

## Comparison of microorganisms from the glacial and interglacial periods in Antarctic ice cores

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Bacterial diversity in Antarctic ice core samples was estimated using 16S rDNA clone library methods.

Two ice core samples were collected in the northern Antarctic during the Japanese Antarctic Research Expedition. One of the samples was taken near Mizuho Base and the other in the Yamato Range. By counting the layers of volcanic fallout of the historically-known eruptions and observing the patterns of delta 18O and of CO<sub>2</sub> flux, we were able to date the Mizuho Base and Yamato range samples to 2,000-4,000 and 20,000-30,000 years old, respectively.

A surface portion (1-2 cm thick) of the ice block was removed with a sterilized ceramic knife. Melted ice-core samples (approximately 1 liter) were filtered at 0.22µm before extracting the DNA. Bacterial 16S rDNAs were amplified using universal primer set and then cloned into cloning vector and partial (500bp) sequences from 5' terminal of 16S rDNA sequences were determined.

A broad range of bacteria were detected in the samples, including soil, psychrotrophic, and enteric bacteria. The 16S rRNA gene clone library from the glacial period sample consisted of Actinobacteria, Bacillus /Clostridium group, CFB, and Deinococcus-Thermus and a-, b-, and r-proteobacteria. In contrast, the gene clone library from the interglacial period sample consisted of Actinobacteria, Bacillus/Clostridium group, CFB, cyanobacteria, and a-, b-, r-, and d-proteobacteria. This indicated that the bacterial community had changed between the glacial and interglacial periods.