

Fine-scale analysis of bacterial community structures in a sediment core of the Mendeleev Ridge in the western Arctic Ocean

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Detailed sedimentological and organic-geochemical studies of marine sediments in high-latitude areas can yield important information on paleoenvironmental changes during the glacial-interglacial climate cycles. A sediment core (PS72/396-3GKG), taken from the Mendeleev Ridge in the western Arctic Ocean during the Polarstern Arctic expedition (ARK-23/3) in 2008, was investigated to establish a precise chronostratigraphy using multi-proxies for reconstruction of glacial history and paleoenvironmental changes during the late Quaternary. Here, in a parallel study, we made an attempt to find if the change in bacterial communities within a relatively well-dated sediment core (spanning ca. 100 ka) could be used a proxy for drastic alterations in sedimentation conditions. Fine-scale distributions of bacterial community were examined using 454 pyrosequencing of the hypervariable regions of V1 to V3 of the 16S rRNA gene in a depth resolution of 1 cm from the surface to 33 cm. In 31 samples showing the success of polymerase chain reaction amplification, 87,015 sequence reads were obtained and clustered 2,532 different operational taxonomic units (OTUs) at the 97 % identity level. Four bacterial phyla including *Firmicutes* (31-49 %), *Proteobacteria* (10-39 %), *Actinobacteria* (20-34 %) and *Bacteroidetes* (3-7 %) were dominant near the surface (0-3 cm). In most samples below the surface, *Firmicutes* became a predominant group accounting for up to 86 % of bacterial communities, except for the sample of 8-9 cm depth where it was unexpectedly low (0.1 %). It was also notable that *Acidobacteria* was dominant (11-25 %) in discrete depth samples (4-5, 6-7 and 14-15 cm), while undetectable or minor (< 1.4 %) in the other samples. The major shifts in abundant phylotypes presumably reflected the distinct sources of bacteria and/or the differences in availability of substrates that were accumulated under different paleoclimatic and paleoenvironmental conditions. As minor bacterial groups (< 3 %), diverse phylotypes affiliated with the recognized phyla (*Planctomycetes*, *Verrucomicrobia*, *Chloroflexi*, *Cyanobacteria*, *Gemmatimonadetes*, *Nitrospira*, *Deinococcus-Thermus*, *Lentisphaerae*, *Spirochaetes* and *Fusobacteria*) and the candidate phyla (BRC1, OP10, OP11, TM7 and WS3) were sporadically detected throughout the sediment core. Overall, our study demonstrated the presence of the high diversities and the sharp discontinuities of bacterial community in the western Arctic sediment core analyzed. In the presentation, co-occurrence of phylotype groups putatively linked to benthic ecosystem processes and biogeography in phylotypes of interest will be discussed.