

Link between microbial populations and iron reduction in methanic sediments of the Helgoland mud area, North Sea

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Iron reduction in subseafloor sulfate-depleted and methane-rich marine sediments is currently a subject of interest in subsurface geomicrobiology. However, little is known about the microbes (if any) potentially driving iron reduction in such environments. A shallow sulfate-methane transition at 50 cm sediment depth and elevated dissolved iron concentrations (up to 350 μM) measured in the methanic zone of the Helgoland mud area provided an avenue to investigate the relationships between depth-wise profiles of dissolved iron, QPCR-derived copies of, and the distribution of pyrosequencing-based 16S rRNA genes of microbial populations in a 5m-long sediment core. We found that gene copy numbers of bacteria and archaea were specifically higher around the peak of dissolved iron in the methanic zone (250-350 cm sediment depth). The higher copy numbers at these depths were also reflected by the relative sequence abundances of members of the candidate division JS1 bacteria (SB45 lineage), methanogens and *Methanohalobium*/ANME-3 related archaea. Our data suggest that yet-unknown metabolic interactions among JS1 bacteria, methanogenic archaea and *Methanohalobium*/ANME-3-related archaea may be important for iron reduction and methane cycling in deep methanic sediments of the Helgoland mud area and perhaps in other methane-rich depositional environments.