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Unexpected microbial diversity in anaerobically methane-oxidizing mats of the Black Sea

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Sediments of the Black Sea harbour consortia of anaerobically methane-oxidizing microorganisms in dense microbial mats, incrusted in large chimney structures consisting of carbonate precipitate. A number of convincing facts collected previously suggests that anaerobically methane-oxidizing Archaea (ANME) as well as delta-proteobacterial sulphate-reducing bacteria are the key players in anaerobic methane oxidation in Black Sea Mats: their presence has been shown by fluorescent-in-situ hybridization (FISH) with 16S rRNA-targeting probes, lipid biomarkers have typical, low delta13C ratios in archaeal and bacterial lipids, a methyl coenzyme M reductase-like protein was purified from the mat, and mat samples exhibit anaerobic methane oxidation. Here, we show that the diversity of Bacteria in both, pink and black mat samples, is larger than previously known. T-RFLP analysis of 16S rRNA and 16S rRNA genes and cloning and sequencing of randomly selected clones revealed the presence of taxa hitherto unknown to be present in anaerobically methane-oxidizing consortia. Besides the previously known delta-proteobacterial sulphate reducers, clones fell into 7 and 5 different phyla in pink and black coloured mats, respectively. Our findings suggest that the turnover of carbon in anaerobically methane-oxidizing communities might involve a larger diversity of microorganisms than was previously assumed.