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Environmental controls on microbial community composition and methane oxidation in the water column above shallow gas flares in the Arctic Ocean

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Global change related temperature rise in the Arctic and its impact on the environment is more severe than for any other region on Earth. Methane (CH_4) has a >23-fold higher global warming potential than CO_2, and the Arctic Ocean holds vast reservoirs of this greenhouse gas, which potentially could be released into the atmosphere. Along the continental shelf at Western Svalbard in the Arctic Ocean, numerous active gas flares were discovered within the last few years. Streams of CH_4 bubbles, released from the seabed to the water column, were found to almost reach the ocean surface in shallow waters (~90 m water depth), but a significant increase in the atmospheric CH_4 level in that region could not be measured. The seemingly mitigated methane release to the atmosphere can, at least in parts, be related to the activity of methane oxidizing bacteria (MOB) that thrive in surface sediments and the water column. These organisms utilize CH_4 by using its carbon source for their energy and biomass production. This contribution will address the following research questions: How much CH_4 is utilized by the MOB community in the Arctic Ocean water column? What controls MOB abundance and their activity? Which microbes are the key players in the aerobic CH_4 oxidation process? In order to address these questions, we carried out gridded biogeochemical measurements in a study area of 30 x 15 km west of Prins Karls Forland (West Spitsbergen margin), partly covering an active gas flare field. At the 64 hydro-cast stations, we measured vertical distribution of conductivity, temperature, salinity, CH_4 concentration and microbial methane oxidation (MOx) rates at 4 different time points (July 2015, May/June 2016, May 2017) covering Arctic winter, spring and summer conditions. We performed 16S rRNA gene sequencing analysis on selected water samples to characterize the microbial community composition. Known MOB are represented only as minor part of the total microbial community, but are highly active at moderate concentrations of dissolved CH_4. For example, we found MOx hot spots with values up to 7 nM d^1 at bottom water depth with CH_4 concentrations of less than 84 nM. In contrast, at stations where bottom CH_4 concentration values reached 640 nM, MOx rates were often lower than 1 nM d^1. The most dominant methylotrophic group identified in most samples with elevated MOx activity is the gammaproteobacterial Marine Methylotrophic Group 3. The verrucomicrobial genus *Haloferula* seems to play a major role within the MOB community. Our results indicated that seasonal effects like organic matter input and meltwater control microbial diversity, but that the oceanographic settings and circulation patterns in the area have major impact on the distribution of MOB biomass and methane oxidation in CH_4rich bottom water.