



## **Microbial Biogeography on the Legacies of Historical Events in the Arctic Subsurface Sediments**

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The Arctic marine environment consists of various microbial habitats. The niche preference of microbial assemblages in the Arctic Ocean has been surveyed with the modern environmental change by oceanographic traits such as sea-ice dynamics, current circulation, and sedimentation. The North Pacific inflow from the shallow and narrow Bering Strait is highly susceptible to sea-level fluctuations, and thus the water mass exchange mediated by the history of sea-ice between the North Pacific and the Chukchi Sea in the Arctic Ocean. Over geological timescale, the climate change may provide putative evidences for ecological niche for the Arctic microbial assemblages as well as geological records in response to the paleoclimate change. In the present study, the multidisciplinary approach, based on microbiology, geology, and geochemistry, was applied to survey the microbial assemblages in the Arctic subsurface sediments and help further integrate the microbial biogeography and biogeochemical patterns in the Arctic subsurface biosphere. Our results describe microbial assemblages with high-resolution paleoceanographic records in the Chukchi Sea sediment core (ARA02B/01A-GC; 5.4 mbsf) to show the processes that drive microbial biogeographic patterns in the Arctic subsurface sediments. We found microbial habitat preferences closely linked to Holocene paleoclimate records as well as geological, geochemical, and microbiological evidence for the inference of the sulphate-methane transition zone (SMTZ) in the Chukchi Sea. Especially, the vertically distributed predominant populations of Gammaproteobacteria and Marine Group II Euryarchaeota in the ARA02B/01A-GC consistent with the patterns of the known global SMTZs and Holocene sedimentary records, suggesting that in-depth microbiological profiles integrated with geological records may be indirectly useful for reconstructing Arctic paleoclimate changes. In the earliest phase of Mid Holocene in the ARA02B/01A-GC with concentrated crenarchaeol (a unique biomarker for Marine Group I Thaumarchaea), the most abundant archaeal population was Marine Group II Euryarchaeota rather than Marine Group I Thaumarchaea, suggesting that the interpretation of archaeal tetraether lipids in subsurface sediments needs careful consideration for paleoceanography. In conclusion, our findings have important implications for the availability of microbial biogeography in the sedimentary record. The present study offers a deeper understanding of the legacies of historical events during the Holocene and implies that the survey of microbial biogeography may be an appropriate tool to monitor potential effects from the climate change in the Arctic Ocean.