

## Microbial diversity drives specialization in litter decomposition and metabolic products

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Soil C formation and loss is controlled by the chemical complexity of substrate inputs and the ability of microbes to efficiently use those substrates to drive growth and decomposition. Litterbag studies infer that microbes exposed to a wide range of substrate complexity have greater functional diversity in their decomposition pathways than microbes exposed to only simple substrates. Here, we test this theory using DNA stable isotopic probing and metabolomics to quantitatively measure the fate of litters that vary in complexity into microbial biomass and metabolic products. We used trees that differ in mycorrhizal association, ectomycorrhizal (ECM) vs. arbuscular mycorrhizal (AM), as a model system to investigate the extent to which litter complexity and microbial community composition influence microbial product formation. We hypothesized that high quality AM litter would enhance microbial metabolism to a greater extent than low quality ECM litter. Further, we predicted that due to microbial specialization in ECM soils, decomposition of either litter type would be faster than AM soils. To test these hypotheses, we incubated isotopically labeled <sup>13</sup>C AM (tulip poplar, *Liriodendron tulipifera*) and ECM (red oak, *Quercus rubra*) litter in soils from AM and ECM dominated plots in a 100-year-old forest in West Virginia. In contrast to our hypotheses, we found evidence that different microbial groups favor AM vs ECM litter in AM soils leading to divergent decomposition products. Fungi and bacteria decomposing either litter type in AM soils were different and more diverse than microbes in the ECM soils. While overall, fungi incorporated more litter into biomass than bacteria, AM soil fungal communities that decomposed AM litter were distinct from those that decomposed ECM litter. This variable preference for litter shifted the metabolic pathways that were used and produced distinctly different microbial products. In contrast to the AM soils, ECM soil microbes were not flexible in utilizing the added litter substrate, nor did the resulting metabolic products differ with litter type. This may be driven by lower diversity in fungal and bacterial communities in the ECM soils. Moreover, ECM soil communities exhibited little distinction in the type of litter incorporated into biomass, resulting in a single metabolic pathway that produced comparable microbial products. These results challenge our understanding of microbial control on decomposition and suggest that microbial diversity drives substrate use.