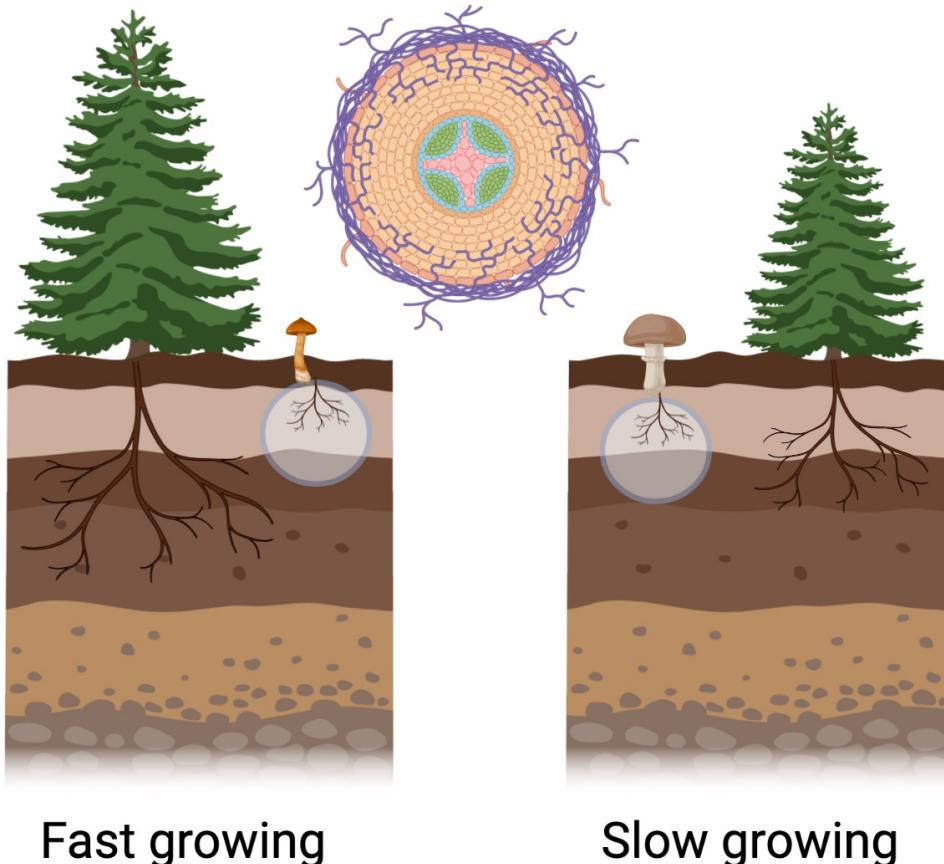


# Ectomycorrhizal fungal communities and functional genes drive forest productivity across the ICP Forest Network

Contact: [mark.anthony@usys.ethz.ch](mailto:mark.anthony@usys.ethz.ch) or @MAnthony02

