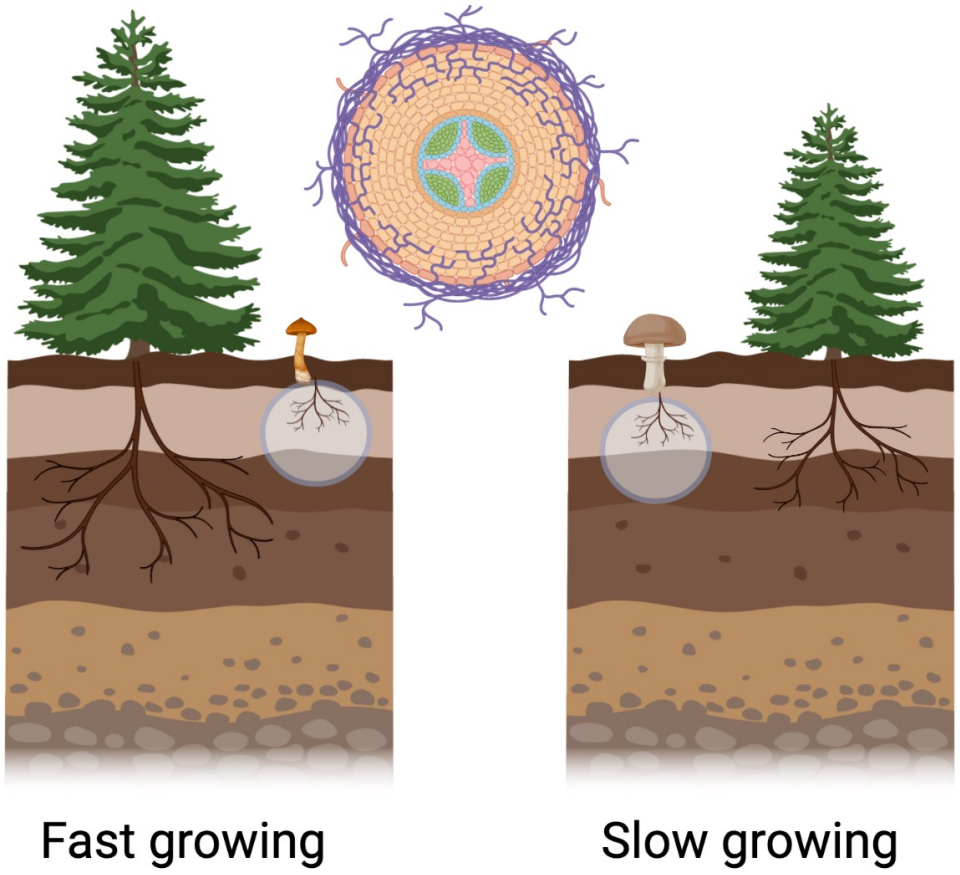
Ectomycorrhizal fungal composition and function predict tree growth across Europe



