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Stabilization of diverse microbial residues in California and Puerto Rico Forest Soils

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The contribution of C from the turnover of diverse microorganisms to stable C pools remains poorly understood. This study follows the turnover of 13C labeled nonliving residues from diverse microbial groups in situ in a temperate forest in California (CA) and a tropical forest in Puerto Rico (PR), during 5 sampling points per site- over a 3 and 2 year period, respectively. Microbial groups include fungi, actinomycetes, Gm(+) bacteria, and Gm(-) bacteria, isolated from CA and PR soils to obtain temperate and tropical isolates. Results indicated that, despite unique biochemical makeup among groups as determined by Py-GC-MS, microbial residues exhibited similar mean residence times (MRTs) within each site. A density fractionation approach isolated: a "light fraction" (LF), non-mineral aggregate "occluded fraction" (OF), and a "mineral bound fraction" (MF). Microbial C inputs were more stable in the OF and MF than the LF throughout the course of the study at both sites. There were no significant differences in 13C recovery among microbes in any PR fractions, despite minor differences in overall MRTs. In CA, there were some significant differences in 13C recovery among microbial inputs in the LF and OF, which related to 13C recoveries in whole soils. In the CA MF, microbial recoveries did not differ, and low variability among treatments was observed. Results support increased protection of microbial C via association with the mineral matrix; however, differential sorption of some microbial isolates over others was not observed. Overall results suggest that inherent recalcitrance of microbial residues may be more important to determining its stability in CA soils when it is 1) unassociated with the mineral matrix (LF); or 2) occluded within aggregates; compared with that strongly associated with mineral surfaces (MF). The overall composition of SOM in fractions also differed, with a greater concentration of benzene and N compounds in the MF; lignin and phenol compounds in the LF; and aliphatics in the OF. Such differences among fractions in OM chemistry suggest unique stabilization mechanisms for the distinct SOM pools. SOM chemistry was most similar in the LF across sites, compared with the OF and MF, suggesting that differences in SOM chemistry between sites may be more attributed to differential decomposition processes rather than unique litter quality inputs. Compound-specific turnover for temperate fungal isolates suggested conservation and transformation of compounds from input residues. A greater 13C enrichment of N-compounds and polysaccharides in soils relative to other compounds indicated that the composition of original inputs continued to influence the chemistry of residual and/or decomposition products, even after 2 and 3 years in CA and PR, respectively. Evidence for transformation of input compounds was observed in the form of 13C enrichment of novel compounds in soils (that were not present in original residues). Further, several compounds exhibited little change to an increase in 13C/12C over time in soils, serving as further evidence for differential stability of unique compounds at the molecular level.