Bacteria Potentially Involved in Iron-Cycling in Surface Marine Sediments Revealed by Pyrosequencing

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Iron is one of the most abundant elements reduced by microorganisms in anoxic sediments, and besides manganese it is the most important solid-phase electron acceptor. The reduction of iron can occur abiotically with sulphide or be mediated by microorganisms capable of transferring electrons from organic carbon substrates to a solid iron-phase. Hence microbial mediation of iron reduction may be an essential factor for the global iron cycle. To gain insight into the bacterial communities involved in iron-(Fe) cycling under marine conditions, we analysed sediments with Fe-contents (0.5–1.5 wt %) from the suboxic zone at a marine site in the North Sea and a brackish site in the Baltic Sea using 16S rRNA gene pyrosequencing. Several bacterial families, including *Desulfobulbaceae*, *Desulfuromonadaceae* and *Pelobacteraceae* and genera, including *Desulfobacter* and *Geobacter*, known to reduce Fe, were detected and showed highest abundance near the Fe(III)/Fe(II) redox boundary. In contrast, the sulphate (SO_4^{2-}) reducing bacteria *Desulfococcus* and *Desulfobacterium* were more abundant at greater depths concurring with a decrease in Fe-reducing activity. The communities revealed by pyrosequencing, thus, match the redox stratification indicated by geochemistry with the known Fe-reducers coinciding with the zone of Fe-reduction. Being able to link the presence and distribution of bacteria to reactive iron phases in marine sediments is a major step forward in understanding how biological processes influence iron cycling in the environment.