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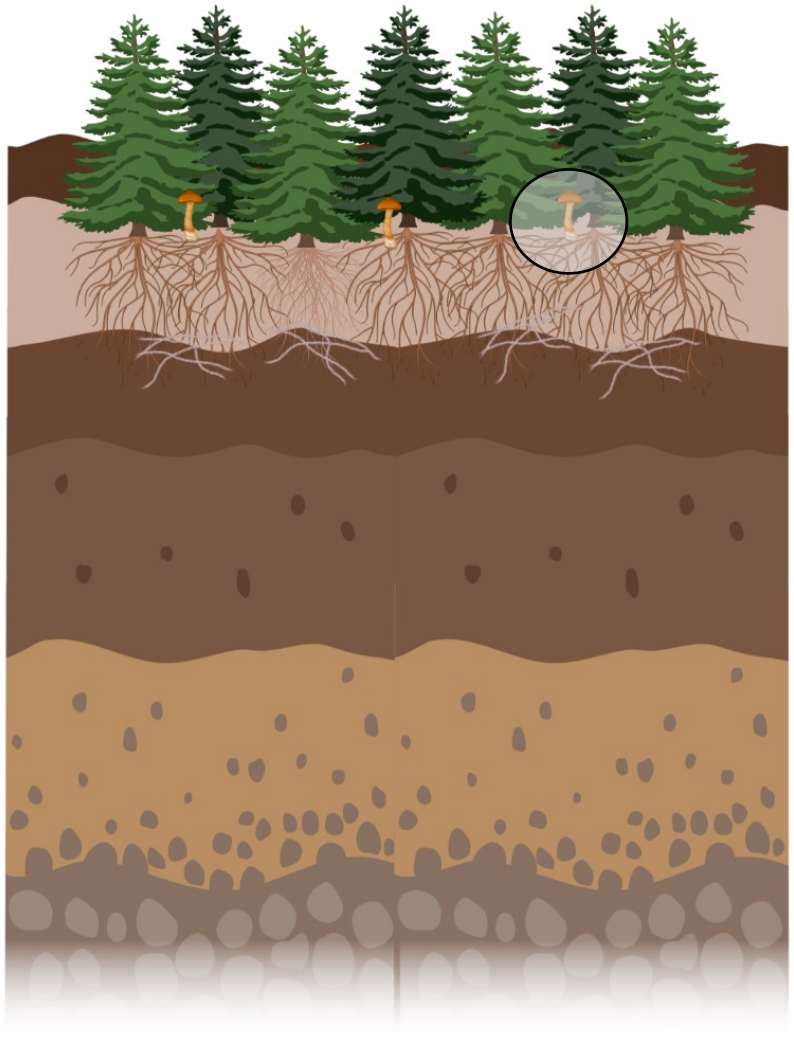
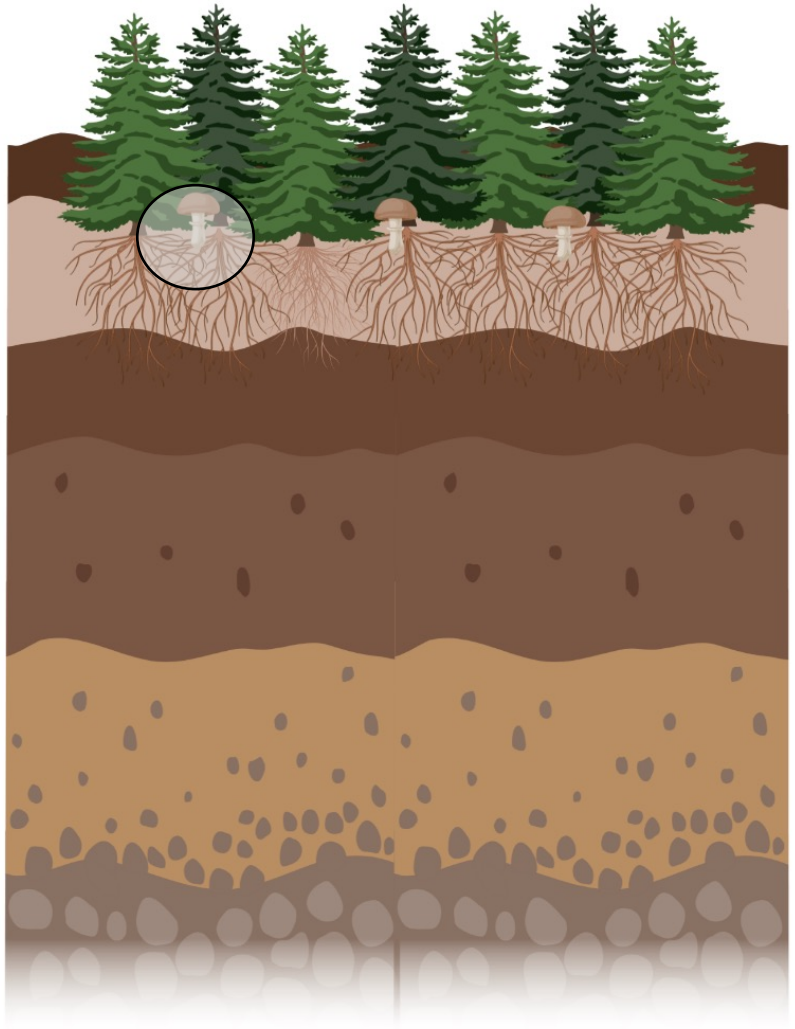
