

Vertical distribution of bacterial communities in the Greater Khingan Mountain permafrost region

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March 28, 2022

Abstract

Soil microorganisms are crucial contributors to the function of permafrost ecosystems, as well as the regulation of biogeochemical cycles. However, little is known about the distribution patterns and drivers of high-latitude permafrost microbial communities subject to climate change and human activities. In this study, the vertical distribution patterns of soil bacterial communities in the Greater Khingan Mountain permafrost region were systematically analyzed via Illumina Miseq high-throughput sequencing. Bacterial alpha diversity varied significantly at different soil depths, and the bacterial diversity and richness in the active layer were significantly higher than in the permafrost layer. The relative abundance of the dominant phyla Chloroflexi (17.92%–52.79%) and Actinobacteria (6.34%–34.52%) was significantly higher in the permafrost layer than in the active layer, whereas that of Acidobacteria (4.98%–38.82%) exhibited the opposite trend, and the abundance of Proteobacteria (2.49%–22.51%) generally decreased with depth. More importantly, the abundance of microorganisms linked to human infectious diseases was significantly higher in the permafrost layer according to Tax4Fun prediction analysis. Redundancy analysis (RDA) showed that NH₄⁺-N, TOC and TP were major factors affecting the bacterial community composition. Collectively, our findings provide insights into the soil bacteria at different depths in high-latitude permafrost regions, as well as their vertical distribution patterns and major environmental drivers, which is key to grasping the response of cold region ecosystem processes to global climate changes.

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