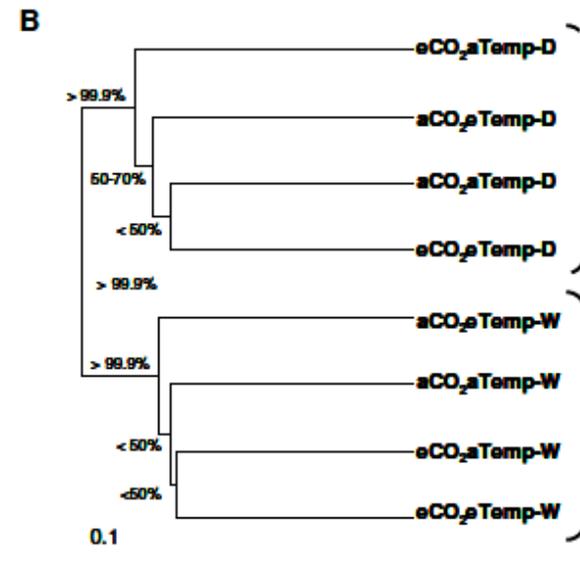
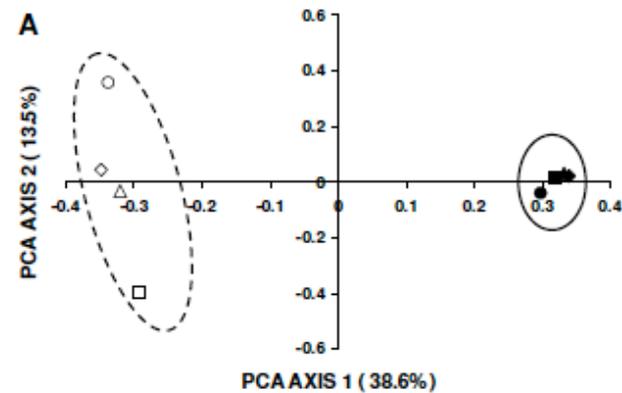


# Soil Microbial Community Responses to Multiple Experimental Climate Change Drivers

Contact: Chris Schadt, 865-576-3982, [schadtcw@ornl.gov](mailto:schadtcw@ornl.gov)

Funding: DOE Office of Science, Biological and Environmental Research



- Ecosystem responses to individual climate change factors are variable but well documented, however multi-factorial studies are rarer and the responses of soil microbial communities virtually undocumented

- Soil bacterial and fungal community structure were investigated in old field communities subjected to altered [CO<sub>2</sub>], precip and temp in a multi-factorial design

- Changes in soil microbial community structure were found to be primarily driven by precip changes and included changes in overall bacterial and fungal abundance and the relative distribution of specific groups such as Acidobacteria and Proteobacteria

- It is unclear what such changes might forebode for the long term biogeochemical properties of soils and ecosystems under complex global change scenarios.

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**Abstract:** Researchers agree that climate change factors such as rising atmospheric [CO<sub>2</sub>] and warming will likely interact to modify ecosystem properties and processes. However, the response of the microbial communities which regulate ecosystem processes is less predictable. We measured the direct and interactive effects of climatic change on soil fungal and bacterial communities (abundance and composition) in a multi-factor climate change experiment that exposed a constructed old-field ecosystem to different atmospheric CO<sub>2</sub> concentration (ambient, +300 ppm), temperature (ambient, +30C), and precipitation (wet and dry) might interact to alter soil bacterial and fungal abundance and community structure in an old-field ecosystem. We found: 1) Fungal abundance increased in warmed treatments; 2) Bacterial abundance increased in warmed plots with elevated atmospheric [CO<sub>2</sub>], but decreased in warmed plots under ambient atmospheric [CO<sub>2</sub>]; 3) The phylogenetic distribution of bacterial and fungal clones and their relative abundance varied among treatments as indicated by changes in 16S rRNA and 28S rRNA genes; 4) Changes in precipitation altered the relative abundance of Proteobacteria and Acidobacteria where Acidobacteria decreased with a concomitant increase in the Proteobacteria in wet relative to dry treatments; and 5) Changes in precipitation altered fungal community composition, primarily through lineage specific changes within a recently discovered group known as Soil Clone Group I (SCGI). Taken together, our results indicate that climate change drivers and their interactions may cause changes in bacterial and fungal overall abundance, however changes in precipitation tended to have a much greater effect on the community composition. These results illustrate the potential for complex community changes in terrestrial ecosystems under climate change scenarios that alter multiple factors simultaneously.

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