Biogeosciences Discuss., 9, C6080–C6086, 2012
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Biogeosciences Discussions

Interactive comment on "A ^{13}C labelling study on carbon fluxes in Arctic plankton communities under elevated CO_2 levels" *by* A. de Kluijver et al.

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Received and published: 30 November 2012

We thank the reviewer for her/his positive review and constructive comments that helped us to improve the manuscript. The suggestions and comments (s)he raised are answered below.

General comments :

Referee: This study examined the effect of CO2 on the flow of 13C, added as bicarbonate, through various components of the plankton and into sinking material in mesocosm experiments. The authors explored these flows by measuring 13C in lipids specific (more or less) to various types of plankton; the 13C content of large zooplankton was assayed directly with animals picked out by hand. The authors emphasize that

their experiment is novel because it was with Arctic waters, but in fact, it should interest readers working in all environments. This is an excellent, potentially very important study. My main scientific concern is prompted by a stray comment on page 8583, "Heterotrophic (gram-positive) bacteria" (this should be "bacteria", not the adjective, "bacterial"). As mentioned in the specific comments below, this implies that the lipids examined by the authors are found only in Gram-positive bacteria (Gram should be capitalized), which are a small fraction (<10%) of the total bacterial community in the oceans. But the authors observed that a large fraction of 13C was found in these bacterial lipids. How can this be? Are these lipids actually in more than just Gram-positive bacteria?

Reply: The main concern of this reviewer is that we used only markers for gram-positive bacteria as representatives of the bacterial community. We have done this for some reasons. 1) The markers for gram-negative bacteria (16:1ω7c, 18:1ω7c, 18:1ω9c) are not specific for bacteria and also occur in some phytoplankton (Dijkman and Kromkamp 2006). 2) Although branched fatty acids are more abundant in gram-positive bacteria, they are also found in some gram-negative bacteria, at least in soils and in Antarctic marine bacteria (Zelles 1999, Nichols et al. 2005). 3) We looked into the fatty acid labelling pattern of both groups and they showed a similar labelling pattern (figure 1 below). Therefore, we consider the use of the gram-positive markers representative for microbial dynamics. We will add a few lines to material & methods/discussion to communicate this to the reader.

Referee: Another general comment is that the writing is a bit rough at times and often very dense with lots of numbers cited in the text. The Abstract is a disservice to the rest of the paper.

Reply: We will rewrite the abstract and present more numbers in a table, rather than presenting them in the results.

Specific comments:

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Referee: Abstract: The abstract just ends without any “take home” message, without a summing up type conclusion about the authors’ most important finding. To make room for this, the first paragraph can be reduced by 50% by folding in some of the methods mentioned in this paragraph with the results. The second paragraph, which describes how the mesocosms changed over time, can be replaced with a discussion of the model results, which sum up everything. The changes over time are not important enough to highlight in the Abstract.

Reply: We will rewrite the abstract according to the reviewers’ suggestions.

Referee: P8572, line 9 and throughout the paper: The authors can just say “phytoplankton”, instead of phyto 1 and “mixotrophs” instead of phyto 2. They can define those terms for this paper. Especially “mixotrophs” is much more informative than “phyto 2”.

Reply: We will change phyto 1 and phyto 2 into “phytoplankton” and “mixotrophs”.

Referee: P8583, line 3: How do the authors explain why production by phytoplankton increased with pCO2 but POC did not? Phytoplankton were not a small fraction of total POC, right?

Reply: The same trend is present in POC, but this was not significant. A sentence will be added.

Referee: P8583, line 15: This is the only place in paper that mentions “gram positive bacteria”. Are the lipids examined by the authors only found in gram positive bacteria? These bacteria, which are mostly in the Actinobacteria phylum, are not very abundant in the oceans. It is essential that the authors discuss the limitation of looking only at Actinobacteria, if in fact that’s what they did.

Reply: This has been discussed above. We will remove “gram-positive”.

Referee: P8587: This very long paragraph is packed with very interesting numbers about the fluxes calculated by the model based on the authors’ results. All or at least

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most of these numbers should go into a table, and the text can be cut in half, focusing on making a few critical comparisons. A few numbers can be cited in the main text, but the large number of them cited here and elsewhere in the Results makes it difficult to read.

Reply: We agree with the reviewer we will add a table with the numbers and reduce the paragraph.

Referee: P8588: The Discussion opens up with a very long and dense paragraph. The authors should find some place to break up it up, making it easier for readers to follow things and to identify the most important points being made by the authors.

Reply: We agree and will make more paragraphs.

Referee: P8589, top of page: The authors found a very high ratio of bacterial production to primary production (BP:PP), an average of 34%. This high fraction implies an even higher amount of organic carbon being processed by bacteria, because the ratio does not include respiration. The best estimates of growth efficiency (BGE) average <20% and are often around 10%. If it's 10%, then >100% of all primary production would have to be routed through heterotrophic bacteria; Total consumption = BP:PP/BGE. Such imbalances and net heterotrophy are probably common in the Arctic.

