Review of Sihi et al. "*Comparing models of microbial-substrate interactions and their response to warming*," Biogeosciences Discussions, 12, 10857-10897, 2015.

General comments:

In this study, the authors explore a few simple model formulations of soil organic matter depolymerization and microbial substrate acquisition. They start with the 2-pool, substrate-microbe model from German et al. 2011 and add complexity, including partitioning microbial respiration into growth and maintenance terms, limiting increases in microbial biomass, and optimizing enzyme production and costs. They argue that the latter two formulations introduce mechanisms of "diminishing return" which act to limit microbial biomass growth in response to increased plant inputs and diminish oscillatory model behavior. I agree that such mechanisms suppress unlimited microbial growth that could occur from a closed positive feedback loop; however, to draw conclusions on system dynamics a more thorough analysis that explores a range of parameters must be undertaken.

As the authors mention, the behavior of models 1 and 2 is very similar [P10872, L23]. How does the additional complexity mathematically manifest itself in the emergent dynamics? Can the similarity be explained by the structure of the models? In the case of models 1 and 2, it seems that they share the same mathematical structure, in that model 2 can be reduced to model 1 as follows:

$$\frac{dS}{dt} = I + \lambda_d M - D \quad \text{where} \quad D = \frac{V_{max}\, S\, M}{K_E + S} \qquad \text{[same in models 1 \& 2]}$$

$$\begin{aligned}\frac{dM}{dt} &= (D - \lambda_r M)(1-g) - \lambda_d M && \text{[form of model 2]}\\ &= (D - Dg - \lambda_r M + \lambda_r g M) - \lambda_d M\\ &= D(1-g) - M(\lambda_r - \lambda_r g + \lambda_d)\\ &= \alpha\, D - \beta\, M && \text{[same form as model 1]}\end{aligned}$$

where $\alpha = (1-g)$ and $\beta = (\lambda_r - \lambda_r g + \lambda_d)$ for model 2. How do these relate to ε and λ_d in model 1, respectively? The authors briefly discuss concerns associated with adding parameters [P10873]. Is introducing uncertainty through extra parameters warranted here? The temperature sensitivity of the partitioned respiration model is indeed different, but the model structure is the same. Additional discussion on how the models relate when reduced mathematically would be a great addition to this manuscript. For example, why does model 4 with μ=0 behave so similarly to model 5?

Overall, this manuscript is well-written and presents an interesting modeling analysis. It could be improved by providing a perspective on future models and giving specific recommendations that the reader could take away for model development. Specific comments are given below to help clarify the analysis and manuscript.

Specific comments:

P10858, L8: It may be more appropriate to say that you "analyse five microbial decomposition models", as this is not a general analysis of all existing models, nor of models with multiple pools.

P10858, L10-15: How does your proposed model compare to models that explicitly represent enzyme dynamics with finite potential binding sites, such as the MEND and DEB models?

P10858, L15: "fast responses" in relation what?

P10858, L16: Why "short-term adjustment in microbial growth"? From the figures it appears that microbial biomass, as with carbon storage, reaches a new (long-term) steady-state.

P10859, L17: Can add citation for Wieder et al. 2015 here.

P10859, L20: The citation for Li et al. 2014 would be appropriate here regarding CUE response to warming across models.

P10860, L15: Although additional parameters were added to separate microbial respiration sources, the form of model 2 can be reduced back to model 1, as shown in the main comments above. Does the parameterization drive the difference in decomposition dynamics, since the model structure is the same?

P10861, L8: For clarity, it would be good to note that enzyme concentrations and microbial biomass go together and that you do not represent them as separate pools in the simulated differential equations; rather, you focus on the response of 2-pool, substrate-microbe models to warming. Can you confidently capture microbe and enzyme allocation/reaction/production dynamics without an explicit enzyme pool?

P10861, L19: It would be good to clarify that the "tendency" is the "derivative" when you first use it, as I feel that the latter is more commonly used among BG readers.

P10863, L19: To be consistent with the literature, it may be good to mention here that the final form you use for model 3 is a reverse Michaelis-Menten formulation, as in Schimel and Weintraub 2003.

P10865, L3: Is there a negative sign missing in Eq. 14? Otherwise, $\mathrm{dS}/\mathrm{dt} = \mathrm{constant} \cdot \mathrm{S}$ with a constant > 0 would increase exponentially. Also, please check your mass balance: if a $(1-\varepsilon)$ fraction leaves to respiration, then should a net $-(1-\varepsilon)$ be leaving S, since $-kS + \varepsilon kS$ in the mass balance?

P10865, L10: Which are the traditional models (cite a few) and how do they represent the temperature sensitivity of CUE? Often CUE decreases linearly with temperature in simple models and often 'traditional', Century-type models include more than one pool of carbon.

P10865, L21: What do you mean by tuning factors for $V_{max,1}$ and K_E and what are they tuned to for model 1 in addition to the German et al. parameters?

P10866, L7: I think "maintenance estimation" should be "maintenance respiration". Also, why one-third of the death rate? Please provide a reference or more reasoning.

P10866, L16: Here you say that you match the equilibrium values for CUE, M, S and decomposition. Matching equilibrium decomposition rates had not been mentioned before?

P10868, L5-15: This confuses me a little, as the two differential equations are coupled and respond together by necessity. The magnitude of change within each pool differs, as the pool sizes are significantly different. Please provide a bit more explanation and rationalization for this part of your analysis. In calculating the true equilibrium, $dM/dt = 0$ and $dS/dt=0$.

P10870, L22: Can you show mathematically how model 4 reduces to the linear model when $\mu=0$?

