

Soil Microbial Community Responses to Short-term Multiple Experimental Climate Change Drivers

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It is agreed that soil microbial communities are responsible for the cycling of carbon and nutrients in ecosystems; however, the response of these microbial communities to climate change has not been clearly understood. In this study, we measured the direct and interactive effects of climate change drivers on soil bacterial and fungal communities (abundance and composition) in an open-field multifactor climate change experiment. The experimental treatment system was established with two-year-old *Pinus densiflora* seedlings at Korea University in April 2013, and consisted of six different treatments with three replicates: two levels of air temperature warming (control and +3°C) were crossed with three levels of precipitation manipulation (control, -30% and +30%). After 2.5 years of treatments, in August, 2015, soil samples were collected from the topsoil (0-15cm) of all plots (n=18). High-throughput sequencing technology was used to assess the abundance and composition of soil bacterial and fungal community. Analysis of variance for a blocked split-plot design was used to detect the effects of climate change drivers and their interaction on the abundance and composition of soil bacterial and fungal community. Our results showed that 1) only the significant effect of warming on fungal community abundance was observed ($P < 0.05$); 2) on average, warming decreased both bacterial and fungal community abundance by 20.90% and 32.30%, 6.69% and 45.89%, 14.71% and 19.56% in control, decreased, and increased precipitation plots, respectively; 3) however, warming increased the relative bacterium/fungus ratio on average by 14.03%, 37.03% and 14.31% in control, decreased, and increased precipitation plots, respectively; 4) the phylogenetic distribution of bacterial and fungal groups and their relative abundance varied among treatments; 5) treatments altered the relative abundance of Ascomycota and Basidiomycota, where Ascomycota decreased with a concomitant increase in the Basidiomycota across all treatments; and 6) the shift induced by treatments in the dominant fungal group was larger than bacterial group. Since soil microorganisms differ in their susceptibility to stressors, the changes in the soil microbial communities may result from treatment-induced shifts in soil temperature and moisture. Our results indicate that climate change drivers and their interactions may cause changes in abundance and composition of soil microbial communities, especially for the fungal community. These results illustrate climate change drivers and their interactions may select for distinct soil microbial communities, and these community changes may shape the way ecosystems function in the future. This study was supported by National Research Foundation of Korea (NRF-2013R1A1A2012242).