

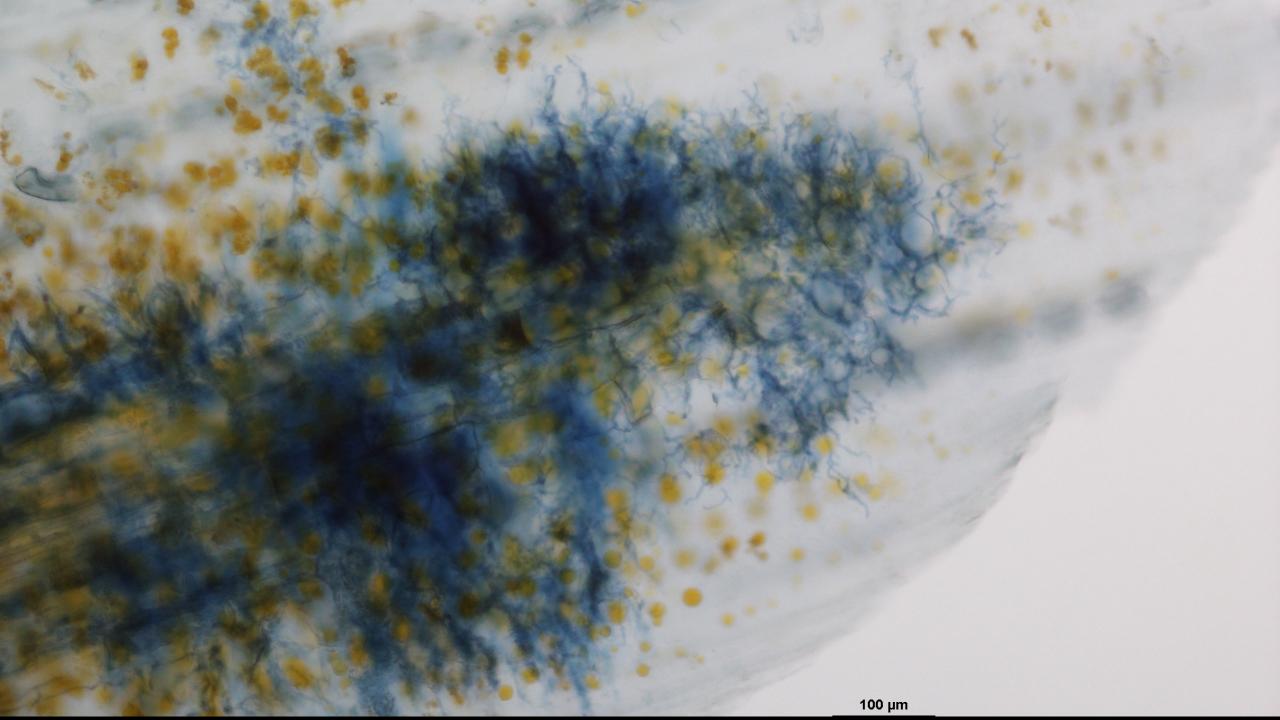
Can we improve western white pine microbiomes to promote resistance to blister rust disease?

