so this comparison is questionable.”

The values have been updated to represent calculations made on the same data.

“Lines 140-144: Although the explanation for these patterns is logical, cause-and-effect relationships are problematic given the complexity of this model, non-linear relationships among variables, and variations in drivers.”

Correct. We have added a sentence reiterating that this is a conjectured driver.

“Line 162: minor issue is the word in parentheses “positive”? ËĞ Figure 1 wasn’t easy to understand, especially the dots. Were they output or illustrative of some specific information? Didn’t figures 1G and 1H contrast fungi and bacteria? The revisions were better, but still confusing. “

Each dot represents a taxon. The figure does not represent model output, but rather is intended to show the experimental design for the simulations (ie whether Ct was fixed or allowed to vary in a scenario, and whether the values possible in the simulation depended on the number of enzymes a taxon had or its status as a bacterium or fungus). Additional text has been added to the figure legend stating that each dot represents one of 10 example taxa in the simulations, although 100 taxa were actually used in the model. We have also updated the figure (attached) as there was a mistake in the representation of fungal and bacterial values in scenarios E-H.

“Lines 182-4: The responses of kinetic parameters to temperature aren’t consistent among the available studies, and most studies report only apparent activities. So, this statement is more speculative than it seems.”

This is an excellent point. We have modified the language to clarify that the stated relationships are assumed in the version of DEMENT we used, although they do not always represent reality.

“Paragraph around line 190: Maybe I missed it but some of this information would help the reader better understand the purpose of some of the selected simulation treatments if provided earlier in the modeling description.”

Additional information has been added into the “Modifications to DEMENT” paragraph to demonstrate that some scenarios were included to maintain distributions of Ct and enzyme counts which were comparable, so that the effect of Ct could be parsed out from other drivers.

“Line 224-5: This sentence seems to conflate competition with CUE and enzyme costs, but this idea seems like it would be limited to differential responses of taxa rather than a generic response of all taxa to temperature. Right? In any case, the results of DEMENT are not necessarily proof of concept for the real world.”

[reference sentence: “Increased CUE is likely needed to offset the costs of extracellular enzyme production that allow taxa to remain competitive at elevated temperatures within the framework of DEMENT; however, there is a paucity of empirical evidence regarding the hypothesized correlations between temperature sensitivity of CUE and enzyme investment in soil systems.]

“Line 234: simulations show the results of a possible synergy within a modeling context, only. “

Agreed. We have added in this clarifying statement.

“Lines 246-9: Again, why were these scenarios chosen?”

A sentence has been added in: “All four scenarios were tested in order to isolate the effect of changing taxonomic domain-Ct relationships from simplychanging Ct or taxonomic domain independently.”

“Line 260: An alternative sensitivity analysis targeting individual model characteristics defining differences between fungi and bacteria would have been appropriate, nor would it take thousands of simulations to explore. “

This is correct. We did not try this, but our experience is that DEMENT becomes very unstable very fast when you tweak anything. Parsing out the drivers of the differences between bacteria and fungi would require not only changing parameters, but also the model itself, as three of the differences between the two groups are hard-coded into the model (motility, nutrient translocation, and how organisms divide). Therefore, we think the suggested sensitivity analysis is outside the scope of the present study.

“Line 267-8: This would be a good place to remind readers of the differences in fungi and bacteria that might explain this result. “

The sentence “Nonetheless, differences in C and nutrient translocation abilities, and in cell size, stoichiometry and turnover rates still defined the two groups.” was added.

“Line 290: Fitting between a range of -48 to +178% doesn’t seem impressive, particularly given some of the omissions. What about the omitted simulations?”

The omitted simulations still have a respiration response to temperature within this range, although the absolute values of respiration are ∼6% lower on average than the simulations which were not excluded. The language has been changed in the text to state that the simulated changes in respiration are narrow compared to the range of observed respiration responses.

“Line 291-3: This is the clearest, simple statement of the study results, and its buried here.”

Thank you. We have now reiterated it in the conclusion.

“Lines 301-3: Although interesting, this statement only adds another level of confusion. This paragraph isn’t needed. “

The paragraph from L296-305 has been removed.

“Fig. 2. Were the temperature responses of soil bacteria isolates on the 4 different media indistinguishable? Ditto for the soil community responses.”

