

Microbial changes regulate function of entire ecosystems

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A major question in ecology has centered on the role of microbes in regulating ecosystem function. Now, in research published ahead of print in the journal *Applied and Environmental Microbiology*, Brajesh Singh of the University of Western Sydney, Australia, and collaborators show how changes in the populations of methanotrophic bacteria can have consequences for methane mitigation at ecosystem levels.

"Ecological theories developed for macro-ecology can explain the microbial regulation of the methane cycle," says Singh.

In the study, as grasslands, bogs, and moors became forested, a group of type II methanotrophic bacterium, known as USC alpha, became dominant on all three land use types, replacing other methanotrophic microbes, and oxidizing, thus mitigating methane, a powerful [greenhouse gas](#), explains Singh. "The change happened because we changed the niches of the microbial community."

The pre-eminence of USC alpha bacteria in this process demonstrates that the so-called "selection hypothesis" from macro-ecology "explains the changes the investigators saw in the soil functions of their land-use types," says Singh. The selection hypothesis states that a small number of key species, rather than all species present determine key functions in ecosystems. "This knowledge could provide the basis for incorporation of microbial data into predictive models, as has been done for plant communities," he says.

"Evidence of microbial regulation of the [biogeochemical cycle](#) provides the basis for including microbial data in [predictive models](#) studying the effects of global changes," says Singh.

Singh warns that one should not take the results to mean that biodiversity is not important. Without microbial biodiversity, the raw materials—different [microbial species](#) with different capabilities—for adapting to changes in the environment would be unavailable, he says.

More information: L. Nazaries, Y. Pan, L. Bodrossy, E.M. Baggs, P. Millard, J.C. Murrell, and B.K. Singh, 2013. Evidence of microbial regulation of biogeochemical cycles from a study on methane flux and land use change. *Appl. Environ. Microbiol.* Published ahead of print 26 April 2013 , [doi:10.1128/AEM.00095-13](https://doi.org/10.1128/AEM.00095-13)

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