

Fungal diversity in Baltic Sea sediment

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Despite the biomass, diversity and metabolic activity for prokaryotic communities in marine subsurface have been intensively studied so far by molecular ecological approaches, subseafloor eukaryotic communities still remain poorly constrained. Here we report fungal communities in deep subseafloor sediments analysed by both cultivation and cultivation-independent molecular ecological approaches. Cultivation of fungi was performed using sediment core samples at the Landsort-Deep site in the Baltic Sea during the International Ocean Discovery Program (IODP) Expedition 347. A total of 6 media with different nutrients and salt concentrations were tested for the cultivation, resulting in 50 fungal colony isolates. The shallower sediment samples showed higher richness of cultivable fungal strains, which trend generally decreased with increasing the depth and burial time. Internal transcribed spacer (ITS)-regions of RNA genes were sequenced, revealing the occurrence of 11 different genera, including *Pseudeurotium bakeri* as the most predominant strain throughout the glacial and interglacial sedimentary sequences. Interestingly, some of the fungal strains were uniquely appeared only in either glacial or interglacial sediments, suggesting that those cultivated strains were originated from different burial sources. Moreover, cultivation-independent analysis of 18S rRNA gene sequencing from the total DNA in the sediments also showed the occurrence of diagnostic eukaryotes that might adjust to high salinity marine environments during the interglacial period, and vice versa, suggesting that those diagnostic eukaryotes sensitively responded to the past depositional and climate changes.