



Ancient DNAs: Influence of Sedimentary Deposition on Bacterial Communities in Arctic Holocene Sediments

Han Dukki¹ and Nam Seung-II²

¹Gangneung-Wonju National University, Gangneung, Republic of Korea (dukkihan@gwnu.ac.kr)

²Korea Polar Research Institute, Incheon, Republic of Korea (sinam@kopri.re.kr)

Community assembly principles driving microbial biogeography have been studied in many environments, but rarely in the Arctic deep biosphere. The sea-level rise during the Holocene (11–0 ky BP) and its resulting sedimentation and biogeochemical processes can control microbial life in the Arctic sediments. We investigated subsurface sediments from the Arctic Ocean using metabarcoding-based sequencing to characterize bacterial 16S rRNA gene composition, respectively. We found enriched cyanobacterial sequences in methanogenic sediments, suggesting past cyanobacterial blooms in the Arctic Mid-Holocene (7–8 ky BP). Bacterial assemblage profiles with a sedimentary history of Holocene sea-level rise in the Arctic Ocean enabled a better understanding of the ecological processes governing community assembly across Holocene sedimentary habitats. The Arctic subsurface sediments deposited during the Holocene harbour distinguishable bacterial communities reflecting geochemical and paleoclimate separations. These local bacterial communities were phylogenetically influenced by interactions between biotic (symbiosis–competition or immigration–emigration) and abiotic (habitat specificity) factors governing community assembly under paleoclimate conditions. We conclude that bacterial profiles integrated with geological records seem useful for tracking microbial habitat preference, which reflects climate-triggered changes from the paleodepositional environment (the so-called ‘ancient DNAs’).