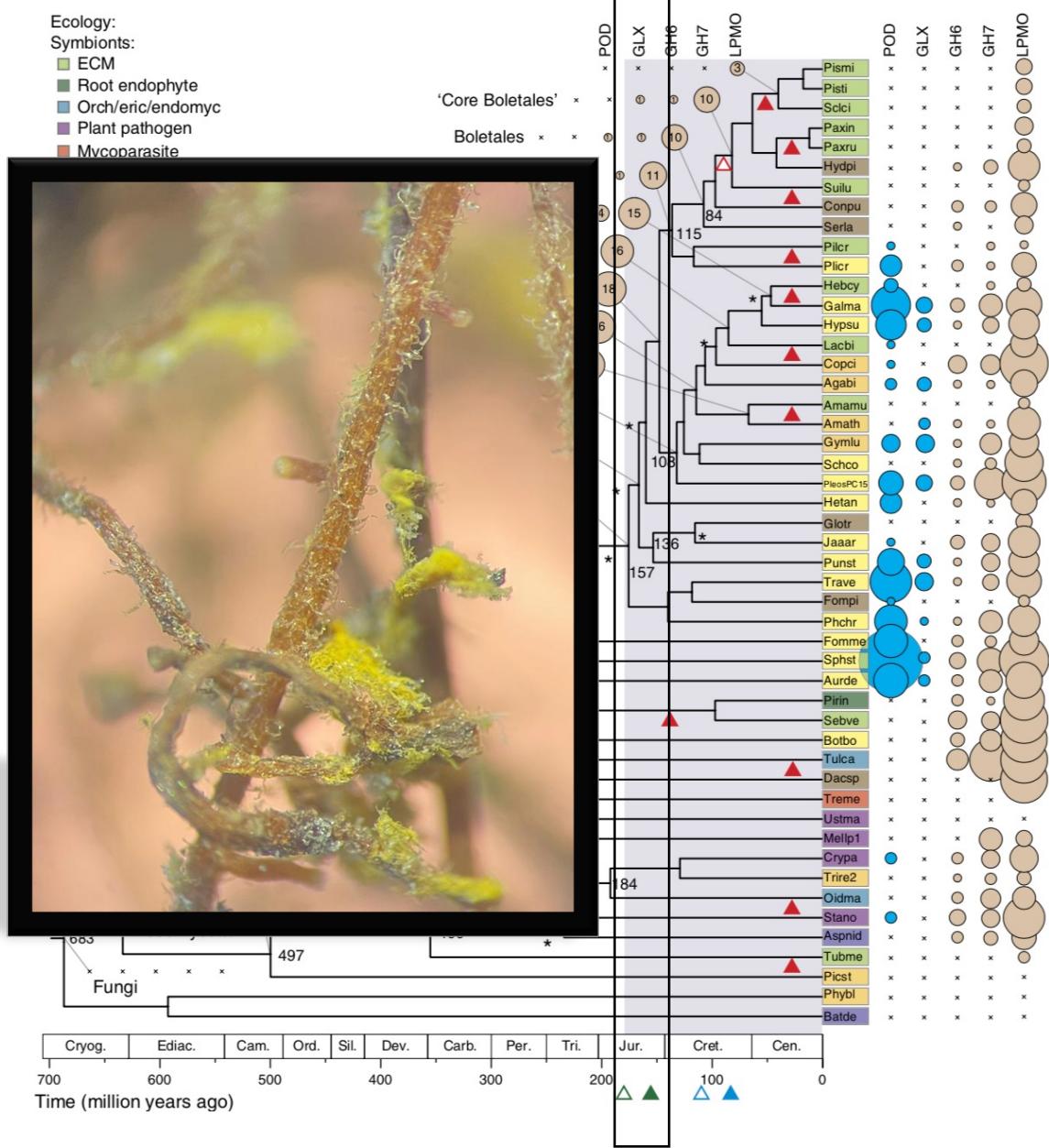
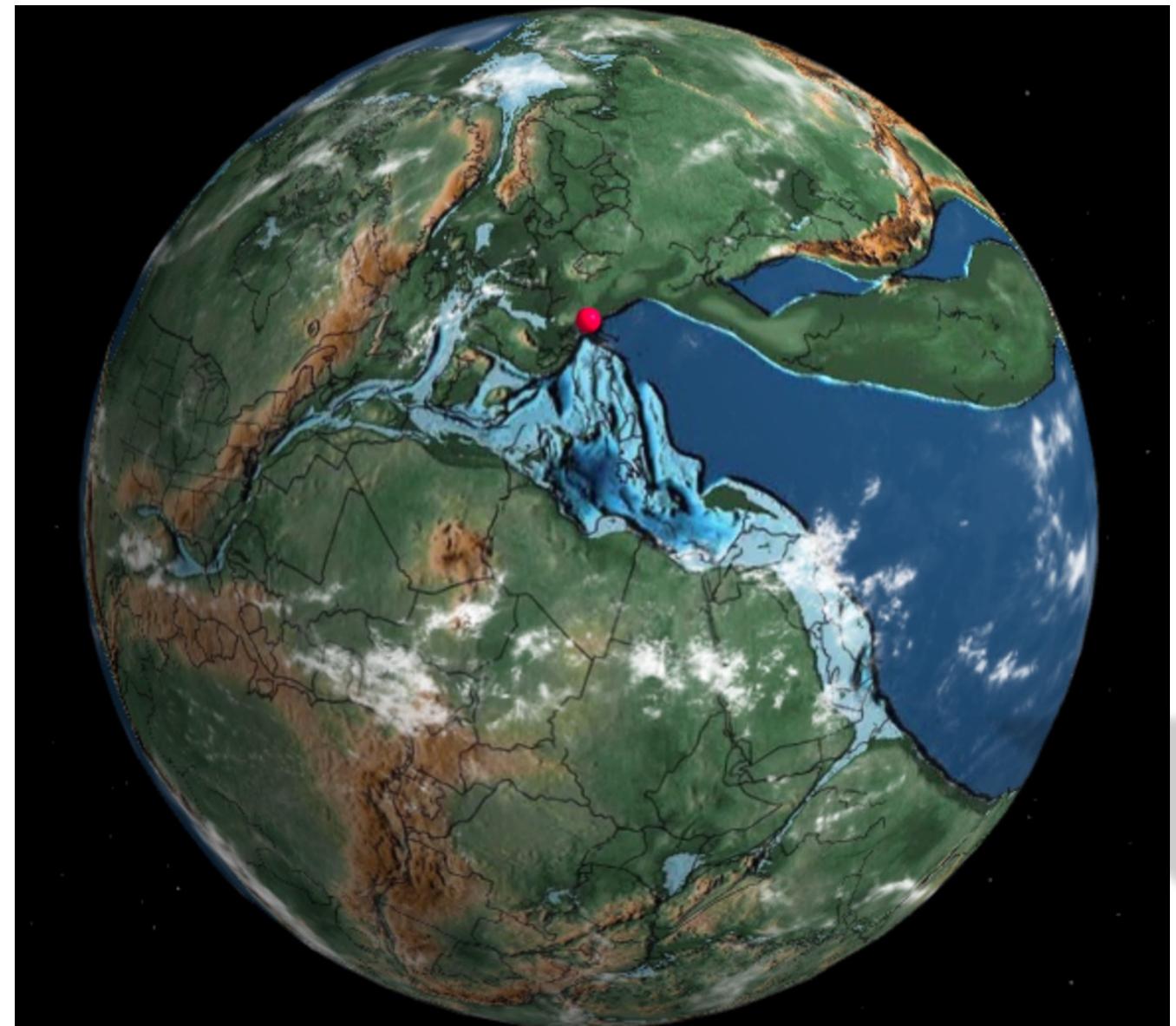


**Mark A. Anthony**, Thomas W. Crowther, Sietse van der Linde, Laura M. Suz, Martin I. Bidartondo, Filipa Cox, Marcus Schaub, Pasi Rautio, Marco Ferretti, Lars Vesterdal, Bruno De Vos, Mike Dettwiler, Nadine Eickenscheidt, Andreas Schmitz, Henning Meesenburg, Henning Andrae, Frank Jacob, Hans-Peter Dietrich, Peter Waldner, Arthur Gessler, Beat Frey, Oliver Schramm, Pim van den Bulk, Arjan Hensen, **Colin Averill**

