

The Effects of Open-top Chamber-simulated Global Warming on Microbial Diversity and Abundance in Tropical Soils

ABSTRACT

Over the years, global warming has become increasingly serious due to its widespread impacts. However, there remains insufficient awareness among people regarding the prolonged effects of temperature rise on terrestrial microbial diversity. Since bacteria have specific temperature ranges for optimal growth and metabolic activity, changes in surrounding temperature may alter their diversity and composition in the soil as well as affect microbial-mediated ecological processes. This study aimed to explore the soil bacterial population from selected areas in Universiti Malaysia Sabah, Kota Kinabalu Campus using a metagenomic approach and subsequently, to monitor the bacterial diversity alterations in response to rising temperatures. Simulated warming was performed using the OTCs that were placed in an open space for maximum exposure to the sun. The average temperature in the OTC was always found to be higher than the average temperature outside the OTC. Three soil samples were collected at six-month intervals from both inside (treatment) and outside (control) the OTC, with soil bacterial DNA extracted and subjected to 16S rDNA metagenomics sequencing and sequence alignment. Among the 39 bacterial phyla found in the soil samples, Proteobacteria dominated the soil samples, followed by Acidobacteriota, Actinobacteriota, Firmicutes, and Chloroflexi. Relative abundance of the soil bacteria showed changes after the first six-month simulation, but there were no significant effects of the treatment on bacterial diversity between the control and treatment plots. Perhaps a longer monitoring period is required to obtain more comprehensive results into the responses of soil bacterial communities to prolonged warming conditions.