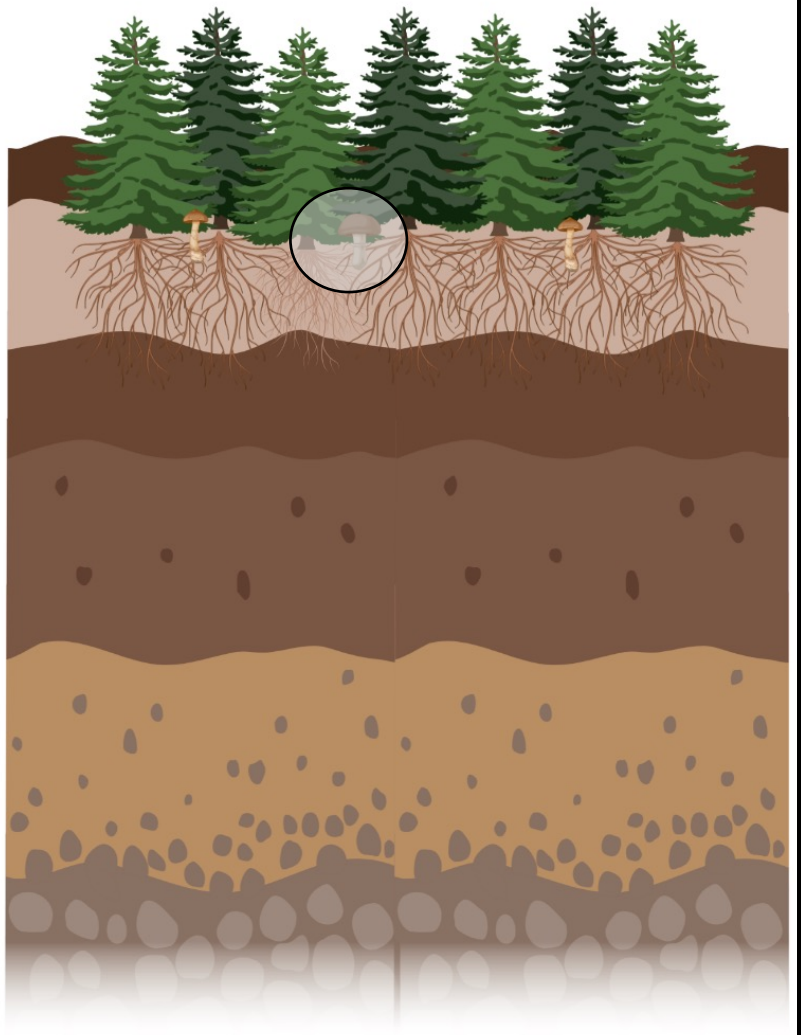
Does variation in the ectomycorrhizal fungal community impact forest productivity?