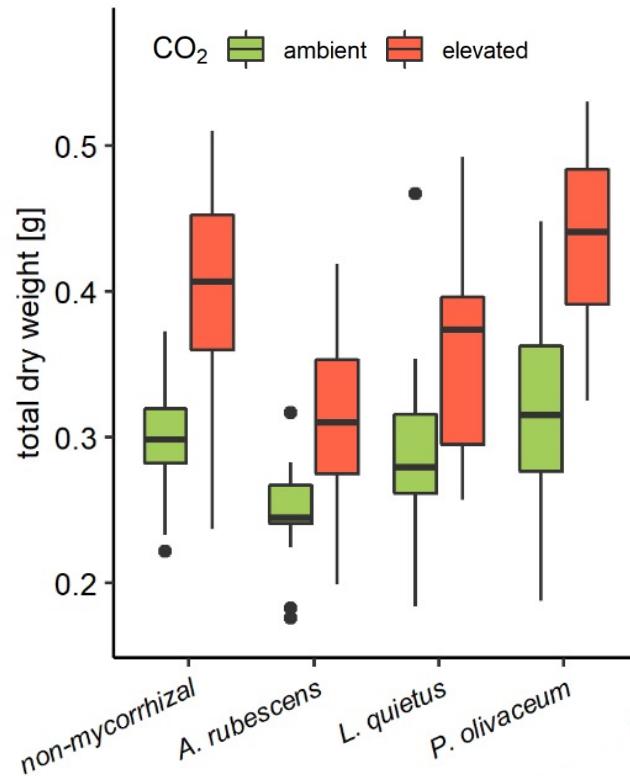
**FNSNF**

FONDS NATIONAL SUISSE  
SCHWEIZERISCHER NATIONALFONDS  
FONDO NAZIONALE SVIZZERO  
SWISS NATIONAL SCIENCE FOUNDATION

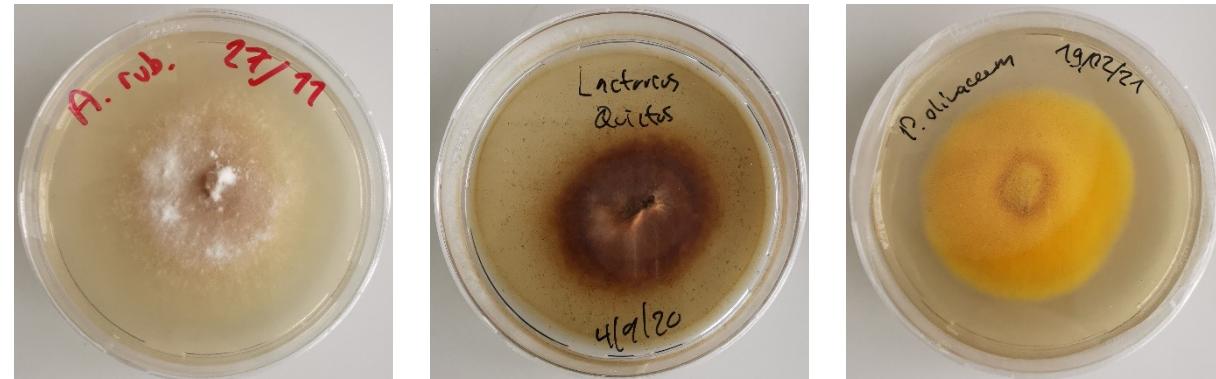
**ETH** zürich



# An estimated 25,000 ectomycorrhizal species worldwide



Vastly differing fungal effects on tree seedling growth



Dettwiler, Anthony et al. (2021; *in prep*)

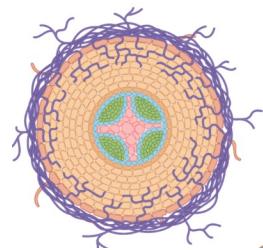
Do insights from mesocosm studies scale up to inform mycorrhizal processes in actual forests?



*Ambiguous ectomycorrhizal species effects increase from petri dishes-to-pots-to-forests*

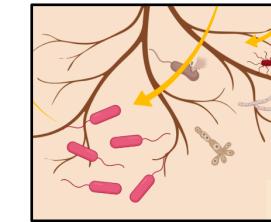
# Two-pronged approach to address this question

Only ectomycorrhizae

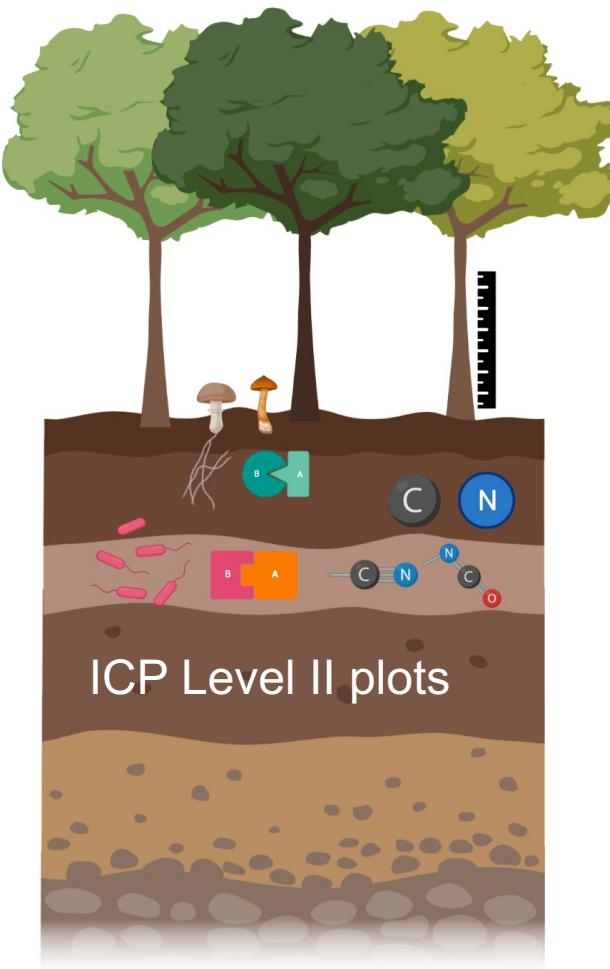


We have root-tip data from 75 plots  
(van der Linde et al. (2018))

