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Interactive comment on "A numerical analysis of the role of the microbial loop in regulating nutrient stoichiometry and phytoplankton dynamics in a eutrophic lake" *by* Y. Li et al.

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Authors response to review comments by A Dietzel.

The authors would like to sincerely thank Dr Dietzel for her constructive comments and suggestions made regarding our manuscript. A detailed response to each of the comments is given below.

GENERAL COMMENTS:

COMMENT: The paper is relevant for the research area of lake water quality modeling, specifically for the aspect of how to describe the processes related to the bacterial

community properly. As typically the effects of the microbial loop are described in a very simplified way in most lake models, the paper is a very valuable contribution to its field. In general, the paper is interesting, well-structured and written well. It seems that the presented study was conducted thoroughly. My main concerns are related to the validation of the model and the related comparison of its three different sub-models/configurations.

RESPONSE: Thank you for the positive comments about the usefulness of this modelling study. The concerns about validation are expanded upon in the individual comments below.

COMMENT: It is not clearly stated, but it seems that the model parameter values for all three configurations are mostly taken from an earlier study (Table 4) of the same lake model (Gal et al. (2009)), which includes the most detailed bacteria model configuration (BAC+DIM). I am wondering if the two newly presented model configurations only perform less well, because they are not calibrated separately and the parameters from the BAC+DIM model do not fit to the alternative model configurations. It should be explained how the older version of the model was calibrated and if and how the newer two model versions were calibrated as well. If there was no additional calibration done, the choice of parameter values for the NOBAC and BAC-DIM configuration should be justified.

RESPONSE: The model was originally calibrated in Gal et al 2009, which furthered earlier attempts (e.g., Bruce et al 2006) and the reviewer is correct that this was equivalent to our BAC+DIM simulation. The parameter choices for this simulation were not arbitrary, but as outlined in the response to Dr Robson, the majority of the parameters were well informed by site-specific research investigations.

In preparing this study, the authors discussed at length about whether to : 1. Use the model calibration as is and compare between the three model configurations, or 2. Calibrate separately for each of the three configurations. While there is merit to entirely

separate calibrations it would not allow a clear comparison between the three configurations as we would be conducting in essence a multi-factor experiment without the ability to hold the rest of the model constant and focus on the role of the microbial loop / bacteria in the model. The chosen strategy is predominantly like 1 outlined above, but with some elements of 2 - therefore we have aimed to keep the model parameters as constant as possible for the alternate configurations (bearing in mind sediment and phytoplankton related parameters and many others would be hard to justify making changes), and re defining some to ensure the general carbon flow pathways in the model configurations were comparable.

This justification for our strategy is provided in Table 4, but we acknowledge we can make this strategy for using the model as a 'virtual laboratory' more clear. That is, it was not our intention to get the structure that gave the minimum error, but to demonstrate – using parameter values that are commonly adopted within the literature – that choices of model structure will lead to different predictions, but also us to isolate different mechanisms within the nutrient cycles.

COMMENT: If the main purpose of the paper is to find out, which model configuration is closest to reality, this should be supported by measurement data. It does not seem to be enough to state that the NOBAC and BAC-DIM configurations had higher errors than the BAC+DIM simulation. This should be shown by a direct comparison with measurement data and/or by a quantitative comparison of errors, e.g. RMSE.

RESPONSE: In response to this concern, we direct the reader to our reply to similar comments to Dr Robson. We also emphasize that our objective was not really to provide a model with the smallest error, but by conducting experiments using the model as a virtual laboratory to build a model that fits with the theoretical workings of the lake ecosystem. We aimed in this paper to demonstrate that the base model simulations were realistic, even if somewhat idealized, and then to try and learn about reality via the questions we raised in the introduction – something that would be extremely difficult to do empirically.

We propose to add the following statement to our introduction to more clearly define the context and motivation for this paper:

"Earlier versions of the model were thoroughly calibrated to field data and process measurements (Gal et al., 2009, Li et al 2013). Here we use the best-calibrated model version to explore the impact of changes in bacterial dynamics on the ecological system. Within a well-validated set of core ecological process parameters determined elsewhere, we vary the structure and function of the microbial loop to assess how these changes would impact broader ecosystem biogeochemistry. While this is essentially a theoretical study, it remains nested in a robust modelling framework that rests on strong process understanding of the Kinneret system."

