

Interactive
Comment

Interactive comment on “Competition for inorganic and organic forms of nitrogen and phosphorous between phytoplankton and bacteria during an *Emiliana huxleyi* spring bloom (PeECE II)” by T. Løvdal et al.

Anonymous Referee #1

Received and published: 6 November 2007

General comments

This paper presents results from a robust study and is, in general, well written. The uptake of various N-substrates by phytoplankton and bacteria is something that has already been studied quite a lot. The number of substrates used is quite limited (ammonium, nitrate and leucine), and the size fractionation method used to discriminate between uptake by algae versus bacteria basically did not work (due to a substantial fraction of the bacteria being attached to larger particles). The more novel features of this study are that uptake was measured during the development of a (artificial) phy-

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toplankton bloom (with changing availability of N and P) and the link of DIN and DON uptake with that of DIP and DOP.

The data presented in this paper feel a bit "over calculated" and more complex than necessary. For me, it would help to also see some figures with rough ("primary") data before making the step to "secondary" parameters like "affinity", "turnover times" and "biomass specific affinity". For example: I find Fig. 4 far more understandable and interesting than the other Figures. The calculation of these "secondary" data includes quite a few assumptions and conversion factors and extra uncertainty due to the methodological limitations discussed at the end of the discussion. In the end, the actual conclusions from these data are quite limited (see abstract). I wonder if these conclusions can also be reached in a more direct way that is easier to understand. In short: I suggest to first present data in a more basic way (e.g. uptake rates and the related contributions of the different substrates to their summed uptake) and then make the step to affinity for the different substrates (and clearly explain what these parameters represent exactly).

I think the use of uptake of a single amino acid (leucine) as a model for total DFAA or even total DON uptake is tricky. Different amino acids may have different uptake pathways and affinities. Also see comment below. In addition, data in Grossart et al. 2006 show that there was a large DCAA pool present, which is not even mentioned in the discussion.

Specific comments

- page 3345, line 4: Why use the term "osmotrophs" instead of just something like "bacteria and phytoplankton" as used in the title?
- page 3346, line 25: Why talk about cyanobacteria in detail here while these are not relevant for this paper?
- page 3350 (M&M uptake 15N compounds): I think the occasions where extra (un-

labeled) NH_4 was added should be specified more clearly since this is where you measured potential NH_4 uptake rates rather than true ambient uptake rates. Specify the " NH_4^+ concentration measurement limit". Later in the paper (page 3353), it is mentioned that NH_4^+ concentrations were always $< 0.02 \mu\text{M}$, indicating that the detection limit was $0.02 \mu\text{M}$ or lower. This means that addition of $0.5 \mu\text{M}$ extra (unlabeled) NH_4^+ was really high.

- page 3351, lines 4-5: "uptake rates were estimated from the regression relationship between uptake and time ... "> how is "uptake" defined here and how was it calculated from $\text{at}\%15\text{N}$?

- pages 3353-3354 (Results nutrients and bloom development): For me, it would help to have the nutrient concentrations, bacterial numbers and Chl a concentrations in one Figure or table for a good overview and direct comparison with the other figures. These data are now hidden in the text or need to be filtered from Grossart et al. (2006).

- page 3355, line 25>: In my opinion, Table 1 does not really add any additional interesting information that is not already included in Fig. 4.

- Discussion: It may be helpful to structure the discussion a bit more. For example by dividing the discussion into subsections (with separate headers) that each deal with one of your research questions.

- page 3359, line 11 to page 3360, line 4 and Figure 6: To me, this section feels a bit too much and not essential/relevant for this paper.

- page 3360: I makes more sense to discuss the various methodological limitations at the beginning of the discussion rather than at the end.

- page 3360, line 20: How long did the filtration take ?

- page 3361, line 4-5: The letswart et al. paper tested individual amino acids as single N substrates. In that case, growth of the bacteria and algae is dependent on their ability to synthesize other AAs required for production of their biomass (proteins)

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from these single AAs. It is quite tricky to translate these results to a field situation where the available DFAA pool has a composition that is similar to that of the microbial biomass as thus requires only very little conversion, making it a much more efficient N substrate.

- page 3361: When you discuss DNA and ATP as potential N substrates, then DCAAs should also be discussed. Fig. 2 in Grossart et al. (2006a) shows high DCAA concentrations!

- page 3362, lines 5-10: This seems like a very general/broad conclusion (DIN v.s. DON) based on uptake of a single amino acid. In addition, the finding that bacteria have a relatively high affinity for amino acids while algae have a relatively high affinity for ammonium is not exactly new.

Technical corrections

- The "(PeECE II)" in the title is not highly relevant so can be deleted.

- page 3350, line 2: "gaze" should be "maze"

- page 3350, line 19-20: "One umol L-1" should be "1 umol L-1"

- page 3352, line 25: I do not think "contributed" is the right word to use here > attributed ?

Interactive comment on Biogeosciences Discuss., 4, 3343, 2007.

BGD

4, S1828–S1831, 2007

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