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Responses of ectomycorrhizal extraradical mycelium and associated bacteria to drought and warming

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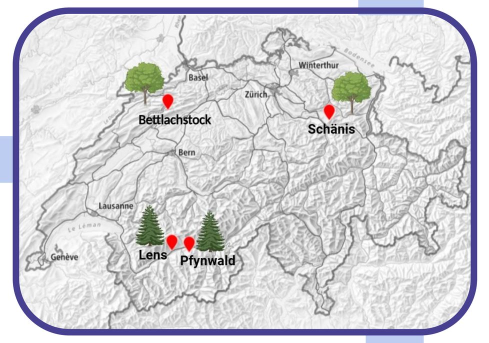
Background

- A recent estimate suggests that global plant communities allocate 9.07 Gt CO_2e per year to **ectomycorrhizal fungi (EMF)**, of which >50% is directed toward production of **extraradical mycelium**, which represents **~30% of the belowground microbial biomass**[a].
- **Rich bacterial communities engage with the extraradical mycelium of EMF**, promoting mycorrhizal-plant symbiosis, enhancing mycorrhizal colonization, and buffer adverse condition[b].
- Forests help to mitigate global change by storing carbon in the soil. However, **forests** themselves are **threatened by global warming and** frequent **droughts**. The way in which forests respond is largely driven by soil microorganisms[c].



Experimental design

Field experiment to assess how **climate change and mycorrhizal network connectivity shape composition of soil microbial community**. The experiment was implemented across 2 *Fagus sylvatica* (beech) and 2 *Pinus sylvestris* (pine) forests. At each site, 3 replicate clusters were established for a total of 576 sampling units. The experiment ran for two years (2023-2025).

Tree seedlings were grown in modified tubes with mesh windows of varying sizes under climate stress.	
Climate treatments: **drought** (1), **warming** (2), **control** (3), **warming x drought** (4)	Mycorrhizal manipulation treatments: • **Full myco** - allow fungal in/out growth, • **Reduced myco** - reduce it, • **No barrier**

In-growth sandbags were buried in the soil in the two beech forests during the growing season and used to **"bait"** the **EMF and their associated bacteria**.

Methods

- Microbial biomass in the in-growth bags was measured by phospholipid fatty acid analysis (PLFA)
- 16S metabarcoding assessed soil microbial community composition
- Plant growth response was measured using basal stem diameter

Microbial biomass analysis in sand bags

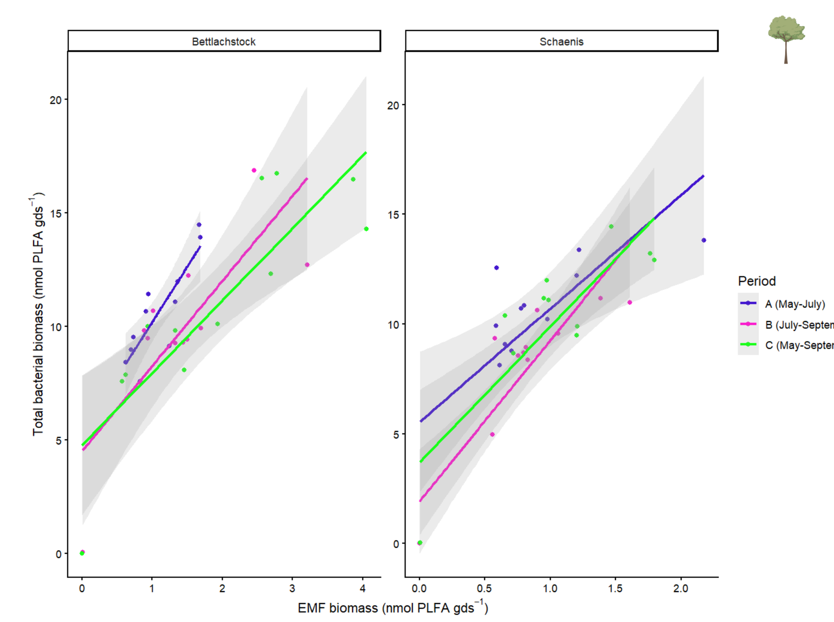


Fig.1: Linear regression of total bacterial and EMF biomass (nmol PLFA gds⁻¹) across sampling periods at Bettlachstock (Bett) and Schänis (Sch) ($R^2 = 0.56–0.79$, $p < 0.01$ for all periods).

