Co-occurrence patterns of soil microbial communities in the low Arctic tundra are affected by the vegetation coverage

Shu-Kuan Wong[1], Yingshun Cui[2], Seong-Jun Chun[3], Ryo Kaneko[1], Shota Masumoto[4], Ryo Kitagawa[5], Akira S. Mori[4], and Masaki Uchida[1,6]

[1] *National Institute of Polar Research, Research Organization of Information and Systems, Tachikawa, Tokyo.*

[2] *Division of Life Science & Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Korea*

[3] *LMO Research Team, National Institute of Ecology, Seocheon, Korea*

[4] *Graduate School of Environment and Information Sciences, Yokohama National University, Tokiwadai, Hodogaya, Yokohama.*

[5] *Kansai Research Center, Forestry and Forest Products Research Institute, Nagaikyutaroh, Momoyama, Fushimi, Kyoto.*

[6] *Department of Polar Science, School of Multidisciplinary Sciences, The Graduate University for Advanced Studies, SOKENDAI, Tachikawa, Tokyo.*

Global climate change is projected to increase the global temperatures, leading to stronger warming in the Arctic regions. Soil microbial communities are actively involved in the biogeochemical cycles in the Arctic region. However, continuous warming will most likely affect the distribution and functions of these microbial communities. This study investigates the soil bacterial community structure and diversity from three different areas with varying vegetation coverage and soil biogeochemical properties in the low Arctic tundra of Salluit and how the bacteria interacts with the different environmental parameters from these environments.

A total of 225 soil samples were collected randomly from three sites. The high elevation transect was set up at the top of the hill with low vegetation coverage, the mid elevation transect was set up mid-hill with intermediate coverage and the low elevation transect was set up in the lower slopes with high vegetation coverage. At each site, three 150 m transects, each situated 50 m apart, were set up at three different environmental conditions with low, intermediate, and high vegetation coverages, respectively. Twenty-five topsoil samples were collected using a sterile scoop from each transect at 6 m intervals and DNA was extracted from each sample. The V3-V4 region of bacterial 16S rRNA gene was amplified and sequenced using the Illumina MiSeq sequencer to determine the bacterial community composition. The resulting sequences were analyzed using QIIME2 pipeline. Microbial co-occurrence networks, structural equation modelling and subsequent statistical analysis were preformed using packages in R software.

Amplicon sequence variants (ASVs) obtained from our samples were categorized into generalist, common taxa and specialist based on their niche breadth index. We found differences within the three bacterial niches (specialist, common taxa and generalist) in terms of the bacterial composition and abundance. Based on detailed network analysis and structural equation modeling, these differences were mainly driven by the different environmental conditions. Plant coverage, especially those of vascular plants which are abundant in low elevation areas, were the main factor controlling the distribution of generalist and to a lesser extent, the common taxa. The distribution of generalist, in turn, controlled the distribution of common taxa. On the other hand, the distribution of specialist was affected by the common taxa but not plant coverage. In short, plant coverage controls the distributions of generalist, which in turn regulates the distribution of common taxa that controls the specialist at the sampling area. Generalists, mainly Rhizobiales, acts as bridges to connect the different microbial communities and assists the surrounding microbes. Specialists, dominated by Ktedonobacterales, on the other hand, only interacts mainly within the group and to a lesser extent, with the common taxa but not the generalist. This result suggested that specialist in the sampling area have a much smaller and limited niche and interacts among themselves to form a close-knit micro-environment to survive in the tundra area. Compared to the generalist and common taxa, these specialists formed a very close-knit and independent microbial cluster within a specific microenvironment; possibly as a strategy to help them persist and survive in the harsh tundra.

In short, we have shown that the distribution of generalist, common taxa and specialist were driven by different environmental factors and these groups have specific interactions among and within each other to help them thrive in the low Arctic. Our results have also revealed that there are complex plant-microbe interactions in the low Arctic tundra. Identifying and studying these interactions are particularly important as climate change will affect both vegetation and microbe; both of which that are particularly sensitive and vulnerable to changing temperatures.