# Fungal pathogen tolerance and geographic variation influence ectomycorrhizal traits of loblolly pine

B.J. Piculell, L.G. Eckhardt, J.D. Hoeksema

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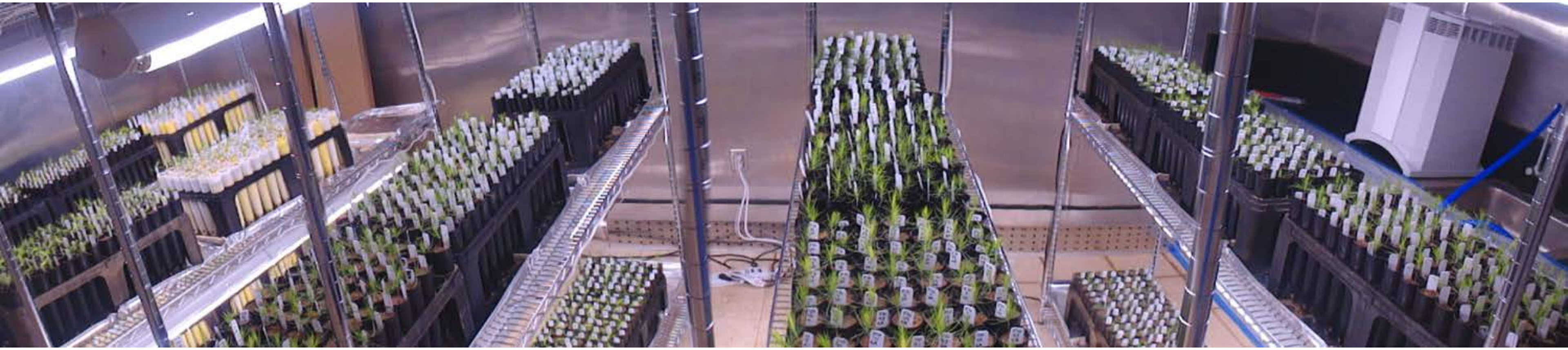

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# How do plants evolve in response to complex environments?

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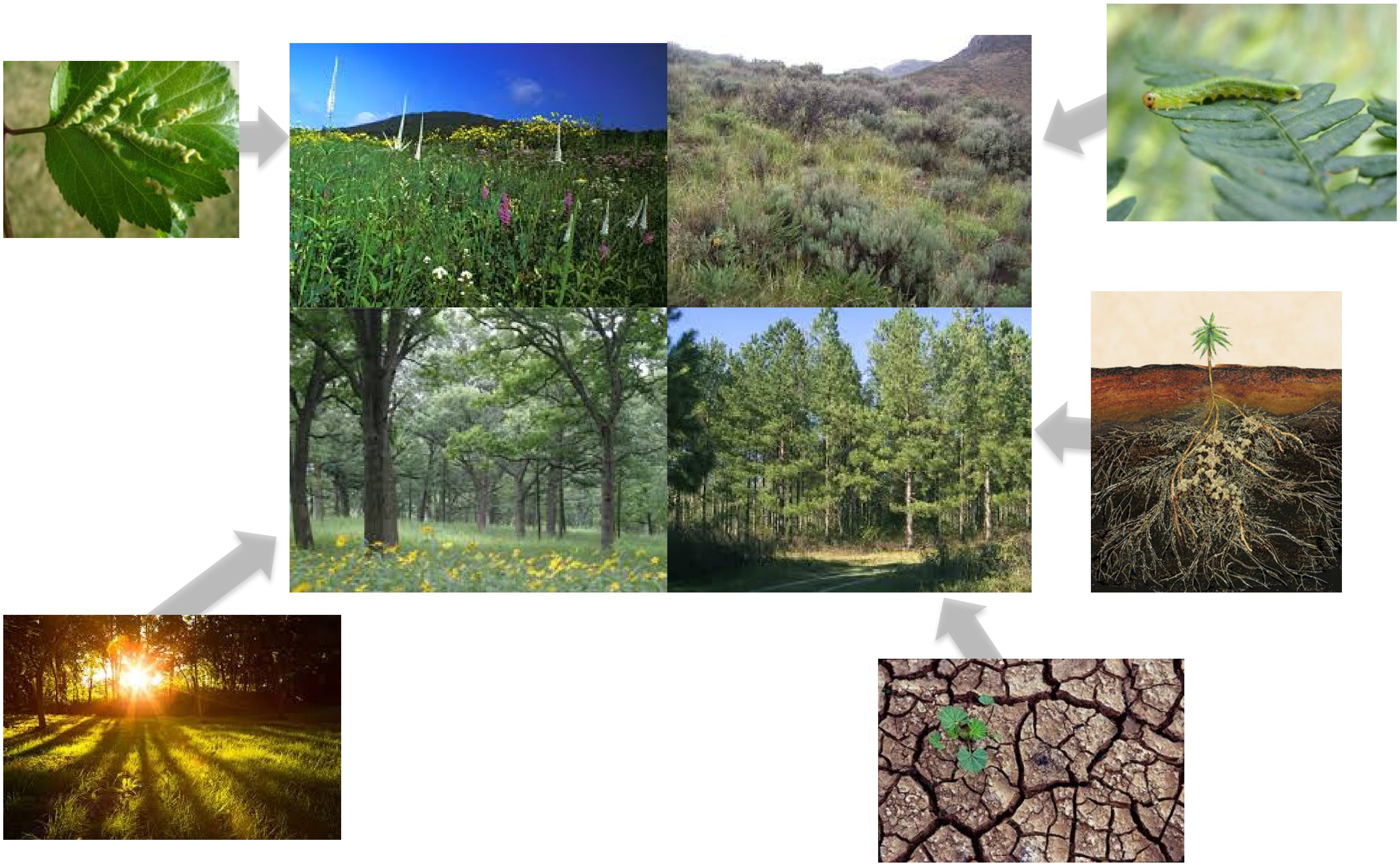
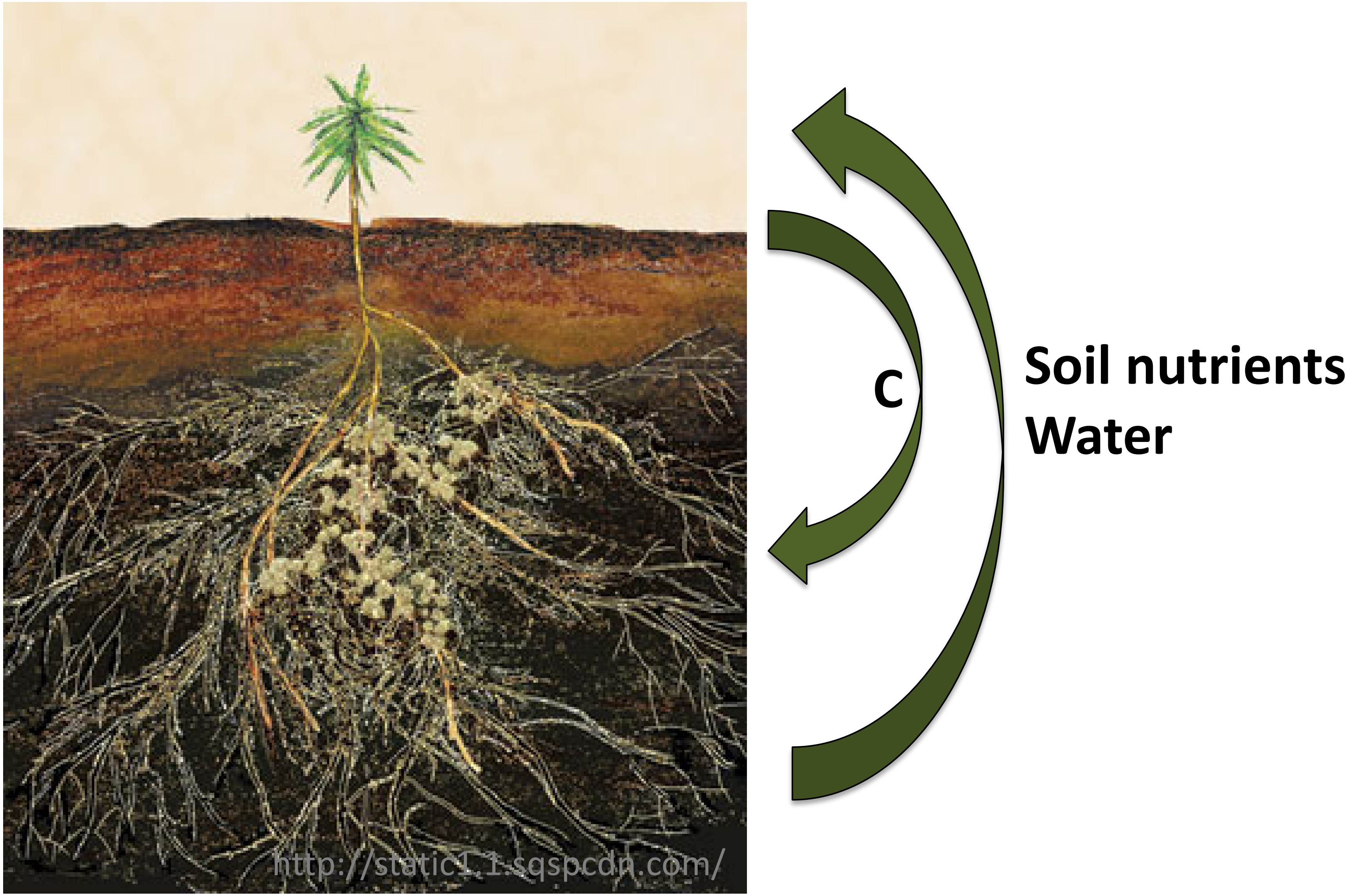


# Loblolly pine (*Pinus taeda*)

# mycorrhizal fungi



# Ectomycorrhizal fungi ⇆ Plants

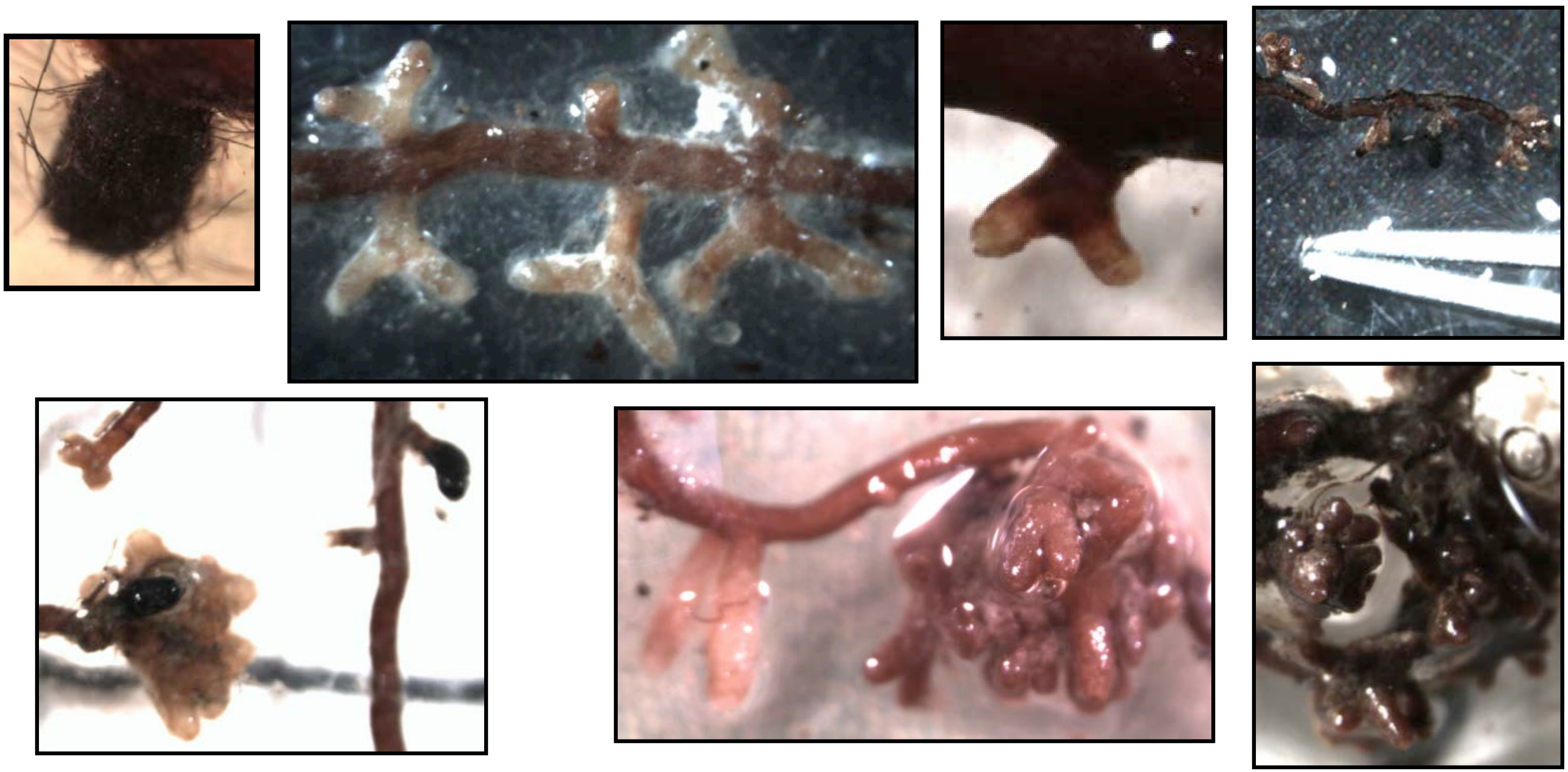
Alter competitive interactions among plants

Multiple fungal species per host plant

Vary in benefit to host plant

# Morphotyping and fungal identification

Root tips colonized by ectomycorrhizal fungi grouped by similar phenotypic characteristics (color, texture, emanating hyphae)



