

## Tagungsnummer

V4

## Thema

Kommission III: Bodenbiologie und Bodenökologie

Biogeochemische Hotspots im Boden

## Autoren

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## Titel

Microbial carbon turnover in the detritusphere

## Abstract

Microbial decomposition processes at the soil-litter interface involves a complex food web including fungi, bacteria, and archaea that compete for the organic matter. During the decomposition, the nutrient quantity and quality changes as well as the microbial community composition. It is still a challenge to identify and quantify active microbial species in concurrency with their absolute contribution to the carbon (C) turnover. In the frame of the DFG-Project (FOR 918) "Carbon flow in belowground food webs assessed by isotope tracers" we determined the C flow and turnover of differently aged maize litter in bacteria and fungi of an arable soil. A microcosm experiment was set up with C-13-labeled and unlabeled maize litter on top of soil cores. A reciprocal transplantation of the labeled litter on soil cores with unlabeled litter allowed us to follow the C flow into different microbial groups at the early (0-4d), intermediate (4-12d) and late stage (28-36d) of litter decomposition. We analyzed microbial CO<sub>2</sub> respiration, microbial biomass and PLFA pattern in the top 3 mm of the soil cores. To identify and quantify microbial species feeding on the substrate and to assess their degree of C-13 assimilation, DNA stable isotope probing followed by gene-targeted sequencing of bacteria and fungi are currently performed on the soil metagenome. We expected specific microbial communities (copio- and oligotrophic) involved in maize litter decomposition at the different stages of litter decay. During the initial days of the experiment, up to 17% of the CO<sub>2</sub>-C was maize-derived C. The C-13 content in the CO<sub>2</sub> decreased with continuous decomposition of the litter. The highest absolute amount of maize-derived C was found in gram-positive bacteria in the early stage of litter decomposition. For fungi, the highest maize C incorporation was in the intermediate stage of litter decomposition. We calculated a faster C turnover in the fungal biomass than in the bacterial biomass for all three decomposition stages. But during the later stage of litter decomposition, maize-derived C was less utilized by both bacteria and fungi. These results will be concluded by the quantitative DNA-SIP method to provide a species-resolved contribution to the C turnover in the microbial food web at different decomposition stages in the detritusphere.