



The role of plant functional group diversity on soil carbon cycling processes in a simple model soil

Marie-Louise Spalinger^{1,2}, Pascal A Niklaus², David Sebag³, Eric Verrechia⁴, Anna-Liisa Laine^{2,5}, Luiz A Domeignoz-Horta^{2,6}

¹Graduate Program in Quantitative Environmental Sciences, University of Zurich, Zurich, 8057, Switzerland

²Department of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, 8057, Switzerland

³IFP Energies Nouvelles, Rueil-Malmaison, 92852, France

⁴Faculty of Geosciences and the Environment, Institute of Earth Surface Dynamics, University of Lausanne, Lausanne, 1015, Switzerland

⁵Research Centre for Ecological Change, Organismal and Evolutionary Biology Research Programme, Faculty of Biological and Environmental Sciences, University of Helsinki, Helsinki 00014, Finland

⁶Université Paris-Saclay, INRAE, AgroParisTech, UMR EcoSys, 91120 Palaiseau, France

Abstract:

The transformation process of plant biomass into soil organic carbon (SOC) is driven by soil microorganisms. Meanwhile particulate organic matter derived from plants shape the belowground microbial communities and influences their activity and growth. Understanding how microorganisms converge labile plant compounds into more persistent soil organic matter is central to foster our knowledge about the terrestrial C-cycling. Microbial carbon use efficiency (CUE) represents an informative parameter as it captures the efficiency at which carbon is incorporated into new microbial biomass. Plant diversity seems to play a crucial role when it comes to carbon storage in soils, as previous studies showed that increasing plant diversity was associated with higher carbon stocks. While those previous studies showed that plant diversity is associated to higher SOC stocks, we still lack in understanding the role of distinct plant functional types and their combinations in driving soil C cycling. This study is based on a laboratory incubation experiment, that focuses on the mechanisms influencing the microbial-derived SOC formation and its persistence in soils. Above and below ground biomass from distinct plant functional types (N fixers and no N fixers, deep rooting- and shallow rooting plants, composed of eight plant species) and their combinations were added to a model soil and inoculated with a microbial community extracted from an agricultural soil. Their decomposition through time is being evaluated. We hypothesize that different qualities of plant biomass influence microbial communities regarding their activity and composition. We further hypothesize that the molecular diversity of different kinds of plant material added to the model soil are expected to affect the composition and persistence of SOC. In this ongoing decomposition experiment, we analyze at different points in time the plant phytochemical signature, the soil microbial community composition and diversity, the cumulative respiration, CUE, the thermal-stability and composition of SOM. Contrary to the hypothesis, our first results show that respiration rates were higher in soils with a more diverse combination of plant functional groups compared to the ones with a lower level of diversity. Our following up measurements will help us better understanding how plant functional groups influence soil C-cycling.