

Soil bacterial communities and environments in the Canadian subarctic tundra

Ryo Kaneko¹, Ryo Kiatagawa², Keita Nishizawa², Shota Masumoto², Akira Mori², Jun Uetake³, Masaharu Tsuji¹ and Masaki Uchida^{1,4}

¹*National Institute of Polar Research*

²*Yokohama National University*

³*Colorado State University*

⁴*SOKENDAI*

We investigated bacterial communities in surface soils from principal tundra vegetations around Kuujjuarapik-Whapmagoostui (55.31°N, 77.75°W) in the Canadian subarctic. The bacterial communities, assessed by high-throughput sequencing of 16S rRNA gene fragments (V3-V4 region), were dominated by various uncultured members related to six phyla; Acidobacteria, Proteobacteria, Actinobacteria, Chloroflexi, Verrucomicrobia, and Planctomycetes. Bray-Curtis dissimilarity index showed that bacterial communities were divided into four distinct clusters. Each cluster significantly correlated to the type of tundra vegetation and soil properties (pH, soil moisture, NH₄ and carbon - nitrogen ratio). Bacterial communities in Cluster 1, mainly Acidobacteria and Actinobacteria, were equally distributed throughout the sampling area. Bacteria from Cluster 2 dominated by Chloroflexi and Actinobacteria, were found in high moisture environments and high cryptogam coverage. Cluster 3 which consisted mainly of Acidobacteria and Planctomycetes thrives in environments with high C/N ratio, relatively low pH and high coverage of dwarf-shrubs of Ericaceae (e.g. *Empetrum nigrum*, and *Vaccinium vitis-idaea*). Verrucomicrobia, Planctomycetes and Acidobacteria abundantly found in Cluster 4 significantly related to high pH, high NH₄ concentration and high coverage of graminoids (e.g. *Carex spp.*). The results from this investigation suggest that subarctic soil bacterial communities also be affected by vegetation and soil properties. Therefore environmental changes would affect directly and indirectly bacterial communities.