Bacterial diversity and function in the soil at Canadian Arctic

Masaki Uchida[1,2], Shu Kuan Wong[1] and Ryo Kaneko[3]

[1]National Institute of Polar Research
[2]*The Graduate University for Advanced Studies, SOKENDAI*
[3]*Bioinsight Co., Ltd.*

Soil microbes are one of the significant components in the Arctic tundra ecosystem. These microbes play an important role in the tundra biogeochemical cycles such as the cycling of carbon and nitrogen. However, there still remains a lot of uncertainties on the microbial diversity and function in the Arctic soil. In this paper, we report the bacterial biodiversity and functions in the soil collected from the Canadian Arctic.

A total of 231 mineral soil samples from three transects at different elevations were collected at Salluit (62°1′N 75°4′W) in the summer of 2017. The soil samples were frozen immediately upon collection and shipped in the frozen state back to the National Institute of Polar Research for further analysis. DNA was extracted from the soil sample to investigate the soil bacterial composition, diversity and function. The V4 region of the 16SrRNA gene was subjected to MiSeq sequencing to determine the soil bacterial composition and diversity. The resulting raw sequences from MiSeq sequencing were analyzed using QIIME2 (Ver. 2019.10). Briefly, sequences were clustered into amplicon sequence variants (ASVs) using the DADA2 algorithm and the taxonomic classification of ASVs were carried out using SILVA v132 database as a reference. The functions of soil bacteria from five selected DNA samples were investigated by hybridizing the DNA with functional gene probes available on the GeoChip 5.0M microarray.

Approximately 473−1130 ASVs (Average: 850 ASVs) were detected from the samples. A total of 59% sequences from all the samples were classified as uncultured bacteria at the genus level. Proteobacteria, Acidobacteria, Actinobacteria, Chloroflexi and Verrucomicrobia were the main bacterial phylum in the soil samples collected from this area. Principal component analysis (PCoA) showed that the bacterial communities in the sampling area can be seperated and clustered according to the elevation where the samples were collected. Compared to samples from the lower elevations, samples from high elevations have lower or lack of members from the phylum Gemmatimonadetes and Rokubacteria but higher proportions of Cyanobacteria. On the other hand, members from the phylum Nitrospirae and Firmicutes were found in higher proportions from samples in the lower elevation. GeoChip 5.0M microarray detected $90{,}811 \pm 3977$ different functional genes from the soil DNA samples. Most of the detected functional genes originated from bacteria, but genes from Ascomata, Basidiomycota and Viruses were also detected. Metal homeostasis and stress were the main functional genes detected from the soil samples. The number of functional genes involved in the carbon dynamics was higher than that of nitrogen, sulphur and phosphorus dynamics. These tendencies were similar to the functional genes from soil samples collected from Whapmagoostui-Kuujjuarapik at Canadian sub-Arctic.