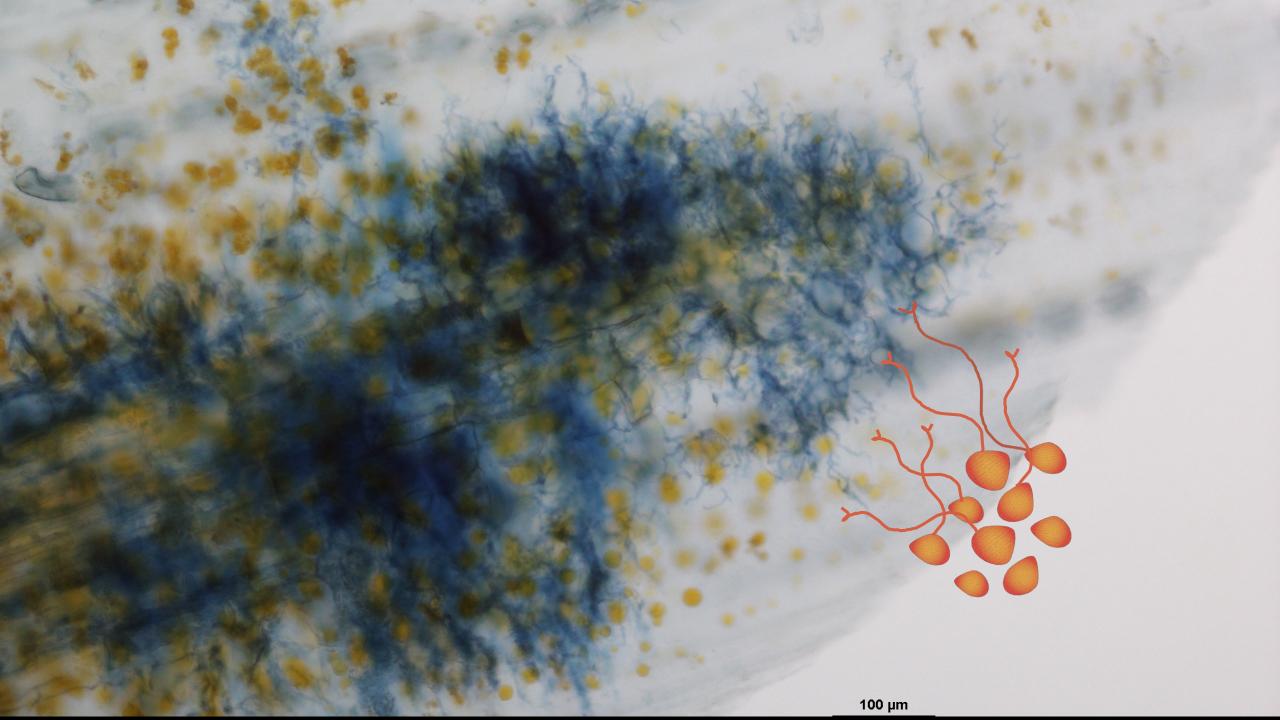
Lorinda Bullington ^{1,2}, Emily Martin², Nadir Erbilgin³, Peter Kennedy⁴, Richard Sniezko⁵

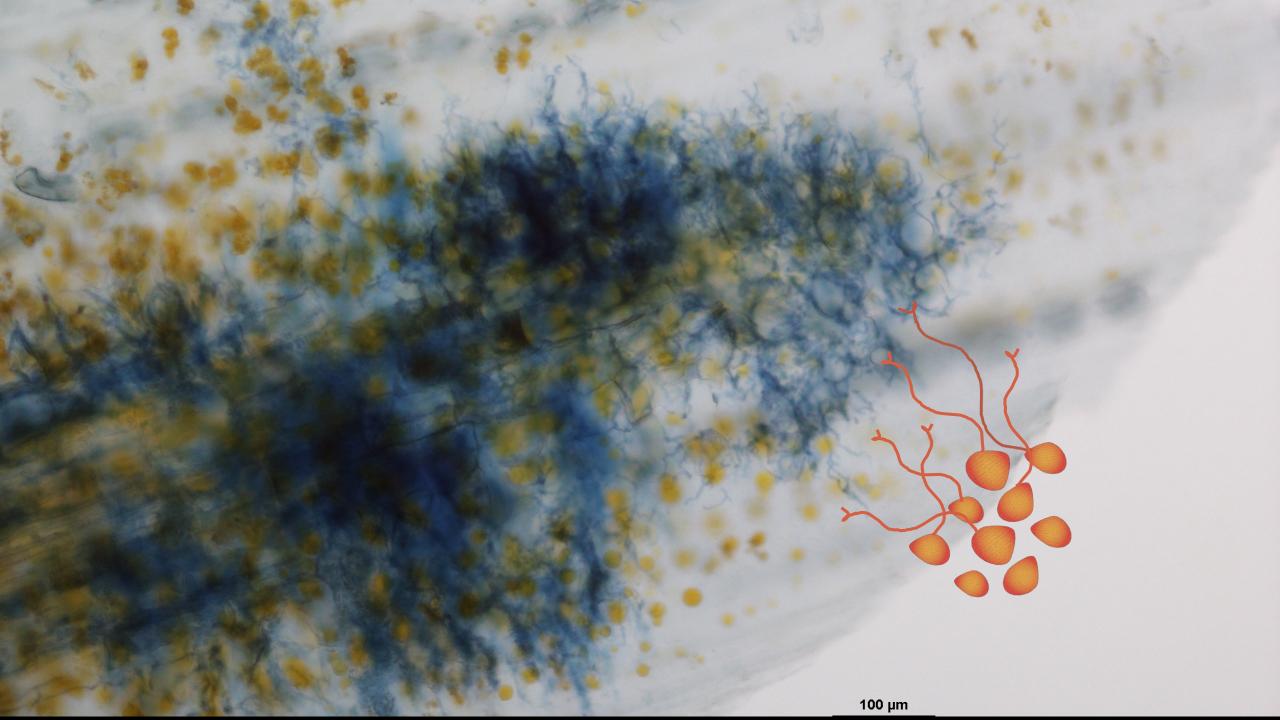
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Lorinda Bullington