P10875, L18: Considering putting ($\mu=0$) for the negligible costs scenario, just to be clear.

P10876, L1: How realistic are the equilibrium values you fit to and how much do these vary in reality? If the parameters are fit to different values, how much might the dynamics and conclusions change? For example, the enzyme-substrate model in Allison et al. 2010 may or may not oscillate depending on the parameters.

P10878, L2: Is there a $+k_r[ES]$ term missing from the expression given for $d[E]/dt$? If the reversibility of enzyme binding removes $-k_r[ES]$ from $d[ES]/dt$, then where does it go? Also, reversibility is not shown in the diagram of Fig. 1.

P10878, L6: Please explain a little more in the text what P is and that it changes; i.e., that it is a rate proportional to microbial biomass.

P10878, L13: Why are you most interested in E_t? The Michaelis-Menten derivation using the quasi-steady state approximation for short-lived intermediates (i.e., d[ES]/dt = 0) is very standard in textbooks, but could be better explained here.

P10878, L15-16: This sentence seems to cut off prematurely, in which E_t … is?

P10878, L17-19: Consider using S_t for total sites instead of [S] which is also used as the transient free sites and is certainly not constant, otherwise d[S]/dt=0 would defeat the purpose. I think that the condition on S or S_t is not necessary for the derivation; Eq. (A2) = 0 by the quasi-steady state assumption of fast-reacting intermediates. Also note the missing period.

P10879, L10: Similarly to what? I would suggest moving P10879 L18 – P10880 L5 to above P10879 L10. It might be better to introduce the previous method and then what you do, instead of switching back and forth.

P10879, L13: Is Eq. (A7) missing a term? From $[E_t]$ = [E]+[ES], taking the derivative and substituting Eq. (A1) and (A2), you would get $\frac{d[E_t]}{dt} = P - \lambda_{E1}[E] - (k_{cat} + \lambda_{E2})[ES]$. This would then add a term to the denominators of (A8) and (A9) and carry through the expressions presented to (A25), etc. It would also be good to be consistent with your E_t and $[E_t]$ notation, as they are used interchangeably in the appendix.

P10882, L4: It would be nice to keep consistent notation for [S]; for example, $S_t = \theta([S] + [ES])$ where [S] represents free (available) sites.

P10882, L8-9: Can you explain a bit more why you take a Taylor series expansion (linearize) around the total sites S=0 versus linearizing around the equilibrium S? Also, you alternate between k_E and K_E.

P10882, L12: Could you explain why the S/θ term is much smaller than E_t and K_E (as on P10883, L1) and dropped from the denominator of Eq. (A24)?

P10884, L5: Is the final expression missing an M in the numerator?

P10885, L1-3: If P is a function of M as before, then M can also be written as a function of P. When taking the derivative of G in Eq. (A32) with respect to P, does the $\lambda_r M$ term come into play? Similarly with substituting a function of M for P in the denominator of D (A35) when determining if an optimum exists.

P10892, Table 2: For model 4, the value of K_p is not given, does this mean that it carries over from the fitting of the other models? For clarity, please add μ to the table where Pc/D is given for model 4.

P10893, Table 3: Should the short/fast time scale and long time scale have the same conditions (namely, S = eq. S) in the caption? Please clarify the methodology in the caption.

P10895-10897, Figures 2-4: Could you include a short descriptive model name for the four models in the legend or in the captions and briefly discuss why you chose a logarithmic x-axis? The log axis makes it harder to think through the dynamics and build intuition for shorter time scales; consider changing to a regular axis. 1,000 years is very long! Also, it looks like models 4 and 5 have the same orange color in the legend. Please make sure the five colors used are clearly distinguishable.

P10897, Figures 4: Could you include a short description of "apparent Q10" in the figure caption, as in the main text?

Technical corrections:

P10858, L5: “sufficient” should be “sufficiently”

P10859, L11: Remove the word “a” to read “to more complex dynamics”

P10860, L20: Sentence fragment – consider revising to: “models, each of which carries a single soil organic matter pool…”

P10862, L1: “represented” might be a better word choice instead of “parameterized” when referring to the mathematical form (structure) of a process.

P10862, L21: Consider changing “They dynamics…” to “The microbial pool is characterized by…” or if keeping the current sentence, change “is” to “are”

P10864, L11: Consider changing “parameterized” to “represented” again.

P10867, L8: Remove “the” from before model 4 and consider replacing “…and expressed them as…” by “expressed as”

P10868, L14: “response” to “respond”

P10868, L23 – P10869, L1: Check sentence punctuation and rephrase; e.g., “response to warming: all catalytic…”

P10869, L13: Consider changing to “… biomass also converges…”

P10870, L19: Consider changing to “warming-induced increase”

P10874, L8: Missing the word “of” in “a surplus of free enzymes”

P10874, L23: Remove the word “they” from “that relate to”

P10874, L27: Add the word “with” in “occur with infinite enzyme…”

P10875, L7: Add the word “the” in “found in the…”

P10875, L21: “… by introducing a variable…”

P10878, L1: Dynamics is plural, so “dynamics… are”

P10878, L6: [S] “is” instead of “are”

P10879, L6: Note the missing space.

P10879, L6: Remove the comma in “we assumed that DOC…”

P10881, L3-4: Are $\lambda_{E1,0}$ and λ_{E1} the same? It looks like there may be a notation typo.

P10882, L14: No need to capitalize “Equations”

P10883, L4: Consider changing the wording of “evaluate end member” to, for example, “evaluate the following scenarios”

P10883, L15: The word enzymes should be plural.

P10884, L11: Change wording to “where P is the…” and also V_{max} “is…” versus “may be…”