

FUNCTIONAL GROUPS, ACTIVITY & INTERACTIONS IN TROPHIC NETWORKS

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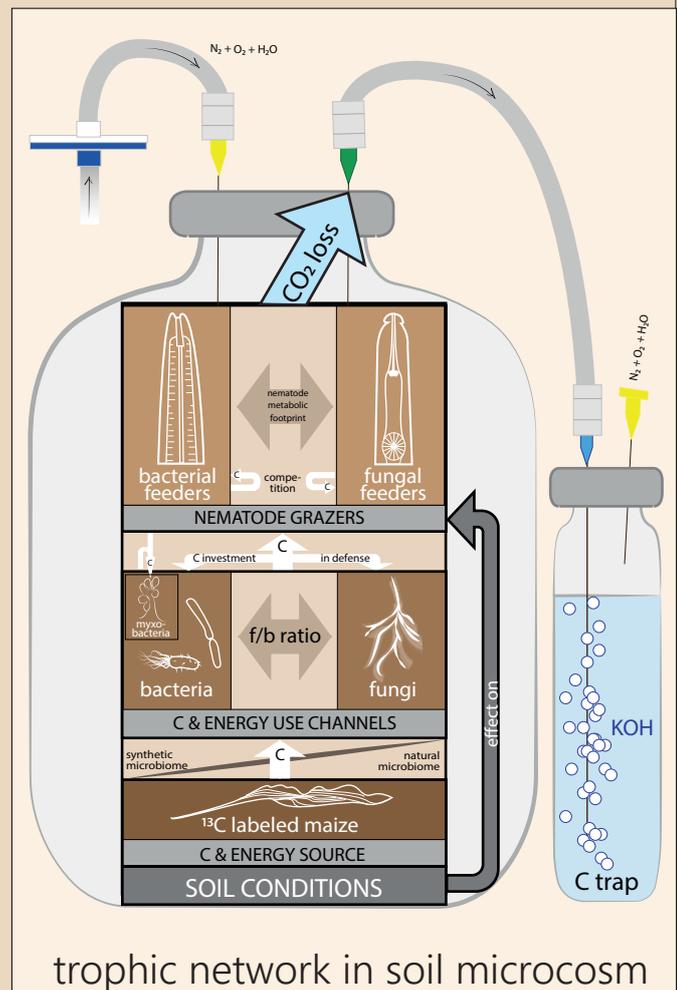
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INTRODUCTION

The aim of the SPP 2322 „Systems ecology of soils – energy discharge modulated by microbiome and boundary conditions is to integrate a thermodynamic description of the soil system to gain a systemic view on energy and matter fluxes and their interactions with living and non-living soil components. Within this scientific consortium the present project investigates the carbon (C), nutrient and energy flow in soil microbiome. Among these microbiota, nematodes are the most abundant and diverse multi-cellular organisms, with functional groups at each trophic level of the micro-food web. The combination of their life history traits with functional guilds allows for determination of decomposition pathways, food web disturbance, enrichment, and structure. Further, metabolic footprints, i.e. trait-based measurements of morphological (body mass) and physiological (respiration) characters, correlate with environmental properties and mirror e.g., the responsiveness to resource pulses. Nematodes are therefore an ideal model group to assess the C flux to and activity of higher trophic levels in the microbiome and to relate this to energy dissipation.



OBJECTIVES

Goal 1 Determine the impact of functional groups of grazers as well as their interactions (e.g. competition) on the C and energy flux along the bacterial & fungal channel (**WP1**).

Goal 2 Assign the changes in grazer diversity, activity and C flux to higher trophic levels induced by different soil environmental conditions (soil type, SOM content, substrate, moisture, temperature). (**WP2**)

SAMPLING

To establish C pools, C fluxes & carbon use efficiency (CUE), ¹³C labeled maize, non-labeled maize and no maize are introduced to 50 g farmyard-manure fertilized sandy loam soil in microcosms with circulating air-flow. The soil is kept at 20 °C, its water potential is pF 2,5 and bulk density 1,15 g/cm³. Sampling occurs destructively in triplicates at 4 time points i.e. day 4, 8, 16 & 32. Released CO₂ is measured regularly. Nematode abundance, trophic and taxonomic diversity is assessed post-sampling.

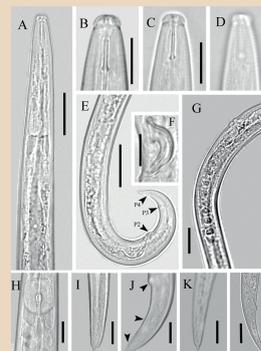
NATURAL MICROBIOME

The natural microbiome of dried & re-watered soil is amended with bacteriovores, fungivores, or no nematodes.



bacterivore
Acroboloides buetschlii

no additional
nematodes



fungivore
Aphelenchoides saprophilus

Calorimetric measurements are performed to relate the interactions in the soil microbiome to energy turnover. By PLFA- & DNA-SIP (stable isotope probing), amplicon & metagenome sequencing it is possible to establish microbial identities, succession & functional niche partitioning. C pools are calculated via $\delta^{13}\text{C}$ signatures of CO₂. $\delta^{13}\text{C}$ bulk analysis of nematodes provides C assimilation rates.

SYNTHETIC MICROBIOME

To gain a mechanistic understanding of interactions in soil microbiota, soil with a defined microbial & nematode community is used (30 bacterial species (Gram+ & Gram-), 2 fungi species, *Acroboloides buetschlii*, 3 species of myxobacteria). Myxobacteria are known for their 'pack-hunting' strategy, feeding on bacteria as well as nematodes, therefore introducing more complexity into the soil micro-food web. The impact of ecological interactions among bacterial grazers on energy & matter turnover in the soil microbiome is further investigated.