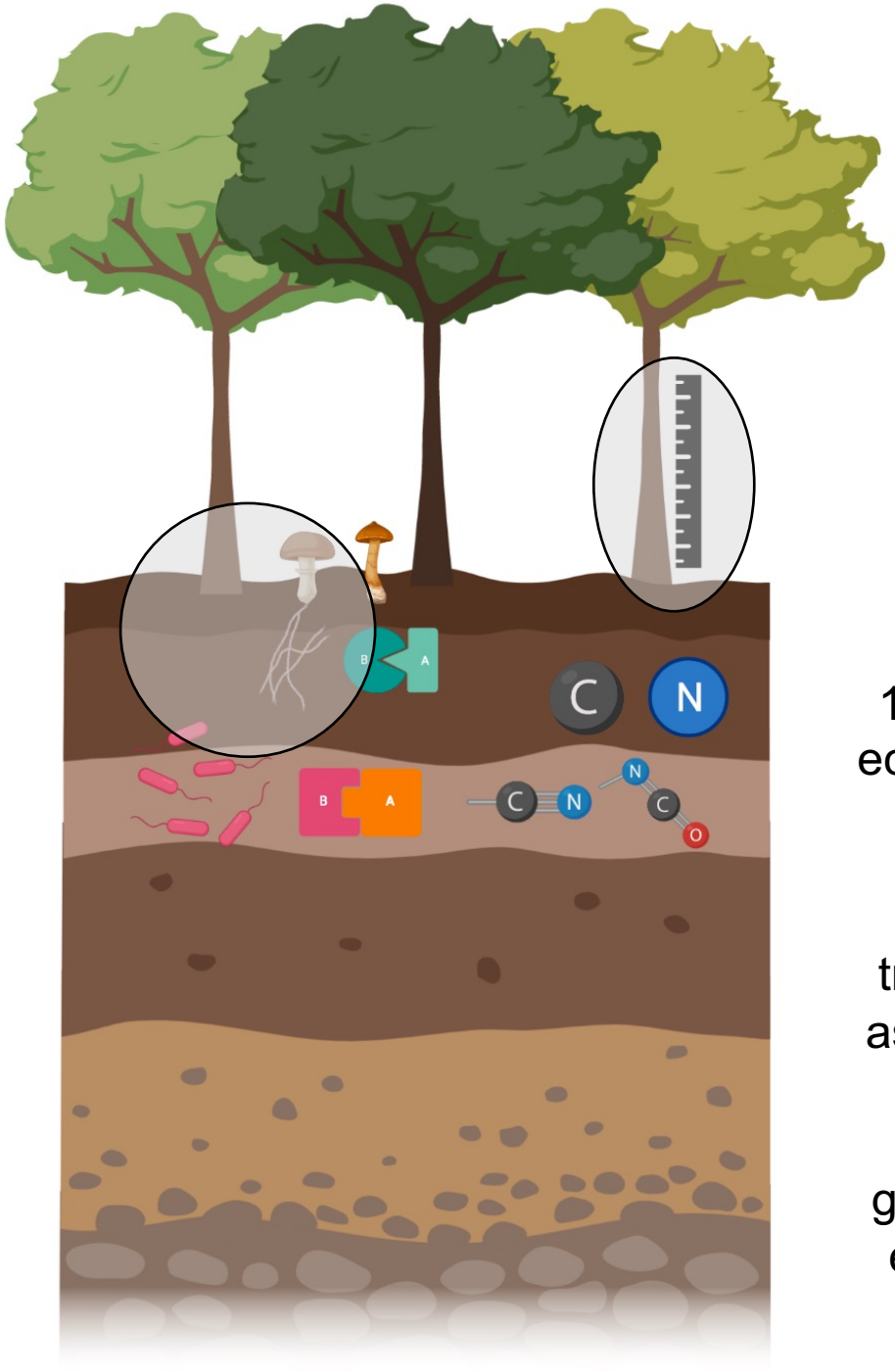
Possible scenarios

Yes - mesocosm evidence

No - functional redundancy

Not much – compared to other factors (e.g. climate)

