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Leaf litter decomposition by microbial communities compared among forest stands dominated by arbuscular versus ectomycorrhizal fungi

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Trees are the dominant primary producers in forest ecosystems and play a central role in global carbon (C) cycling. A substantial fraction of tree-assimilated C enters the soil as leaf litter, where it is decomposed by diverse microbial consortia. Whether C from litter is rapidly mineralized to CO_2 or accumulates as soil organic matter largely depends on the functional traits and activities of soil microbes. Understanding the factors shaping litter-decomposing microbiomes is therefore essential for predicting the capacity of forest soils to act as C-sinks.

Most tree species form symbiotic associations with either arbuscular mycorrhizal (AM) or ectomycorrhizal (ECM) fungi. Litter from AM-associated trees typically contains more accessible nutrients and decomposes faster than the more recalcitrant litter from ECM-associated trees. ECM fungi possess broad enzymatic repertoires and, in some taxa, oxidative mechanisms for nutrient mobilization, whereas AM fungi largely depend on interactions with other microbial taxa. Although these contrasts are well established, the multipartite interactions among trees, mycorrhizae, and other soil microorganisms, and particularly the functional differences of decomposer microbiomes in AM- and ECM-dominated forests, remain insufficiently understood.

To address this, we conducted an *in-situ* incubation experiment using litter from *Acer saccharum* (AM-associating) and *Quercus alba* (ECM-associating) in AM- and ECM-dominated forest stands in south-central Indiana, USA. We assessed the changes in the composition of decomposer microbiomes with progressing litter decay and seasonal dynamics in the litter and adjacent soil by metabarcoding of the 16S rRNA and ITS2 regions after 1, 3, 6, and 12 months. Additionally, we performed metatranscriptomic analyses for decomposer communities after 3 months. Combined with existing metagenomic data, these approaches will enable us to identify microbial taxa and processes driving litter decomposition, C- and nutrient processing across contrasting mycorrhizal contexts.

Initial results indicate that fast-growing, opportunistic *Aspergillaceae*, known to utilize readily available, labile substrates, dominated the early decomposition of AM-litter. In contrast, *Sordariomycetes*, capable of degrading recalcitrant compounds, were more abundant in ECM-

litter. These patterns are consistent with our expectations and demonstrate the potential of our experimental setup to resolve the functions of microbiome members beyond mycorrhizal fungi. Ultimately, this study will enhance our understanding of the microbial taxa that are critical for C cycling in forests and of how decomposer microbiome dynamics are shaped by dominating mycorrhizal types.