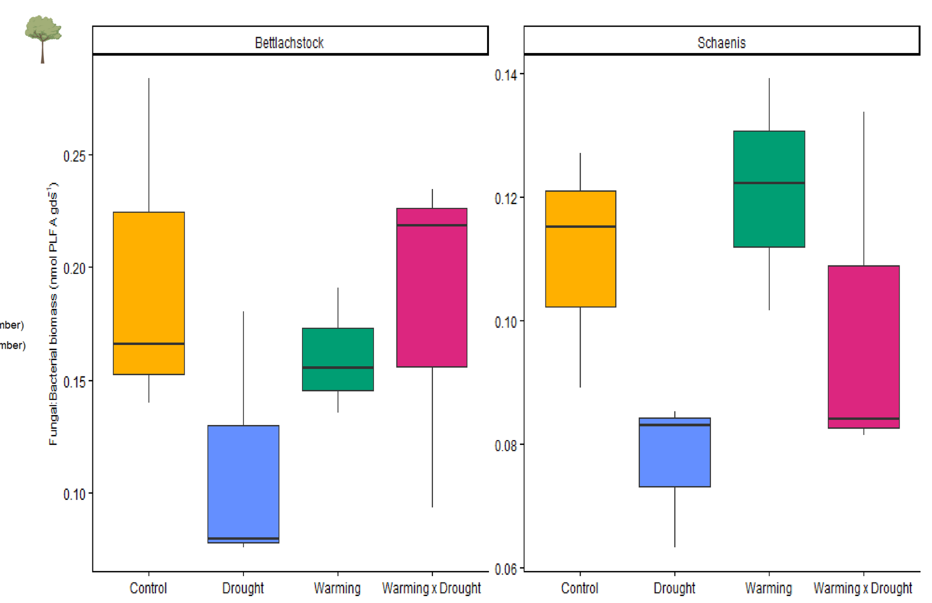


Fig.2: Fungi-to-bacteria biomass ratio across climate treatments at Bett and Sch (LME, Type II Anova). At Sch, drought significantly reduced the ratio ($p = 0.0016$). No significant effects were detected at Bett.

- Across treatments and sampling windows, bacterial biomass was positively correlated with EMF biomass in the in-growth bags (Fig.1)
- After the entire growing season, **drought reduced the fungal-to-bacterial biomass ratio** in the in-growth bags (Fig. 2)
- Across treatments and experimental sites (beech forests), **plant growth and fungal-to-bacterial biomass** were **positively correlated** (Fig. 3)