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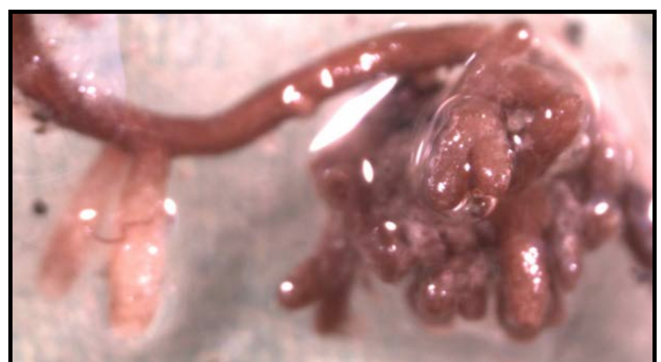
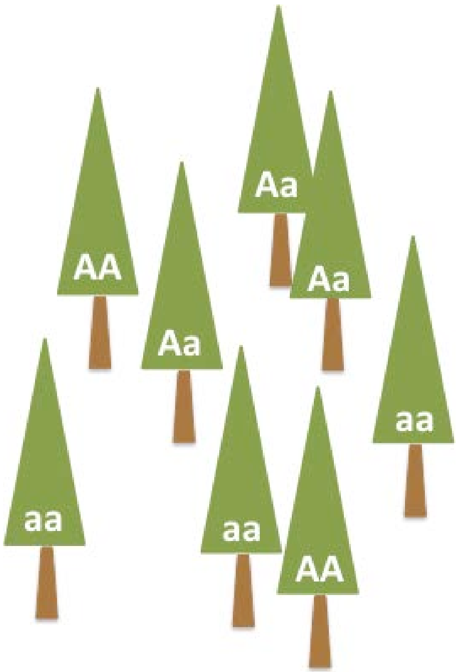
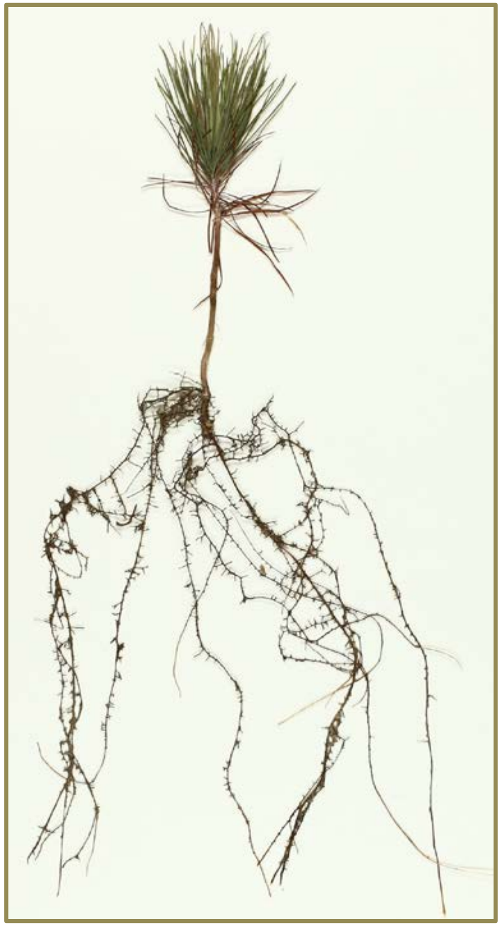
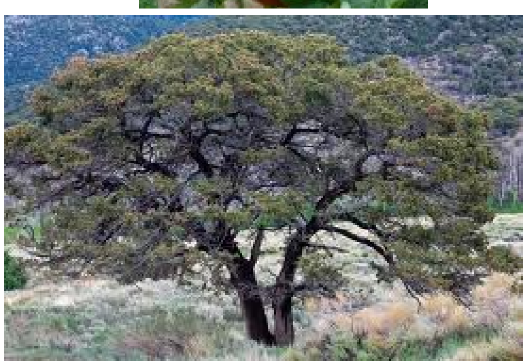



# Understanding the genetic basis of mycorrhizal traits



# Evidence for genetic correlations between mycorrhizal and other plant traits



Modern wheat vs older cultivars
(Zhu *et al.*, 2001)

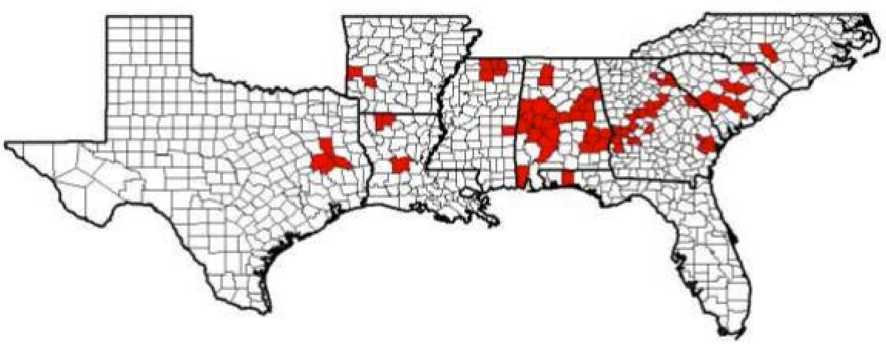
Cultivated tomato vs wild strains
(Bryla & Koide, 1990)

Herbivore resistant Pinyon pine
(Sthultz *et al.*, 2009)

**Pine decline**

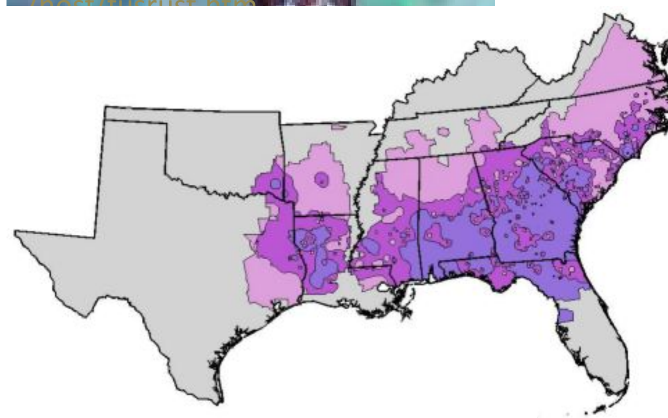
*Leptographium* and *Grosmannia*

from Eckhardt *et al.,* 2007



**Fusiform rust**

*Cronartium*


Forest Ecology and Management 349 (2015) 134–148

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Forest Ecology and Management

journal homepage: www.elsevier.com/locate/foreco

ELSEVIER

Review

## A review of southern pine decline in North America

David R. Coyle [a,*], Kier D. Klepzig [b], Frank H. Koch [c], Lawrence A. Morris [a], John T. Nowak [d], Steven W. Oak [d,1], William J. Otrosina [e,1], William D. Smith [c,1], Kamal J.K. Gandhi [a]

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## Managing Fusiform Rust on Loblolly and Slash Pine in Forest and Landscape Settings

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## Loblolly Pine Decline

James Johnson, Forest Health Coordinator

A phenomenon known as Loblolly Pine (*Pinus taeda*) Decline is now used to describe drastic decreases in tree health, growth rates, and ongoing mortality in stands. Stands suffering from LPD are characterized by thinning and yellowing crowns, reduced radial growth, deterioration of fine feeder root systems, and increased mortality rates on

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UofA DIVISION OF AGRICULTURE
RESEARCH & EXTENSION
University of Arkansas System

Agriculture and Natural Resources

FSA7543

# Fusiform Rust in Arkansas

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## ASSESSMENT OF LOBLOLLY PINE DECLINE IN CENTRAL ALABAMA

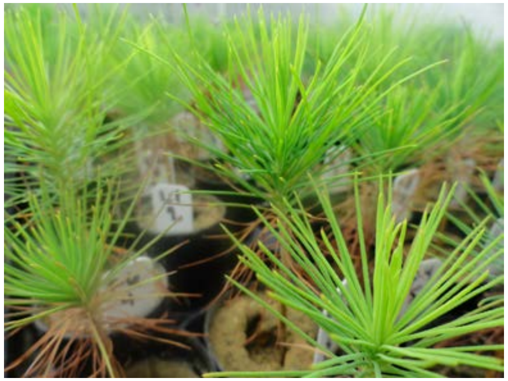
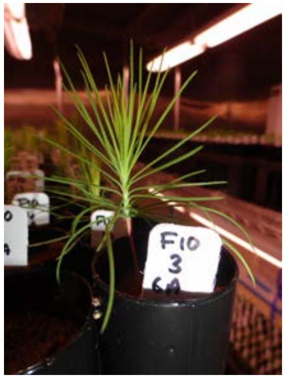
**Nolan J. Hess, William J. Otrosina, Emily A. Carter, Jim R. Steinman, John P. Jones, Lori G. Eckhardt, Ann M. Weber, and Charles H. Walkinshaw[1]**

**Abstract**—Loblolly pine (*Pinus taeda* L.) decline has been prevalent on upland sites of central Alabama since the 1960's. The purpose of this study was to compare Forest Health Monitoring (FHM) standards and protocols with root health evaluations relative to crown, stem, and site measurements. Thirty-nine 1/6 acre plots were established on loblolly decline sites in nine central Alabama counties. Sites were selected on federal, state, and private industrial lands to measure variables of decline symptoms, age classes and management

# Fungal pathogen tolerance and geographic variation influence ectomycorrhizal traits of loblolly pine

Q1: Do different locations within the natural range of loblolly pine yield different mycorrhizal fungal communities?

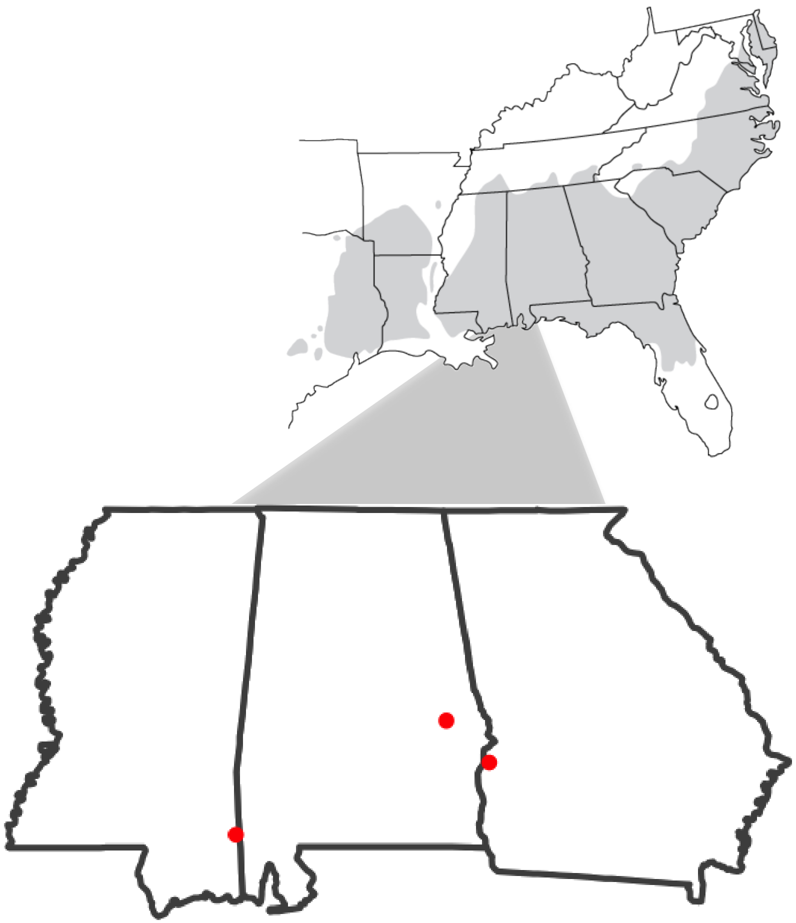
Q2: Do individual EM fungi respond differently to host genetic variation in pathogen tolerance and does this response depend on origin of the fungal community?

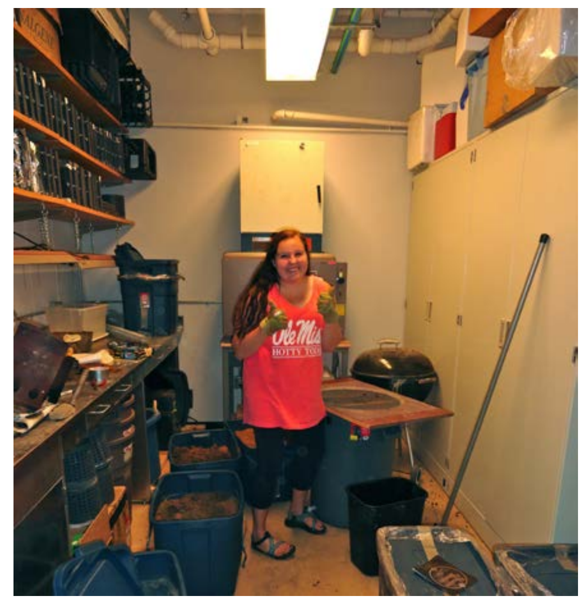




Seedlings from loblolly pine families either *tolerant* or *susceptible* to Pine decline (PD) or Fusiform rust (FR)

Tolerant | Susceptible

# 3 soil sources





seedlings: 4 categories

**Fusiform rust: t or s**

**Pine decline: t or s**

| | # Individual seedlings | | |
|---|---|---|---|
| **Category** | **AL** | **MS** | **GA** |
| FR-t | 52 | 42 | 37 |
| FR-s | 63 | 54 | 55 |
| PD-t | 48 | 50 | 23 |
| PD-s | 50 | 43 | 41 |
| Total | 213 | 189 | 156 |

