

Distribution of eukaryotic DNA in global deep subseafloor sediments: Potential for reconstruction of paleo-ecosystems

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Scientific ocean drilling has advanced our understandings of the deep biosphere. Bacteria and Archaea in the subseafloor sediments are known to have nearly equal numbers to that in the whole ocean, and they play significant ecological roles in the global biogeochemical cycling. Compared to Bacteria and Archaea, less attention has been paid to eukaryotic communities in the deep subseafloor biosphere because their survival under such extreme energy-limiting environments is not likely. Nevertheless, fungal DNA has been often observed in surface marine sediments, and also in deep subseafloor sedimentary environments down to 2 km (Ciobanu et al., 2014). Furthermore, some fungi in deep subseafloor sediments were successfully revived and cultivated in the laboratory, which were considered to survive for millions of years as spores (Liu et al., 2017). During the past decade, in addition to these viable fungi, paleo-environmental DNA is a trace to reconstruct the ancient biodiversity in Holocene sediments (Capo et al., 2017). However, biogeographical distribution and diversity composition of the deeply buried eukaryotic cells (and genomes) in deep subseafloor sediments remain still largely unknown. In this study, we investigated the distribution of 18S rRNA gene in the remaining palaeoenvironmental DNA in millions of years old sediment. We attempted to amplify 18S rRNA gene fragments using extracted DNA from 300 subseafloor sediment samples globally collected from the past ocean drilling projects. DNA was extracted by hot-alkaline and commercial kit-based methods, resulting in more than 600 DNA extracts. PCR using domain specific primers successfully amplified 18S rRNA gene fragments from 175 DNA extracts that are mainly from sediments down to 100 mbsf. Using those amplicon, iTag sequencing was performed to characterize eukaryotic (palaeo-) biodiversity. As a result, fungal DNA was abundant in the obtained sequence libraries, nevertheless those fungi are known to be revivable or not. Algae related 18S rRNA sequences including *Ochrophyta*, *Dinoflagellata*, and *Chlorophyta* are also prevalent in all samples though the relative abundances decreased with depth. These results suggested that palaeoenvironmental DNA was preserved in deep subseafloor sediments. In this presentation, we will discuss the correlation between the eukaryotic diversity and sedimentological and/or palaeoenvironmental setting, and also the potential of palaeoenvironmental DNA for reconstructing paleoecosystem.

Keywords: IODP, sediment, environmental DNA