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Substrate Complexity Dictates Metabolic Strategy: Multi-Omics Analysis of Soil Sugar Catabolism

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Soil microbial communities drive global carbon cycling, with complex polymers constituting an important component of soil organic matter (Fig. 1). Yet the metabolic mechanisms underlying the utilization of these polymers by soil microbes remain poorly understood compared to the catabolism of labile monomers[1,2]. This knowledge gap is critical given that complex polysaccharides play essential roles in carbon cycling and long-term persistence in soils[3–6]. Research from the last fifteen years suggests that organic matter persistence depends on ecosystem-scale properties such resident microbial populations rather than intrinsic chemical recalcitrance[7,8], yet substrate molecular complexity clearly influences degradation rates and pathways, suggesting chemical structure retains importance. This motivates addressing a fundamental scaling challenge: How does metabolism differ across molecular complexity gradients from monomers to polymers[10,11]?

In this study, we amended California grassland soils with ^{13}C-labeled sugars and hemicellulose and traced carbon flow through microbial metabolism at the community level. By integrating metatranscriptomics, ^{13}C-exometabolomics, and ^{13}C-quantitative stable isotope probing (qSIP) of microbial DNA over one month, we identified correlations among microbial gene expression patterns, exometabolite ^{13}C-labeling dynamics, and taxon-specific growth responses, which highlighted that the same soil microbial community exhibited distinct metabolic responses to substrate pulses across molecular complexity gradients. Our results demonstrate that microbial communities coordinate complex, substrate-dependent metabolic responses that are beyond the predictions derived from pure culture studies alone. These findings advance mechanistic understanding of how microbial genomic traits scale to ecosystem-level biogeochemical cycles.

References

1. Costa et al. (2018), Front. Microbiol. 9, 1636.
2. Schimel & Schaeffer (2012), Front. Microbiol. 3, 348.
3. Nadell et al. (2016), Nat. Rev. Microbiol. 14, 589-600.
4. Tisdall & Oades (1982), J. Soil Sci. 33, 141-163.
5. Redmile-Gordon et al. (2020), Geoderma 363, 114143.
6. Sokol et al. (2022), Nat. Rev. Microbiol. 20, 415-430.
7. Schmidt et al. (2011), Nature 478, 49-56.
8. Lehmann et al. (2020), Nat. Geosci. 13, 529-534.
9. Cordero & Datta (2016), Curr. Opin. Microbiol. 31, 227-234.
10. Berlemont & Martiny (2015), Appl. Environ. Microbiol. 81, 1513-1519.
11. Nuccio et al. (2020), ISME J. 14, 999-1014.

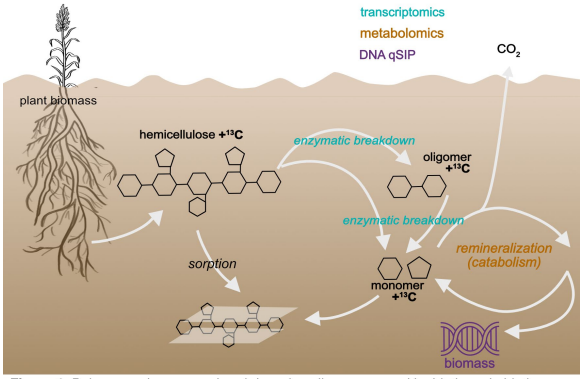


Figure 1. Polymer and monomer breakdown in soil are governed by biotic and abiotic processes, which together determine whether the SOM is respired, recycled, or stabilized into persistent pools. qSIP = quantitative stable isotope probing.