

## ***Interactive comment on “Modeling transient soil moisture limitations on microbial carbon respiration” by Yuchen Liu et al.***

**Yuchen Liu et al.**

liu305@illinois.edu

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Major concern 1: My first major concern is the lack of measurements and evaluation of microbial biomass that is not difficult to do at all. Microbial biomass is one of the keywords in this study. However, I only saw an example (Fig.7) showing the transition between active and dormant biomass. The authors did not say if the biomass was measured values or just an illustration. By the way, the total biomass (6250 gC/m<sup>3</sup>) is pretty high according to Cleveland & Liptzin (2007), Wang et al., (2013) and Xu et al. (2013).

We thank the reviewer for their insight regarding the quantification of biomass and agree that the model we have developed points to the significance of this parameter

C1

value. Despite not having microbial biomass data for our incubations, we feel our modeling results are insightful and informative. In designing our experiments, we specifically sought to test the influence of variable soil moisture content on otherwise identical samples taken from the same soil core and depth, which supports the assumption that the biomass content of all subsamples is the same. Although the reviewer is correct in that the microbial biomass measurement is straightforward, our lab did not have the capability to make these measurements at the time that we conducted these incubations. Perhaps more importantly, our results point to is not the need for quantification of active vs. dormant vs. dead biomass through time, which is unfortunately more complex than measuring total biomass (as pointed out by anonymous referee #3).

To address this concern, however, we will add to section 5.1 stating that a key outcome of the present model is the need for measurement of active vs. dormant vs. dead biomass as a calibration for the DM model to natural settings. However, in the scope of this paper, model application to specific environmental conditions is not the emphasis. As such, we think the model (especially DM1 and DM2) treatment of the transition between active and dormant biomass under changing soil moisture is more important than the actual number of active and dormant biomass, since the model is capable of achieving any number of active and dormant biomass by modifying the parameters (a, b, and Sehalf). In Fig. 7, we show an illustration of the transition between simulated active and dormant biomass as the model responds to modification of the moisture content. This transient behavior of the biomass is a novel and vital contribution of the current study, since it uniquely produces Birch-type behavior rather than the simple monotonic decrease generated by simpler models.

We thank the reviewer for pointing out that the number of total biomass (6250 gC/m<sup>3</sup>) used in Fig. 7 is larger than reported in some studies. In fact, this is a typo from an earlier version where we were reporting the total biomass integrated across all depths. We have now corrected and updated the figure and associated text, where the total biomass is actually much lower and varies as a function of the soil depth (as a

C2

fraction of the total organic carbon in each depth interval). The correct values are 3037 gC/m<sup>3</sup> for shallow soil, 2126 gC/m<sup>3</sup> for intermediate soil, and 1367 gC/m<sup>3</sup> for deep soil, which are consistent with prior literature. In addition, we state that the fraction of active biomass is dependent on the soil moisture content regardless of the biomass population size. Based on the reviewers' suggestions, we will adjust Fig. 7 in order to better emphasize this point, such that the active respiring biomass is simply a fraction between 0 and 1 instead of an absolute value.

Major concern 2: Another major concern is the unusual organization of the manuscript. Generally, the model description should also be included in the 'Materials and methods' section, and the modeling results in the "Results" section.

We thank the reviewer for this observation and completely agree that there is a broad range of organizational approaches used in such model development papers. The reason we settled on this structure is that the development of the 4 models in increasing complexity is only justified when the datasets are already presented and used as a point of comparison to the simulations. Thus, we thought that splitting model development into an earlier section would leave readers with a poor understanding of why this hierarchical model framework is being developed. However, since all three anonymous referees have explicitly pointed out this problem, we've decided to change the structure to the more traditional model development within the earlier 'materials and methods' section and the model results within the latter 'results' section. The model description will be shortened, emphasizing the differences between the four models, and some of the currently detailed information will be moved into supplementary. In addition, the subtitles of the "Discussion" section will be modified to directly state the main take-home point of each subsection, focusing more on the big-picture questions. A new paragraph will be added after line 377 as a summary containing the key points of the discussion section. Another paragraph will be added to section "5.4 Future direction" specifically about how we are going to upscale the reactive transport model with the application of the DM2 model, for improved simulation of hillslope to watershed scale

C3

carbon cycling.

Minor comments: Please insert a citation to justify the 'Se dependent inhibition factor' (Line 466-485). The authors stated 'K-selection microbial subcategory ... utilize both labile and recalcitrant carbon', however, I did not see an equation like Eqs. 10-11 for the use of labile carbon by K-selection microbes. Did you assume there is no inhibition for (U<sub>i</sub>=lab, j=K)? The inhibition factor is used for (U<sub>i</sub> = lab, j = K) as well. Another equation is added to specify that. 
$$U_{(i=lab,j=K)} = k_{(up,K)} \times Bio_{(active,K)} \times C_{(sol,lab)} / ((C_{(sol,lab)} + C_{(half,lab)}) \times O_{(2(aq))} / ((O_{(2(aq))} + K_{half})) \times (((2Se_{sample})^{(1/3)} + 1) / 2)$$

Abstract: Though the authors addressed the 'dormancy model' was better than the first-order model, they did not explicitly emphasize the 'DM2' version that was actually the focus of this study. We will modify this statement (line 37) in the abstract to: "...we conclude that a dormancy-incorporated model featuring two distinct microbial strategists performs better..."

We will modify the last sentence (line 43) of the abstract to: "Thus, the multi-population dormancy-incorporated model may better simulate respiration of the whole soil, and is the main focus of this study"

Introduction: please add a brief review of dormancy models in addition to Manzoni et al. (2014). Another paragraph will be added to the introduction section to review the background of the dormancy model.

Line 315 & 374: I think, in both places, 'm' & 'n' should be 2 as there are 'two microbial communities along with two subcategories of organic carbon'. In both places, 'm' and 'n' are corrected to 2.

Line 358: please insert a citation for 'the Brooks-Corey equation' A citation is added for 'the Brooks-Corey equation' (line 361).

Fig.1: I didn't see the 'red star'. A star is added in Fig. 1.

C4

Table 4: I understand that the authors used 'effective saturation' instead of 'soil water matric potential' in Eqs. 8-9. Please justify the values for parameters 'a' & 'b' in Eqs. 8-9. The authors stated 'the b value employed by Manzoni et al. (2014) is used'; however, Manzoni et al. (2014) used  $b=4$ . We double checked the Manzoni paper and verified that the b value used in Manzoni et al. (2014) is 4.9 (Table 2 of Manzoni et al. 2014).

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