Our Approach: ICP Forest Network

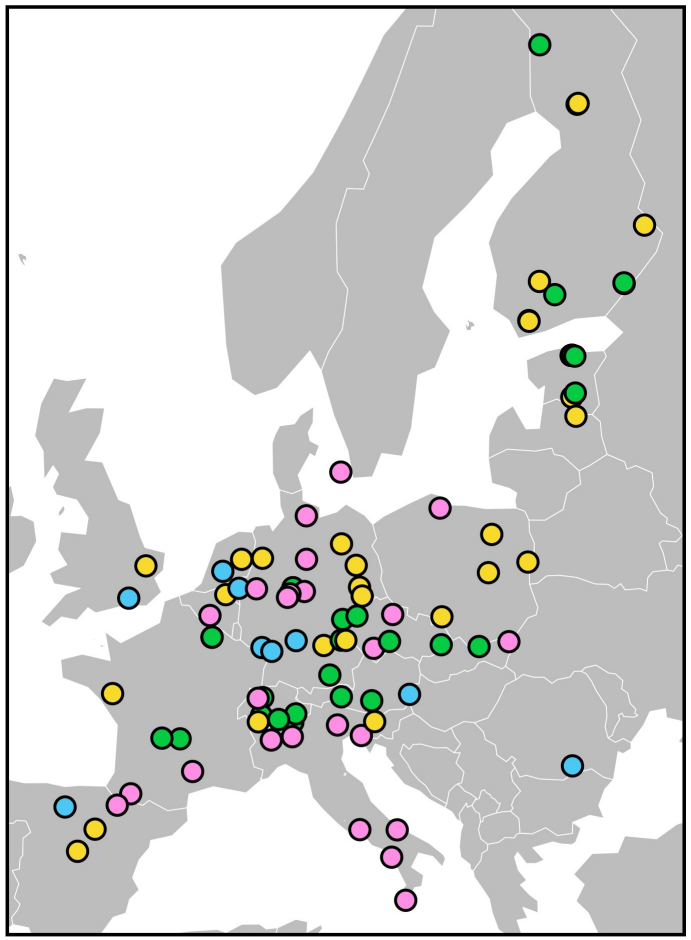


Methods

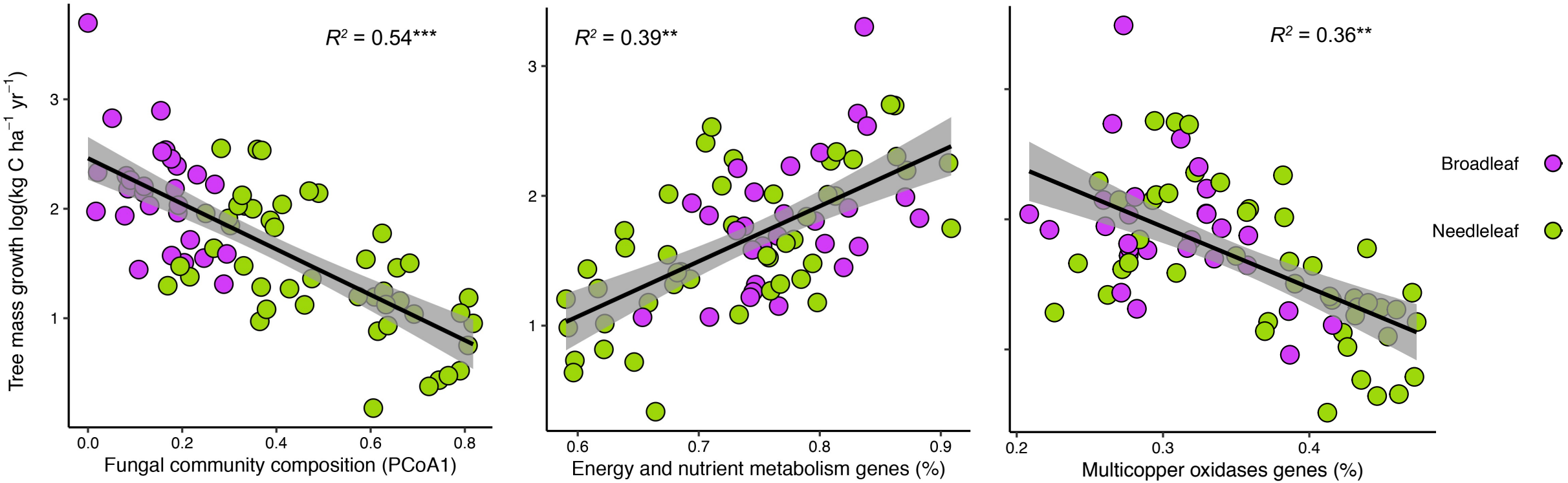
1. Pair tree growth & ectomycorrhizal fungal community data

