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

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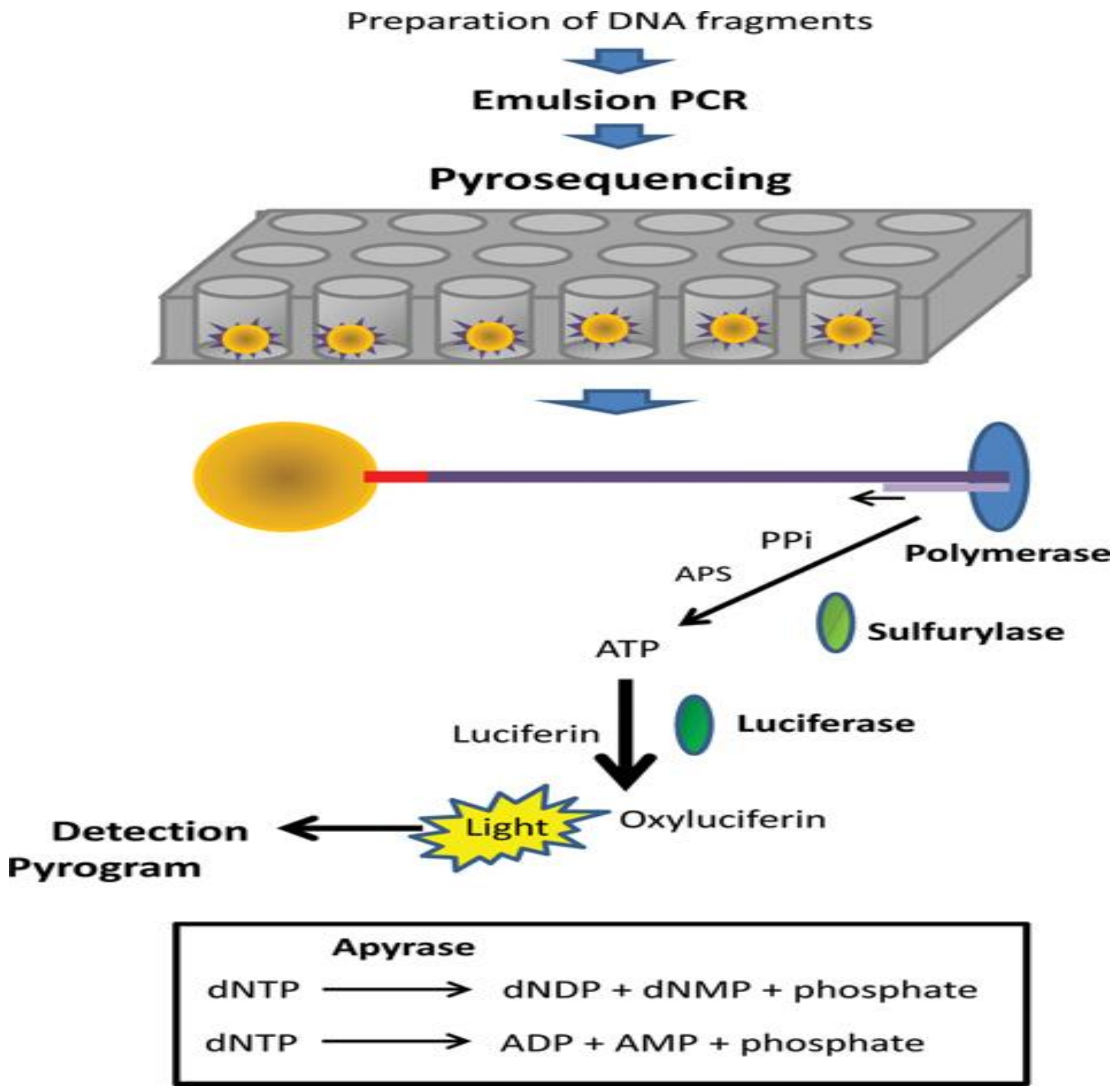
Keywords: Pyrosequencing, LTRAS, organic, conventional, soil, agriculture