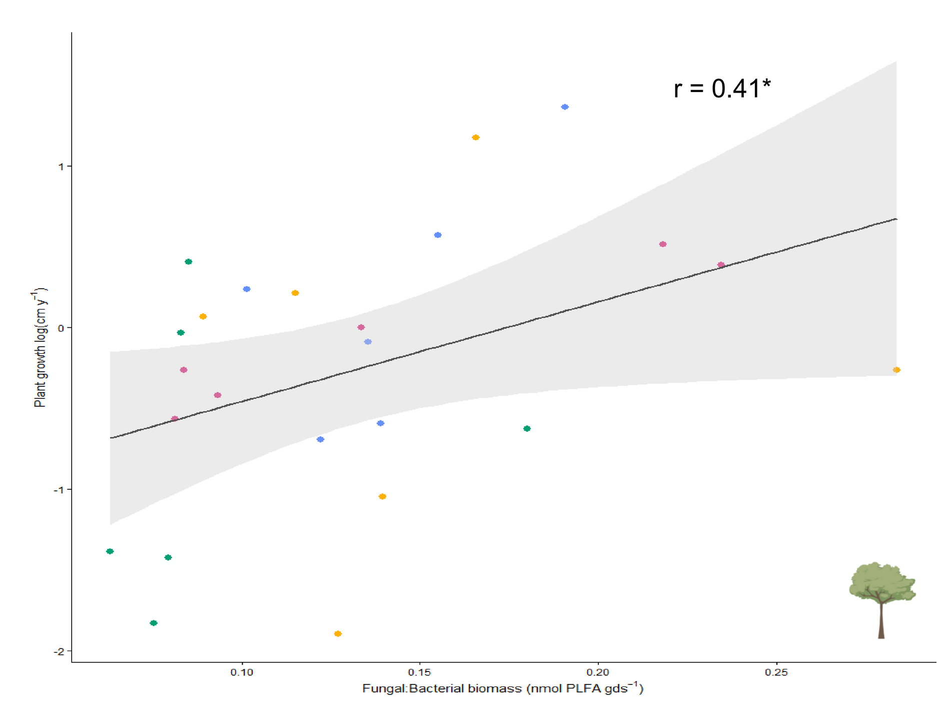


Fig.3: Linear regression of fungi-to-bacteria biomass (nmol PLFA gds⁻¹) and plant growth log (cm y-1) in Bett and Sch.

Conclusions

- Tight coupling between extraradical mycelium and bacterial communities under climate stress
- Bacteria associated with the extraradical mycelium of EMF are comparatively less sensitive to drought than the fungi

Soil bacterial community composition analysis

- **Strong warming/drought effect** on the bacterial community composition (Fig.4)
- In the **pine forests** there is a **significant mycorrhizal connectivity effect** (Fig.4)
- The main climatic driver of bacterial community composition varies even within the same forest type (Fig.5)

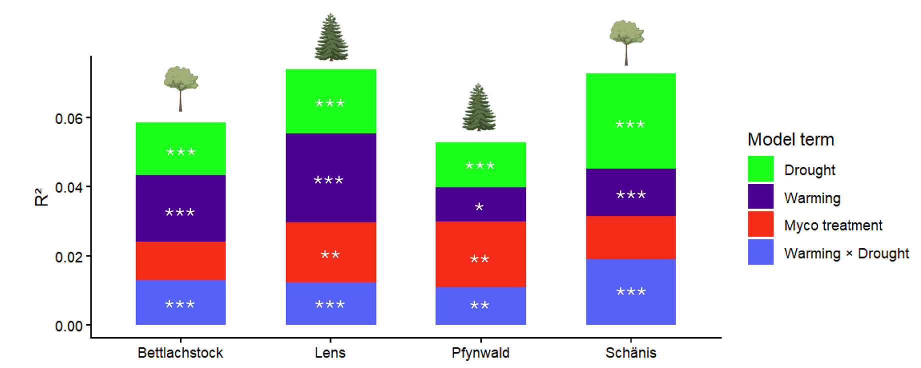


Fig.4: Stacked bar plot showing the proportion of variance (R^2) and p-value (*, **, ***) in bacterial community composition explained by warming, drought and mycorrhizal manipulation treatment as estimated by PERMANOVA, for each experimental site.

Conclusions

- Local factors modulate bacterial community responses to climate change
- Mycorrhizal connectivity emerges as a key driver of bacterial community assembly in pine forests