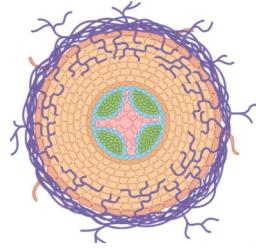
The full microbiome



We have soil from 300 plots  
-fungi  
-bacteria  
-functional genes

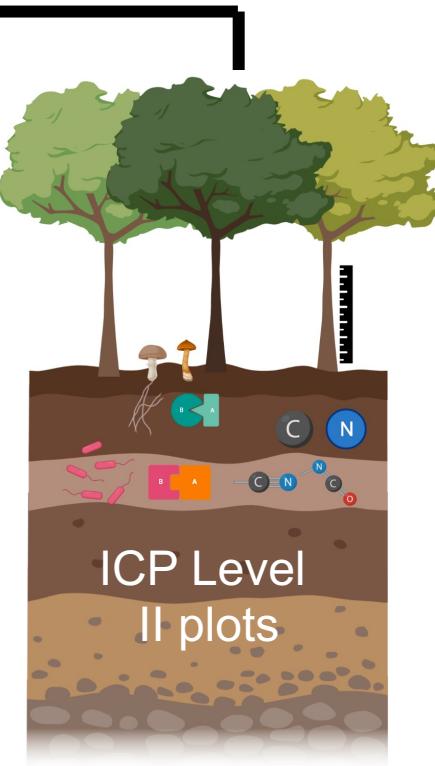


# Ectomycorrhizal-focused analysis

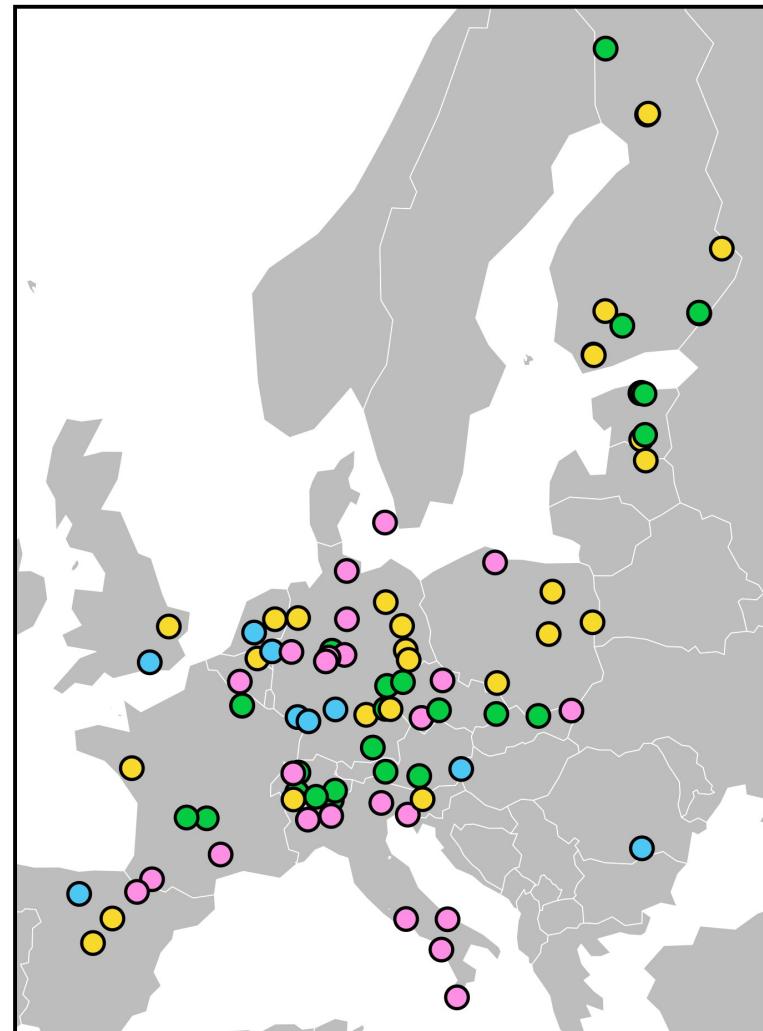
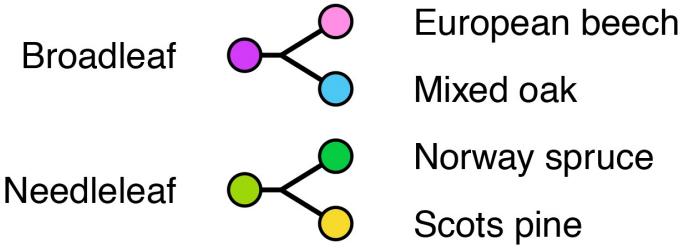