# Fungal pathogen tolerance and geographic variation influence ectomycorrhizal traits of loblolly pine

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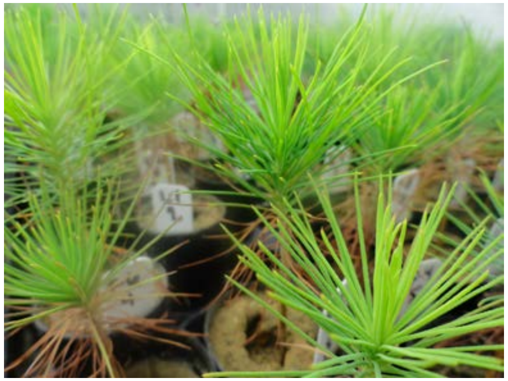
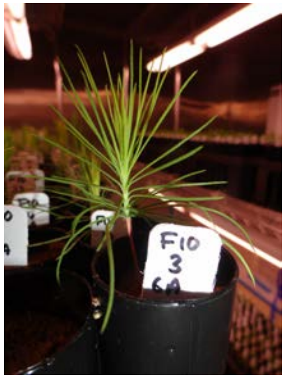
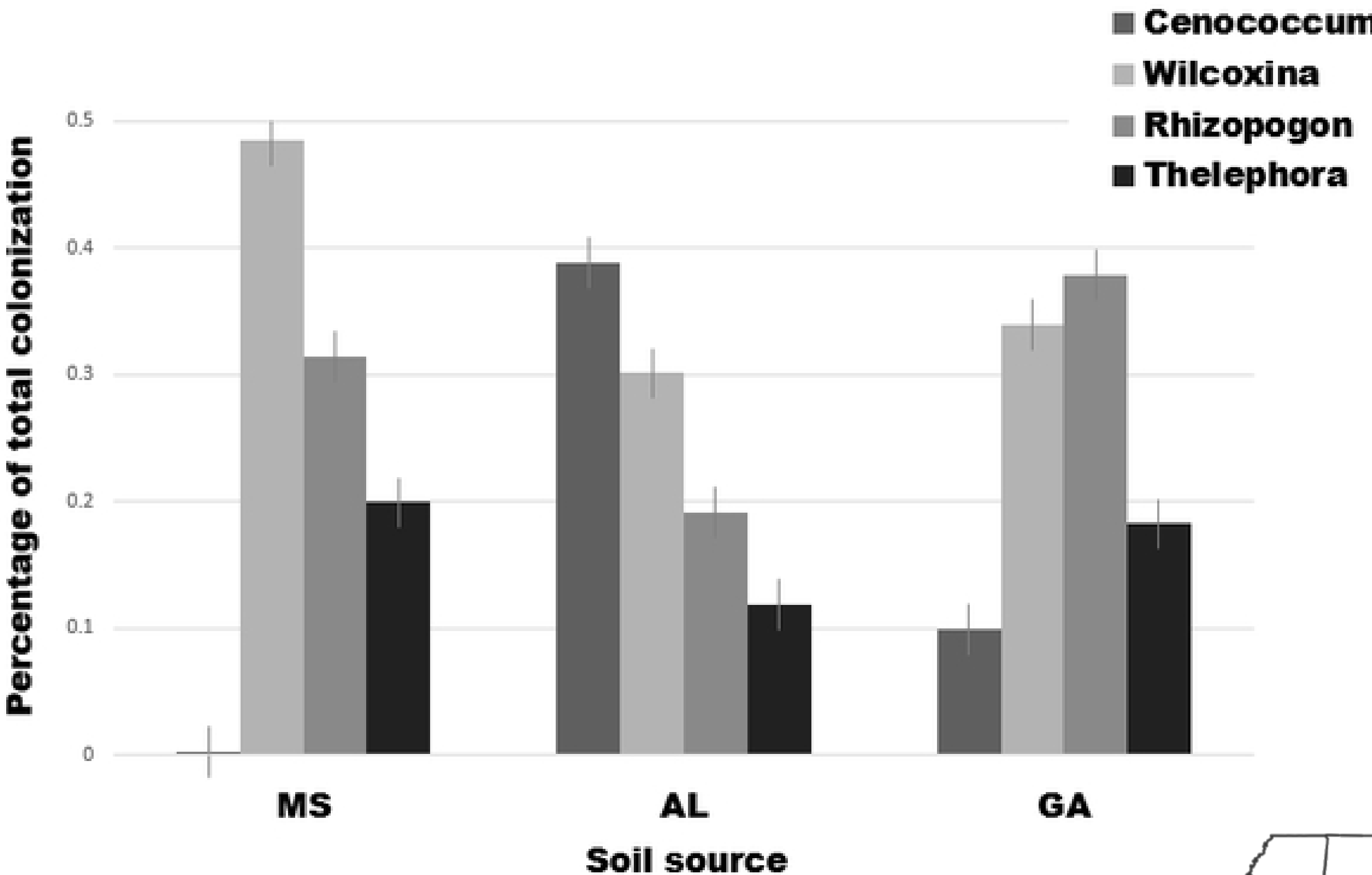



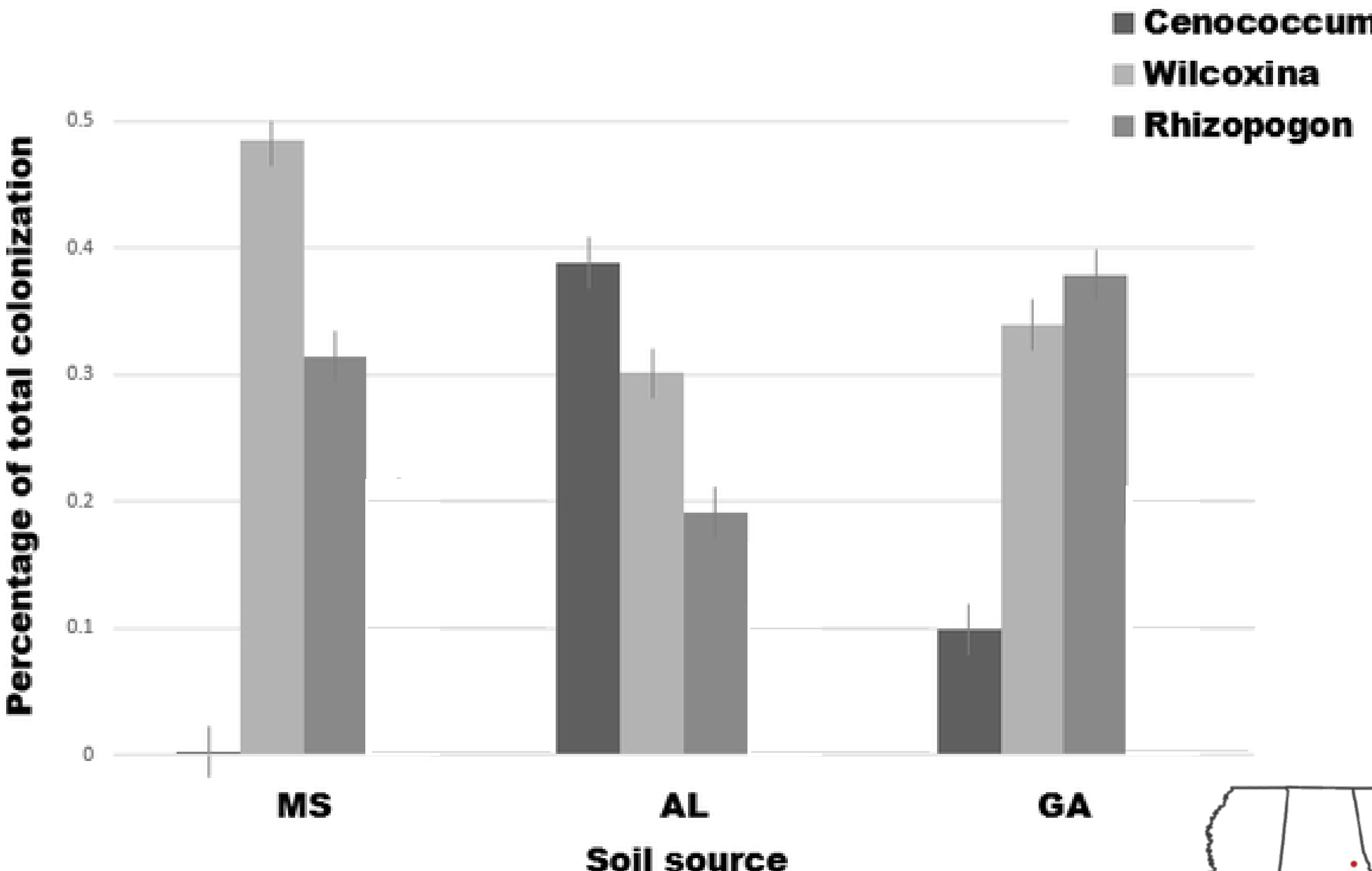

# Different locations within the natural range of loblolly pine yield different dominant mycorrhizal fungal communities

($F_{2,560} = 36.754$, $p = 0.01$)



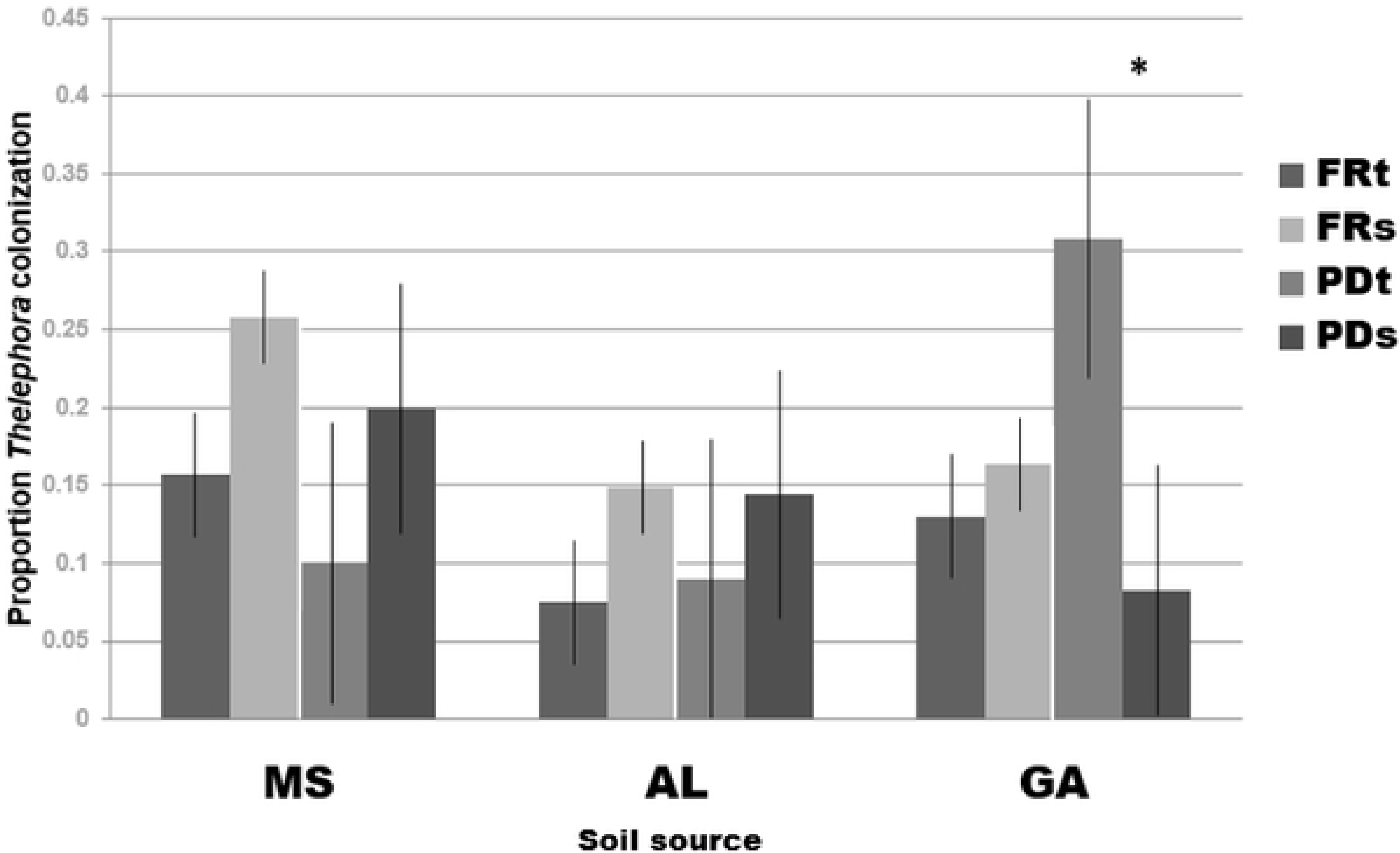

# Three of the four dominant fungal colonizers respond only to soil inoculation source

*Rhizopogon* ($F_{2,532}$= 19.342, $p$ = 7.787 e-09), *Cenococcum* ($F_{2,532}$= 120.840, $p$ = <2.0 e-16), and *Thelephora* ($F_{2,532}$= 12.5084, $p$ = 4.91e-06)




# Colonization of *Thelephora* determined by interaction of plant family resistance category and soil inoculation source

($F_{6,536} = 3.691$, $p = 0.00132$)



