

Microbial communities in agricultural soils have the potential to increase atmospheric concentrations of greenhouse gases

Tracy K. Teal^{1*} (tkteal@msu.edu), Vicente Gomez-Alvarez², **Thomas M. Schmidt**^{1,3}

¹Michigan State University, East Lansing, MI; ²Environmental Protection Agency ORD-NERL, Cincinnati, OH; ³Kellogg Biological Station, Hickory Corners, MI

Project Goals: The conversion of land to agricultural use has resulted in an increased production of carbon dioxide and nitrous oxide from soils and a decreased consumption of methane– all changes that exacerbate the problem of rising concentrations of greenhouse gases in the atmosphere. As the flux of nitrous oxide and methane are almost entirely microbially-mediated, this shift is due to changes in microbial community structure and function. We aim to survey microbial communities under different land management strategies to determine how communities differ, with a particular focus on traits linked to N₂O production and CH₄ consumption. Towards this aim we are studying soil from the Kellogg Biological Station (KBS) Long Term Ecological Research (LTER) study site, focused on field crop ecosystems, as well as the GLBRC network where potential biofuel crops are assessed for their sustainability and productivity. We are combining metadata with metagenomic data and targeted-gene surveys to address specific questions about the relationships between the genetic structure of microbial communities in soil and their production and consumption of greenhouse gases.

The expansion of land under agricultural management has significantly increased atmospheric forcing from greenhouse gases – carbon dioxide, methane and nitrous oxide. Agricultural soils now contribute approximately half the anthropogenically derived N₂O in the atmosphere¹, and soils that are typically a sink for methane consume little to no methane when converted². Microbial communities are almost entirely responsible for catalyzing nitrous oxide flux, reducing nitrate to nitrous oxide and nitrogen in a process known as denitrification³. Although present at low abundances, methanotrophs in soil oxidize methane, with higher diversity communities consuming up to 8 g CH₄-C per hectare per day⁴. In an effort to assess changes in the taxonomic composition and metabolic potential of microbial communities, metagenomic and targeted genomic surveys across a gradient of land uses at the KBS LTER and Michigan GLBRC sites were conducted. We have found that microbial communities take approximately 20 years to recover, both taxonomically and functionally, from agricultural management, concomitant with soil biogeochemistry, and that denitrifier communities are particularly affected by agricultural practices. Under agriculture, the denitrifier community increases from approximately 10% of the community to 33%. Additionally the community composition of denitrifiers changes to an increased proportion of ammonia oxidizing bacteria that lack the capacity to reduce N₂O to N₂. It is likely that fertilization is having a primary affect on this shift⁵ and further studies on a

switchgrass fertilization gradient are being conducted. Our data suggests that both the abundance of denitrifiers in a community, and their structure, determine the rate of nitrous oxide production in soils and that an understanding of denitrifier communities could lead to solutions for mediation or more accurate models of terrestrial nitrous oxide fluxes.

As methanotrophs are rarer community members, targeted gene approaches for *pmoA* were used and revealed that among agricultural management, perennial crops – switchgrass and prairie – maintain a higher diversity of methanotrophs suggesting higher methane consumption at these sites.

As we strive to develop biofuel crops, the sustainability of these crops and their effect on ecosystem services is an essential component. Our work suggests that land management has important implications for soil microbial communities and the greenhouse gas fluxes they catalyze. An enhanced knowledge of the effects of agriculture on microbial community composition that drives N₂O production and CH₄ consumption is the first step towards managing or restoring microbial biodiversity in soil to mitigate the production of this potent greenhouse gas.

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