## Calculated tree growth

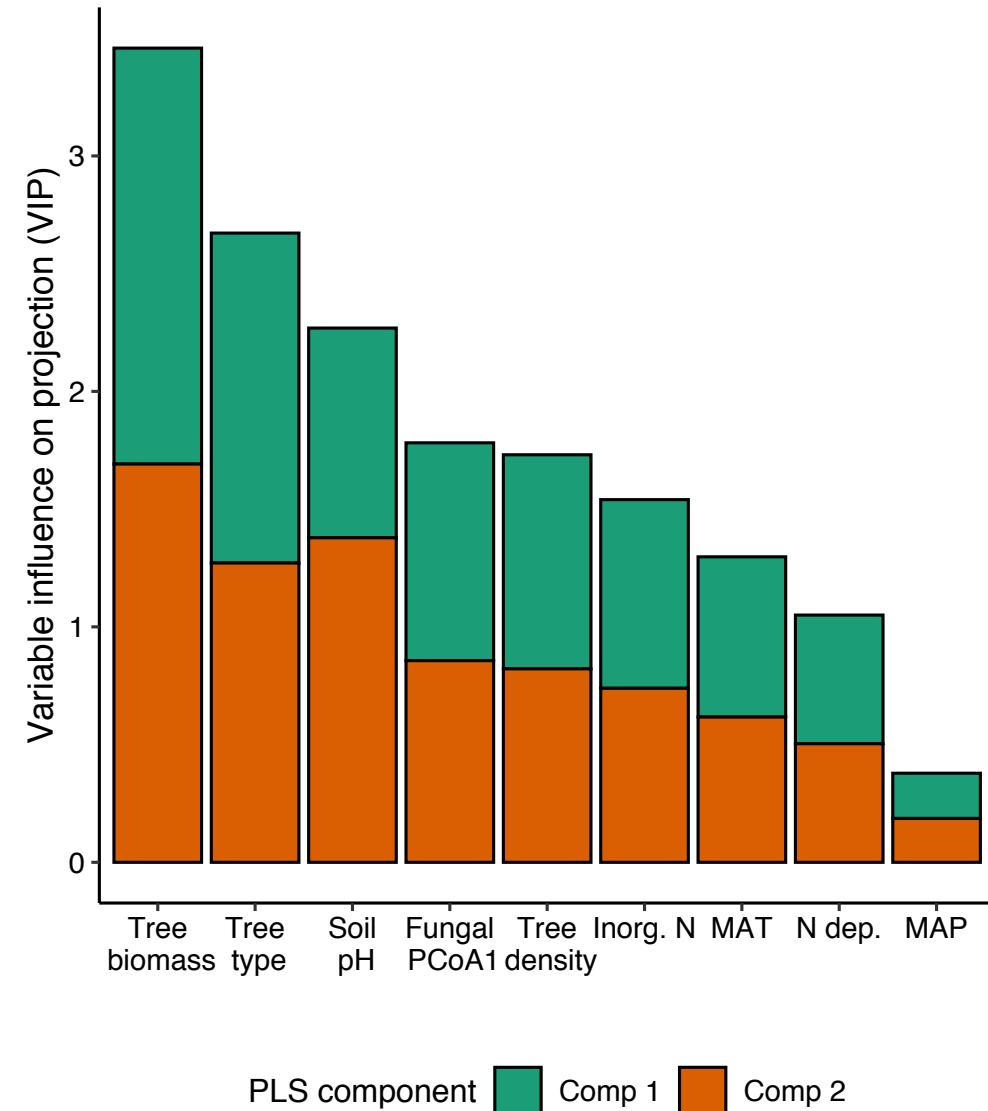
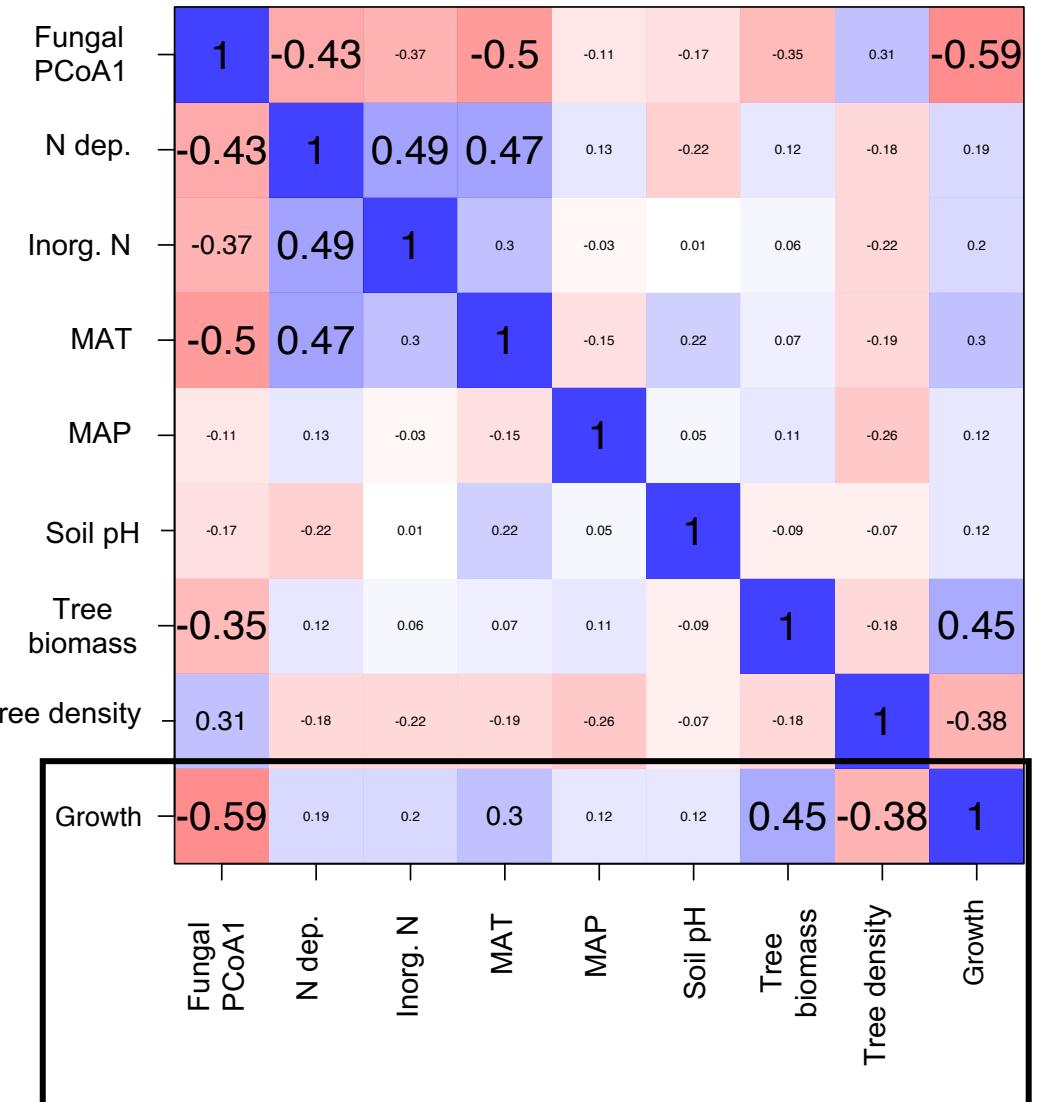
1.  $\Delta$  DBH (mean 5.5 year window).
2. Allometric questions  $\rightarrow$  kg C yr<sup>-1</sup>



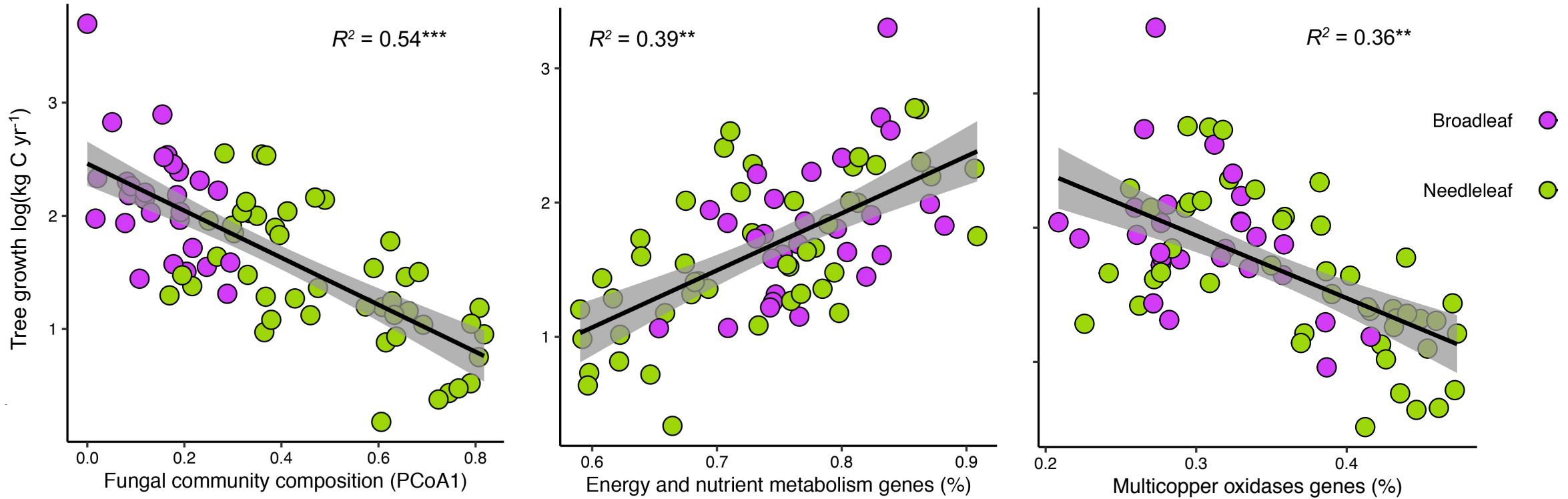
*Tree growth ~ Fungal predictor + MAT + MAP + N deposition + soil inorganic N contents + soil pH + stand density + tree size + tree type*



