

Interactive comment on “Methane oxidizing seawater microbial communities from an Arctic shelf” by Christiane Uhlig et al.

Anonymous Referee #1

Received and published: 7 December 2017

This is the first study to use next generation sequencing techniques to study methane oxidizing bacteria in Arctic seawater and sea ice, combining community analysis with measurement of methane oxidation rates and incubation experiments with varying methane concentrations and incubation time. Methane oxidizing bacteria can play an important role in reducing methane flux to the atmosphere, but relatively little is known about what controls their abundance and activity, so this paper makes a nice contribution to the literature. The methane-oxidizing microbial communities in seawater and sea ice are different, but in both environments their relative abundance is fairly low. Relative abundance remained low even after incubation at elevated methane concentrations, though total abundance increased. I have no major criticisms of this paper.

Specific comments: P6, L25: how many contaminant sequences were removed, rela-

C1

tive to total sequences?

P9, L16: 16S rRNA gene

P14: I'm not sure this means copper couldn't be limiting methane oxidation

Figure S5: Is there a list of candidate OTUs somewhere? Figure S5 doesn't show many of these very clearly- I can't even tell what group of proteobacteria is shown in the first panel. Any theories on what's going on with these organisms if they're not oxidizing methane?

Interactive comment on Biogeosciences Discuss., https://doi.org/10.5194/bg-2017-410, 2017.

C2