



## **The role of soil microarchitecture on microbial processes and community structure in different soil depths**

Victoria Martin (1), Philipp Gündler (1), Bruna Imai (1), Stefan Gorka (1), Alberto Canarini (1), Christina Kaiser (1,2), Andreas Richter (1,2)

(1) Department of Microbiology and Ecosystem Science, University of Vienna, Austria, (2) International Institute for Applied System Analysis (IIASA) Evolution and Ecology Program, Laxenburg, Austria

Soil aggregates are a key component to understand soil organic carbon (SOC) dynamics on the scale at which microbes interact. Indeed, occlusion within structural aggregates is thought to be an important mechanism mediating SOC persistence. However, detailed information relating C cycling to microbial communities via a mechanistic understanding of their physiology within different aggregate size classes is often lacking. Also it is known that the mean residence time of SOC increases strongly with soil depth. Therefore, depth might modulate the contribution of aggregates to soil C turnover due to the different environmental conditions affecting soil microbes. In this study we aimed at analysing parameters related to soil C processing, microbial physiology and community structure for three different aggregate classes at three different soil depths.

Soil cores from three different depths (0-10 cm, 20-30 cm, 35-45 cm) were taken at a beech forest in Vienna. After air drying and subsequent dry-sieving into three different aggregate size fractions (macroaggregates 2 mm-250  $\mu\text{m}$ , microaggregates 250-63  $\mu\text{m}$ , aggregates in the silt- and clay-size <63  $\mu\text{m}$ ), soils were rewetted and pre-incubated for seven days, before microbial carbon use efficiency (CUE), and gross growth and turnover rates were analysed using a method based on the incorporation of  $^{18}\text{O}\text{-H}_2\text{O}$  into microbial DNA on each aggregate class. Additionally, we measured C and N pools, microbial community composition based on phospholipid fatty acids (PLFAs) and the carbon isotope composition of aggregates carbon and PLFAs. We also measured activity of key extracellular enzymes involved in SOC turnover.

Increasing soil depth significantly decreased C and N concentration which did not differ among different aggregate size classes. Additionally, no change in the distribution of aggregate sizes with depth was detected. Soil  $\delta^{13}\text{C}$  values were more enriched with depth and in the smallest aggregates of the top soil, clearly reflected a higher degree of OM turnover. Enriched  $\delta^{13}\text{C}$  values with depth were also found in microbial PLFAs. Higher bacterial and fungal biomass and substrate concentrations in the top soil horizon resulted in generally higher enzymatic activities. However, we observed a higher contribution of enzymes degrading microbially-derived substrates with decreasing aggregate size. Microbial mass specific respiration decreased in deeper soil layers but did not change between different aggregate sizes. However, mass specific growth rates and turnover times did not change in different aggregate size classes or soil layers. Microbial CUE values were not different between soil depths and higher values were only found in the smallest aggregate group of the top soil layer.

Taken together, our results suggest that even though differences in extracellular activities were found, there are no intrinsic differences concerning microbial physiology in terms of mass specific respiration- and growth-rates, CUE, and turnover for the examined aggregate size classes. Moreover, soil depth seems to be a more important control for shaping microbial community structure than soil microarchitecture in our study.