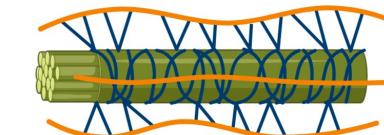
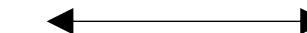
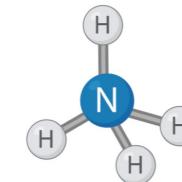
# Fungal composition emerges as a key predictor

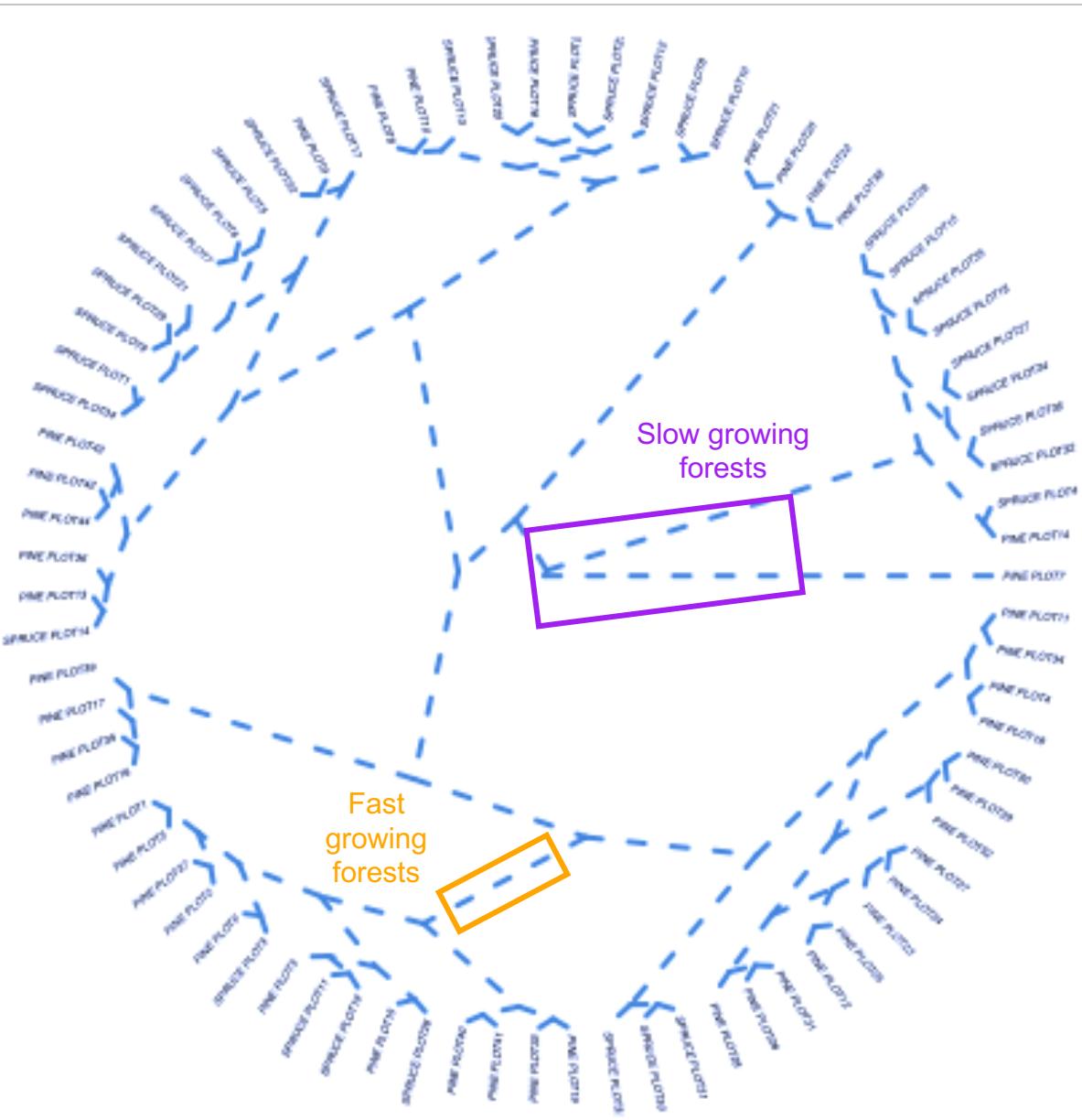


