

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.

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This study targeted the overarching question of how CUE variability across taxa mediates microbial community in decomposing litter under increasing temperature. This question reflects a broad issue in microbial system modelling in particular and experimental studies in general, that is, an either intentional or unavoidable ignorance of CUE variation among individuals in microbial community.

To address the question, Pold et al. modified the DEMENT, a spatially explicit trait- and individual-based microbial modelling framework, and explored a series of scenarios of variability of temperature sensitivity of CUE across taxa (Ct). These scenarios, con-

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strained by observed CUE variation, account for functional group (bacteria and fungi) and taxon-specific enzyme production variability. However, a few spots in the methods section could be further clarified. First, it would be better to provide an explicit equation showing how CUE is calculated in DEMENT:

$CUE = C_i + (T-15)*C_t$, where C_i is the intrinsic CUE, which is calculated as a function of baseline CUE and numbers of enzyme and transporter. This equation, though simple, would first make the writing much easier to organize and follow with regard to what specific changes have been modified in this study. This equation could be listed around line 80 on page 4. In addition, the first sentence in section 2.3 about Running DEMENT could be moved above to the very beginning of section 2.2 to introduce the modifications. Also, it might be better to include the DEMENT GitHub repository URL.

The results of Pold et al. clearly indicate the role of CUE variability in regulating the fate of litter C in response to temperature (and likely moisture). Although I overall agree with all of the results and discussions, there is one spot in the very beginning of the results section was particularly not clear to me: in the paragraph around line 130, first, to my understanding references to Figure. 1A and Fig.1B should be reversed. As regards the homogeneous scenario, the authors stated “all taxa had an identical temperature sensitivity that was equivalent to the cross-taxon mean (0°C-1)...”. I am not sure what exactly the constant C_r value is across taxon, 0, some value positive or negative, as illustrated in Fig.1 A, A_i , A_{ii} ? Also, throughout the discussion and results, the terms used to describe heterogeneity in the specific parameter C_r and homogeneous community are not easy to follow, and are sometimes confused with descriptions of other microbial models that are not microbial explicit. I recommend being explicit and consistent throughout the ms when using heterogeneity and homogeneity to describe the variation in C_r and across-taxon variability, as well as different models.

Overall, I believe this work sheds light on bench work and in particular modelling efforts in terms of great needs in better dealing with microbial system complexity. More specifically, I see this piece as a very helpful exercise facilitating the further development of

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DEMENT and other microbial explicit models .

A final note is regarding the definition of CUE. CUE in theory is an emergent property. However, CUE in DEMENT and other models, considering a modelling tradeoff of complexity vs. efficiency, is still more like a prescribed parameter. This means current modelling framework largely cannot address causes underpinning CUE variability. Therefore, if Pold et al. could acknowledge the difference between CUE in this study and emergent CUE somewhere in the manuscript, that would make this paper even more informative, though it already is. Combined, from the novelty and implication of question addressed through soundness of methodology to writing I support the publication of this study after addressing the minor concerns above.

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