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Disentangling the drivers of soil organic matter decay as temperature changes by integrating reductionist systems with soil data

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Accurately predicting decomposition rates of soil organic matter (SOM) as temperature increases is critical for projecting future atmospheric [CO_2]. SOM decay is catalyzed by exo-enzymes (EEs) produced by microorganisms and secreted into the soil. Microbes take up liberated resources for metabolic processes and release diverse compounds, including CO_2. Historically, investigations of the influence of temperature on heterotrophic CO_2 release have focused on CO_2 response, including its isotopic composition; recent studies also assess EE activity and microbial community composition. However, it is difficult to generalize from such studies how temperature will influence SOM decay and CO_2 release because the responses of EEs, microbial resource demand, biomass production rates, and respiration rates are not parsed. Quantifying the individual temperature responses of all of these processes in unaltered soil is not tractable. However, we can use experimentally simplified systems to quantify fundamental biochemical and physiological responses to temperature and compare these results to those from environmental samples. For example, we can quantify the degree to which EE kinetics in isolation induce changes in availability of microbially assimilable resources as temperature changes and calculate associated changes in relative availability of assimilable carbon and nitrogen (C:N flow ratio), in isolation from altered microbial resource demand or uptake. We also can assess EE activity and CO_2 release at different temperatures in diverse soils, integrating temperature responses of EE kinetics and microbial communities. Discrepancies in the temperature responses between real soils and isolated enzyme-substrate reactions can reveal how adaptive responses of microbial communities influence the temperature responses of soil heterotrophic CO_2 release.

We have shown in purified reactions that C:N flow ratios increase with temperature at pH 4.5, but decline between pH 6.5 and 8.5. If soil microbes exhibited no change in resource demand or C allocation with altered C:N flow ratios and if relative C availability was tightly coupled to respiration, we would expect variation in C:N flow ratios predicted by purified solutions to be expressed in analogous, relative patterns of C mineralization. However, the positive response of heterotrophic CO_2 release to similar temperature increases in five strongly acidic forest soils (three boreal, one cool temperate, and one warm temperate) was much smaller than in a neutral-pH grassland or an alkaline desert, the opposite of what we might predict if C:N flow ratio was the only driver of respiratory responses to temperature. We also observe distinct d13C of CO_2 respired from pure cultures in which substrate composition and availability are strictly controlled as temperature changes, reflecting fundamental shifts in C flux through metabolic pathways. These changes in d13C-CO_2 with warming are greater than those observed in soils. Combined, these CO_2 and d13C-CO_2 data suggest that soil microbial adaptation to temperature is a meaningful driver of heterotrophic respiratory responses to temperature. We highlight the utility of reductionist experimental systems for characterizing fundamental SOM decay rates and changes in microbial C metabolism at different temperatures, and integrating them with analogous data derived from soils to quantify the role of microbial adaptation as a driver of SOM decay.