# Fungal community and nitrogen cycling gene correlations



Inorganic vs. organic nitrogen trade-off

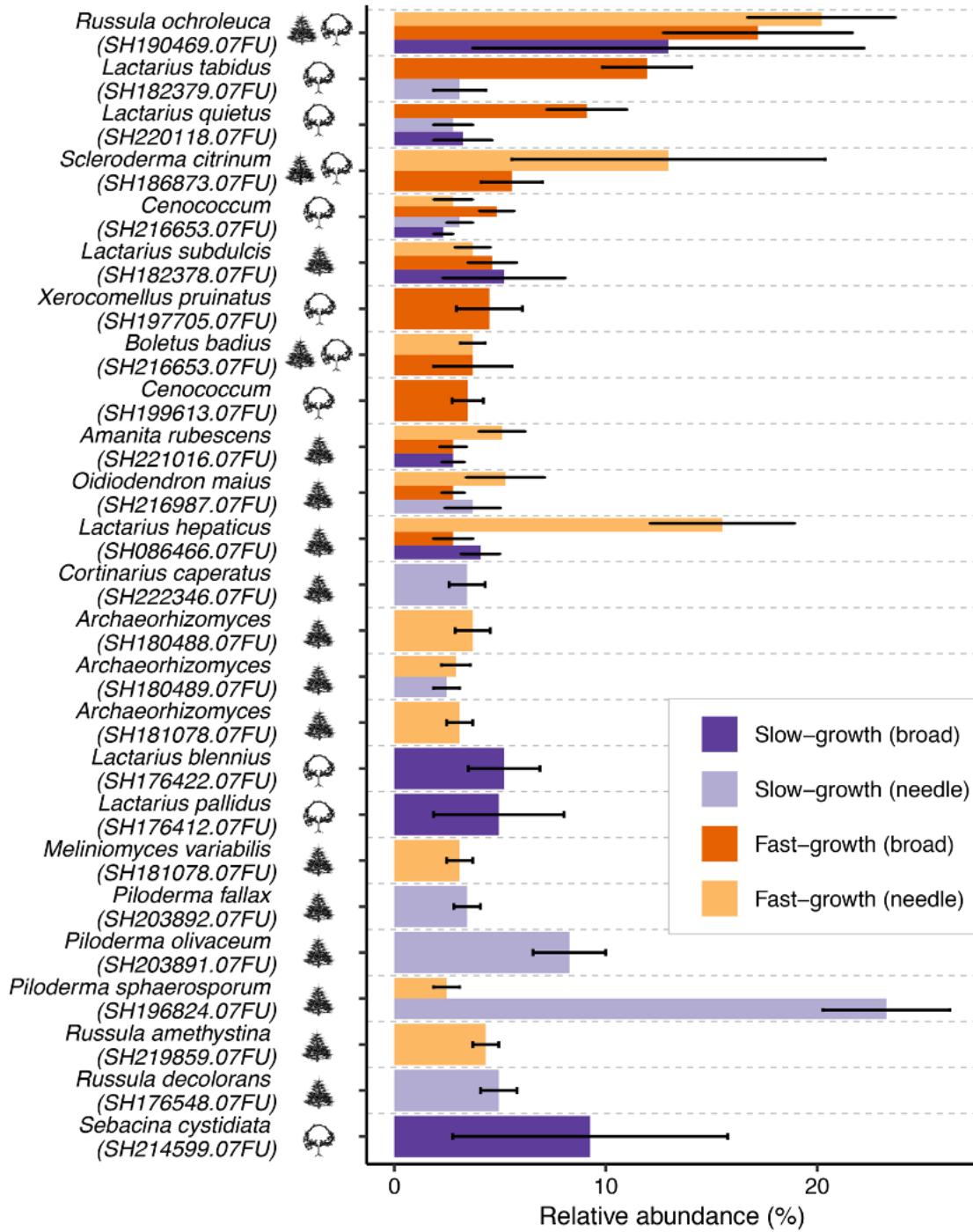
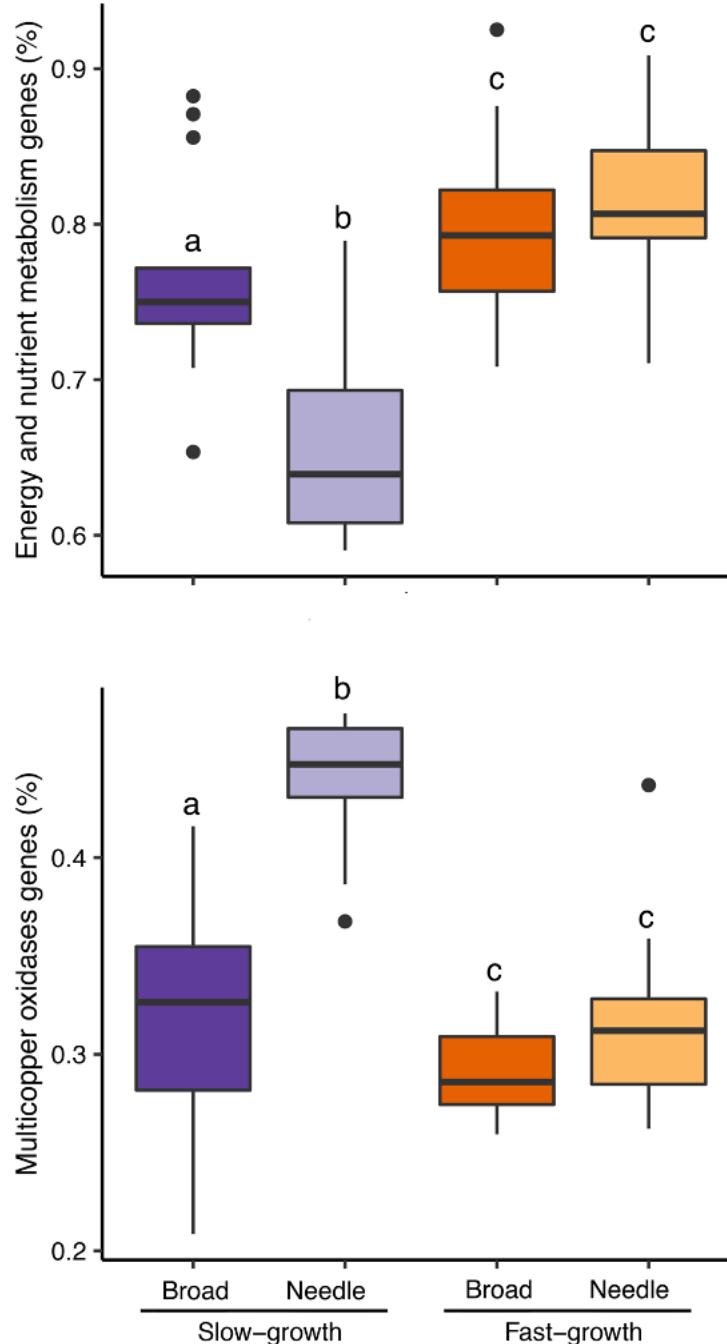




