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# ***Interactive comment on “Multiple soil nutrient competition between plants, microbes, and mineral surfaces: model development, parameterization, and example applications in several tropical forests” by Q. Zhu et al.***

**Q. Zhu et al.**

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Response Letter

Title: Multiple soil nutrient competition between plants, microbes, and mineral surfaces: Model development, parameterization, and example applications in several tropical forests

General Response: We would like to thank the two anonymous referees and T. Wutzler for their constructive comments. Special concerns came from the two anonymous

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reviewers about the “constant enzyme abundance assumption”. In this revision, we modified our model so that plants are able to dynamically adjust their nutrient carrier enzyme abundance according to their fine root biomass. Sensitivity analysis, model calibration, and evaluations were completely re-done. Since the fertilization experiments we examined were short-term (24 or 48 hours), plants were not able to adjust their competitiveness and we therefore did not see large difference between the new and original models. However, allowing the plants to adjust their competitiveness did affect plant nutrient uptake over longer time periods (e.g., seasonal). The model modifications suggested by the reviewers give the model great potential to better represent nutrient competition among various nutrient consumers.

The response letter is organized by (1) reviewers’ major comments; (2) authors’ response. Minor reviewer comments (e.g., typo) are not listed here. We have carefully checked the entire paper and incorporated those specific minor comments.

1. Zhu et al. (2015) did an excellent job at developing the N-COM model. I enjoyed reading their manuscript starting with their motivation on why current ESMs do not represent the competition between different microbial groups, plants and soil matrix for nutrients realistically. Their innovative ECA approach (Equilibrium Chemistry Approach) is very well suited for dealing with the multiple interactions between nutrients, plants, microbial groups and soil minerals. Overall, the manuscripts is well structured and a delight to read. It will be exciting to see N-COM implemented in a microbe mediated SOM decomposition model.

Response: Thanks so much for your positive feedbacks.

2. From the description in section 2.3 you cannot tell, if the Bayesian calibration of N-COM is entirely proper. It seems that you ran one Monte Carlo Markov Chain for 50000 iterations. You claim that you reached convergence, but you could provide the readers with a trace plot of the MCMC (e.g. in the Appendix).

Response: To address this reviewer concern, we added a tracer plot (Figure A1) that

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shows the evolution of model parameters during MCMC sampling. We also performed two replicated MCMC calibrations (with different random number seeds).

We noticed that the some of the parameters were not well constrained, which was reflected in their relatively large posterior uncertainty and small uncertainty reduction. We argued that the non-convergence resulted from data paucity rather than a short MCMC chain. For example,  $k^{\text{plant\_NO3}}$  is the least constrained parameter because there were no NO<sub>3</sub>- pool size data. We have added more discussion about this issue in Section 3.1.

3. In section 3.1, you state that the posterior parameters were irregularly distributed. Nevertheless, you fitted a normal distribution to the posterior sample ( $n = 1000$ ) of parameters. You can, however, directly use your sample from the posterior to make inferences about the mean and standard deviation (or maybe better median and interquartile range). I would recommend to use the second halves (your last 25000 iterations) of your chains to directly calculate your  $\sigma_{\text{posterior}}$  for the estimation of the uncertainty reduction.

Response: Thanks for your recommendation. In the revised manuscript, we used the last 25000 samples of the MCMC chain to infer our posterior model parameters (mean and standard deviation).

4. In Figure 2, your binning of the posterior sample is quite broad. Could you use smaller bins and maybe use a larger sample from your MCMC (e.g. second halves of the chains) to construct this plot?

Response: We updated Figure 2: (1) prior model parameters distributions (log-normal) were plotted for comparison; (2) posterior model parameters were divided into more bins. We also added another figure (Fig. A2) to show the fitting of posterior model parameters to Gaussian distribution, based on which the mean and variance were obtained.

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5. I would welcome some additional discussion, if a dynamic simulation of enzyme abundances for the different consumers could result in a time-varying apparent relative competitiveness. For the purpose of the present study, you assumed that all consumers have the same enzyme abundances (P4068,L15). Does this assumption simply eliminate the time-component from competition between the different consumers? Does this mean that with your approach you are able to represent the long-term competition between consumers?

Response: To address this, and the other two reviewer similar concerns, we modified our model structure so that plants and decomposing microbes were able to adjust their nutrient carrier enzyme abundance (as described above). The enzyme abundance of plants and decomposing microbes were scaled by the fine root biomass or potential immobilization rate, respectively.

6. You could try to improve how you introduce the structure of the five SOC pools. In Equation 4 you introduce  $F_{moveC\ i,j}$ , but the link to  $f_{ij}$  and  $g_i$  (Table 2) could be presented more clearly to the reader.

Response: Sorry for the confusion. Following Equation 4, we added more detailed description about how to calculate  $F_{moveC\ i,j}$  based on  $f_{ij}$  and  $g_i$ .

7. In Figure 1, you use the terms “MIC NH<sub>4</sub> uptake” and “MIC NO<sub>3</sub> uptake”; in the text, however, you mostly use the term “immobilization”. It would be great if you updated Figure 1 to match the terminology used throughout the paper.

Response: Thanks. To ensure consistency, we updated the entire manuscript (including Figure 1). “Microbial NH<sub>4</sub> and NO<sub>3</sub> updates” were replaced by “NH<sub>4</sub> and NO<sub>3</sub> immobilization”.

8 other minor comments In line 21, p 4064, you state that carbon has the units “g C m<sup>-3</sup>”, while in Table 2 it is “g C m<sup>-2</sup>”. Please clarify.

Response: In line 21, p 4064, that was a typo, we have corrected it. The model is not

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vertically resolved. All the fluxes and state changes are calculated in terms of “g m<sup>-2</sup>”.

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