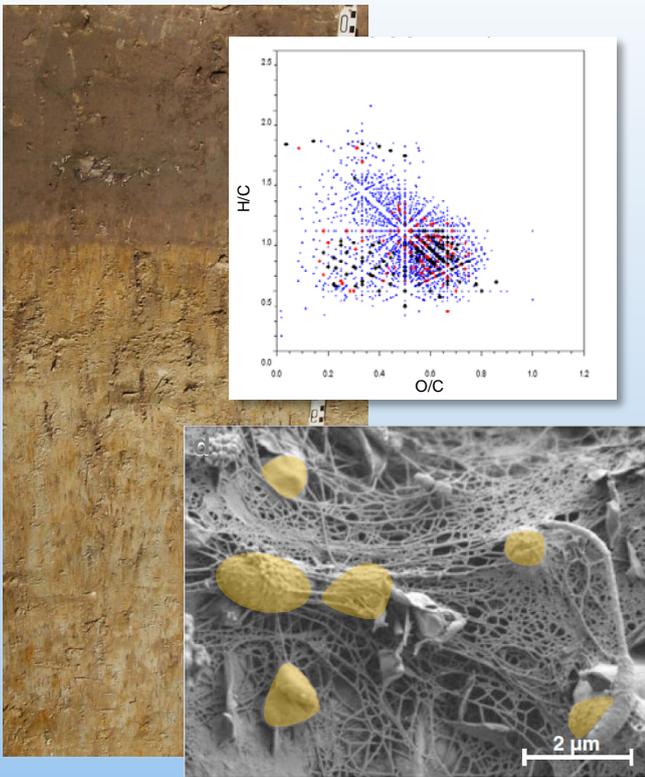


SOM_{mic}

Microbial Contribution and Impact on Soil Organic Matter, Structure and Genesis



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addition that goes beyond simple eco-enzyme C:N:P stoichiometry with unclear consequences for soil C sequestration.

IP17 Soil microbial carbon use efficiency and biomass mean residence times depending on soil depth and stoichiometry

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KEYWORDS Soil microbial carbon use efficiency, soil depth, soil stoichiometry, ecophysiology

The ratios of bioavailable elements in soils hardly ever meet the nutritional demands of soil microbial communities. Yet, the microbial biomass stoichiometry is relatively constant. To maintain their biomass stoichiometry, microbial communities might adjust their carbon use efficiency (CUE), defined as the organic C taken up that is allocated to growth. So far, it is not well understood how microorganisms adjust their CUE and the mean residence time (MRT) of the microbial biomass to ratios of available elements in soil due to a lack of suitable methods. Microbial CUE has been measured by determining the incorporation and respiration of C from specific ¹³C-labeled substrates. However, this approach confounds microbial CUE with the specific use efficiency of a given substrate. Moreover, the approach is associated with a large uncertainty since soil microorganisms do not only take up C from the labeled compound that is added, but also from the soil organic matter, and they may use both sources at very different rates.

We developed a method to determine both microbial CUE and MRT of the microbial biomass independently of substrate. The new method is based on the labeling of microbial genomic DNA with ¹⁸O from ¹⁸O-H₂O. Since genomic DNA is only synthesized when cells are dividing, the incorporation of ¹⁸O into genomic DNA can be used to calculate the microbial growth rate. Based on the growth rate and the respiration rate, microbial CUE is estimated. Moreover, the method can be used to assess the MRT of the microbial biomass C in soil. We show results on microbial CUE and MRT of the microbial biomass in soil profiles and in grassland soils of a long-term fertilization experiment. With increasing soil depth, the rates of C uptake into the microbial biomass decreased, and the MRT of the microbial biomass increased. However, the microbial CUE did not change with soil depth. In the grassland experiment, we found that nitrogen but not phosphorus or potassium fertilization decreased microbial C uptake and increased microbial CUE, while the MRT was not affected by fertilization. We will discuss the implications of soil microbial CUE and MRT of the microbial biomass for C cycling.

IP18 Are plants or microbiota regulating SOM stoichiometry in forest soils?

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KEYWORDS SOM elemental analysis, recultivated soil, forest, dominant tree species.

The tree species influence on soil C accumulation and soil organic matter (SOM) stoichiometry is still not fully clear. We compared soil organic carbon (SOC) stocks, N, S, H, O as well as microbial (C_{mic}) and fungal C mass (C_{fung}) for the organic layer and three mineral horizons (0-5 cm, 5-10 cm, 10-30 cm) under five widely distributed tree species in the temperate region: Black pine (*Pinus nigra*), Common spruce (*Picea abies*), Douglas fir (*Pseudotsuga mienziessii*), European beech (*Fagus sylvatica*) and Red oak (*Quercus rubra*). The study was carried out at the spoil heap and recultivation area Sophienhöhe with