The role of Common Mycorrhizal Networks for nutrient allocation in *Fagus sylvatica* (European beech) trees

Bruna Imai[1], S. Gorka[1], J. Wiesenbauer[1], W. Mayerhofer[1], C. Kaiser[1]

[1]Department of Microbiology and Ecosystem Science, University of Vienna, Austria.

bruna.imai@univie.ac.at

Background

- Mycorrhizal fungi connect multiple plants belowground forming Common Mycorrhizal Networks (CMNs).
- CMNs facilitate mutualistic interactions between plants providing channels to exchange carbon and nutrients.
- The terms of trade and mechanisms in which plants and their fungal partners interact are still not fully understood.

Is there C transfer between the root systems of plants connected via a CMN?

Do CMNs amplify or alleviate belowground competition for nutrients?

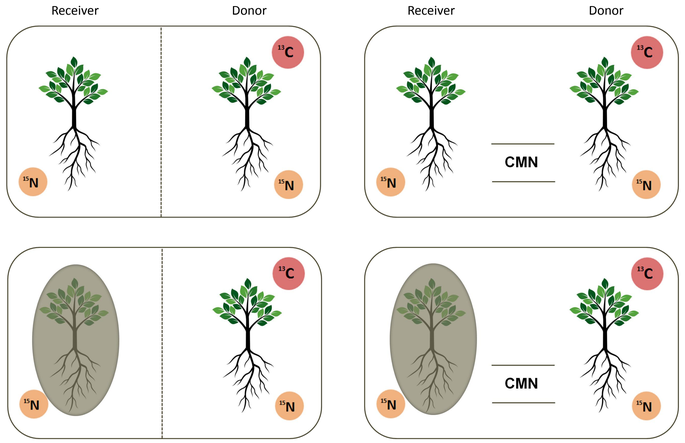

Figure 1. Fully factorial experimental design varying 2 factors: presence/absence of CMN and equal/unequal conditions (i.e. shading of one tree). The full setup was replicated 6 times.

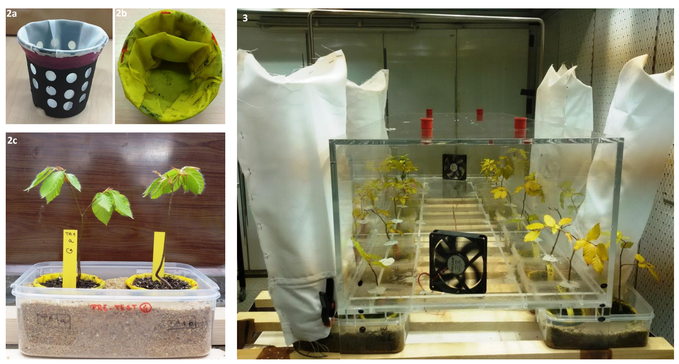

Figure 2. Experimental set up. (a) perforated pots wrapped in a fine mesh (49µm) to allow hyphae but not root growth. (b) Mycorrhiza-exclusive ^{15}N-labelled peat in 49µm mesh bags buried in each pot. (c) Pots positioned in pairs in plastic boxes filled with sand, to allow CMNs to establish between them.
Figure 3. Labelling chamber where the aboveground plant parts were incubated in a ^{13}C-CO_2 enriched atmosphere (approximately 90 atom% ^{13}C)

Methods

- Young beech trees were transferred along with native soil and natural mycorrhizal inoculum into perforated pots wrapped in a fine pored (49µm) mesh allowing hyphae, but not roots to pass (Figure 2a).
- ^{15}N-labelled peat (δ^{15}N=400‰) was enclosed in 49µm mesh bags and buried in each pot (Figure 2b). Pots were positioned in pairs in plastic boxes filled with sand, to allow CMNs to establish between them for 5 months (Figure 2c).
- After the growing period, and four weeks before harvesting the plants, $^{13}CO_2$ labelling was started. Once a week, one of the plants ("donor") in each box was exposed to a ^{13}C-CO_2 atmosphere for 8 hours (Figure 3).
- Treatments: 1) CMN (some pots were turned around 3x/week to prevent the establishment of CMNs) and 2) Shading (in part of the "receiver" boxes, one of the two plants was shaded) (Figure 1).
- Analyses: tracing of ^{13}C and ^{15}N into above and belowground pools of both donor and receiver plants by isotope ratio mass spectrometry (EA-IRMS) and ^{13}C phospholipid fatty acid (PLFAs) analysis (GC-IRMS).