Temperature response is, on average, the same for all media types for isolates. But substrate does matter for the temperature response of a given isolate. Soil community responses do differ based on substrate (ex Frey et al. 2013, glucose vs. phenol). Thus together, this indicates the potential for either species sorting or differential stimulation of communities at different temperatures. We have a manuscript in review on this.

“Fig. 3. How did continuous and discrete compare to heterogeneous or homogeneous? The revisions helped.”

Thank you. We replaced all the continuous and discrete language with heterogeneous and homogeneous, respectively.

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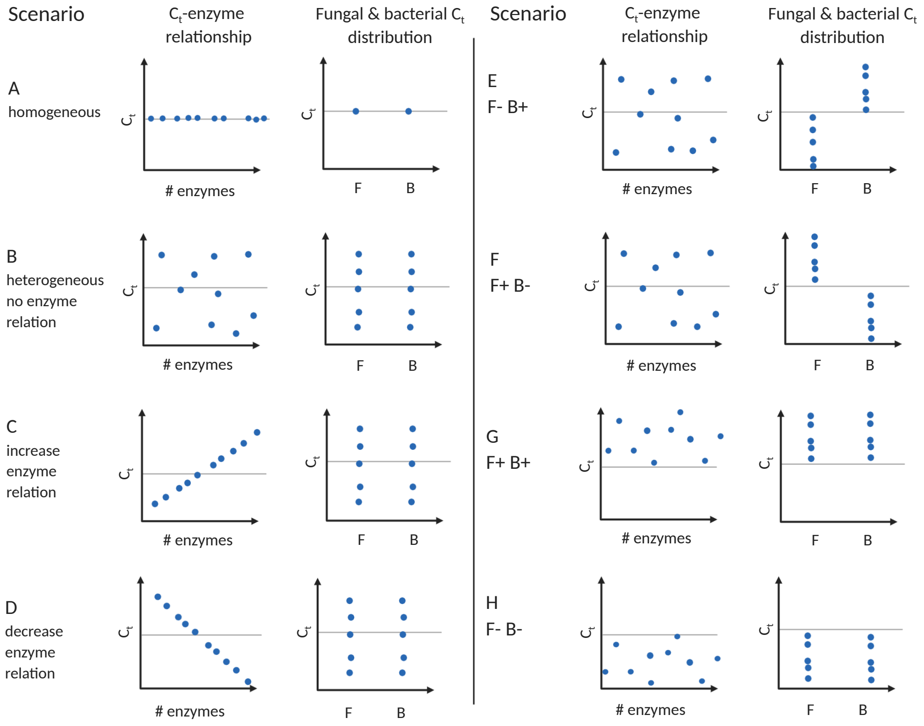

Fig. 1. Revised figure 1

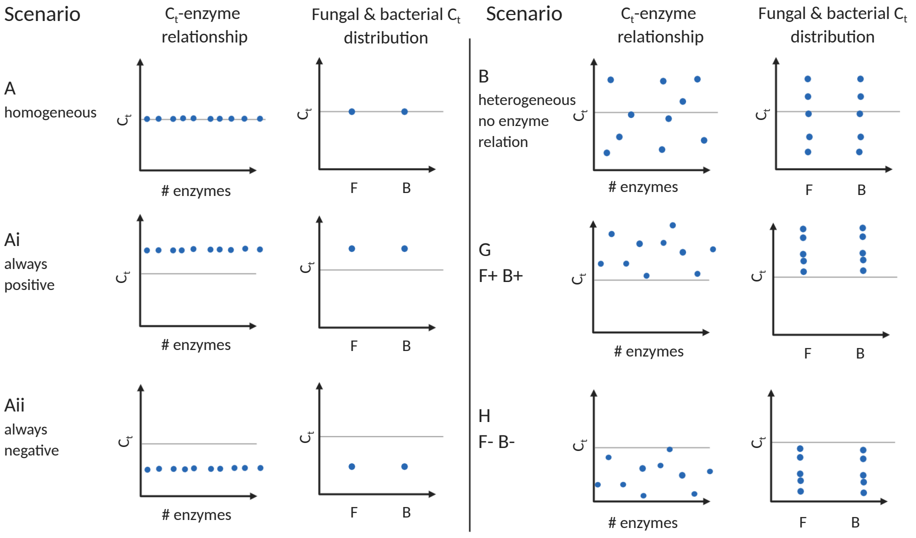

Fig. 2. Revised figure S1