Effects of biodiversity on the flow of carbon from aboveground to belowground systems

(Tracing the photosynthetically fixed $\delta^{13}C$ through soil microbes in a continuous labelling experiment)

[1]Mellado-Vázquez P. G., [1]Lange M., [2]Landais D., [2]Piel C., [2]Escape C., [2]Devidal S., [2]Ravel O., [2]Milcu A., [2]Roy J., [1]Gleixner G.

[1]Max Planck Institute for Biogeochemistry Jena; [2] The National Center for Scientific Research-CNRS, Ecotron

pmellado@bgc-jena.mpg.de

I. Introduction

High plant diversity increases plant biomass, carbon sequestration and microbial activity in soils [1]. The importance of soil microorganisms as mediators of decomposition and accumulation of soil organic matter is well documented [2]. However, the effect of biodiversity on the activity of different soil microbial groups has not yet been studied. The differentiation of processes carried out by diverse microbial groups in soils is important in terms of understanding the belowground carbon cycle. Here, we study the influence of biodiversity on the ability of soil microorganisms to feed from recently photosynthesized carbon. We traced $\delta^{13}C$ into different microbial groups (Table 1), after ~4 weeks of continuous labeling with $\delta^{13}CO_2$, in plant diversity experiment with two diversity levels: 4 (Fig. 2a) and 16 (Fig. 2b) plant species richness (PSR). Abundance, structure and $\delta^{13}C$ values of the microbial community were investigated using phospholipid fatty acid (PLFA) and neutral lipid fatty acid (NLFA) analysis.

Fig.1 Ecotron facility (see methods)

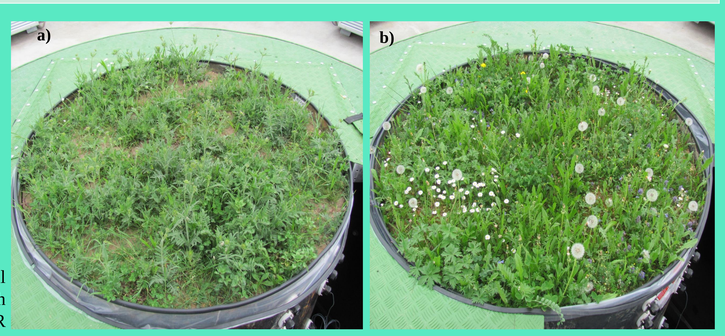


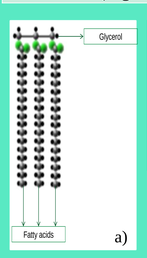
Fig. 2 Soil Monoliths with a) 4 ; b) 16 PSR

III. Results

- **Total amount of PLFA (31.3-36.1 µg g^{-1}) and NLFA (22.3-35.6 µg g^{-1}) were higher in the topsoil layer than in the deeper-soil layer (PLFA= 17.9-18.9 µg g^{-1}; NLFA= 16.6-26.8 µg g^{-1}) (Fig. 3 a, b)**
- **Plant diversity (Fig. 3 a, b, p <0.0019) have a significant effect on NLFA concentrations in both soil layers**
- **The microbial community composition did not varied significantly among soil depths and plant species richness (data not shown)**
- **Among all microbial groups differentiated, AMF (arbuscular mycorrhizal fungi) had the highest ^{13}C enrichment (Fig. 4 a, b) in both soil depths**
- **Higher $\Delta^{13}C$ enrichment values of AMF were found in soil with higher plant diversity (Fig. 4 a, b)**

II. Experimental site and Methods

The Ecotron facility (Montpellier, France) (Fig. 1) allows us to simulate and control ecosystem conditions like: temperature, gas fluxes and precipitation. The application of stable isotopic labeled tracers can also be performed. We installed 12 soil monoliths into individual macrocosms where the environmental conditions of Jena, Germany were reproduced. The application of label $^{13}CO_2$ allowed us to trace the flow of C into soil microorganisms. In July, 2013, 3 soil samples from 0-5 cm and 3 from 5-10 cm depth were collected in each macrocosm. The samples were sieved to > 2 mm; root picked and stored at -20 °C until PLFA (Fig. 5b) and NLFA (Fig. 5a) extraction (Fig. 6) [7, 8]



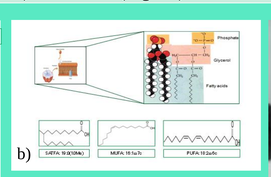
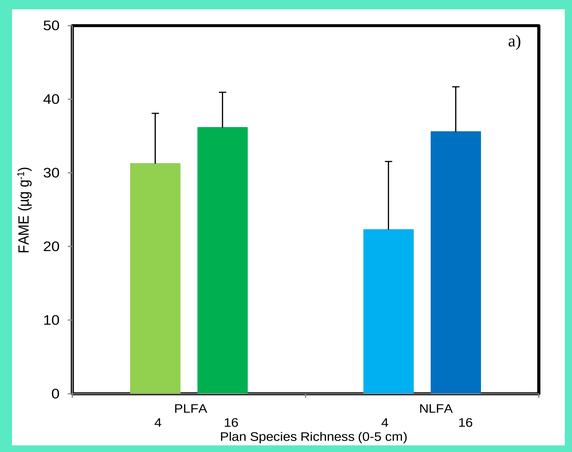


