

Reconstructions of past flora using DNA analysis from ice core samples on Gregoriev Glacier, Kyrgyz Tienshan

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Analyses of ice cores have often been used as a means to reconstruct past environments. The species composition of the organism such as microorganism and plant in the ice cores could reflect the environmental condition at that time. Thus, organisms in ice cores could be useful to reconstruct past environments. However, analysis of the biological contents in ice cores is still highly limited.

We report results of metagenomic analyses of genomic DNA collected from the ice core sample (about 8,000 and 12,500 years old) collected on Gregoriev Glacier, Kyrgyz Tienshan. The ice core samples were melted using a device that enabled us to obtain water only from the inner portion of the cores. Complete separation of the inner and outer cores is required to avoid contamination by bacteria that can adhere to the cores during drilling and storage. We carried out taxonomic and functional binning of the metagenomic DNA by utilizing sequences generated by the 454 FLX sequencer, and attempted to reconstruct the organisms and their interactions within the community and with the environment on the sampled sites. The results implied genomic information used as an environmental marker for past environmental studies.

Keywords: ice core, genome analysis, metagenome, past environmental study, microorganisms