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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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A couple of comments follow about aspects of the paper that could be improved. - Each of S. Giovannoni's comments has been addressed individually as follows.

1. I recommend commenting on the abundance of methylophaga and OM43 in the 454 data, or indicate they were not detected if that is the case. It may be that the relatively low coverage obtained in this study (386 seqs/sample) led to these taxa being undetectable. If this is the case, that should be explained so that readers new to this topic understand the issues. OM43 is not mentioned at all, but perhaps it should be, since it has been shown to be an obligate methylotroph, is one of the dominant taxa in some coastal environments, and has been shown to be a source of abundant XoxF

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peptides in a coastal ocean metaproteome.

The authors recognise this omission in the manuscript and acknowledge that these taxa should be included to reflect our current understanding of marine methanol utilisation. Therefore, we suggest the addition of the following comments:

“Although numerically very rare (1-11 16S rRNA gene sequences per sample), 16S rRNA gene sequences identified as Methylophaga spp., Methylophaga sp. DMS021 (EU001861) and uncultured Methylophaga sp. (EU031899), were found in each of the Atlantic Ocean provinces in this study (at 97% PAR or 200m depth), consistent with previous identification of Methlophaga spp. in these Atlantic provinces using mxaF gene cloning in (Dixon et al., 2013).” (Page 14, lines 14-19).

“Members of Betaproteobacteria, OM43, have been shown to be obligate methylotrophs, with cultivated cells of strain HTCC2181 dissimilating 3.5 times more methanol than was assimilated (Halsey et al., 2012). OM43 were not successfully identified in the 16S rRNA sequences in this study, which could be an artefact of the relatively low sequence coverage (386 sequences per sample) leading to this taxon not being detectable. During a previous coastal study in the western English Channel (16S rRNA pyrosequence data, Sargeant et al., 2016) only a single sequence of the OM43 clade, HTCC2181, was identified. This is a limitation of this type of environmental sequencing effort and should be a consideration in planning any future projects aiming to understand microbial function through process measurements alongside the generation of metagenomic datasets.” (Page 14, line 28 – Page 15, line 6).

This would also require the addition of Halsey et al., 2012 to the full reference list: Halsey KH, Carter AE, Giovannoni SJ (2012) Synergistic metabolism of a broad range of C1 compounds in the marine methylotrophic bacterium HTCC2181. Environmental Microbiology 14:630-640.

2. Amplicon ratios are not as powerful as cell numbers for identifying correlations between taxa and rates, although they are much easier to obtain. So, the correlations

with SAR11 are not with SAR11 cells per unit volume, which would be best, but rather a correlation between the relative success of SAR11 in the community and rates of MeOH oxidation. I suggest the authors revisit the manuscript and choose wording that conveys these issues to oceanographer readers, who often misunderstand this aspect of relative abundance data. –

The authors recognise that this is a limitation and clarity should be provided. We suggest the addition of;

“It should be noted that this correlation has been made with amplicon ratios, relating to the relative success of SAR11 in the community, rather than with SAR11 cell numbers specifically.” (Page 13, lines 10-12).

“More work is required to add clarity and understanding to the role that SAR11 cells play in marine community methanol dissimilation.” (Page 14, lines 3-4).

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