

KBS 89, a bacterial strain from the phylum Acidobacteria that was isolated from KBS LTER soils. Acidobacteria are one of the most abundant groups of bacteria in soils from agricultural and forested sites. Photo Credit: Michigan State University Center for Advanced Microscopy

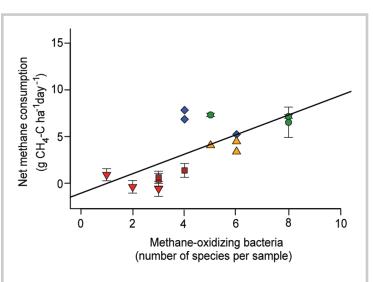
decomposing organic matter in soil. Others consume methane (CH<sub>4</sub>) from the atmosphere, thus helping to mitigate climate change. The magnitude of each of these processes is influenced by human activities and impacts the warming potential of Earth's atmosphere. To better understand the role that agricultural management has on these processes, KBS LTER scientists studied the composition and activity of microbial communities in soils across a variety of cropped and natural ecosystems.

Using contemporary genomic techniques, KBS LTER scientists analyzed DNA extracted directly from soil to assess which microbes were present and their metabolic potential. Communities of microbes were compared from three very different land use types: row-crop agriculture (corn, soybean, and wheat rotations), "old fields" that had been abandoned from agriculture for decades, and deciduous forests. Because these treatments had been in place for 20-50 years, scientists were able to measure the long-term impacts of land management.

## Soil Microbes

SOIL MICROBES AND AGRICULTURE – KBS LTER scientists found that soil microbial diversity is not much affected by land management, except for those groups of microbes involved in specific metabolic processes such as the production and consumption of the important greenhouse gases methane and nitrous oxide. This introduces an interesting potential for managing soil microbial diversity to provide specific ecosystem services such as greenhouse gas mitigation in agriculture.

Microbes in terrestrial environments are important catalysts of global carbon and nitrogen cycles, including the production and consumption of greenhouse gases in soil. Some microbes produce the greenhouse gases carbon dioxide  $(CO_2)$  and nitrous oxide  $(N_2O)$  while



The rate of methane consumption by soils at the KBS LTER is related to the diversity of methane oxidizing bacteria present. Methane consumption is lowest in sites managed for row-crop agriculture (red triangles), and increases in early successional sites (brown squares), managed grasslands (blue diamonds), and both successional (orange triangles) and deciduous forests (green circles). Graph Credit: Levine, Teal, Robertson and Schmidt (2011) ISME Journal.



Fall 2013

Results showed that land management has little influence on general microbial diversity, but greatly affects the diversity of microbes involved in methane oxidation: soils with a greater diversity of methane oxidizing bacteria consume more methane from the atmosphere. These observations suggest that managing lands to conserve or restore the diversity of methane-consuming bacteria could help mitigate climate change.

Likewise, land management also seems to greatly affect the diversity of microbes involved in nitrous oxide production: fertilized soils produce more nitrous oxide and have a very different genetic makeup. KBS LTER scientists are currently working to understand exactly how and why different agricultural practices affect the relationship between the diversity of microbes and nitrous oxide production.

These results demonstrate that agriculture distinctly influences the diversity of bacteria responsible for the production and consumption of two of the three major naturally-occurring greenhouse gases. Understanding the relationship between microbial diversity and the flux of greenhouse gases is the first step to management aimed at sustaining or enhancing soil microbial diversity to provide specific ecosystem services such as greenhouse gas mitigation in agriculture.

## For Further Reading

Levine, U.Y., T.K. Teal, G.P. Robertson and T.M. Schmidt. 2011. Agriculture's impact on microbial diversity and associated fluxes of carbon dioxide and methane. *The ISME Journal* 5:1683-1691.

Eichorst, S.A., C.R. Kuske and T.M. Schmidt. 2011. Influence of plant polymers on the distribution and cultivation of bacteria in the phylum Acidobacteria. *Applied and Environmental Microbiology* 77:586-96.

Xue, K., L. Wu, Y. Deng, Z. He, J. V. Nostrand, G. P. Robertson, T. M. Schmidt, and J. Zhou. 2013. Functional gene differences in soil microbial communities from conventional, low-input and organic farmlands. *Applied and Environmental Microbiology* 79:1284-1292.

Jangid, K., M. A. Williams, A. J. Franzluebbers, T. M. Schmidt, D. C. Coleman, and W.B. Whitman. 2011. Land-use history has a stronger impact on soil microbial community composition than above ground vegetation and soil properties. *Soil Biology & Biochemistry* 43:2184-2193.

