Comparative analysis of microbial communities and soil organic carbon utilization associated with the depth and thawing effects on tundra soil in Alaska

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In high-latitude regions, temperature has risen twice as fast as the global average (0.3°C per decade) and this leads to the increase in microbial degradability against soil organic carbon (SOC). Furthermore, the decomposed SOC is converted into green-house gases (CO₂ and CH₄) and their release could further increase the rate of climate change. Thus, understanding the microbial diversity and their functions linked with SOC degradation in soil-thawing model is necessary. In this study, we divided SOC-rich tundra soil from Council, Alaska into two depth regions (30–40 cm and 50–60 cm of depth) and incubated that for 108 days at 0°C. A total of 111,804 reads were obtained through a pyrosequencing-based metagenomic study during the microcosm experiments, and 574–1,128 of bacterial operational taxonomic units (OTUs) and 30–57 of archaeal OTUs were observed. Taxonomic analysis showed that the distribution of bacterial taxa was significantly different between two samples, while archaea was similar. In detail, the relative abundance of phyla *Actinobacteria* and *Firmicutes* largely increased in 30–40 cm and 50–60 cm of soil depths, respectively. Genera *Oryzihumus* (30–40 cm) and *Desulfosporosinus* (50–60 cm) were predominant in *Actinobacteria and Firmicutes*, respectively. Weight measurement and gel permeation

chromatography of the SOC extracts demonstrated that polymerization of humic acids, main component of SOC, occurred during the microcosm experiments. Taken together our results indicate that these two bacterial phyla could play a key function in SOC degradation and utilization in cold tundra soil.

Key words: Biodegradation, Arctic, Climate change, Soil organic carbon, Soil bacteria