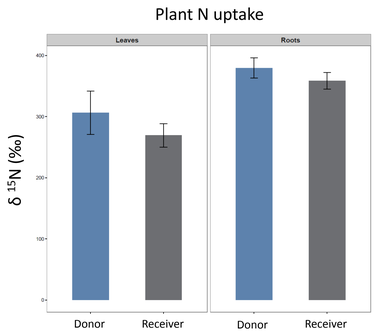

Figure 4. Above and belowground allocation of N in the donor and receiver plants, shown as δ^{15}N. Both pools were significantly different from nat.ab. control plants ($p < 0.05$). Error bars represent standard error; n = 6

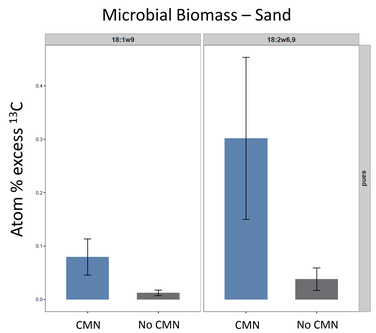

Figure 5. Enrichment of ^{13}C in the fungal PLFAs in the sand between donor and receiver plant pots were significantly different from control ($p < 0.05$). Comparison via Mann-Whitney U test; n = 6.

Results

- On average, 72% of the plant biomass N originated from the labelled peat bags while only 28% were soil derived. No significant differences between treatments were found (Figure 4).
- PLFA biomarkers (fungi and bacteria) became significantly ^{13}C enriched in the peat bags of both donor and receiver pots. In receiver pots, peat bags became highly enriched in ^{13}C compared to the surrounding soil (Figure 6).
- PLFAs were enriched in ^{13}C in the peat bags of the receiver plants regardless of the disruption in the CMN treatment (Figure 5).
- Fungal PLFA biomarker (18:2ω6,9) extracted from the roots of the receiver plants were slightly, but significantly enriched in ^{13}C (Figure 7).

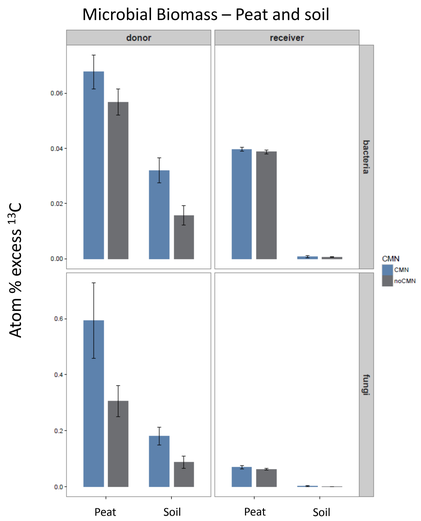

Figure 6. Enrichment of ^{13}C in fungal-specific (18:1ω9 and 18:2ω6,9) and bacteria-specific PLFAs in soil and peat. All microbial groups were significantly enriched compared to nat.ab. controls in peat but only donors were enriched in the soil. Comparison via Mann-Whitney U test; n = 6.

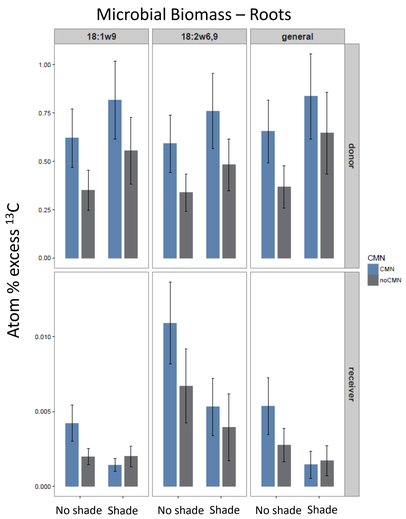

Figure 7. Enrichment of ^{13}C in fungal-specific and general PLFAs in roots of donor and receiver plants. ^{13}C was significantly enriched compared to natural abundance in one fungal-specific biomarker (18:2ω6,9) of the receiver plant, suggesting a ^{13}C transfer via ECM hyphae. Comparison via Mann-Whitney U test; n = 6.

Discussion & Conclusion

- Host plants relied mostly on their fungal partner to acquire nutrients as most of the N allocated in the plant biomass was exclusively accessible by hyphae. We found, however, no effect of CMN on belowground competition for nutrients.
- The significant enrichment in ^{13}C in the peat bag buried under the receiver plant indicates a hyphal transfer of photoassimilated C. This is not only found in the belowground realm of their host plants but also over longer distances into the realm of their neighbors. However, the fact that the enrichment was significant even when the CMN was disrupted suggests a significant long-distance C transfer also via temporarily broken fungal hyphae.
- The ^{13}C enrichment in the fungal PLFA biomarker extracted from the roots of the receiver plants may indicate a translocation of photoassimilated C from the donor plant into the root system of the receiver plant. Whether this C stayed in the fungal tissue or was transferred into plant cells is however unknown.