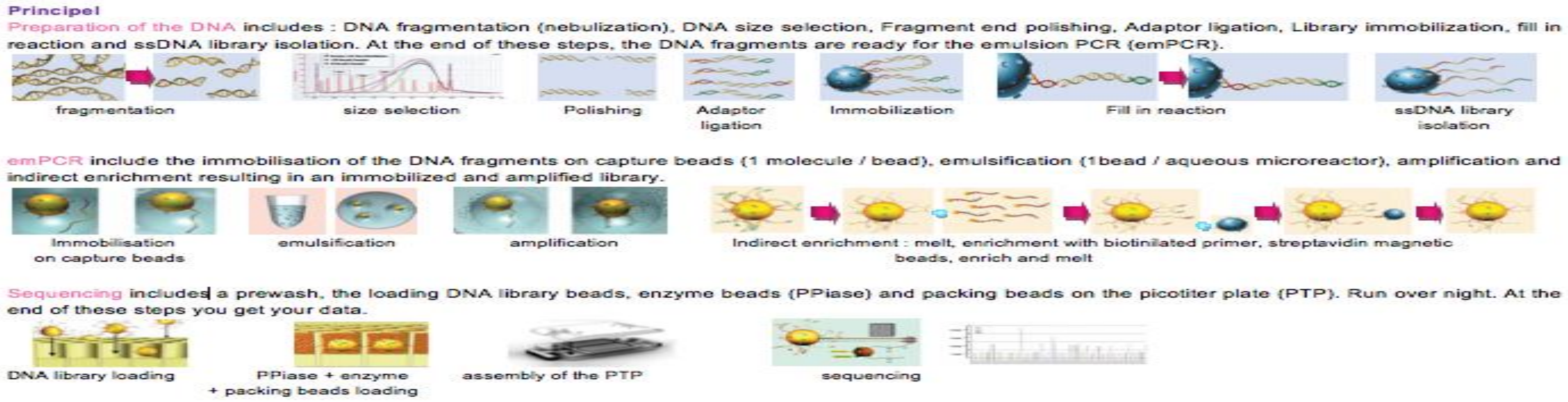
Abstract

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 Pyroseqeuncing 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.

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 js added to the complimentary sequence.



Principel

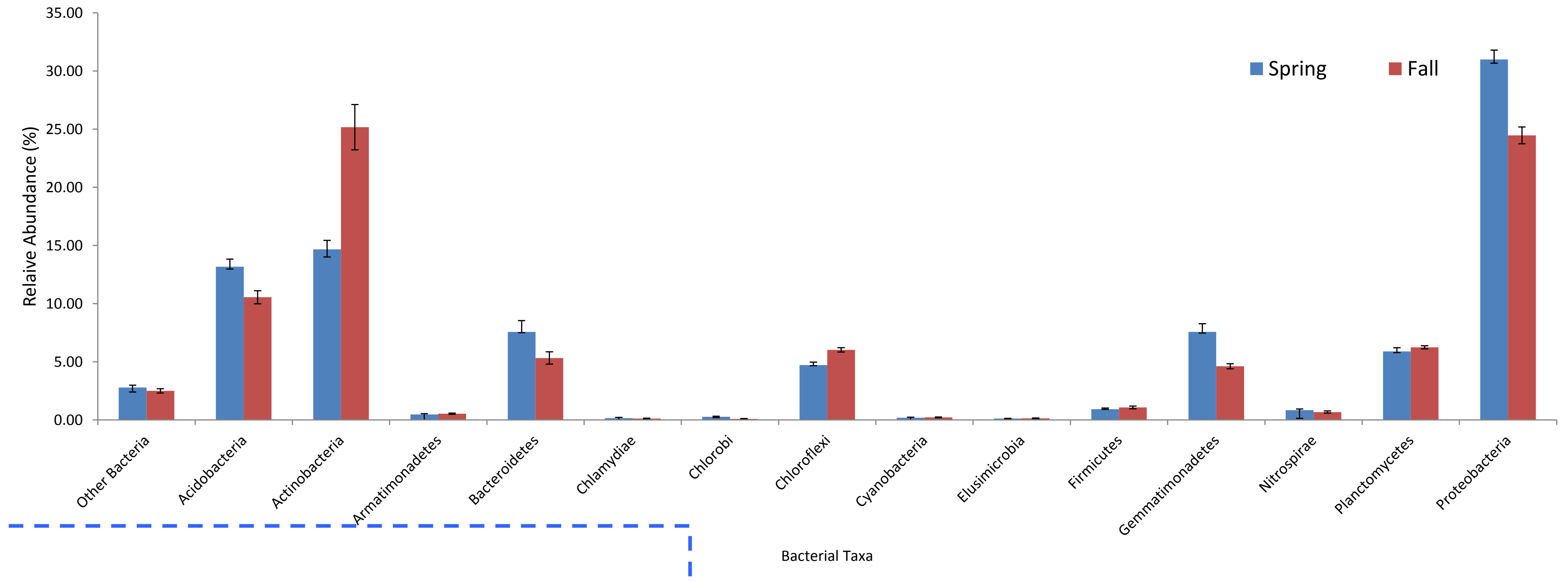
Preparation of the DNA includes : DNA fragmentation (nebulization), DNA size selection, Fragment end polishing, Adaptor ligation, Library immobilization, fill in reaction and ssDNA library isolation. At the end of these steps, the DNA fragments are ready for the emulsion PCR (emPCR).

emPCR include the immobilisation of the DNA fragments on capture beads (1 molecule / bead), emulsification (1bead / aqueous microreactor), amplification and indirect enrichment resulting in an immobilized and amplified library.

Sequencing includes a prewash, the loading DNA library beads, enzyme beads (PPiase) and packing beads on the picotiter plate (PTP). Run over night. At the end of these steps you get your data.

http://www.giga.ulg.ac.be/jcms/prod_178513/de-novo-sequencing

Figure 1: Relative abundance of bacterial taxa in spring and fall



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

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.

Literature Cited

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Acknowledgements: Special thanks to Emma Torbert, Isreal Herrera, Inmyoung Park, Johnny Hsia and Jennifer Denbow