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Pyrosequencing evidence for iron-cycling microbial communities in sediments of the Skagerrak and Bothnian Bay

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The diversity and metabolic pathways of microorganisms linked to Fe cycling in marine sediments are still poorly understood. Marine microorganisms in general are difficult to isolate and those that have been successfully isolated may not represent the main endogenous population. Various culture-independent techniques have been applied to characterize marine microbial communities, but only recently, has high throughput pyrosequencing been applied in marine sediment studies. Initial results are promising in capturing the full complexity of microbial communities in sediments. We performed a pyrosequencing-based study in marine and brackish sediments of the Baltic Sea; to our knowledge this is the first pyrosequencing study focused on the zone of Fe cycling. The goal of this study was to determine the bacterial and archaeal community composition near the sediment surface showing ongoing Fe cycling as a first step in characterizing the microorganisms potentially involved in Fe cycling. Two 35-cm-cores were sampled from ferruginous sediments in the Skagerrak, SK, North-Baltic Sea and the Bothnian Bay, BB, Northern Baltic Sea. Porewater (Fe2+, Mn2+, SO42-) and solid phase (Fe, Mn, total S) concentrations were measured and 16S rRNA genes were analysed using 454-pyrosequencing. Additionally, stable S and O isotope signatures of dissolved sulfate were measured at SK site. Sediment biogeochemistry indicated an intense suboxic zone with accumulation of dissolved Fe in the top 30 cm but only minor net sulfate (SO42-) reduction at both sites. Pore water profiles showed Fe2+ and Mn2+ levels of $\sim$140-150 μM throughout the core below a 6 cm thick oxidized surface layer in SK sediments and $\sim$300 μM below a 2 cm thick surface layer in BB sediments. Dissolved sulfide levels were below the detection limit in both sediments. Stable S and O isotope signatures suggest only minor net sulfate reduction. Fe reduction in the studied sediments is dominated by microbial dissimilatory Fe reduction, while cryptic Fe-S-cycling can be largely excluded. 16S rRNA gene sequences indicate Proteobacteria dominated both sites. Beta diversity, i.e. diversity differences between sites, were attributed to Chloroflexi, δ-, γ-Proteobacteria, candidate division OP8, Acidobacteria, Euryarchaeota YLA114 and Thermoplasmata E2 in SK. Unclassified Archaea, Acidobacteria, Chlorobi, α-, γ- and δ-Proteobacteria were taxa that showed significant values of Spearman correlation with Fe2+ concentrations. In the BB β-Proteobacteria and Cenarchaeaceae contributed to β-diversity and Spearman correlations showed that β-Proteobacteria correlated with Mn2+ concentrations. Potential Fe and Mn reducers including Desulfobacteraceae, Desulfuromonadaceae, Desulfobulbaceae, Geobacteraceae, Pelobacteraceae, Clostridiaceae, and Bacillaceae (between $\leq$0.1-12% relative abundance) as well as the archaeal Methanosarcinaceae were detected. Fe oxidation occurring near the sediment surface was supported by the presence of Fe oxidising Mariprofundus in SK and Gallionella in the brackish BB sediments reflecting their adaptation to the prevailing salinity. Although Spearman correlations showed several groups correlate with Fe/Mn, specific microorganisms could not be determined. Thus, an unclassified and abundant microbial community may carry out Fe/Mn cycling or alternatively, microorganisms that are known for Fe/Mn cycling, but are less abundant, could be involved.