Microbial diversity, community composition, and abundance of functional groups of over a gradient of C and N agricultural inputs

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Abstract

Soils representing a gradient of C and N inputs from agriculture from a long term agricultural research field were analyzed for total microbial abundance, diversity, community composition and abundance of specific functional groups of N and P cycling organisms using 454 Pyrosequencing technology qPCR. Treatments did not differ in total diversity according to Pyrosequencing data analyses; however, there are key differences in community composition including higher abundances of organisms like Proteobacteria, Acidobacteria and Bacteriodetes in the organic and conventional treatments compared to the no input and uncropped treatments as well as higher abundances of Acidobacteria, Bacteriodetes, Proteobacteria, and Gemmatimonadetes in the spring compared to the fall. Canonical correspondence analysis reveals that amount of C and N inputs are strongly correlated with variation in bacterial and archaeal taxa in spring and fall samples. The organic and conventional systems are more similar in terms of community composition in the spring compared to the fall while the no input and uncropped systems are similar in the spring and fall. Additionally, the abundance of key N cycling genes AmoA and NirS are also correlated with the variation seen in bacterial and archaeal taxa. This study demonstrates a stronger correlation with microbial community composition including higher abundances of Proteobacteria, Acidobacteria and Bacteriodetes that is stronger in the fall samples compared to spring samples indicating the importance of seasonality and agricultural management in determining microbial community composition.

Conclusions

- Microbial communities composition is different in the different types of agricultural systems compared. High inputs seem to select for specific groups of microorganisms that prefer high levels of organic substrates.
- Microbial community composition seems to change from the spring to the fall indicating that water availability and temperature greatly influence the soil microbial community in addition to management practice.

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What is pyrosequencing?

Pyrosequencing is a method of sequencing DNA via synthesis of a complimentary strand of DNA. A specific intensity of light is emitted depending on the type of nucleotide that is added to the complimentary sequence.

Organisms that prefer high organic substrates like Bacteriodetes and Proteobacteria are more abundant in fall samples compared to spring samples. These organisms are also more abundant in the organic and conventional systems/

Literature Cited