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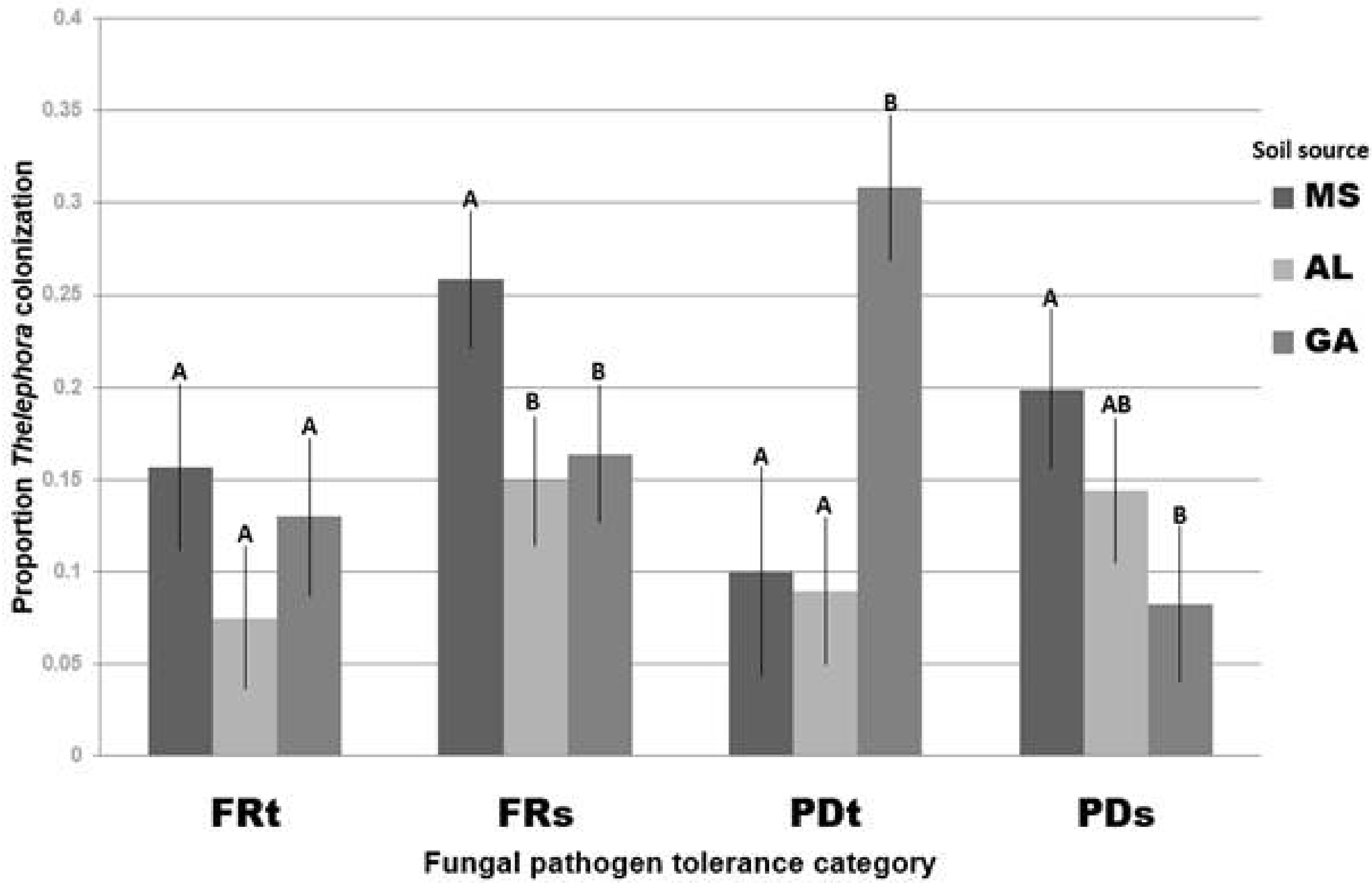
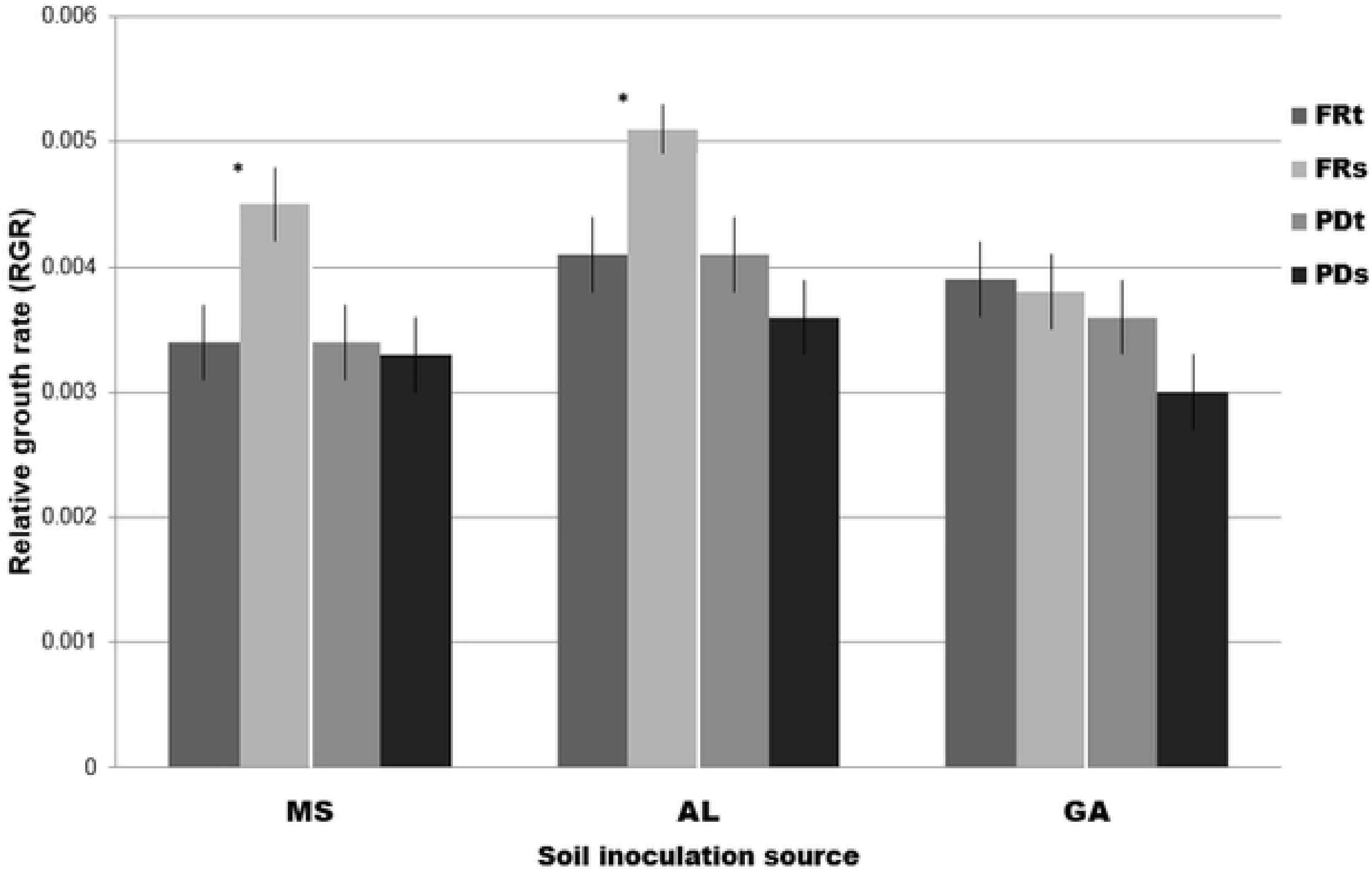


# Relative growth rate of seedlings determined by interaction of plant family resistance category and soil inoculation source

($F_{6,532} = 3.342$, $p = 0.0031$ )



## Relative growth rate of seedlings determined by interaction of plant family resistance category and soil inoculation source

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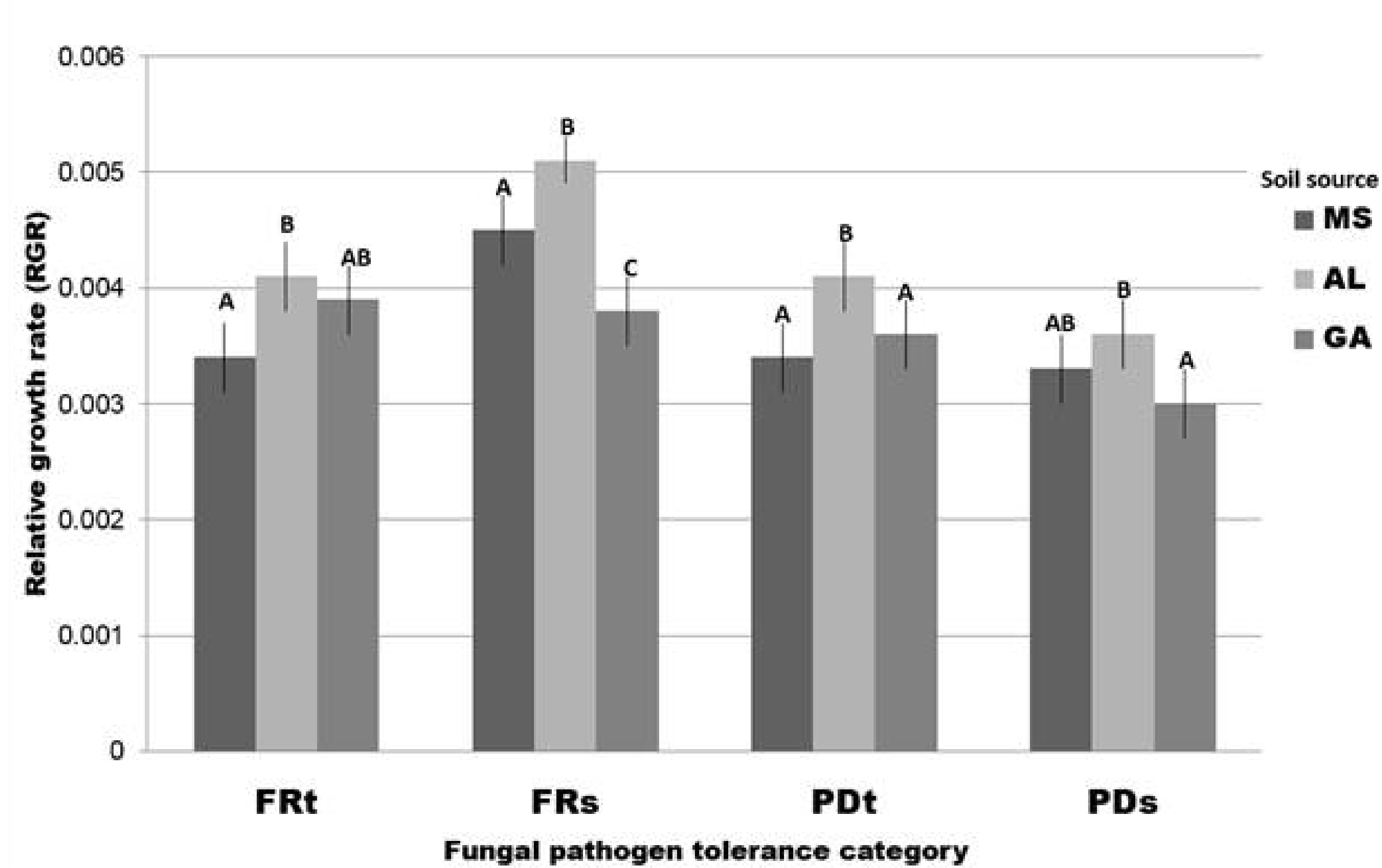
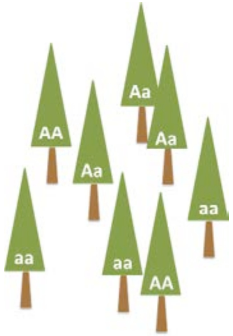
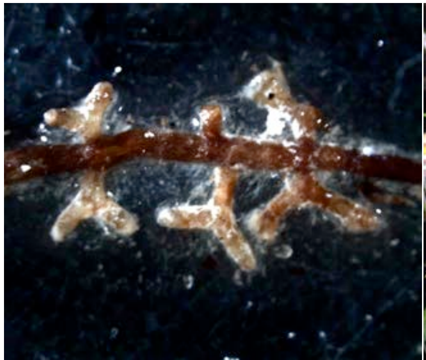


# Conclusions

- Evidence of genetic correlations between fungal pathogen tolerance and *Thelephora*
- Evidence of genetic correlations between fungal pathogen tolerance and relative growth rate
- outcome of genetic correlations differs among soil environments
- Loblolly pine interacts with EM species differently



# Association mapping of ectomycorrhizal traits in loblolly pine

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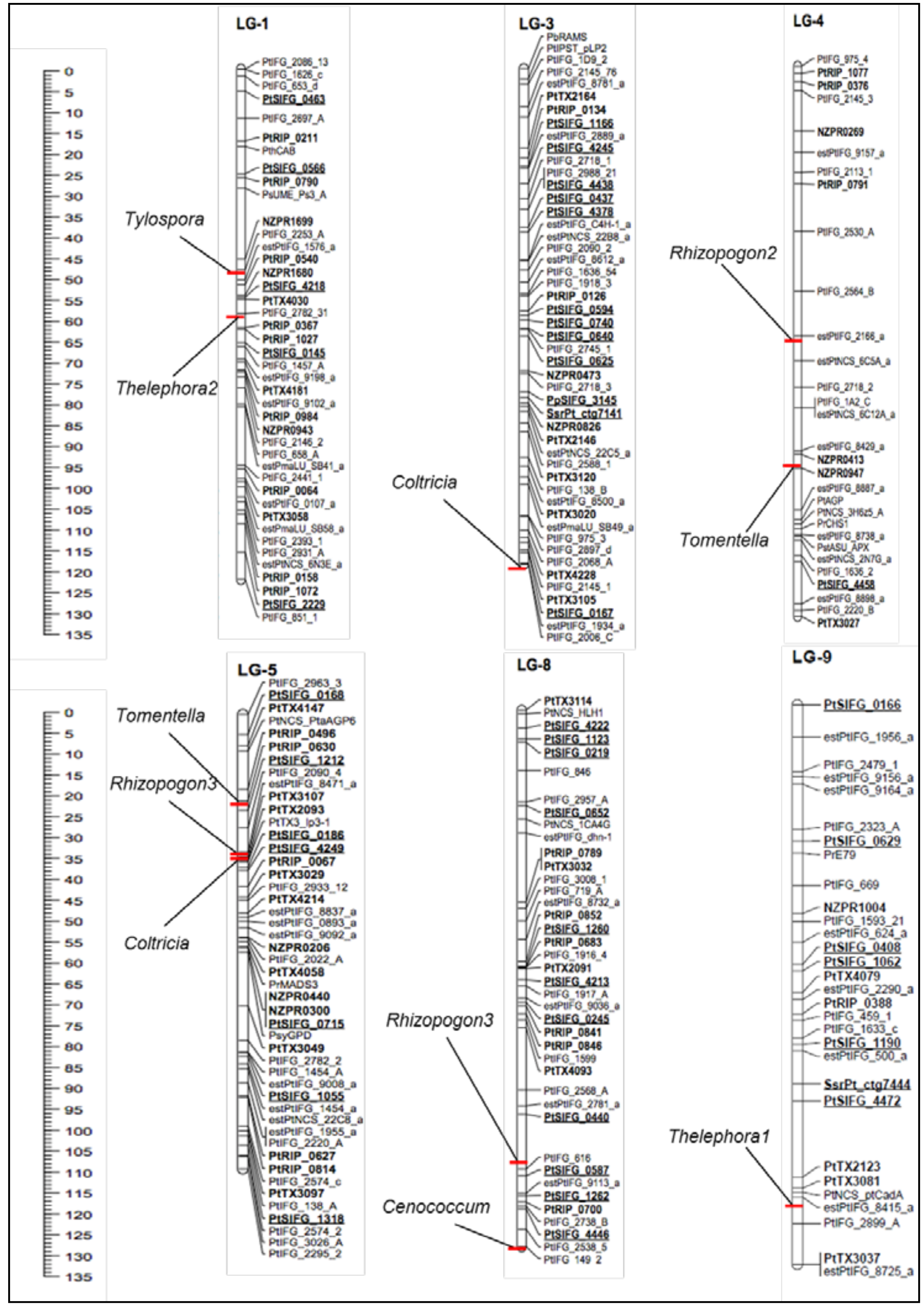
# Ectomycorrhizal traits mapped to loblolly pine genome