Nonetheless, we acknowledge the issue of validation and as highlighted in our response to Dr Robson, we will endeavor to improve the level of detail in the model error statistics but highlight we feel this wont add a lot of extra weight to the message over and above the model error analysis already presented in Gal et al 2009 but will extend the understanding of the different microbial loop alternatives

SPECIFIC COMMENTS:

1) p. 19733, lines 10-12 / p. 19734, lines 22-27 / p. 19738, lines 10-17: I found it difficult to find out which mechanism is described in which microbial loop sub-model. Table 2 helps a lot to find out, but it should be also clarified in the text. For example, the order of the listed potential mechanisms is not the same in the abstract and in the introduction, numbering could be done consistently and it could be stated that the bacterial provision of an alternative food source for zooplankton is somehow integrated in all three sub-models.

RESPONSE: Thankyou for this suggestion, we will endeavour to improve the clarity of the simulations so readers can more clearly distinguish between them.

2) p. 19743, lines 3ff: for a thorough comparison of the three model configurations and evaluation of the importance of specific processes, the parameters sensitivity analysis should be conducted for the three model configurations and not only one.

RESPONSE: We argue throughout the paper that the BAC+DIM is the most compatible model structure with theory and (based on parameters) provides the best-fit with data. We therefore used this section of the paper to then highlight the most sensitive parameters and pathways in

the microbial loop based on this particular model configuration. Whilst it would be ideal and is certainly possible to do a sensitivity analysis for all simulations, we felt this would add an extra 6 sub-plots that would not be of a lot of value since we argue those configurations are not capturing the essential dynamics.

3) p. 19744, lines 6ff: As mentioned above, "matching the field data" should be proven.

RESPONSE: As outlined earlier, we will add validation information as supplementary material to the revised manuscript and modify this section to point to that material so the model comparison with observed data is possible.

4) p. 19744, lines 11ff: It is not clear to me what the comparisons like "reduced", "higher", "increased" refer to in this section. Is that the comparison of the three model configuration simulations among each other or to field data?

RESPONSE: These are referring to changes of simulation results relative to the BAC+DIM simulation. We will clarify to avoid confusion.

5) p. 19744, lines 16/17: the errors or a direct comparison of model results and measurement data (e.g. added to Fig.2) should be shown.

RESPONSE: Refer to above comments.

6) P. 19755: the final conclusions of the shown results could be presented a bit more clearly and pronounced (as done on the following page).

RESPONSE: Thankyou for this suggestion. We will endeavour to clarify as we update the discussion to the review comments in the revised version.

7) Table 4: Are the parameters, for which the authors refer to the earlier study, the same for all three model configurations? How were those parameter values chosen (manual/automatic calibration)?

RESPONSE: The parameters are the same for the 3 configurations except for the differences outlined in Table 4 (eg see Kz), and the rationale for this is as summarised above. The original calibration was manual (refer to our response to Dr Robson) and we will clarify and update this in the revised manuscript through addition of a validation section as supplementary material.

8) Fig. 2: As mentioned above, a comparison with data would help.

RESPONSE: As above.

TECHNICAL CORRECTIONS:

1) p. 19737, line 25: for clarification, "A" as the specification of the phytoplankton state variables should be added after "five phytoplankton groups", as done for zooplankton in line 2 on the following page.

RESPONSE: Agree, will be amended in the revision.

2) p. 19741, line 17: "DOC" should be a subscript in UDOC

RESPONSE: Agree, will be amended in the revision.

3) p. 19749, line 18: there is one "accurately" too much in this line 4) p. 19751, line 20: "increases" should be "increase"

RESPONSE: Agree, will be amended in the revision.

5) p. 19755, line 18: "therfore" misses an "e"

RESPONSE: Agree, will be amended in the revision.

6) Table 1: Are "N_A" and "N_Z" also "simulated variables"?

RESPONSE: Thanks for highlighting this. They are "parameters" of the model but not state variables – we will update the terminology in the table.

7) Table 1: Where "CAEDYM names" are missing, are they the same as written in "Notation"?

RESPONSE: Where they are missing that means they are not "state variables" subject to advection and mixing, but either derived from state variables (for the purposes of the analysis or comparing with data) or as above in point 6.

8) Table 4: "N" = "N/A"?

RESPONSE: Yes, will be corrected

Interactive comment on Biogeosciences Discuss., 10, 19731, 2013.