2. Make statistical tree growth models, assess fungal effects

3. Conduct a greenhouse study to experimentally test

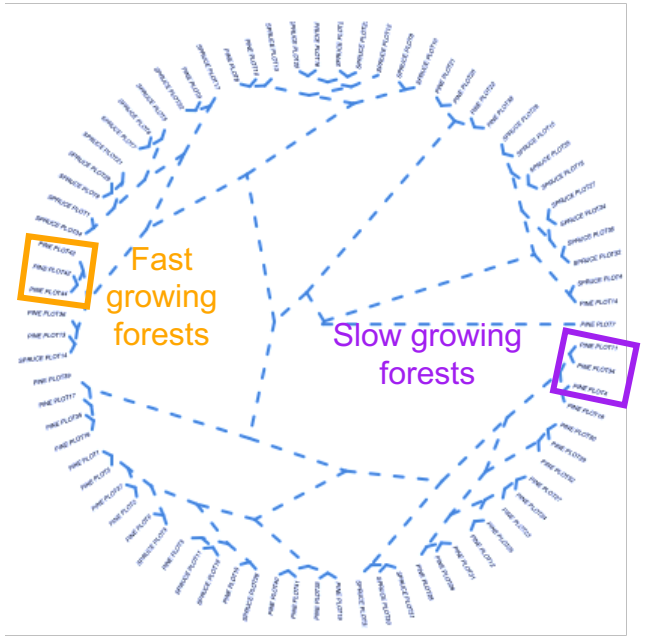


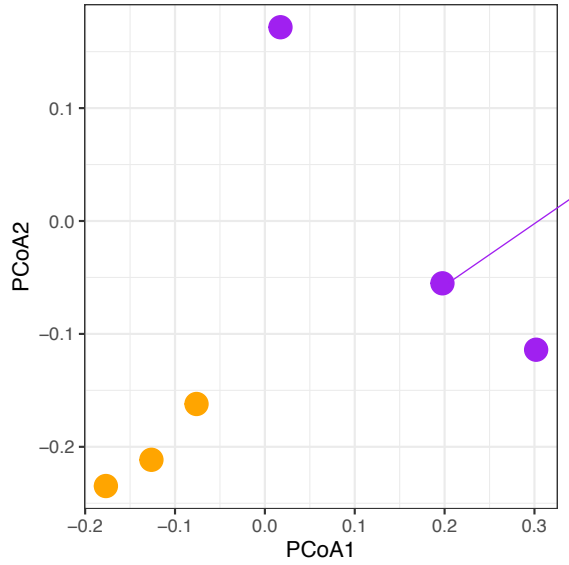
Variation in ectomycorrhizal composition is linked to **three fold** variation in tree growth rates



Fungal energy & nutrient (inorganic N) metabolism genes are positively correlated with tree growth rate - multicopper oxidase gene proportions are negatively correlated –
inorganic vs. organic N strategies

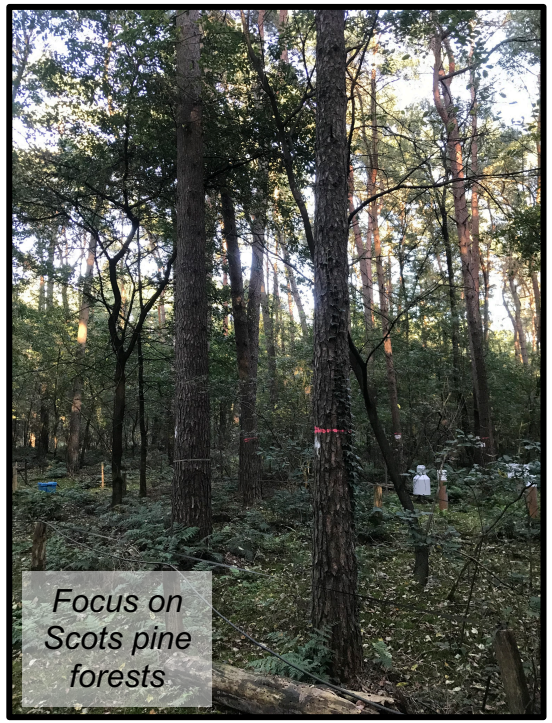
1. Identified fungal communities characteristic of “slow” and “fast” tree growth