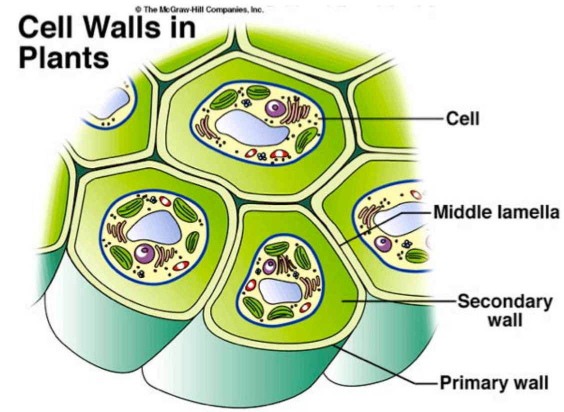
Percentage of phenotypic variance in mycorrhizal traits attributed to marker effects ($R^2$) ranged from 13% to 55%

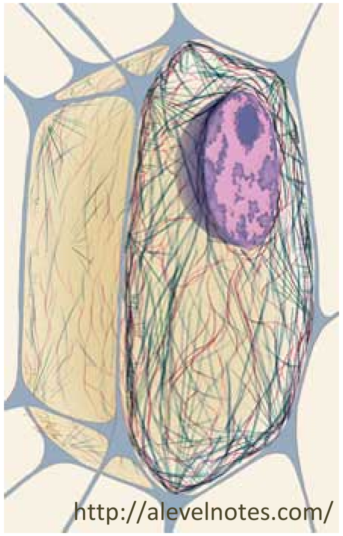


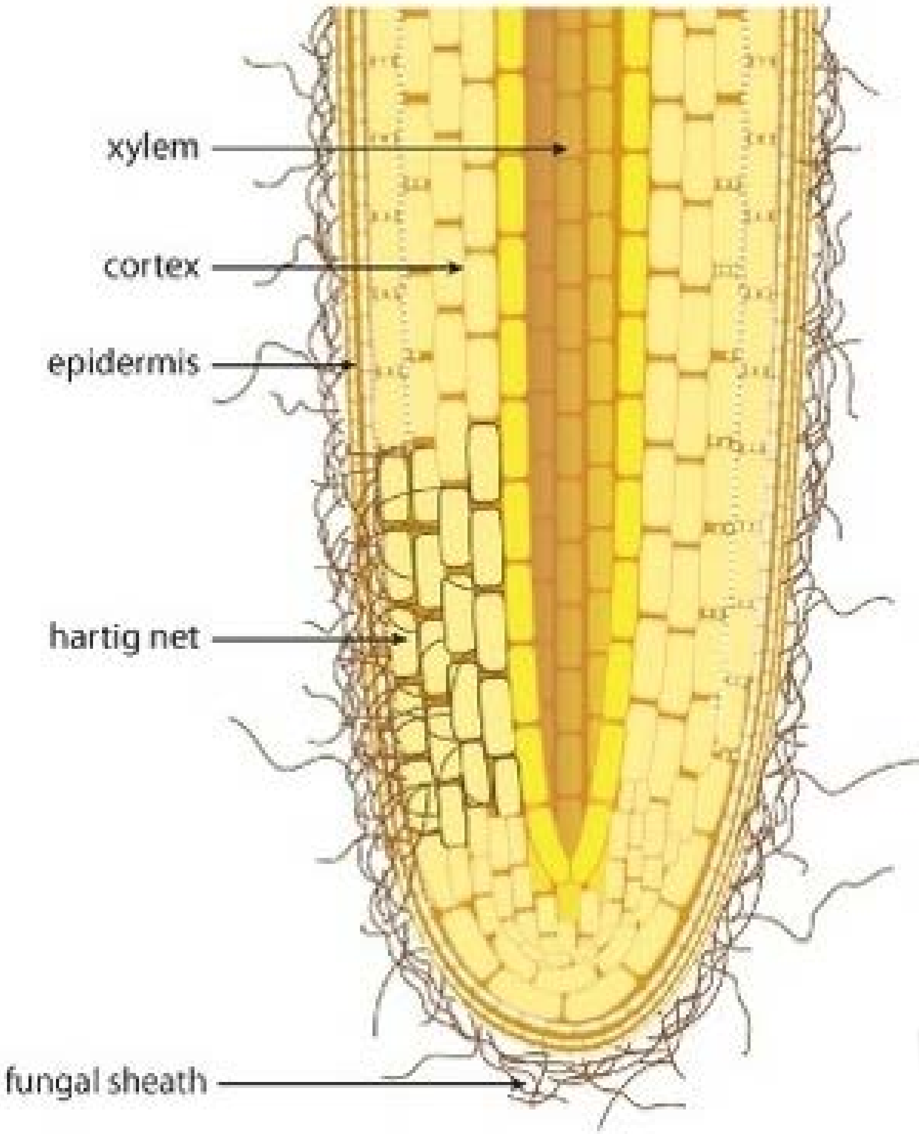

modified from Echt *et al.*, 2011

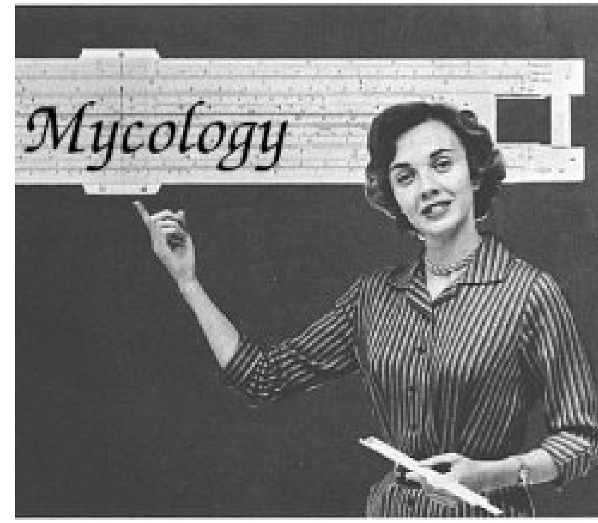
# Host plant cell structural components influence abundance of certain EM fungi

| Trait | Annotation | Putative function |
|---|---|---|
| **Rhizopogon3** | Protein domain found in the Ovate family protein (OFP) | In *Arabidopsis, OPF4* has a role in regulating **secondary cell wall formation** (Li *et al*., 2011) |
| **Rhizopogon3** | Glycosyl transferase, family 8 (GT8) | In *Arabidopsis,* the activity of three members of the GT8 family are involved in the synthesis of xylan (Rennie *et al*., 2012), an integral component of plant **secondary cell walls** |
| **Tomentella** | Actin family of proteins | Involved in formation of filaments that are a major component of the **cytoskeleton** |




xylem
cortex
epidermis
hartig net
fungal sheath


Mycology

# Conclusions

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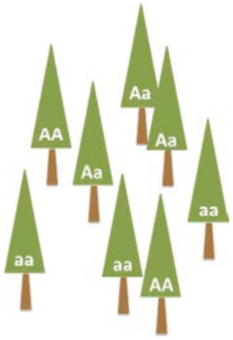
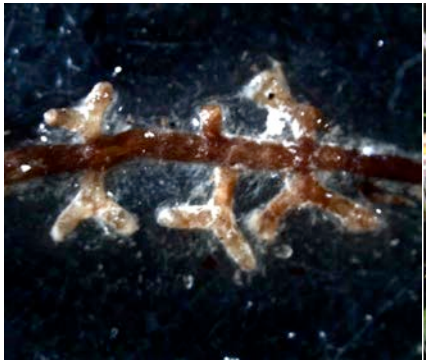
- association analysis suggests fewer genes of large effect
- mycorrhizal traits associated with host plant cell structural components

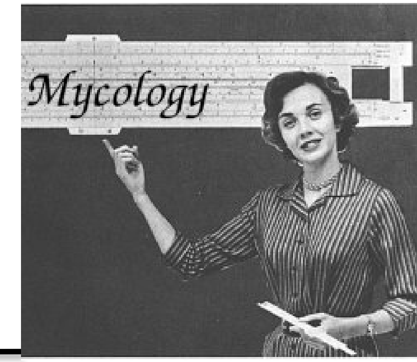







*Mycorrhizal fungi influence*

- **Carbon sequestration**
- **Water stress mitigation**




REPORT

## Roots and Associated Fungi Drive Long-Term Carbon Sequestration in Boreal Forest

K. E. Clemmensen[1,*], A. Bahr[2], O. Ovaskainen[3], A. Dahlberg[1,4], A. Ekblad[5], H. Wallander[2], J. Stenlid[1], R. D. Finlay[1], D. A. ...
+ See all authors and affiliations

*Science* 29 Mar 2013:
Vol. 339, Issue 6127, pp. 1615-1618
DOI: 10.1126/science.1231923

Research review

## Mycorrhizal fungi have a potential role in soil carbon storage under elevated $CO_2$ and nitrogen deposition

K. K. TRESEDER* AND M. F. ALLEN
*Center for Conservation Biology, University of California at Riverside, Riverside, CA 92521, USA*
*Received 9 November 1999; accepted 7 March 2000*

Global Change Biology

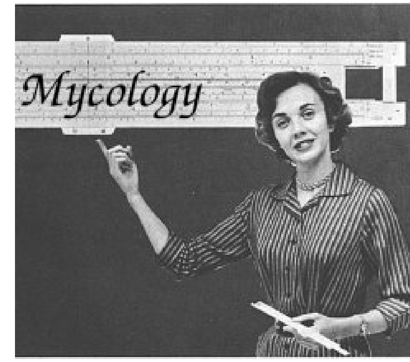
PRIMARY RESEARCH ARTICLE | Free Access

## Mycorrhizal fungi enhance plant nutrient acquisition and modulate nitrogen loss with variable water regimes

Timothy M. Bowles, Louise E. Jackson, Timothy R. Cavagnaro

First published: 01 September 2017 | https://doi.org/10.1111/gcb.13884 frontiers in Microbiology

ORIGINAL RESEARCH
published: 11 June 2018
doi: 10.3389/fmicb.2018.01248




# The Response Patterns of Arbuscular Mycorrhizal and Ectomycorrhizal Symbionts Under Elevated $CO_2$: A Meta-Analysis

*Yuling Dong[1,2], Zhenyu Wang[3], Hao Sun[1,2], Weichao Yang[1] and Hui Xu[1]**

*[1] Key Laboratory of Pollution Ecology and Environmental Engineering, Institute of Applied Ecology, Chinese Academy of Sciences, Shenyang, China, [2] University of Chinese Academy of Sciences, Beijing, China, [3] School of Biological and Chemical Engineering, Liaoning Institute of Science and Technology, Benxi, China*

"Our results demonstrated that eCO2 increased mycorrhizal plants biomass (+26.20%) . . . and mycorrhizal fungal growth (+22.87% in extraradical hyphal length and +21.77% in mycorrhizal fungal biomass)"

## Acknowledgements

Jason Hoeksema (Ole Miss)
Lori Eckhardt (Auburn)
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Jim Roberds (USFS)
Pedro Jose Martinez Garcia (UC Davis)
Seth Pritchard (C of C)
Allan Strand (C of C)
Chuck Burdine (USFS)

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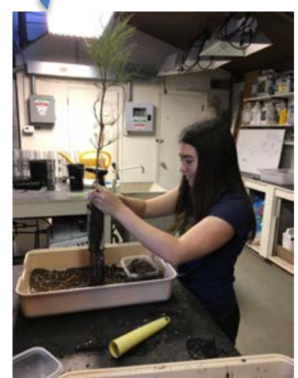
THE UNIVERSITY OF MISSISSIPPI
GRADUATE SCHOOL
2003, 2007 Council of Graduate Schools Peterson Inclusiveness Award Recipient


## Awesome Undergrads!

Whitney Sephaus

Sophie Kreutz

Julie Raguel




## *Questions?*

***Bridget Piculell***
***piculellb@cofc.edu***

# Conclusions

- environmental variation has more influence on mycorrhizal community than genetic variation ****** New analysis needed with corrected pedigree!
- genetic correlations between mycorrhizal traits and other traits

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- association analysis suggests fewer genes of large effect
- shared chromosome regions confirmed by quantitative genetic analysis
- mycorrhizal traits associated with host plant cell structural components

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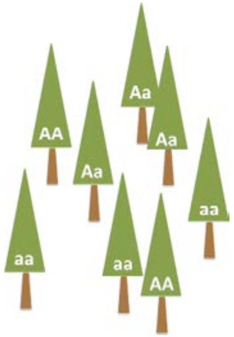
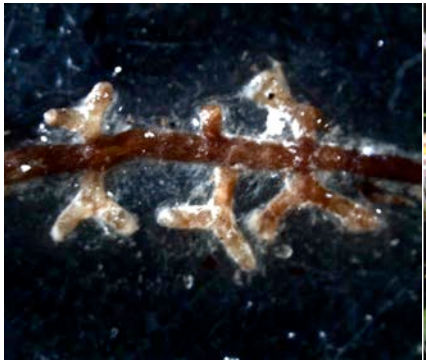
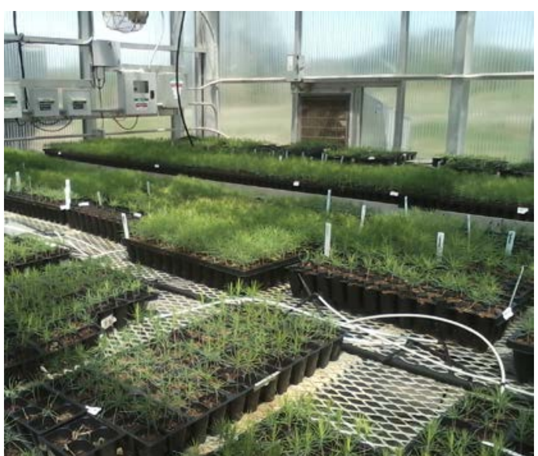


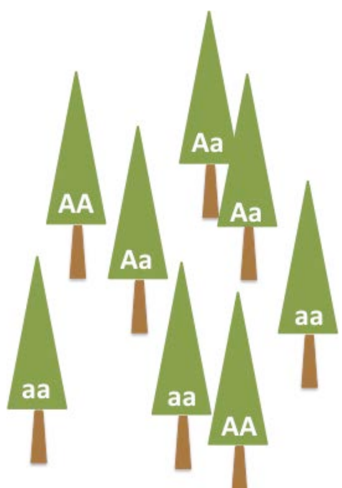


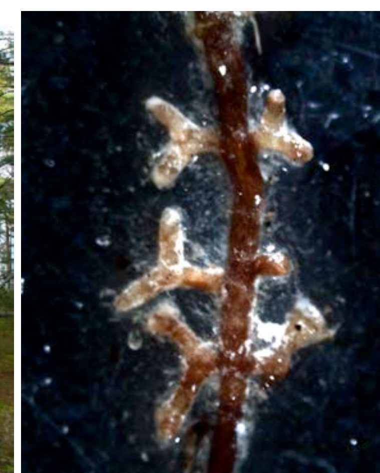

1: Heritability and genetic correlations of above- and belowground traits in loblolly pine

2: Association mapping of ectomycorrhizal traits in loblolly pine

3: Current work at College of Charleston





## What happens when roots die?

Fine root senescence is understudied

- Soil carbon pools are much larger than most other carbon pools on the planet
- Fine root turnover represents the most significant mode of carbon flux from plants into these pools, outstripping the role of leaves and other aboveground litter.