Fungal antagonist assays



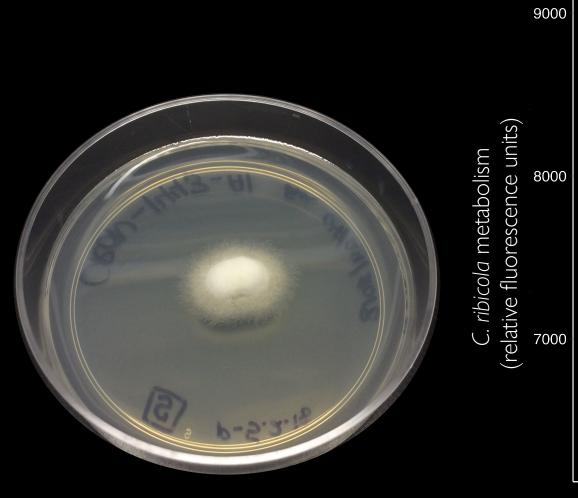
VS.



Cronartium ribicola (pathogen)

Fungal symbionts

Fungal antagonist assays



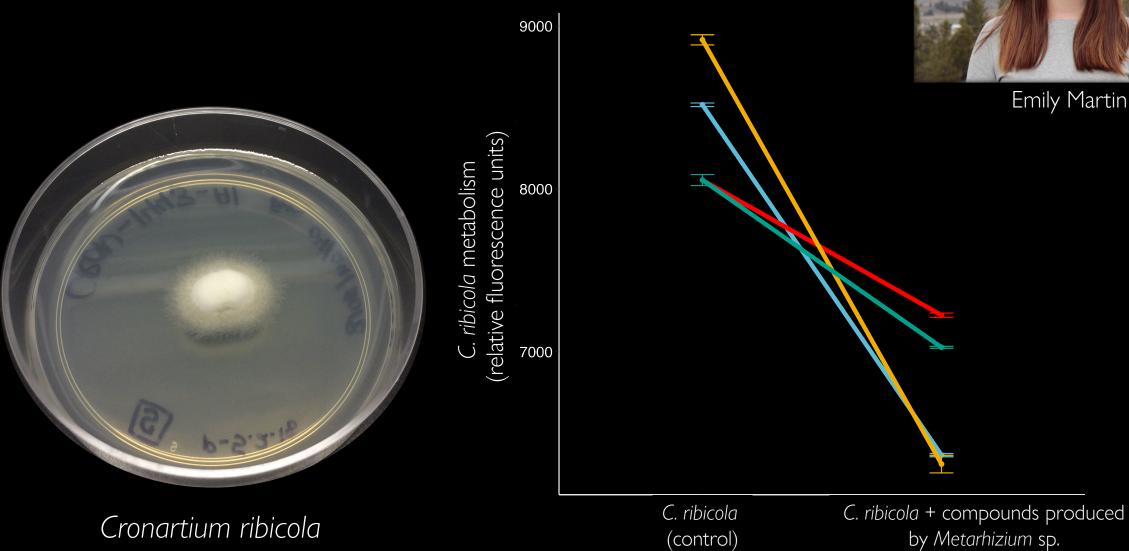
Cronartium ribicola

C. ribicola (control) C. ribicola + compounds produced by Metarhizium sp.



Emily Martin

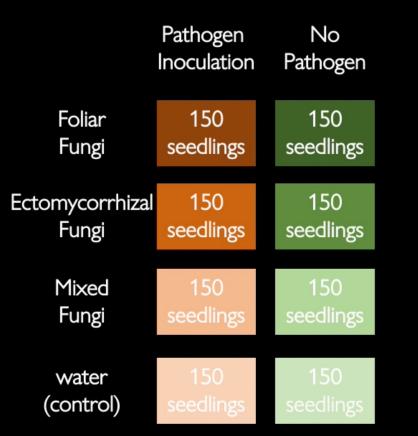
Fungal antagonist assays



Suillus sibiricus



Full-factorial Experimental Design





