

Ecological factors driving microbial community assembly in response to warming

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Researchers from the OU Institute for Environmental Genomics and Department of Microbiology and Plant Biology lead a study that aims to better understand ecological community assembly mechanisms in response to climate warming.

"Understanding community assembly rules is a longstanding issue of ecologists," said Jizhong Zhou, the director of the Institute for

Environmental Genomics and a George Lynn Cross Research Professor in the OU College of Arts and Sciences. "We developed a novel framework to quantitatively infer community assembly mechanisms by phylogenetic bin-based null model analysis i.e., iCAMP."

Using the iCAMP framework, the researchers revealed new findings on the dynamic changes of ecological processes from 2009 to 2014 in grassland bacterial communities under long-term experimental warming.

"In simulated data, iCAMP shows outstanding performance in terms of precision, sensitivity, specificity, accuracy, and robustness," Zhou said.

"Using iCAMP, we showed that climate warming increased homogeneous selection in soil bacterial community assembly, which was also related to the changes in drought and plant productivity."

Zhou adds that the general framework used in this study has potential to benefit not only [microbial ecology](#), but also plant and animal ecology and that their findings have important implications for predicting and mitigating the ecological consequences of climate [warming](#).

More information: Daliang Ning et al, A quantitative framework reveals ecological drivers of grassland microbial community assembly in response to warming, *Nature Communications* (2020). [DOI: 10.1038/s41467-020-18560-z](#)

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