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Biochemistry of hexose and pentose transformations in soil analyzed by position-specific labeling and ^{13}C-PLFA

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ABSTRACT

Microbial transformations are key processes of soil organic matter (SOM) formation, stabilization and decomposition. Combination of position-specific ^{13}C labeling with compound-specific ^{13}C-PLFA analysis is a novel tool to trace metabolic pathways. This combination was used to analyze short-term transformations (3 and 10 days after tracer application) of two key monosaccharides: glucose and ribose in soil under field conditions. Transformations of sugars were quantified by the incorporation of ^{13}C from individual molecule positions in bulk soil, microbial biomass (by CFE) and in cell membranes of microbial groups classified by ^{13}C-PLFA.

The ^{13}C incorporation in the Gram negative bacteria was higher by one order of magnitude compared to all other microbial groups. All of the ^{13}C recovered in soil on day 3 was allocated in microbial biomass. On day 10 however, a part of the ^{13}C was recovered in non-extractable microbial cell components or microbial excretions. As sugars are not absorbed by mineral particles due to a lack of charged functional groups, their quick mineralization from soil solution is generally expected. However, microorganisms transformed sugars to metabolites with a slower turnover. The ^{13}C incorporation from the individual glucose positions into soil and microbial biomass showed that the two main glucose utilizing pathways in organisms – glycolysis and the pentose phosphate pathway – exist in soils in parallel. However, the pattern of ^{13}C incorporation from individual glucose positions into PLFAs showed intensive recycling of the added ^{13}C via gluconeogenesis and a mixing of both glucose utilizing pathways. The pattern of position-specific incorporation of ribose C also shows initial utilization in the pentose phosphate pathway but is overprinted on day 10, again due to intensive recycling and mixing. This shows that glucose and ribose – as ubiquitous substrates – are used in various metabolic pathways and their C is intensively recycled in microbial biomass.

Analyzing the fate of individual C atoms by position-specific labeling deeply improves our understanding of the pathways of microbial utilization of sugars (and other compounds) by microbial groups and so, of soil C fluxes.

1. Introduction

Soil organic carbon (SOC) plays a major role within the global C cycle as soils can function as a source or sink of atmospheric C. Plant residues and rhizodeposits are the main sources of organic matter in soils (Rasse et al., 2005). Therefore, many studies have focused on decomposition, microbial utilization and stabilization processes of C from these sources in soils.

The low molecular weight organic substances (LMWOS) play a crucial role within the C cycle in soil. Although their portion of SOC is quite low, they represent the SOC pool with the highest turnover (1–10 h mean residence time) and a quantitatively relevant gross flux of C passes through this pool (30% of total CO_2 efflux) (van Hees et al., 2005). LMWOS are defined as the lightest components of dissolved organic carbon (DOC) with a molecular weight lower than 250 Da (Boddy et al., 2007). Their main sources are exoenzymatic depolymerization of above- and belowground litter as well as rhizodeposition. Microorganisms determine the fate of LMWOS in

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