## An attempt to reconstruct air temperature in the past using DNA information in ice core samples on Gregoriev Glacier, Kyrgyz Tienshan

\*Segawa Takahiro<sup>1</sup>, Koji Fujita<sup>2</sup>, Ayumi Akiyoshi<sup>3</sup>, Nozomu Takeuchi<sup>4</sup>

1. University of Yamanashi, 2. Nagoya University, 3. National Institute of Polar Research, 4. Chiba University

Ice cores drilled from glaciers can provide a means of direct analysis of microbes in the past. The species composition of microorganisms in the ice core could reflect the environmental condition at that time. Ancient DNA analyses help clarify the phylogenetic relationships among organisms with branching dates. However, the DNA in these samples is often highly degraded and fragmented. Therefore, to analyze the small amount of DNA preserved in these samples, an effective technique to extract total DNA, shotgun sequencing, and molecular evolution analysis is required. Several recent studies have focused on glacier microorganisms such as snow algae and bacteria on glacial ice melting. Snow microorganisms are currently attracting a great deal of attention as they accelerate glacier melting. Despite the ecological importance in glacial environments, little is known about what kind of snow microorganisms lived in the past and their evolutionary dynamics because of the lack of knowledge regarding past microbial information.

We report the cyanobacterial community structure results and their evolution by molecular DNA analysis collected from the ice core samples collected on Gregoriev Glacier, Kyrgyz Tienshan. We successfully reconstruct the cyanobacterial community living on the modern glacier surface in the ice core samples. We also present detailed pictures of global distribution patterns of glacier cyanobacteria over the Arctic, Antarctic, and Asian high mountains, using the sequences of the nuclear rDNA internal transcribed spacer 2 (ITS2) region. Furthermore, we attempted to reconstruct air temperature in the past based on cyanobacteria's genetic information detected in ice cores and glacier surfaces' temperature conditions in various regions where the cyanobacteria live. Our results enhance understanding of the enigmatic time scale of cyanobacterial microevolution, which has the potential to elucidate environmental responses of them to the drastic climatic change events of the Quaternary.

Keywords: ice core, microorganism, DNA