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Ectomycorrhizal fungal composition and function predict tree growth across Europe

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Ectomycorrhizal fungi are central members of the forest fungal community, forming symbiosis with most trees in temperate and boreal forests, enhancing plant access to limiting soil nutrients. Decades of greenhouse studies have shown that specific mycorrhizal fungi enhance tree seedlings growth and nutrient uptake rates, and that these effects are sustained when seedlings are out-planted into regenerating forests. Whether these relationships scale up to affect the growth of mature trees and entire forests harboring diverse fungal communities remains unknown. In this study, we combined a continental set of European forest inventory data from the ICP forest network with molecular ectomycorrhizal fungal community surveys to identify features of the mycorrhizal mycobiome linked to forest productivity. We found that ectomycorrhizal fungal community composition was a key predictor of tree growth, and this effect was robust to statistically accounting for climate, nitrogen deposition, soil inorganic nitrogen availability, soil pH, and forest stand characteristics. Furthermore, ectomycorrhizal fungi with greater genomic investment in energy production and inorganic nitrogen metabolism, but lower investment in organic nitrogen acquisition, were linked to faster tree growth. Lastly, we sampled soils from fast and slow growing forests and introduced their microbiomes into a sterilized growth medium to experimentally isolate microbiome effects on tree development. Consistent with our observational analysis, tree seedling growth was accelerated when inoculated with microbiomes from fast vs. slow growing forests. By linking molecular community surveys and long-term forest inventory data in the field, and then pairing this with a microbiome manipulation study under controlled conditions, this work demonstrates an emerging link between the forest microbiome and dominant European tree growth rates.

