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Iron cycling microbial communities in sediments of the Baltic Sea

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The biogeochemical cycling of iron is a key early diagenetic process. However, limited information exists about the diversity and metabolic pathways of microorganisms linked to iron cycling in marine sediments. The goal of this study was to determine the bacterial community diversity in sediments showing ongoing dissimilatory iron reduction using 454-pyrosequencing as a first step in characterizing microorganisms potentially involved in iron reduction. For this purpose, two 35 cm cores were sampled from ferruginous sediments in the Skagerrak (SK) and the Bothnian Bay (BB) from the North-Sea Baltic Sea and the northern Baltic Sea respectively. 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 sulphide levels were below detection in both sediments. No significant depletion of SO42- occurred at both sites, further supported by stable S and O isotope analyses of dissolved sulfate at SK site. Only very minor net sulfate reduction is suggested here from the trend in sulphur isotope signatures, in agreement with previously reported gross microbial sulphate rate measurements (Canfield et al., 1993;GCA). Based on these biogeochemical constraints, Fe reduction in the studied sediments is therefore dominated by microbial dissimilatory iron reduction, while cryptic Fe-S-cycling can be largely excluded.

16S rRNA gene sequences indicate Proteobacteria as the dominating microbial group in these sediments. Potential iron and manganese reducing bacteria included Geobacteraceae, Pelobacteraceae, Shewanellaceae, and Oceanospirillales. Additionally, Actinobacteria and Bacteroidetes were present.

Also, Fe-oxidizers were present and their occurrence correlated in depth with a Fe-oxide-rich layer, most likely a former buried Fe-oxidation front. Gene sequences point to the presence of Mariprofundus in SK sediments and Gallionella in the brackisch BB sediment, hence, Fe oxidizers are adapted to the prevailing salinity. Beta diversity indicates that most diversity between the two sites is due to Gaiellaceae and Ellin6529 groups in BB and Phycisphaerae and Desulfobacteraceae in SK sediments. Considering the entire community in these zones of Fe reduction, it is clearly distinct from communities commonly found in sulphate reduction zones.