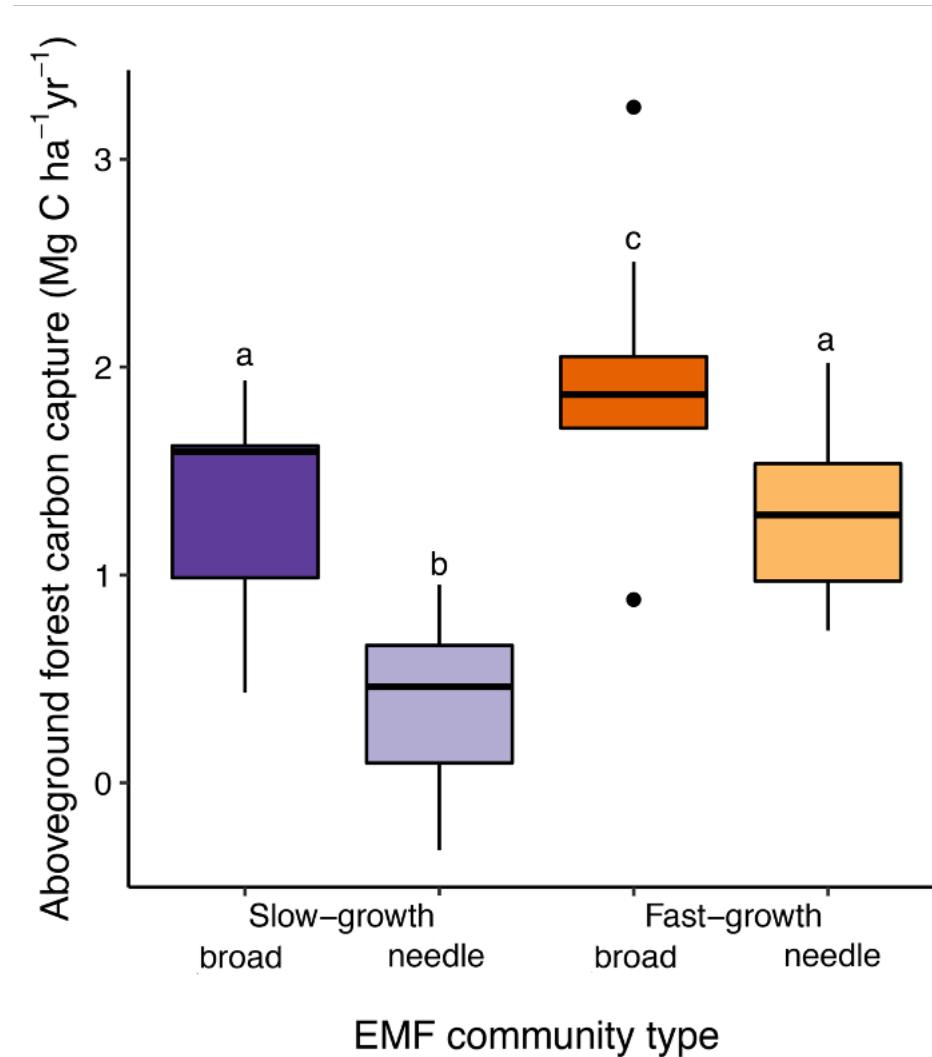
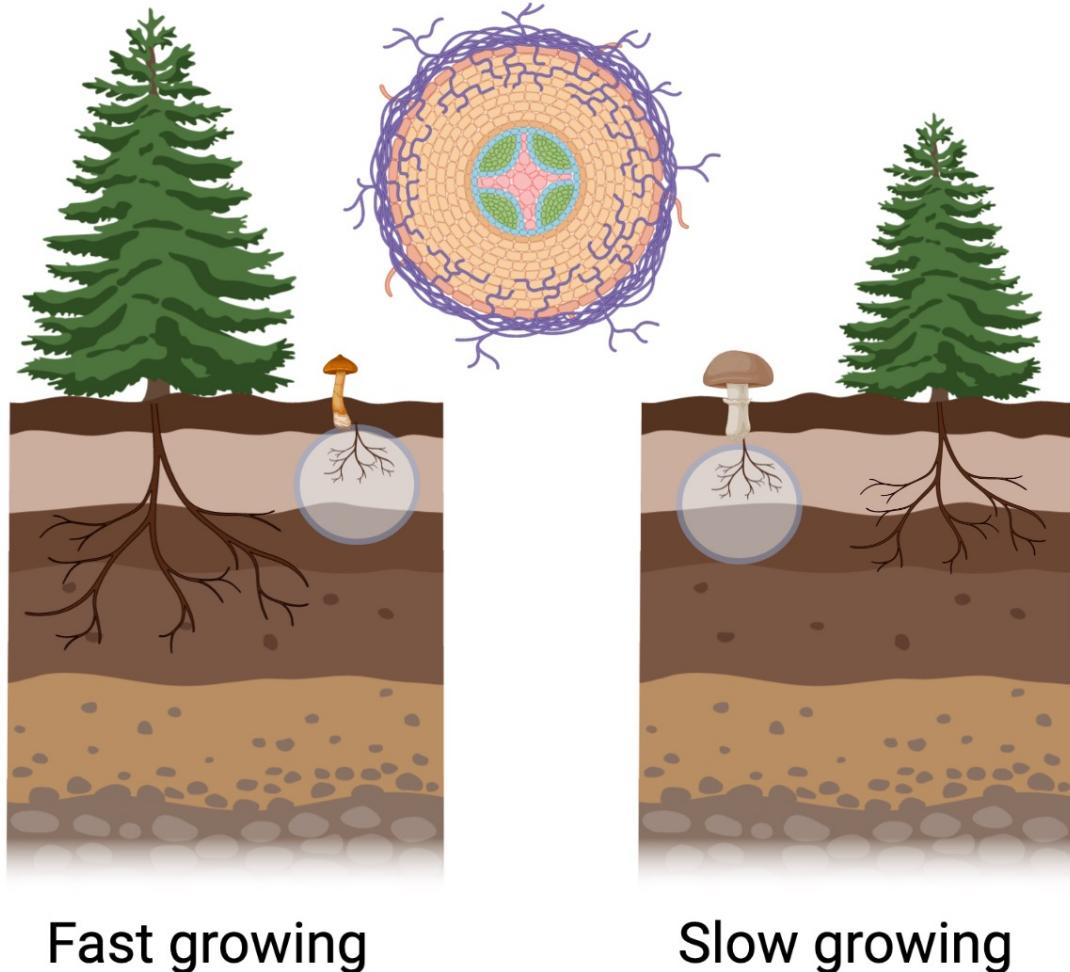
## Identifying species indicative of slow and fast tree growth

Are there community clusters indicative of slow and fast tree growth (i.e. clusters of similar fungal communities in forests with significantly greater or lower mean tree growth rates than the overall average)?

- ‘Slow tree growth associated EMF’
- ‘Fast tree growth associated EMF’



# Assessing aboveground carbon capture at the forest scale under different fungal scenarios



# Conclusions, future work, collaborations

- Fungal composition and N cycling genes emerge as top predictors of tree growth
- Fungal effects were robust to other large-scale drivers of tree growth
- Opportunities to conserve habitat for ecologically important fungi or develop better mycorrhizal forest inoculations
- Higher resolution microbiome analysis – **we have extra soil.**
- We are also conducting greenhouse studies sourcing microbes from 'slow' vs. 'fast' growing forests – **we have extra soil and plant materials**
- Screening different ectomycorrhizal fungi - **cultures to share? Will you find mushrooms in your forests?**