Biogeosciences Discuss.,
https://doi.org/10.5194/bg-2018-30-SC1, 2018

Biogeosciences
Discussions

Interactive comment on "Basin-scale variability of microbial methanol uptake in the Atlantic Ocean" *by* Stephanie L. Sargeant et al.

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Received and published: 8 March 2018

This study provides an inventory of measurements relevant to methanol consumption by microbial communities across the Atlantic, a rare basin-wide evaluation. The description is somewhat monotonous, but it is what it is. A great variability is uncovered across provinces and across depths, but little correlation is found of methanol oxidation/assimilation with respect to where it happens. In general, dissimilation is somewhat correlated with the presence of SAR11, and, in general, assimilation is two orders of magnitude lower than dissimilation. Which means SAR11 uses some other carbon source(s) for building biomass, and these remain unknown. In general, I think, even if many questions remain unanswered, this is a useful benchmark study.

Improvements that I would like to suggest:

Page 14, line 15, please say tetrahydrofolate-linked C1 transfer pathway, there are various oxidation levels and none of them are methyl- level after methanol oxidation.

Same page, lines 15-18. You do not see any bona fide methylotrophs in your 16S libraries. How can you conclude that they are active, along with SAR11? Either elaborate or remove this statement. PCR amplification of specific genes does not compare with 16S analysis, and you do not do any in this study anyway.

Meantime, an interesting question: while true methylotrophs do inhabit marine waters, why are they so sparse and apparently uncompetitive compared to SAR11? Can you elaborate?

Fig. 5 would greatly benefit from introducing colors, would be so much easier to compare guild distribution. Also, please order the taxa in a uniform way, i.e. use the same taxon order in each panel.

Table 1. Specify that you show ranges below averages/means, specify which. Specify what NA means.

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