Geophysical Research Abstracts
Vol. 17, EGU2015-6335-1, 2015
EGU General Assembly 2015

Distinct fungal and bacterial $\delta^{13}C$ signatures can drive the increase in soil $\delta^{13}C$ with depth

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Soil microbial biomass is a key precursor of soil organic carbon (SOC), and the enrichment in ^{13}C during SOC diagenesis has been purported to be driven by increasing proportions of microbially derived SOC. Yet, little is known about how the $\delta^{13}C$ of soil microbial biomass - and by extension the $\delta^{13}C$ of microbial inputs to SOC - vary in space, time, or with the composition of the microbial community. Phospholipid fatty acids (PLFA) can be analyzed to measure the variation of the natural abundance $\delta^{13}C$ values of both individual groups of microorganisms and the microbial community as a whole. Here, we show how variations of $\delta^{13}C_{PLFA}$ within the soil profile provides insight into C fluxes in undisturbed soils and demonstrate that distinct $\delta^{13}C$ of fungal and bacterial biomass and their relative abundance can drive the increase of bulk $\delta^{13}C_{SOC}$ with depth.

We studied the variation in natural abundance $\delta^{13}C$ signatures of PLFA in podzolic soil profiles from mesic boreal forests in Atlantic Canada. Samples from the organic horizons (L,F,H) and the mineral (B; top 10 cm) horizons were analyzed for $\delta^{13}C$ values of PLFA specific to fungi, G+ bacteria, or G- bacteria as proxies for the $\delta^{13}C$ of the biomass of these groups, and for $\delta^{13}C$ values of PLFA produced by a wide range of microorganisms (e.g. 16:0) as a proxy for the $\delta^{13}C$ value of microbial biomass as a whole. Results were compared to fungi:bacteria ratios (F:B) and bulk $\delta^{13}C_{SOC}$ values.

The $\delta^{13}C$ values of group-specific PLFA were driven by differences among source organisms, with fungal PLFA consistently depleted (2.1 to 6.4‰) relative to and G+ and G- bacterial PLFA in the same sample. All group-specific PLFA, however, exhibited nearly constant $\delta^{13}C$ values throughout the soil profile, apparently unaffected by the over 2.8‰ increase in $\delta^{13}C_{SOC}$ with depth from the L to B horizons. This indicates that bulk SOC poorly represents the substrates actually consumed by soil microorganisms in situ. Instead, our results suggest that soil microorganisms primarily consume substrates that exhibit constant $\delta^{13}C$ values throughout the soil profile, like root litter or dissolved organic carbon from litter leachates or root exudates that percolates through the soil column.

$\delta^{13}C$ values of PLFA produced by both fungi and bacteria, in contrast to the group specific PLFA, strongly increased with depth and were tightly correlated to F:B ratios (R^2 > 0.84), which decreased with depth. Because group-specific PLFA did not exhibit increased $\delta^{13}C$ with depth, the increase observed in the general biomarker $\delta^{13}C$ values, associated with the aggregated microbial community, was not the consequence of microbial incorporation of more ^{13}C enriched SOC at greater depth. Rather, the increase in community $\delta^{13}C$ reflects a shift in community structure towards more ^{13}C enriched bacteria with depth. Our results indicate that, higher $\delta^{13}C$ values associated with microbial biomass at a greater depth likely contributes to the increase in $\delta^{13}C_{SOC}$ with depth via more 13C enriched contributions from necromass to SOC.