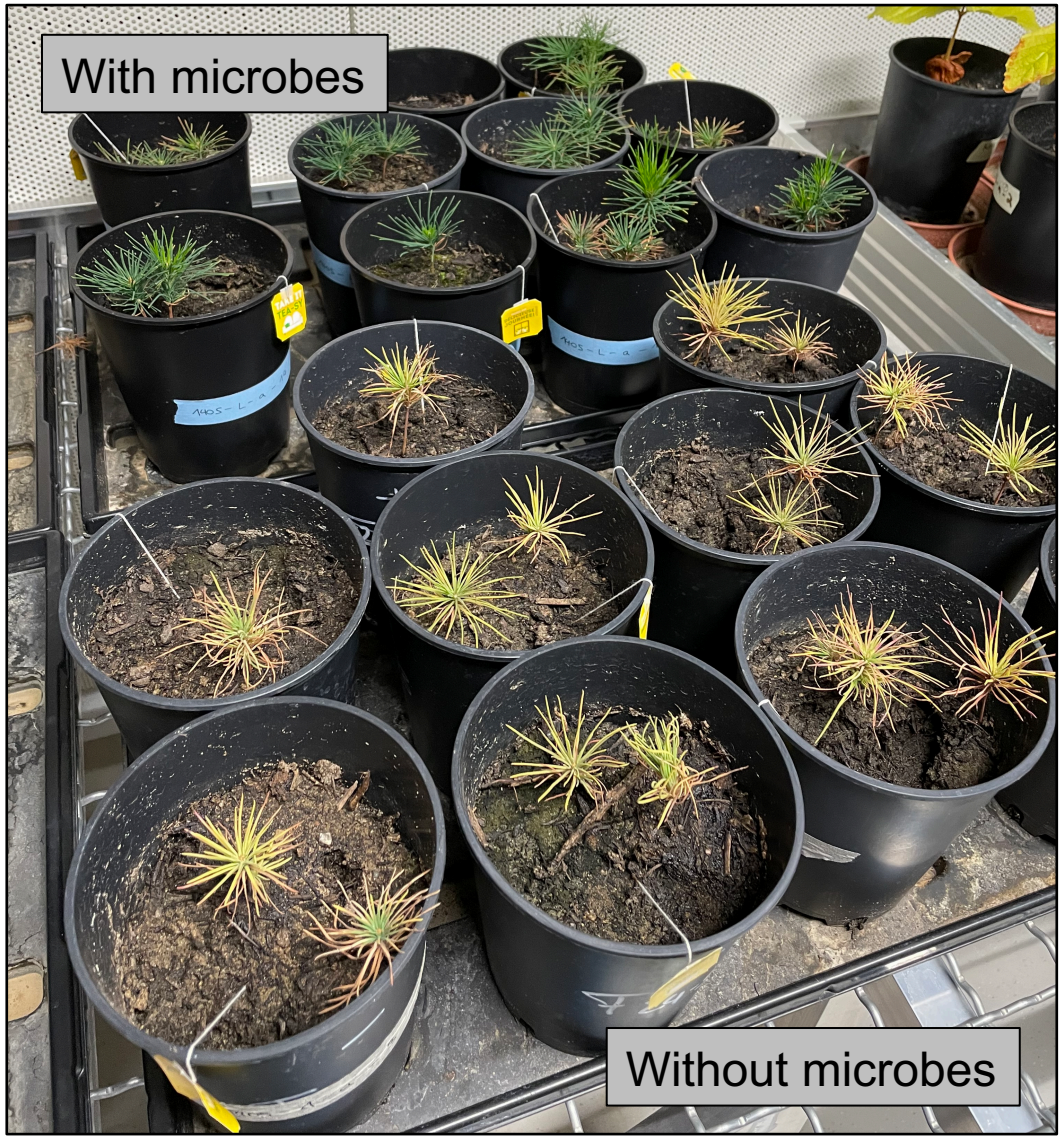


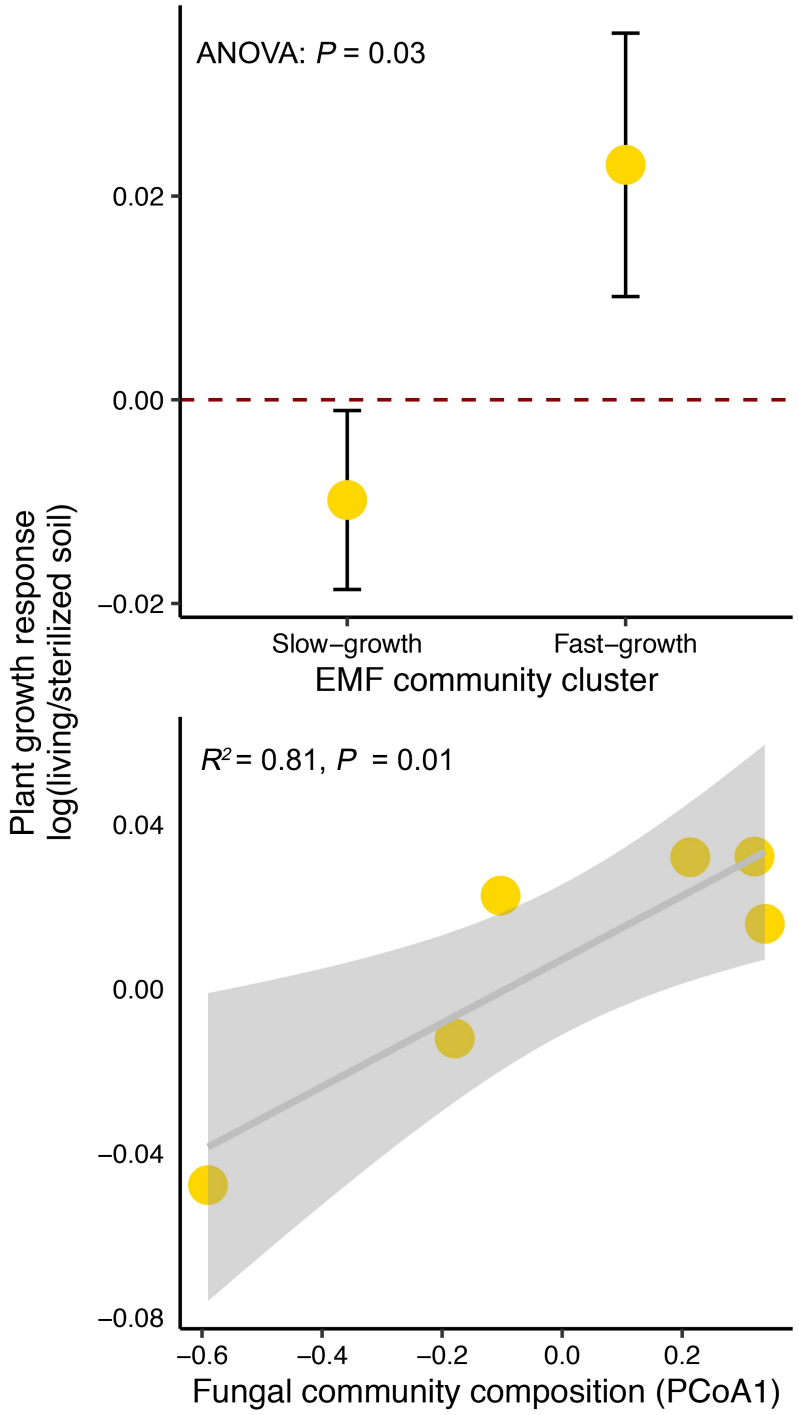
2. Collected soil from six forests to serve as microbial inoculant.