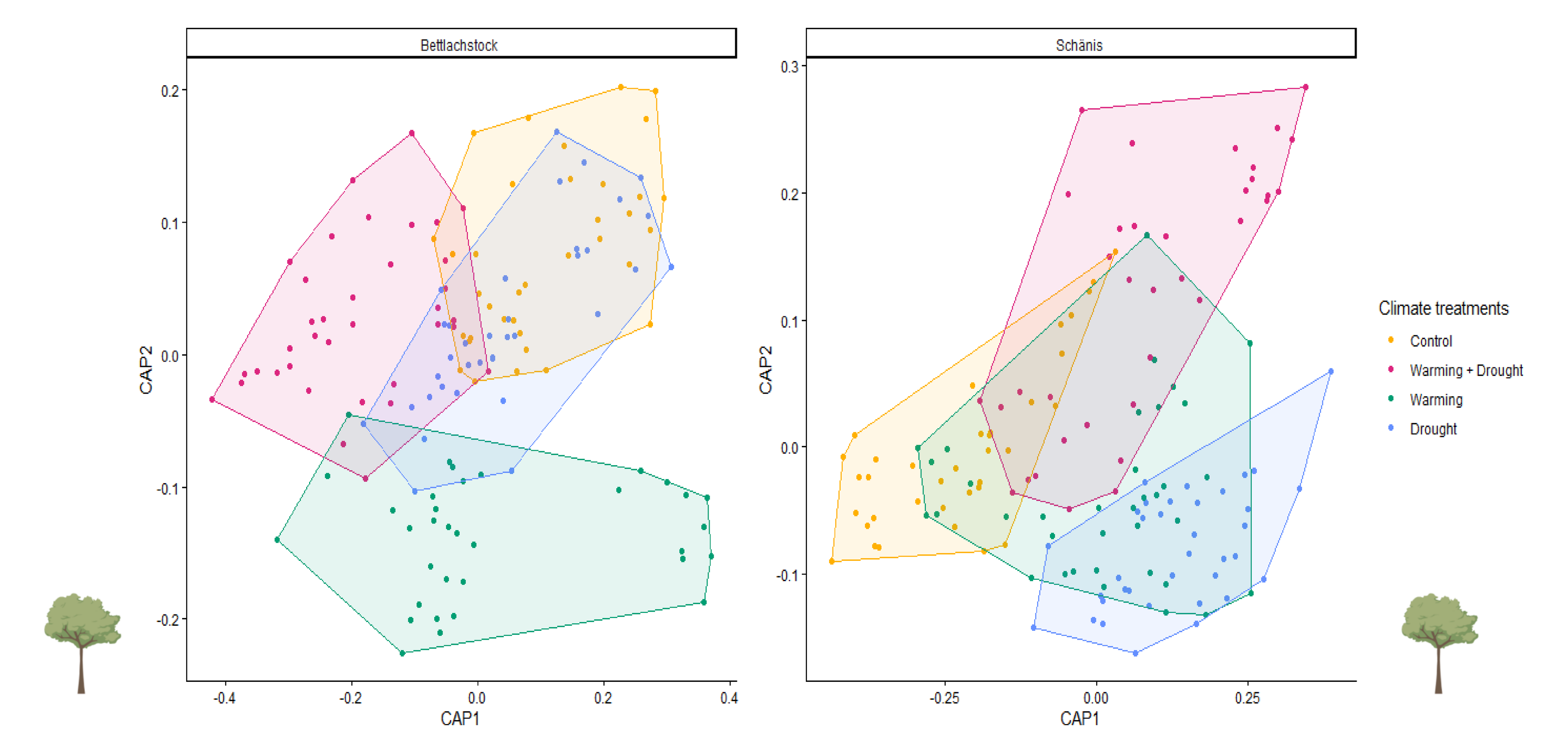


Fig.5: db-RDA of bacterial community composition at Bett and Sch. Polygons represent climate change groups. At both sites, warming (Bett: $F = 3.24$, $p < 0.001$; Sch: $F = 2.01$, $p < 0.001$) and drought (Bett: $F = 2.65$, $p < 0.001$; Sch: $F = 4.16$, $p < 0.001$) and their interaction (Bett: $F = 2.15$, $p < 0.001$; Sch: $F = 3.03$, $p < 0.001$) significantly drove bacterial community composition.

Take-home message

Warming and drought reshape soil microbial communities in a site-specific manner, with drought emerging as the primary driver of EMF and their associated bacteria decline, threatening the below-ground networks that support forest ecosystem functioning.

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WSL

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a. Hawkins, Heidi-Jayne, et al. "Mycorrhizal mycelium as a global carbon pool." *Current biology* 33.11 (2023): R560-R573
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c. Baldrian, Petr, Rubén López-Mondéjar, and Petr Kohout. "Forest microbiome and global change." *Nature Reviews Microbiology* 21.8 (2023): 487-501.