

# Isolating a functionally relevant guild of fungi from the root microbiome of *Populus*

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## Background

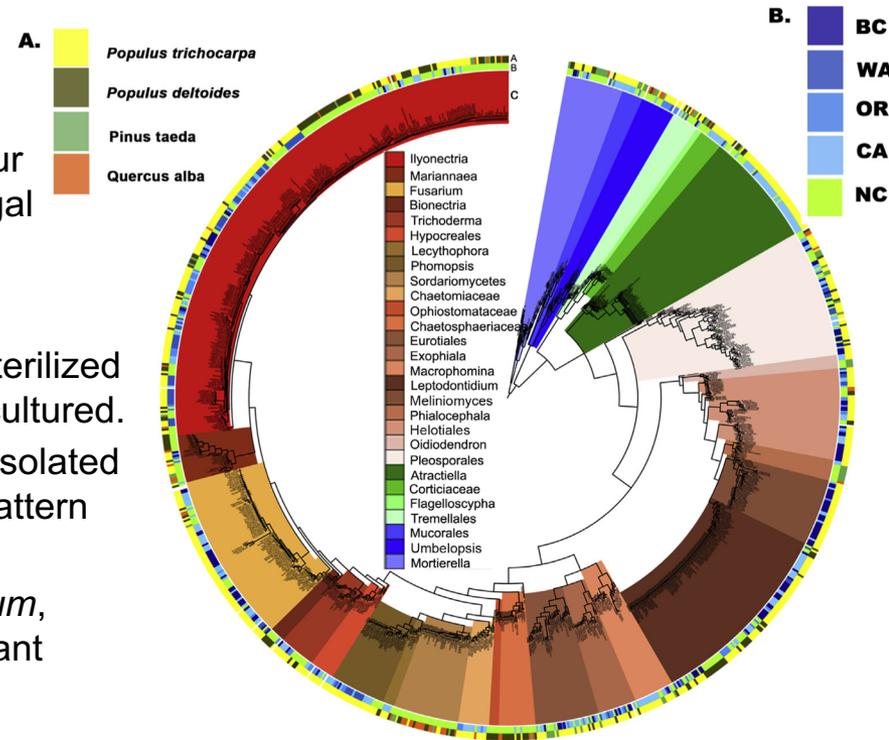
- Plant roots interact with a complex community of root-associated bacteria and fungi that are essential for maintaining plant health. This work sought to improve our understanding of the structure and function of plant-fungal interactions in the rhizosphere of *Populus*.

## Science

- Over 1800 fungal isolates were obtained from surface sterilized roots of *Populus*, many of which are unique and rarely-cultured.
- The most dominant taxa associated with *Populus* were isolated from both eastern and western US soils, with no clear pattern of biogeographical provenance.
- Most of the isolated fungal OTUs included *Leptodontidium*, *Cylindrocarpon*, *Atractiella*, and *Ilyonectria*. Low abundant ones included *Rhizoctonia*, *Cadophora*, *Corticaceae*, *Mortierella*, and *Flagelloscypha*.
- Many of the sequenced fungal isolates represent previously uncultured fungi.

## Significance

- This research makes a significant contribution to establishing baseline resources for understanding the core members of the endorhizal guild of fungi able to live inside *Populus* roots.



**Phylogenetic affinities of fungal isolates based on 28s rDNA analysis.** Plant host from which root-associated fungi were isolated from is color-coded on outer ring; region from where the isolates originate is color coded in middle ring; taxonomic affinity of isolates are color-coded as indicated by the inner key.