Reply: We agree with the reviewer that this is an interesting point. Our experiment was initiated after a bloom has happened. High community respiration was shown by Tanaka et al. and Silyakova et al. (this issue). Motegi et al. (this issue) estimated BGE in the first part of the experiment to be ∼15%, indicating that bacterial carbon demand exceeded primary production. However, a comparison between whole community bacterial carbon demand and primary production cannot be directly made because our study focussed on recently fixed 13C rather than total carbon.

Referee: The very old review by Cole et al. (1988) is not worth citing. The most recent

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review is by Fouilland and Mostajir (2010). I don't think the authors need to have much about this topic, but something needs to be said.

Reply: We will change the reference.

Referee: P8592, line 8: Rather than "dorming", the authors probably mean "dormant".

Reply: We will change it.

Referee: P8592, line 9: The authors should stick to their assumption about bacteria using only DOC and not complicate the discussion by raising the possibility of these microbes using POC. Earlier, the authors said that detritus was a small fraction of POC, implying that most of the POC is in living organisms, the carbon of which is unlikely to be used by bacteria. The 13C in bacteria could be similar to that of POC because these microbes may make up a large fraction of total POC. Perhaps more likely, 13C in POC reflects what's in phytoplankton which in turn have a huge impact on bacteria.

Reply: We agree and this will be removed.

Referee: P8592, line 19: Nearly all of the paragraph starting here should be deleted. The reader doesn't learn anything new, except perhaps the difficult of these measurements.

Reply: We will maintain this paragraph, because we believe it's important to mention the potential problems with DOC measurements for future labelling experiments.

Referee: P8954, line 14: Why would sedimentation lead to lower grazing? The authors need to make their logic clearer here.

Reply: Because if more phytoplankton ends in detritus and sinks out, there is less available for grazing, this will be clarified.

References Dijkman, N. A., & Kromkamp, J. C. (2006). Phospholipid-derived fatty acids as chemotaxonomic markers for phytoplankton: application for inferring phytoplankton composition. Marine Ecology Progress Series, 324. Nichols, C. M., Lardière, S. G.,

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Bowman, J. P., Nichols, P. D., AE Gibson, J., & Guézennec, J. (2005). Chemical characterization of exopolysaccharides from Antarctic marine bacteria. Microbial ecology, 49(4), 578-589. Zelles, L. (1999). Fatty acid patterns of phospholipids and lipopolysaccharides in the characterisation of microbial communities in soil: a review. Biology and Fertility of Soils, 29(2), 111-129.

Interactive comment on Biogeosciences Discuss., 9, 8571, 2012.

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Interactive Comment

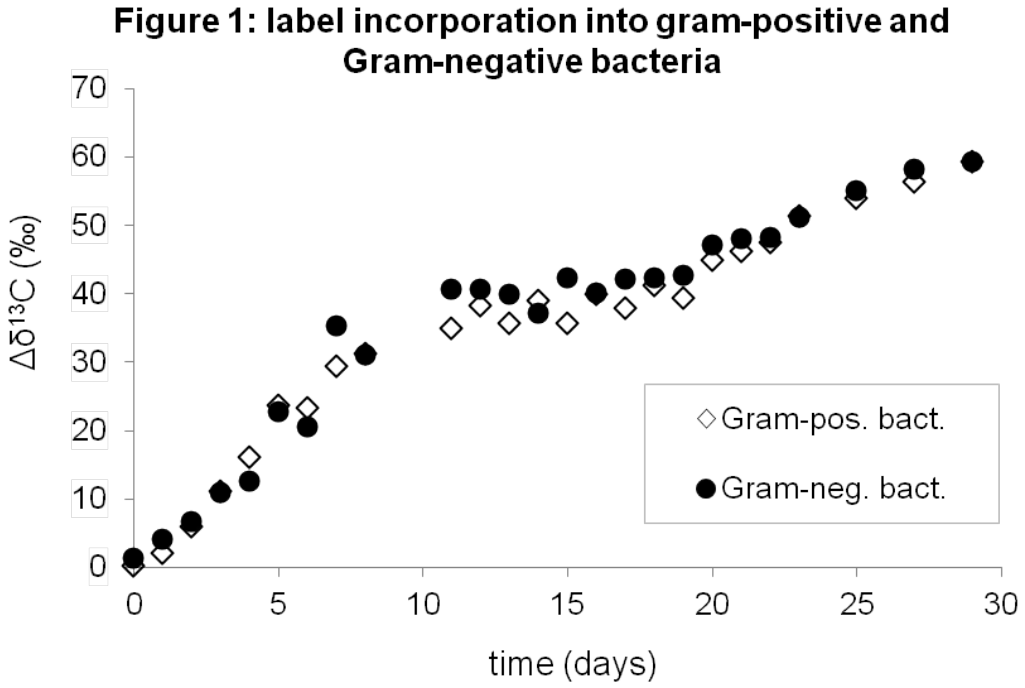

Fig. 1.

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