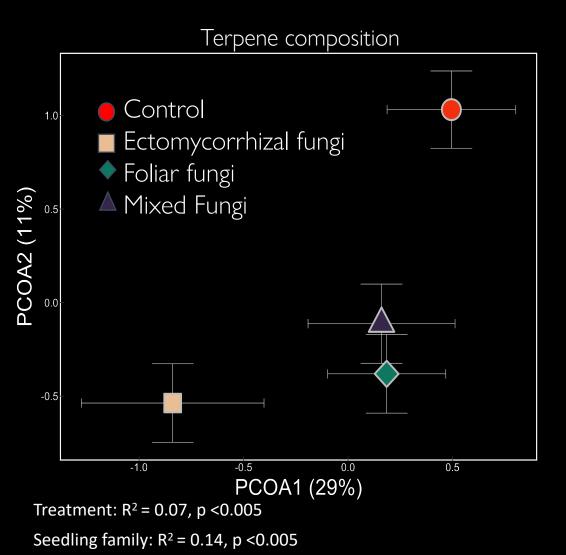


Inoculation with Cronartium ribicola

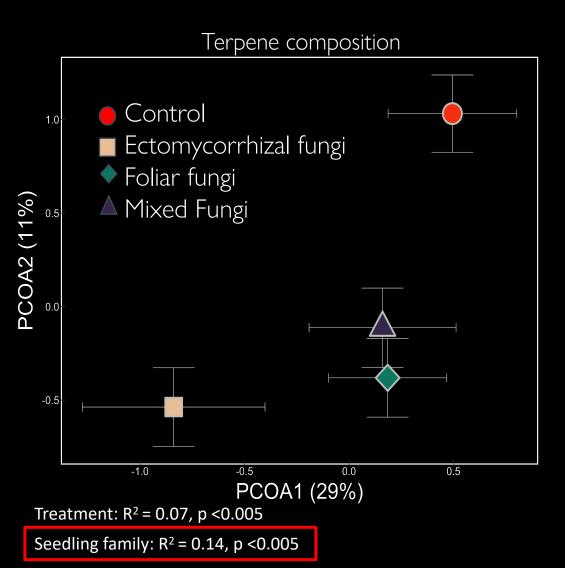
• Six seedling families (seeds collected from the same parent tree) were included to determine the genetic variation of fungal microbiome interactions.

• Seedling families represented seed lots with known resistance to Cronartium, as well as those with known susceptibility.

