

Interactive comment on “Dissolved organic matter release by phytoplankton in the context of the Dynamic Energy Budget theory” by Eleni Livanou et al.

Anonymous Referee #2

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This work presents a DEB-based model purporting to describe the production of DOM by phytoplankton under N or P stress. The general topic is important, and does align with the subject areas of the journal.

The model is shown to broadly align with a single data set for N-limitation, and is then operated under different conditions with an aim to consider differential consequences of N vs P limitation. I have the following general observations upon this work which I am afraid makes me question the usefulness of the approach and application.

Firstly, the structure of the model, as shown in Fig.1, is contrary to that which aligns with the physiology of real phytoplankton. Indeed the structure, with its partitioning of

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inorganic N and P and within different organic structures appears most strange. I find this very worrying. The model is complex, and claims to be mechanistic (as are DEB models), but it just does not tally.

There are also other facets of the model description that are of concern to me: the stoichiometry of cellular components (which is not shown to collectively reproducing observed changes in cellular C:N:P); the explanation of internal ammonium (which in reality is essentially zero) and of internal nitrate (which is also usually very low, and indeed contrary to some reports can never attain a significant % of cell-N because of nitrate-solubility issues) and the interactions between ammonium and nitrate usage (which perpetuate various classic misleading literature articles); the whole rational for DIN and DIP release (perhaps a hangover from the heterotrophic origins of the DEB concept?) appears to be unsupported unless the simulations are running in a light-dark cycle (are they?); comments about cell size variation gloss over the fact that P-limited cells are very much larger than nutrient-replete cells, and N-limited cells are much smaller; and so on.

I therefore have a serious problem with the conceptual basis of the model. The authors have also not explained why their approach has any benefits over any other approach.

The model is shown to fit against only one data set, for a diatom, growing under N-limitation. That data set comes from one of those presented in Flynn et al. 2008, who also conducted a (solely N-based) exploration of the description of DOM release. Very strangely there is no comparison with the utility of this model with that of Flynn et al for N-based scenarios; why have the authors not done this?

Further, while this article considers P-limitation (Flynn et al did not) it does so using a framework that is unproven, and hence one that must remain speculative. Indeed, no evidence is presented for how the model handles P-limitation, or indeed how cellular C:N:P varies under N and P limitation. If the DEB model had at least been shown to handle general C-N-P interactions (there are various data sets available to which to

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conduct such a comparison) then this would not be of such concern.

The model is sold for potential deployment in ecosystem simulators but it appears incomplete for such usage, lacking acclimative Chl:C (which is important in DOM modelling as a failure to rapidly modulate C-fixation promotes DOM release) and indeed it has not been shown how the model reacts to light-limitation (which is of importance during bloom development and thence to DOM release).

In section 4.2 there is a commentary about P vs N –limitation; I suggest this requires some common basis for reference (perhaps u/Umax?). As it stands the statements appear ambiguous and potentially incorrect.

In section 4.3 is a discussion about forms of DOM. I find the description of DOC, DON, DOP used in this article somewhat confusing; DON and DOP are also components (subsets) of DOC. The discussion lacks a consideration of CNP of DOM forms, and also (again) a comparison with the outputs of the Flynn et al. effort. Just now it is not clear to me what advantages this DEB-based approach may have over any other model. There are also some strange (to me) comments concerning glucose and polysaccharides in this section.

There are various detailed comments that I could give to help the authors, but just now I think that I need to see:

- i) a more acceptable conceptual basis (I do not believe that Fig.1 does this),
 - ii) a demonstration that the whole model can describe dynamic C:N:P experimental data series,
 - iii) a more rigorous set of comparisons with Flynn et al (whose data they use, but then for some reason never further discuss in comparative terms even in the context of N-limited growth) and indeed with the functionality of other models (ERSEM springs to mind).
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