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

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Each of L. Chistoserdova's comments has been addressed individually as follows.

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. - "methyl-THF linked oxidation pathway" will be changed to "tetrahydrofolate-linked C1 transfer pathway" (Page 14, line 15).

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. –

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Specific gene amplification, using mxaF functional gene primers, has been conducted previously on the same samples as the current study looking at 16S rRNA analysis. The mxaF functional gene analysis identified classic methylotrophic bacteria from these samples, these results are published in a previous manuscript Dixon et al. (2013). To clarify this in the text we propose the amendment of "Methylotrophic bacteria such as Methylophaga sp., Methylococcaceae sp. and Hyphomicrobium sp. have been previously identified, using mxaF functional gene primers (which encode for the classical methanol dehydrogenase), from the upper water column of Atlantic Ocean provinces (Dixon et al., 2013)" to "Previously methylotrophic bacteria such as Methylophaga sp., Methylococcaceae sp. and Hyphomicrobium sp. have been identified, using mxaF functional gene primers (which encode for the classical methanol dehydrogenase), from the same DNA samples analysed for 16S rRNA genes in this study, from the upper water column of Atlantic Ocean provinces (Dixon et al., 2013)" (Page 14, lines 7-10).

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? –

The authors agree this is an interesting question and more work is needed to unpick this. We don't have an answer for this based on published literature and knowledge currently available, however we can speculate that it may be down to the shear abundance and evolutionary strategy of SAR11 in comparison to true methylotrophs. SAR11 are the most abundant, free living, heterotrophic bacteria in open ocean systems and are often the most abundant organisms in oligotrophic waters. The competitiveness and high abundance of SAR11 cells in open ocean waters could be one part of a reason why true methylotrophs are relatively sparse in comparison. SAR11 have been shown to have one of the smallest genome sizes of any replicating cell and Giovannoni et al., (2005) suggest that the streamlining hypothesis may provide an explanation for this. The streamline hypothesis, assumption that selection reduces genome size due to the

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metabolic burden of replicating DNA without adaptive value, could be the strategy responsible for the dominance and success of the SAR11 clade in oligotrophic waters.

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. –

We will change shading of Figure 5 to coloured taxa for clarification and amend the order of taxa presented within the Figure.

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

A comment will be added to the end of the Table caption to clarify what these values are “Values given are average $\pm$ standard deviation (range). NA denotes that data is not available.”

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