



## Microbial carbon turnover in the plant-rhizosphere-soil continuum

Ashish Malik (1), Helena Dannert (1), Robert Griffiths (2), Bruce Thomson (2), and Gerd Gleixner (1)

(1) Max Planck Institute for Biogeochemistry, Jena, Germany, (2) Centre for Ecology and Hydrology, Wallingford, Oxfordshire, United Kingdom

Soil microbial biomass contributes significantly to maintenance of soil organic matter (SOM). It is well known that biochemical fractions of soil microorganisms have varying turnover and therefore contribute differentially to soil C storage. Here we compare the turnover rates of different microbial biochemical fractions using a pulse chase  $^{13}\text{C}$  plant labelling experiment. The isotope signal was temporally traced into rhizosphere soil microorganisms using the following biomarkers: DNA, RNA, fatty acids and chloroform fumigation extraction derived microbial biomass size classes. C flow into soil microbial functional groups was assessed through phospholipid and neutral lipid fatty acid (PLFA/NLFA) analyses. Highest  $^{13}\text{C}$  enrichment was seen in the low molecular weight (LMW) size class of microbial biomass ( $\Delta\delta^{13}\text{C} = 151\text{‰}$ ) and in nucleic acids (DNA: 38‰ RNA: 66‰) immediately after the pulse followed by a sharp drop. The amount of  $^{13}\text{C}$  in the high molecular weight (HMW) microbial biomass (17-81‰) and total fatty acids (32-54‰) was lower initially and stayed relatively steady over the 4 weeks experimental period. We found significant differences in turnover rates of different microbial biochemical and size fractions. We infer that LMW cytosolic soluble compounds are rapidly metabolized and linked to respiratory C fluxes, whereas mid-sized products of microbial degradation and HMW polymeric compounds have lower renewal rate in that order. The turnover of cell wall fatty acids was also very slow. DNA and RNA showed faster turnover rate; and as expected RNA renewal was the fastest due to its rapid production by active microorganisms independent of cell replication.  $^{13}\text{C}$  incorporation into different functional groups confirmed that mutualistic arbuscular mycorrhizal fungi rely on root C and are important in the initial plant C flux. We substantiated through measurements of isotope incorporation into bacterial RNA that rhizosphere bacteria are also important in the initial C conduit from plants. Other saprophytic fungi and bacteria show a delayed  $^{13}\text{C}$  incorporation pattern which could suggest secondary  $^{13}\text{C}$  assimilation often indicative of trophic interactions. Thus, different soil microbial biochemical fractions as well as functional groups show differential C turnover which could have implications on soil C storage.