## What happens when roots die?

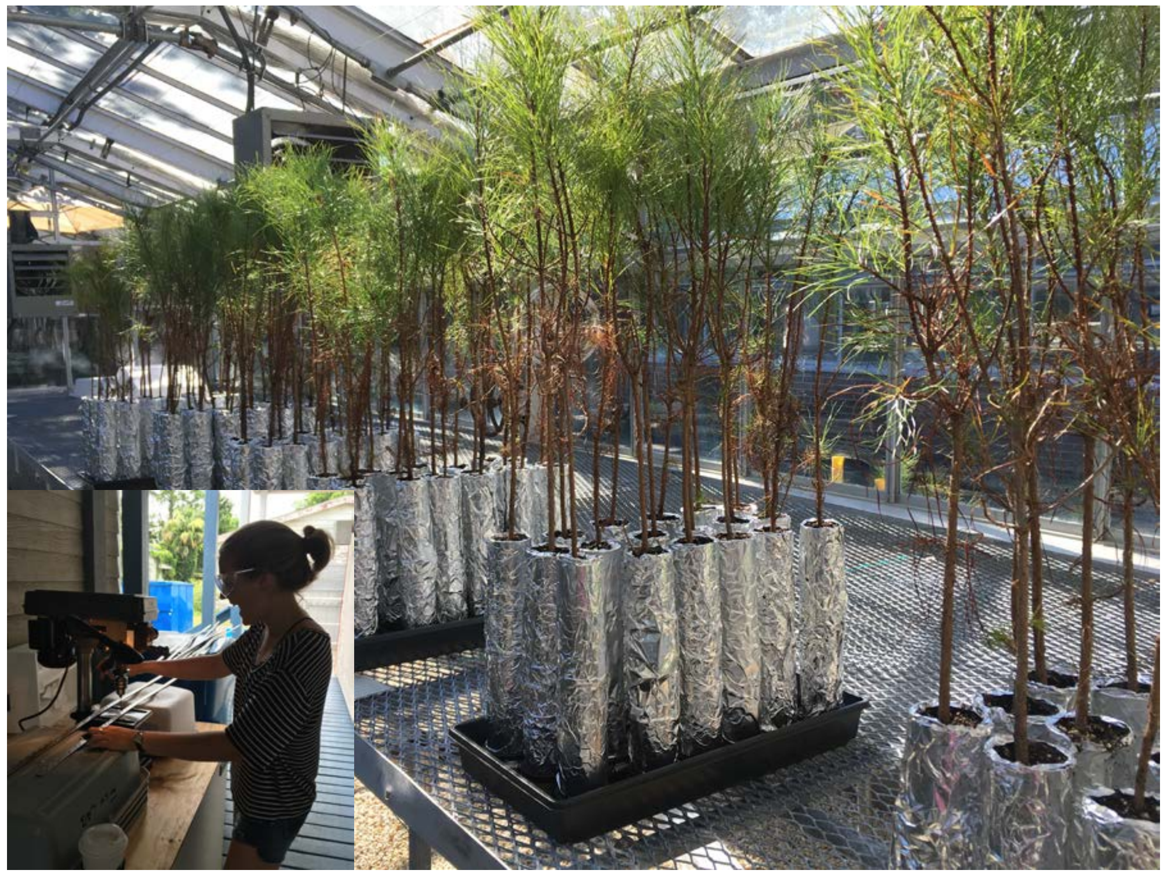
Fine root senescence is understudied

- To track fine roots through time and access them for manipulations in the field, we have installed 100 30x30cm plastic "root windows" at a site in coastal SC

# What happens when roots die?

Fine root senescence is understudied

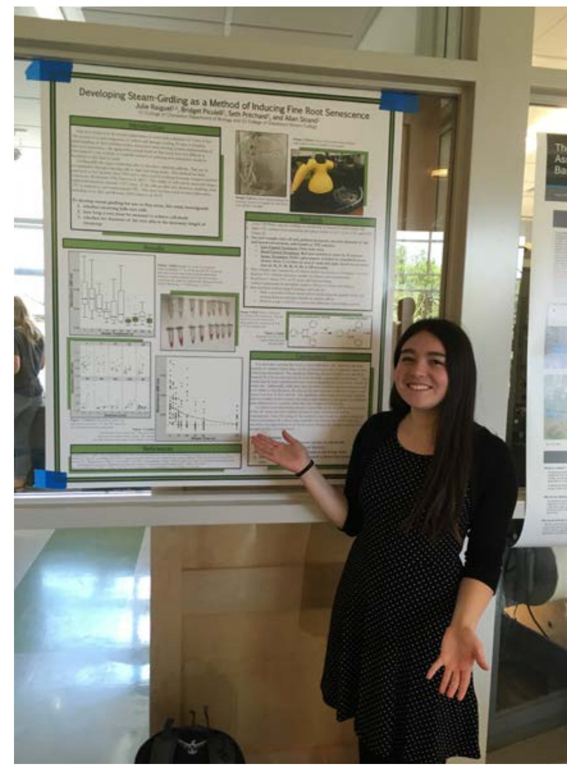
- Toobis (tractable observation of biotic interactions*)



**What happens when roots die?**

Fine root senescence is understudied

- Steam girdling as a method to induce root senescence



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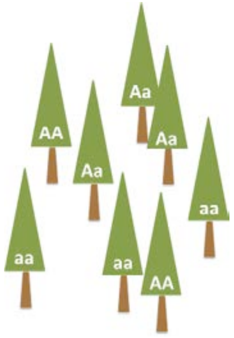
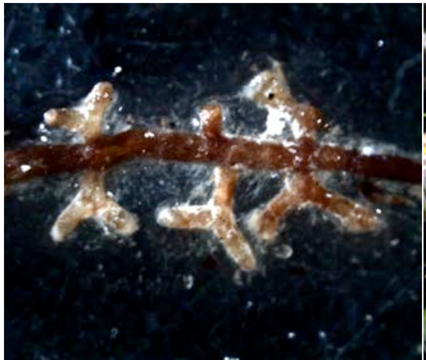
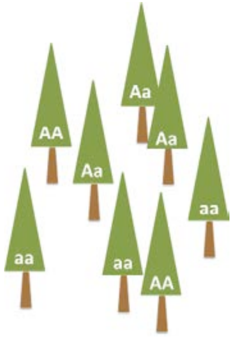


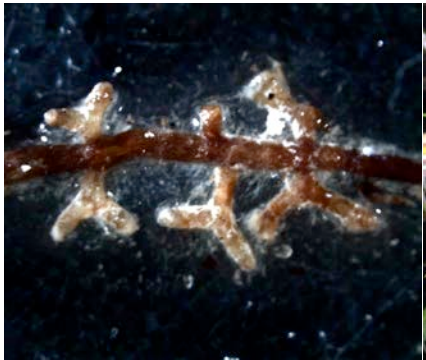



# Synthesis

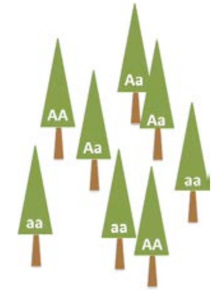
- Loblolly pines evolve independently in their interactions with different EM fungi
- Genetic correlations exist both among EM traits and between EM and other traits
- There is variation in the expression of genetic correlations
- Genetic determination of EM traits may be linked to cell structure





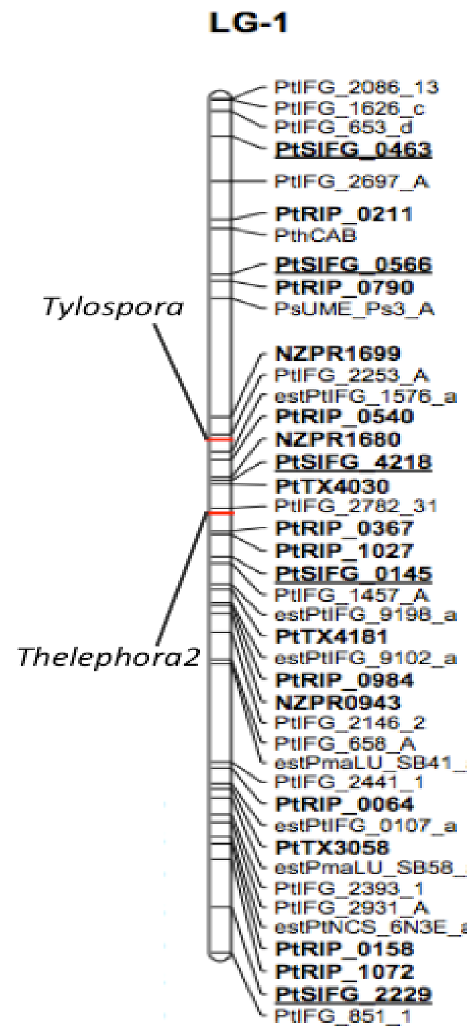



## Quantitative genetic analysis

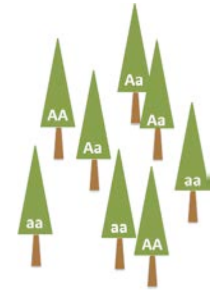



## SNP association analysis

| Chromosome | trait - trait | Pearson's r | *p* value |
|---|---|---|---|
| 1 | Tylospora - Thelephora2 | 0.27 | 0.00011 |

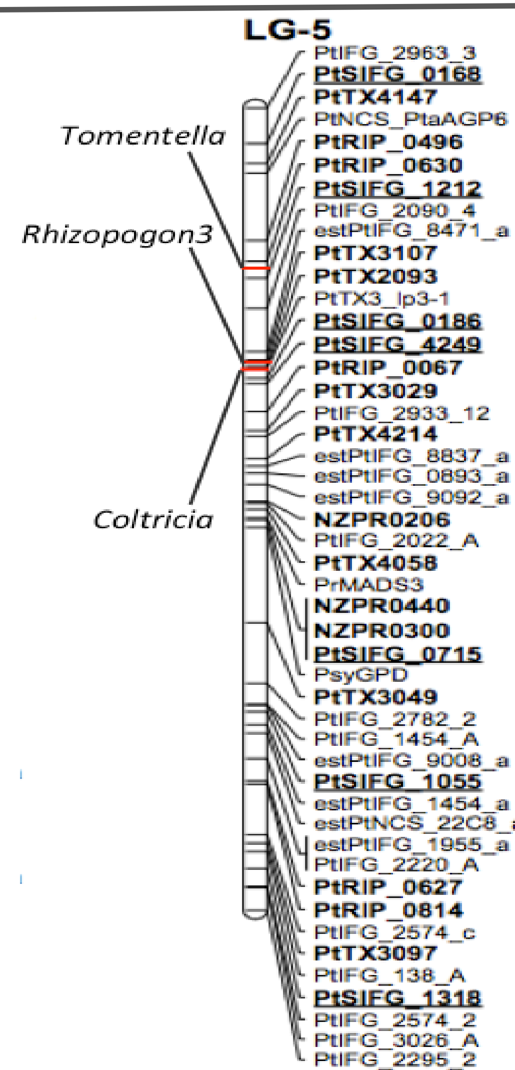


## Quantitative genetic analysis

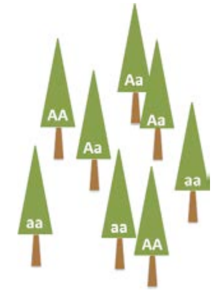



## SNP association analysis

| Chromosome | trait - trait | Pearson's r | *p* value |
|---|---|---|---|
| 1 | Tylospora - Thelephora2 | 0.27 | 0.00011 |
| 5 | Tomentella - Rhizopogon3 | 0.34 | 1.02 E -6 |
| | Coltricia - Rhizopogon3 | 0.19 | 0.00011 |
| | Coltricia - Tomentella | 0.28 | 8.5 E -5 |



