

Effects of sedimentary redox conditions on Eukaryotic DNA recorded in deep-sea sediments

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Eukaryotic DNA in marine sediments can be a useful indicator of both ancient marine ecosystem in water column and living microbial eukaryotes in sediments. However, the environmental factors that influence the composition and preservation of eukaryotic DNA in marine sediments are poorly characterized. In this study, we examined effects of sedimentary redox conditions on the diversity of eukaryotic communities recorded in deep-sea surface sediment samples from 8 sites of the Japan Sea (from oxygenated abyssal sediments to sulfidic sediments in methane seeps) using a combination of various geochemical and molecular-biological tools. Sedimentary redox conditions were characterized by depth profiles of pore water (oxygen, nitrate, iron, sulfide, etc.) and bulk sedimentary organic matter (TOC, TN, $\delta^{13}\text{C}$, $\delta^{15}\text{N}$). The concentration and diversity of 18S rDNA in the sediment samples were investigated by qPCR and pyrosequencing. Decreases in 18S rDNA concentration with sediment depth were rapid in the oxic sediments, while decreases were moderate in the anoxic sediments and the sulfidic sediments. The community composition based on 18S rDNA sequences also varied with the sedimentary redox conditions. These results suggest that redox conditions of surface sediments can be important factors controlling the composition and preservation of eukaryotic DNA in deep-sea sediments.

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