How agricultural management shapes soil microbial communities: patterns emerging from genetic and genomic studies

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Agriculture is a predominant land use and thus a large influence on global carbon (C) and nitrogen (N) balances, climate, and human health. If we are to produce food, fiber, and fuel sustainably we must maximize agricultural yield while minimizing negative environmental consequences, goals towards which we have made great strides through agronomic advances. However, most agronomic strategies have been designed with a view of soil as a black box, largely ignoring the way management is mediated by soil biota. Because soil microbes play a central role in many of the processes that deliver nutrients to crops and support their health and productivity, agricultural management strategies targeted to exploit or support microbial activity should deliver additional benefits. To do this we must determine how microbial community structure and function are shaped by agricultural practices, but until recently our characterizations of soil microbial communities in agricultural soils have been largely limited to broad taxonomic classes due to methodological constraints. With advances in high-throughput genetic and genomic sequencing techniques, better taxonomic resolution now enables us to determine how agricultural management affects specific microbes and, in turn, nutrient cycling outcomes.

Here we unite findings from published research that includes genetic or genomic data about microbial community structure (e.g. 454, Illumina, clone libraries, qPCR) in soils under agricultural management regimes that differ in type and extent of tillage, cropping selections and rotations, inclusion of cover crops, organic amendments, and/or synthetic fertilizer application. We delineate patterns linking agricultural management to microbial diversity, biomass, C- and N-content, and abundance of microbial taxa; furthermore, where available, we compare patterns in microbial communities to patterns in soil extracellular enzyme activities, catabolic profiles, inorganic nitrogen pools, and nitrogen transforming processes. Where genetic data are scarce, we further inform our observations with data from phospholipid fatty acid, ribosomal intergenic spacer, (terminal) restriction fragment length polymorphism, and denaturing gradient gel electrophoresis analyses. By summarizing the most current information about microbial community structure under different agricultural management strategies, we hope to jumpstart a dialogue that could ultimately inspire novel—and sustainable—agronomic approaches that work with and through soil microbes.