## Quantitative genetic analysis

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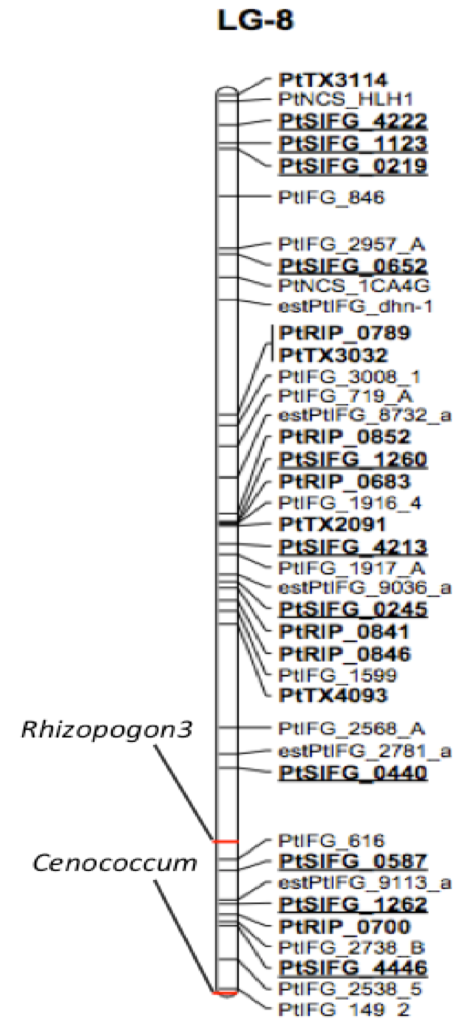
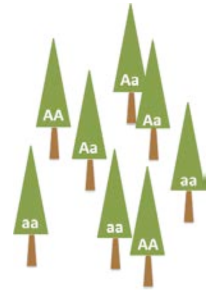
| | Coltricia - Tomentella | 0.28 | 8.5 E -5 |
| 8 | Cenococcum - Rhizopogon3 | -0.17 | 0.017 |

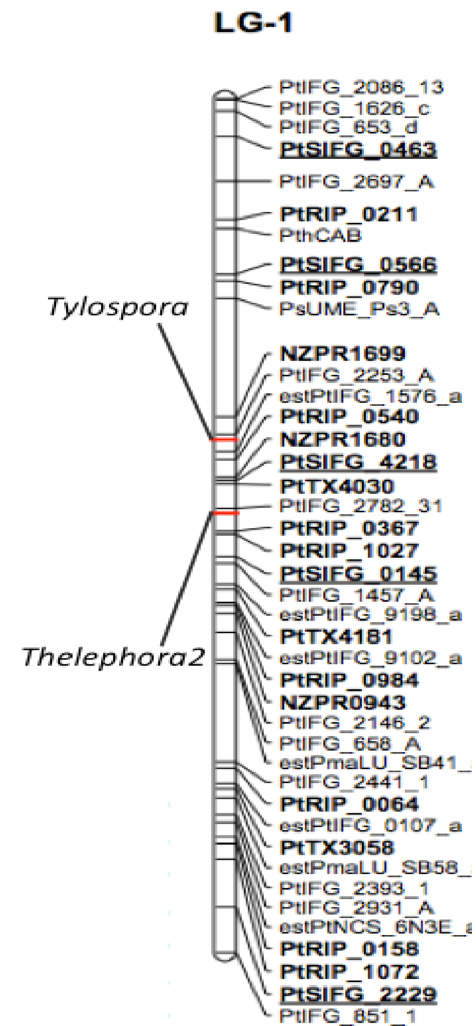


## Quantitative genetic analysis

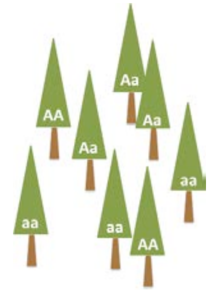



## SNP association analysis

| Chromosome | trait - trait | Pearson's r | *p* value |
|---|---|---|---|
| 1 | Tylospora - Thelephora2 | 0.274 | 0.00011 |

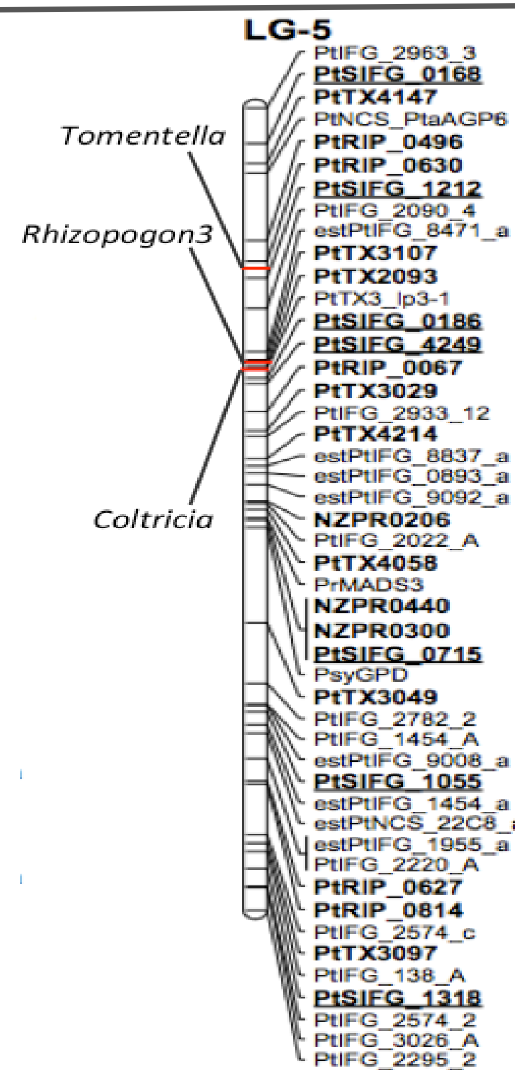


## Quantitative genetic analysis

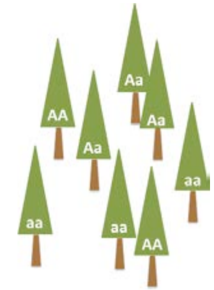



## SNP association analysis

| Chromosome | trait - trait | Pearson's r | *p* value |
|---|---|---|---|
| **1** | **Tylospora - Thelephora2** | **0.274** | **0.00011** |
| **5** | **Tomentella - Rhizopogon3** | **0.34245** | **1.02 E -6** |
| | **Coltricia - Rhizopogon3** | **0.1859** | **0.00011** |
| | **Coltricia - Tomentella** | **0.27836** | **8.5 E -5** |



## Quantitative genetic analysis

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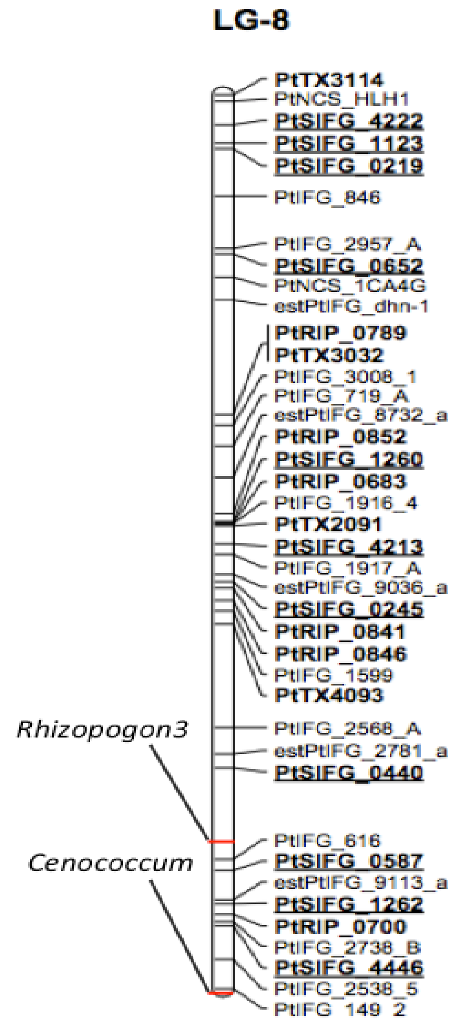
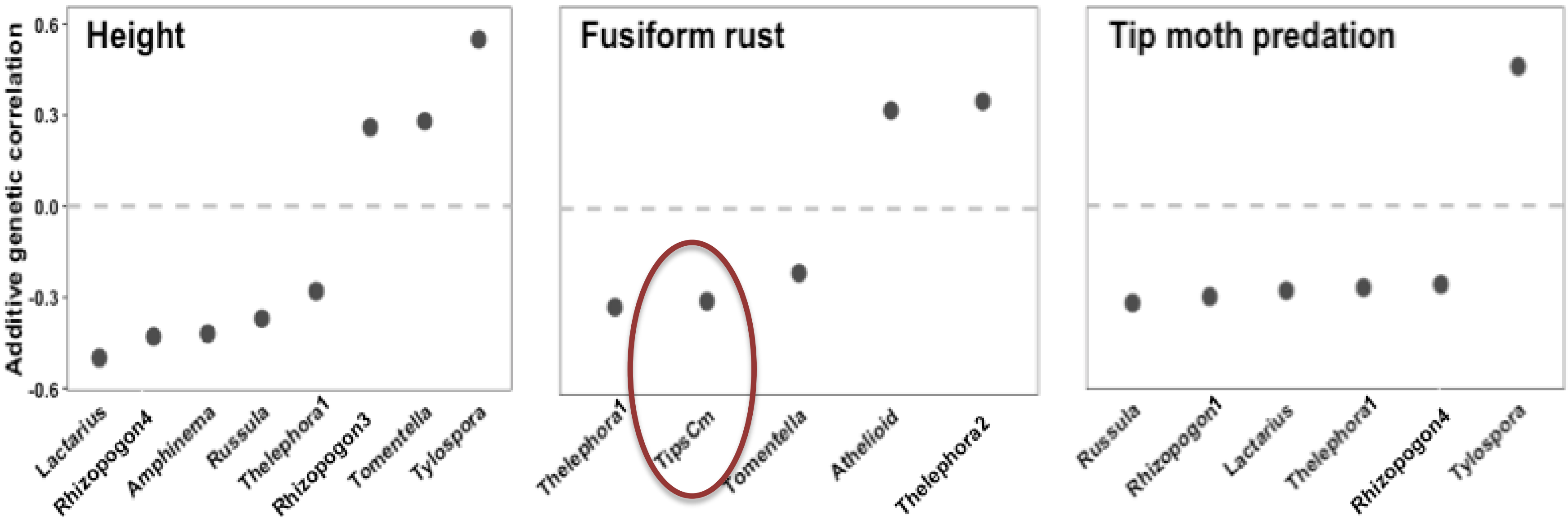
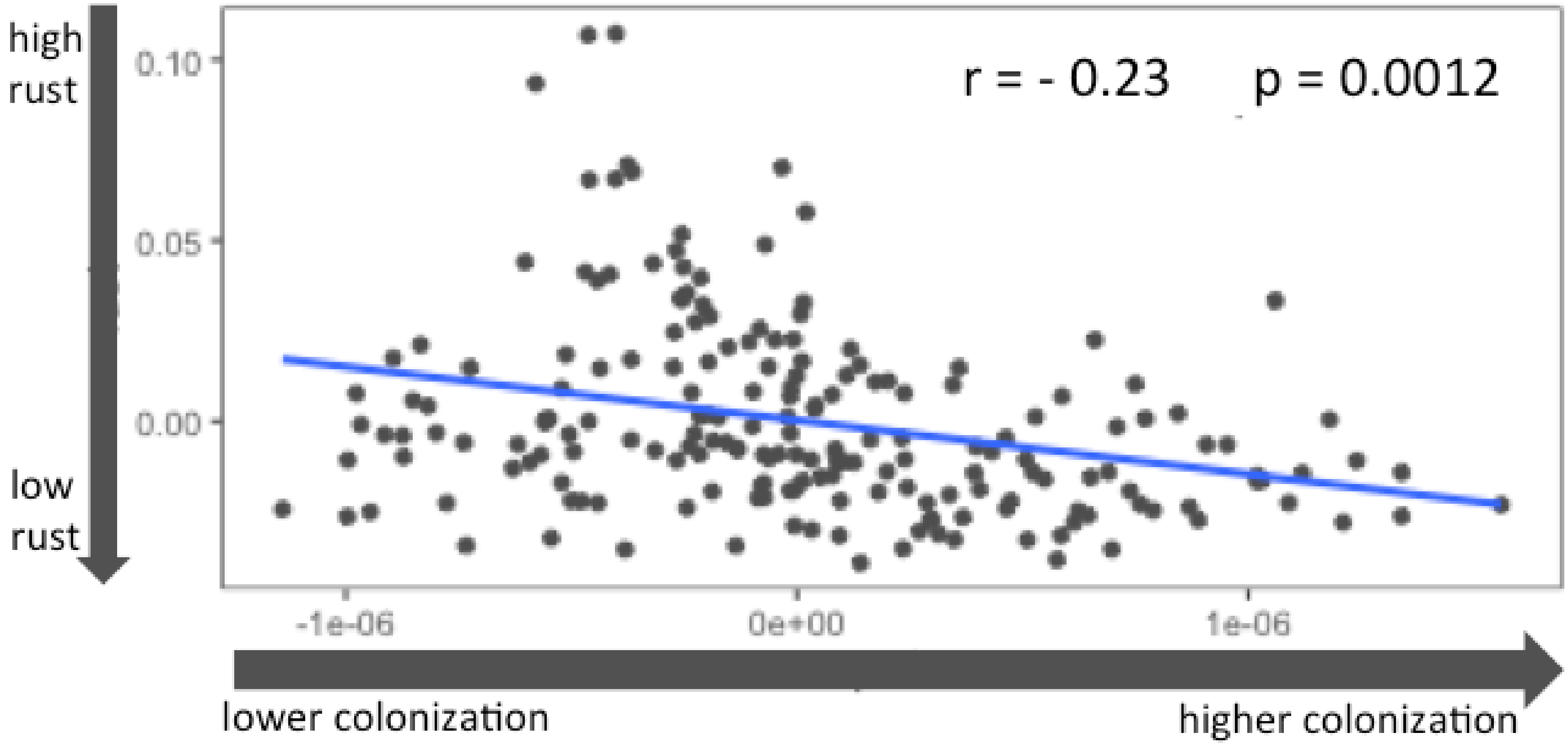


# Genetic correlations between traits in loblolly pine

Pearson's r shown for all significant correlations ($p < 0.05$)