Fig. 5. a) NLFA and b) PLFA representations

Fig. 6 PLFA and NLFA extraction and measurement in GC-FID and GC-IRMS systems

IV. Conclusions

- **Arbuscular mycorrhizal fungi (AMF) are the most important microorganisms for the above-below ground carbon transfer**
- **Biodiversity increases carbon input into the belowground system**



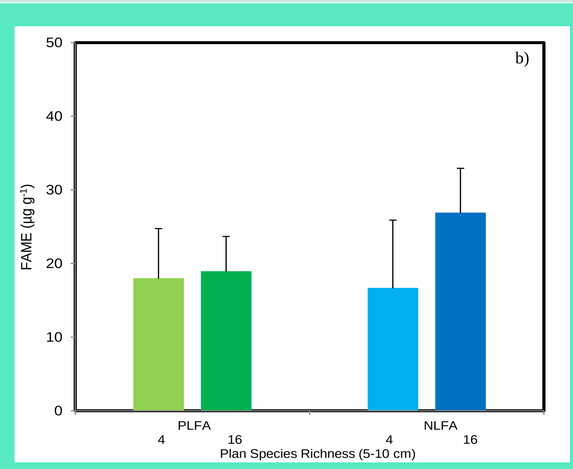
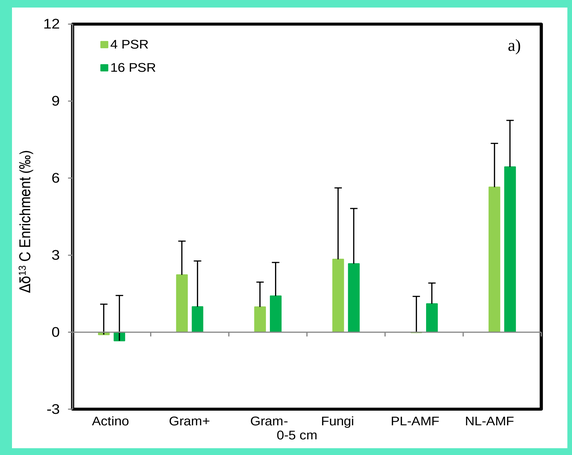


Fig 3. PLFA and NLFA concentration (µg/g) in soils with different plant species richness (4 and 16) in a) 0-5 cm depth and b) 5-10 cm depth.



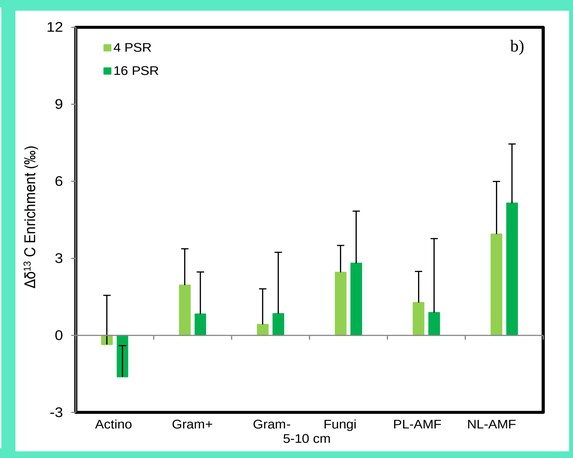


Fig 4. $\Delta\delta^{13}C$ enrichment (‰) in different microbial groups (Actinomycete, gram positive bacteria, gram negative bacteria, saprophytic fungi and arbuscular mycorrhizal fungi) at different soil depths: a) 0-5 cm depth and b) 5-10 cm depth.

Table 1.Contribuition of specific compounds to different microbial groups

Microbial group	Compound
Actinomycetes	16:0(10Me), 18:0(10Me) [3]
Gram positive bacteria	14:0i, 15:0i, 15:0a, 16:0i, 17:0i, 17:0a [1,4]
Gram negative bacteria (rhizosphere related organisms)	16:1ω7, 16:1, 17:1, 17:0cy, 18:1ω7, 19:0cy [4,5]
Saprophytic fungi (rhizosphere related organisms)	18:2ω6 [4]
Arbuscular mycorrhizal fungi (AMF) (rhizosphere related organisms)	16:1ω5 [6]

References

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Friedrich-Schiller-Universität Jena

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