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Microbial diversity, abundance and metabolism in oxic and anoxic abyssal clays from the North Atlantic Ocean.

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Microorganisms extensively populate the water column and sediment and are essential components of marine ecosystems because they regulate cycling of key nutrients. Global distribution of microbial communities in the oceans mainly derives from climatic control on primary production, and the resulting sinking organic matter defines cell abundances in the underlying sediments. Sedimentation rate controls the depth of O_2 penetration into marine sediments, which can extend until the underlying basaltic crust in deep sea abyssal clay. How the presence and absence of O_2 in subseafloor sediments correlates with the diversity and abundance of microbial life is not well understood. We target both DNA (all cells) and RNA (active cells) of microbial communities from sediments of the Northern Atlantic Ocean abyssal plain, focusing on oxic (n=2 sites) and anoxic (n=1 site) subseafloor settings. The drill sites are located below the water depth of carbonate compensation (CCD) and thereby reflect a constant pelagic regime with very low sedimentation rates and organic contents. The cored sediment sequences retrieved display oxic and anoxic conditions that correlate with slower (ca. 1 m per million years) and faster (>3 m per million years) sedimentation rates, respectively. To resolve the diversity and abundance of microbial communities populating the deep abyssal plains, we applied quantitative PCR (qPCR) and high-throughput (Illumina) sequencing targeting the 16S rRNA genes, and qPCR of ammonia monooxygenase and dissimilatory sulfate reductase genes. At the oxic site, 16S rRNA gene copies decreased from 10^7 at the sediment surface to 10^3 at 16 meters below seafloor (mbsf), whereas at the anoxic site 16S rRNA gene copies were generally an order of magnitude higher decreasing to 10^4 at the core bottom (26 mbsf). The taxonomic diversity and microbial abundance at the oxic sites were dominated by benthic groups of ammonia oxidizing Thaumarchaeota, whereas at the anoxic site a single OTU of the Atribacteria (JS1) dominated the entire microbial community throughout the entire core. In the presence and absence of O_2, Chloroflexi was the second most abundant Phylum across all sites, but with different aerobic and anaerobic groups inhabiting the oxic and anoxic sediment, respectively. Sediment slurry experiment showed that extracellular DNA (eDNA) is used as a growth substrate, suggesting that preservation of eDNA from past organisms is minimal and that the DNA recovered from our cores derives primarily from living bacteria. Actively utilized metabolic pathways inferred from metatranscriptomes from the oxic and anoxic sites provide insights into the metabolism that underlies nutrient cycling and cellular survival under these extremely energy limited conditions in the presence, and absence, of O_2.