3. Grew Scots pine in a sterile growth medium with sterilize or live soil from the same forests



Microbes from “fast tree growth” fungal communities in the field accelerate tree growth





Does variation in the ectomycorrhizal fungal community impact forest productivity? ***Yes!***

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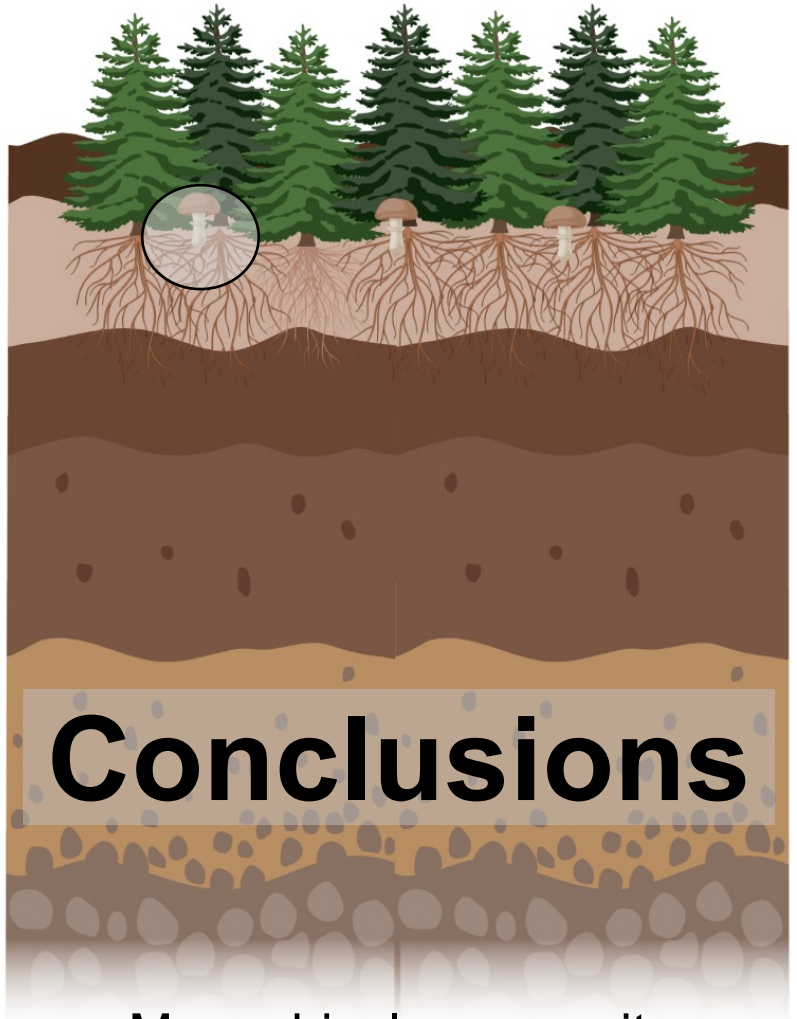
Our results support mesocosm studies and mycorrhizal theory



Conclusions

Mycorrhizal community variation ~ three-fold difference in tree growth rates

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Communities specialized at accessing inorganic, not organic N, accelerate tree growth