**Protein-based stable isotope probing (protein-SIP) - bacteria dominate the short-term decomposition of 15N-labeled plant-derived organic matter**

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Soil inhabiting microbes both decompose plant-derived and create soil organic matter. Fungi are well-known to be the main decomposers of plant-derived material but both synergistic and antagonistic relations to bacteria had been reported.

In this study, we used 16S and 18S rDNA gene profiling and functional metaproteomics (protein-SIP) to characterize the composition of a soil microbial community decomposing 15N-labeled plant-derived organic matter (OM). The genetic results showed an increase in fungi and Proteobacteria affiliated with the utilization of plant-derived material within the first days of exposure. Similarly, metaproteomic analysis revealed Proteobacteria as the most abundant phylum followed by Actinobacteria and Ascomycota.

Finally, protein-SIP revealed copiotrophic behaviour for Rhizobiales belonging to Proteobacteria, Actinomycetales belonging to Actinobacteria and Chroococcales belonging to Cyanobacteria as these phylotypes immediately incorporated 15N-labeled plant-derived OM. Conversely, the fungal taxa Saccharomycetales and the bacterial Enterobacteriales, Pseudomonadales, Sphingomonadales and Xanthomonadales displayed oligotrophic behaviour.

This study unveiled that, in contrast to the dominance of fungi during prolonged leaf litter decomposition, mostly bacteria were involved in the short-term utilization of plant-derived OM.