# Does microbial community composition matter?

## Investigating the microbial ecology of soil C cycling using $^{13}C$ stable isotope probing

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The activity of soil microbial communities is fundamental to several critical unknowns in how terrestrial biosphere-atmosphere C exchange is regulated and will respond to changing climate and anthropogenic inputs. However, most ecosystem scale C models of terrestrial environments do not consider the composition of the indigenous microbial community. For microbial processes regulating the decomposition and transformation of plant litters/exudates in soil, several fundamental questions remain about if and how the composition of the microbial community matters, including C utilization preferences, succession of microbial groups, response to N deposition, the importance of the secondary soil C inputs - microbial bodies to C sequestration, and soil priming events. During the last 12 years, the use of $^{13}C$ isotope tracers in combination with phospholipid fatty acid (PLFA) biomarkers has begun to directly address these questions by enabling researchers to follow labeled substrates into and through microbial communities *in situ* from a variety of sources. The resulting data provide quantitative turnover rates of labeled C pools among 6 groups of organisms that share broad metabolic and physiological similarities. Results from two studies will be presented that addressed three related questions about the microbial ecology of soil C cycling: (i) do distinctly different microbial communities degrade plant litters the same way? (ii) how does plant litter quality affect succession patterns among microbial groups? (iii) which group(s) of microbes control rhizosphere priming of soil organic matter? While significantly less specific than $^{13}C$-RNA/DNA probing techniques, $^{13}C$-PLFA is a rapid and useful approach to determine how microbial community composition can affect ecosystem-scale C exchange processes.