Fungal treatments changed seedling defensive chemistry

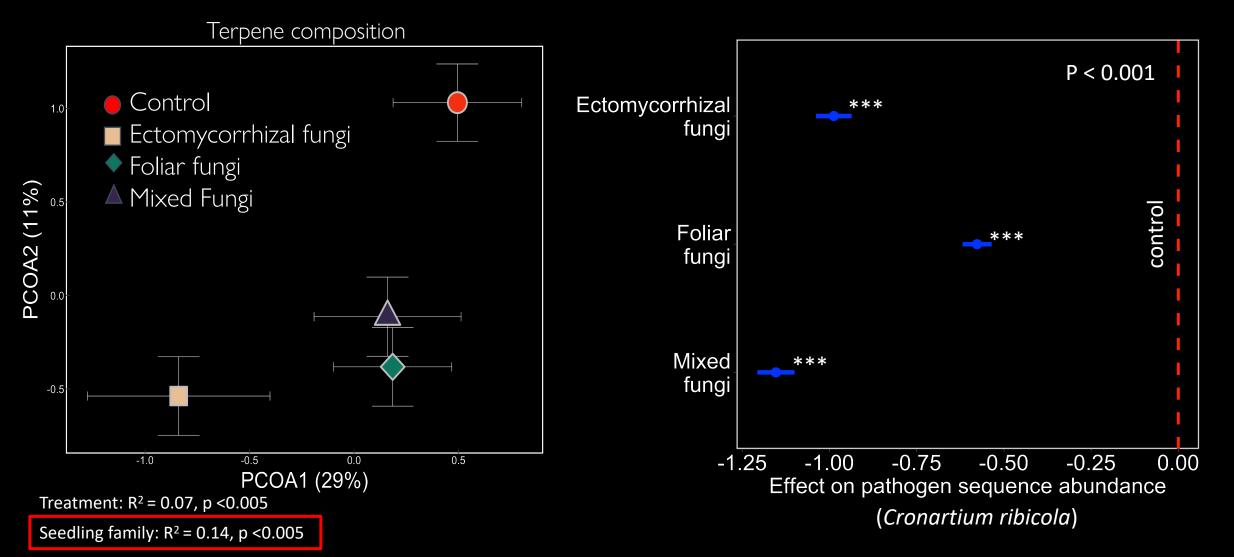


Fungal treatments changed seedling defensive chemistry



Fungal treatments changed seedling defensive chemistry

Fungal treatments reduced pathogen sequence abundance



C. ribicola sequence abundance is positively correlated with disease characteristics

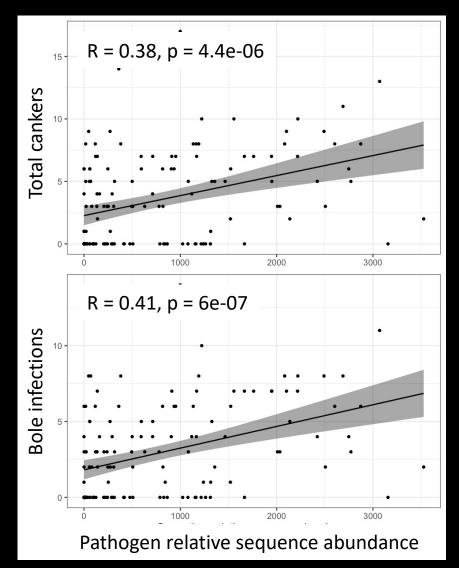




Photo: Richard Sniezko

Summary

- Inoculations with fungal endophytes and ectomycorrhizal fungi altered tree defensive chemistry and reduced pathogen sequence abundance in foliar tissue
- Pathogen sequence abundance was positively correlated with the total cankers and number of stem infections on each seedling
- Treatment effects vary among seedling families. Families known to have greater genetic resistance to *C. ribicola* appear to respond more positively and more strongly to fungal treatments

Thank you for listening!

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