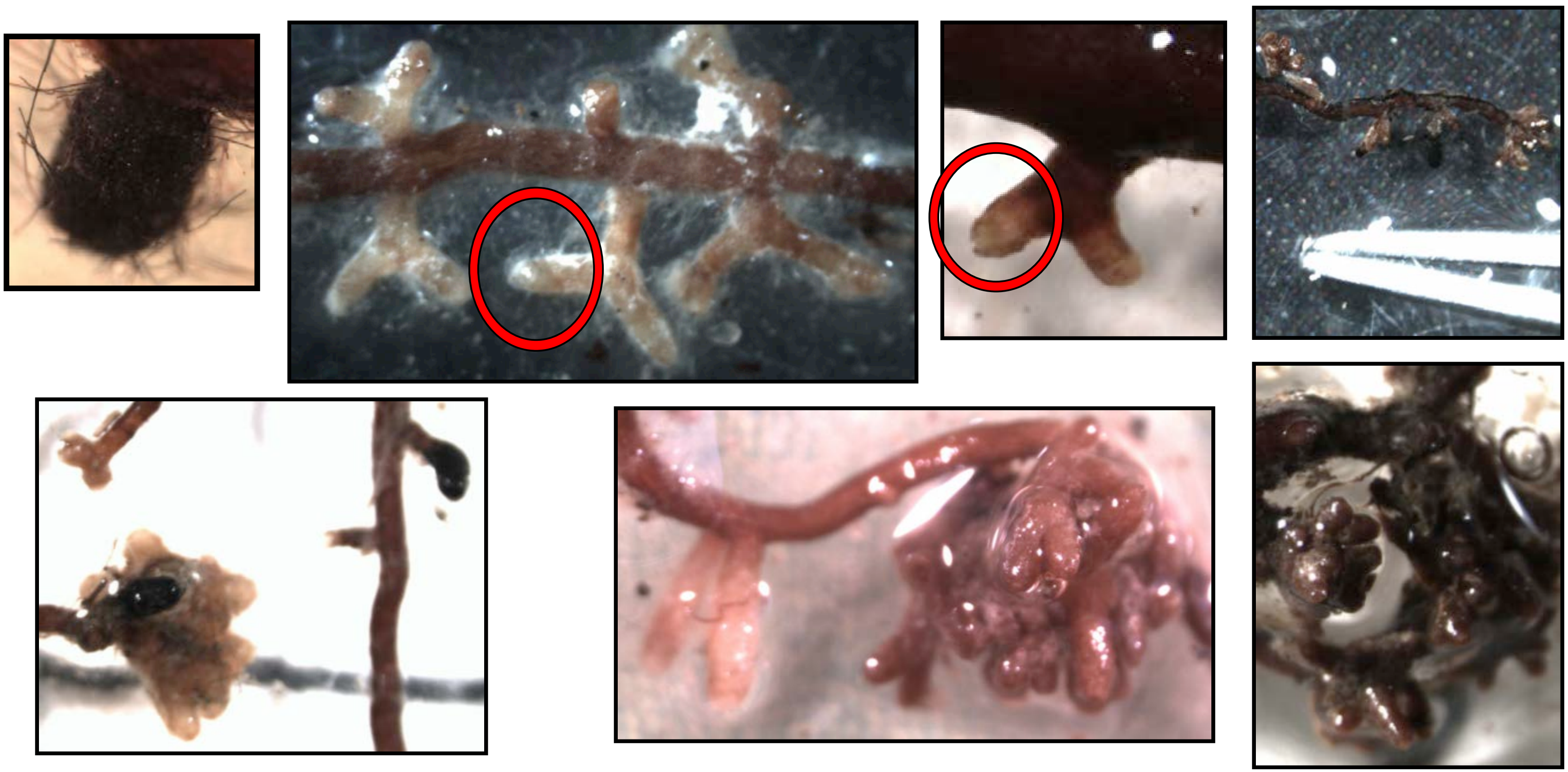


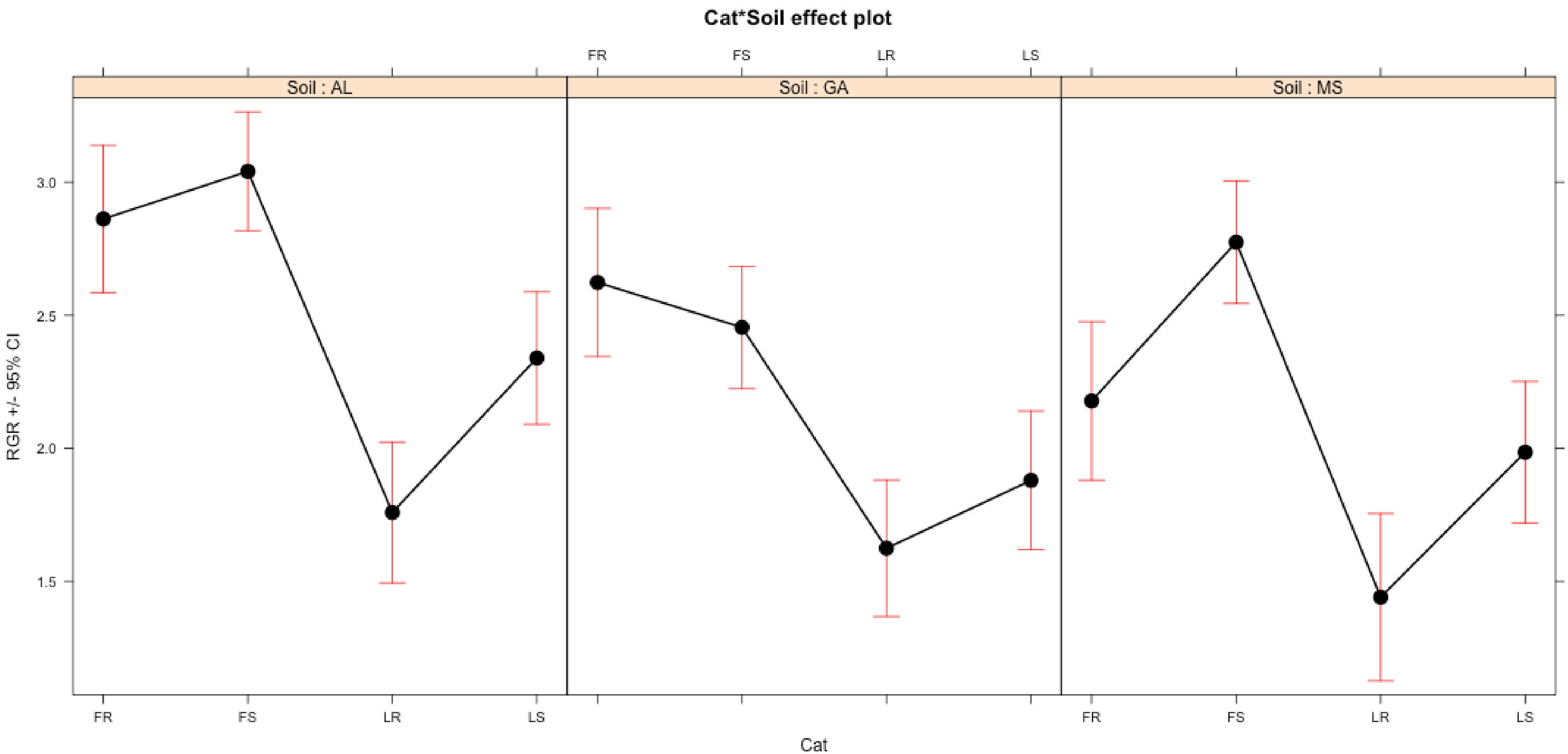
# Genetic correlations between fusiform rust infection and mycorrhizal colonization in loblolly pine



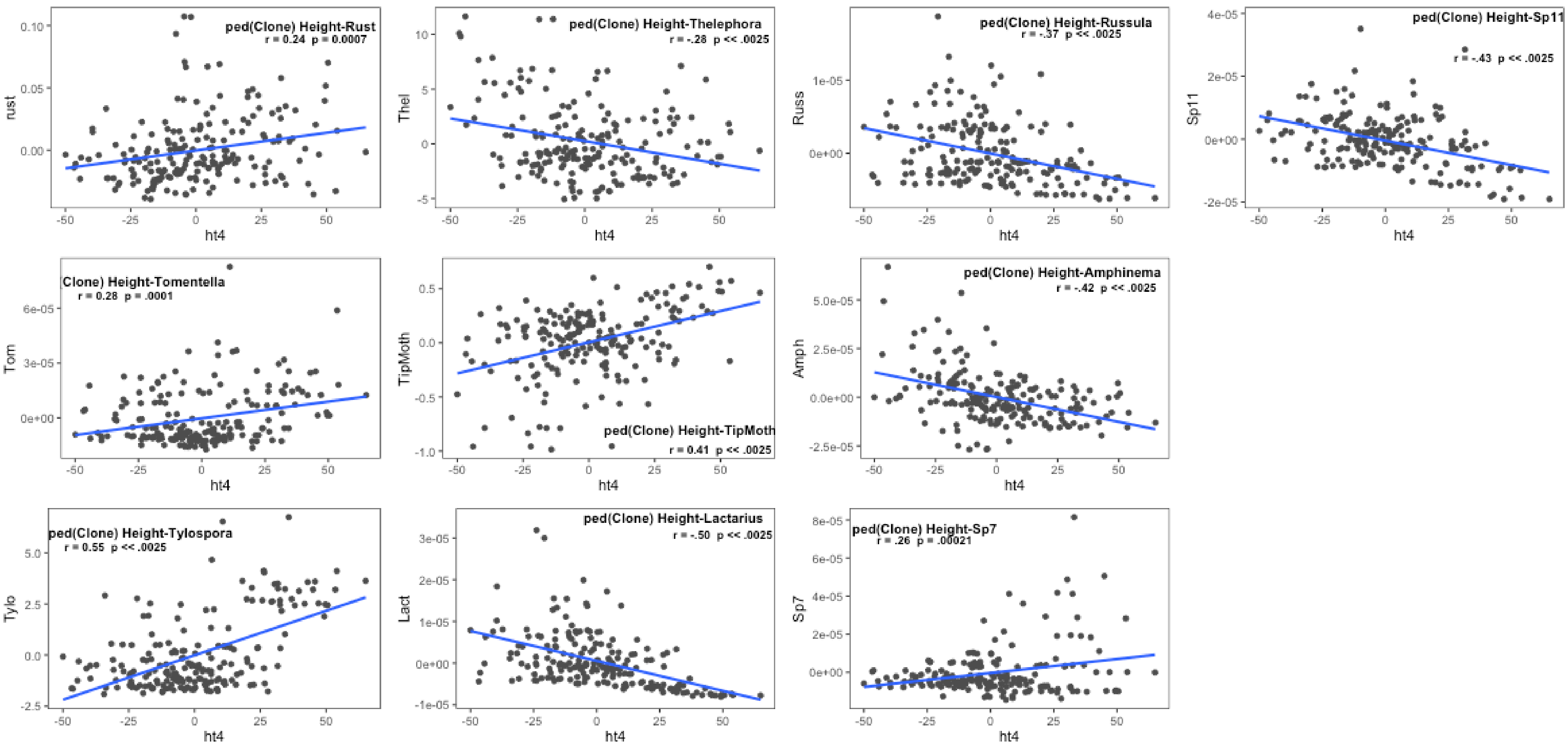
# Morphotyping and fungal identification

Root tips colonized by ectomycorrhizal fungi grouped by similar phenotypic characteristics (color, texture, emanating hyphae)



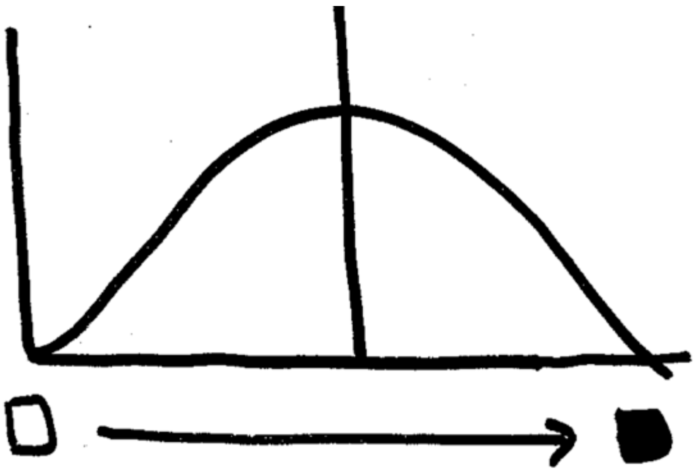


Cat*Soil effect plot
Soil : AL
Soil : GA
Soil : MS
RGR +/- 95% CI
3.0
2.5
2.0
1.5
FR
FS
LR
LS
Cat

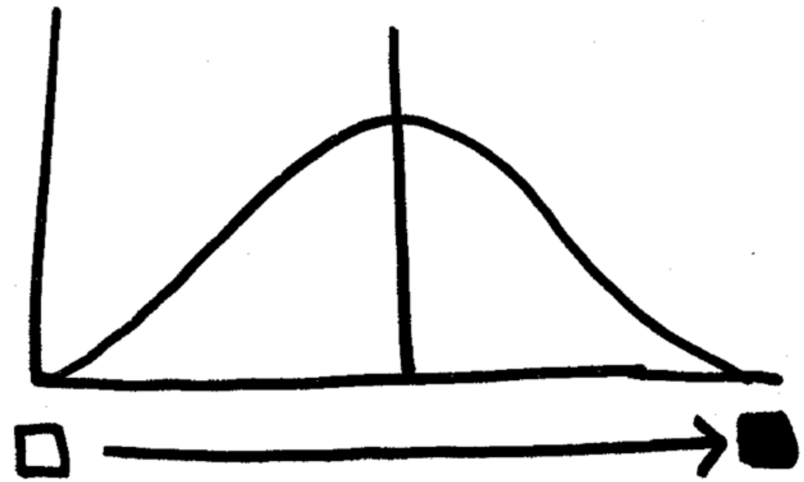


ped(Clone) Height-Rust
r = 0.24 p = 0.0007
rust
ht4
ped(Clone) Height-Thelephora
r = -.28 p << .0025
Thel
ht4
ped(Clone) Height-Russula
r = -.37 p << .0025
Russ
ht4
ped(Clone) Height-Sp11
r = -.43 p << .0025
Sp11
ht4
(Clone) Height-Tomentella
r = 0.28 p = .0001
Tom
ht4
ped(Clone) Height-TipMoth
r = 0.41 p << .0025
TipMoth
ht4
ped(Clone) Height-Amphinema
r = -.42 p << .0025
Amph
ht4
ped(Clone) Height-Tylospora
r = 0.55 p << .0025
Tylo
ht4
ped(Clone) Height-Lactarius
r = -.50 p << .0025
Lact
ht4
ped(Clone) Height-Sp7
r = .26 p = .00021
Sp7
ht4

$$V_P = V_A + V_I + V_E$$

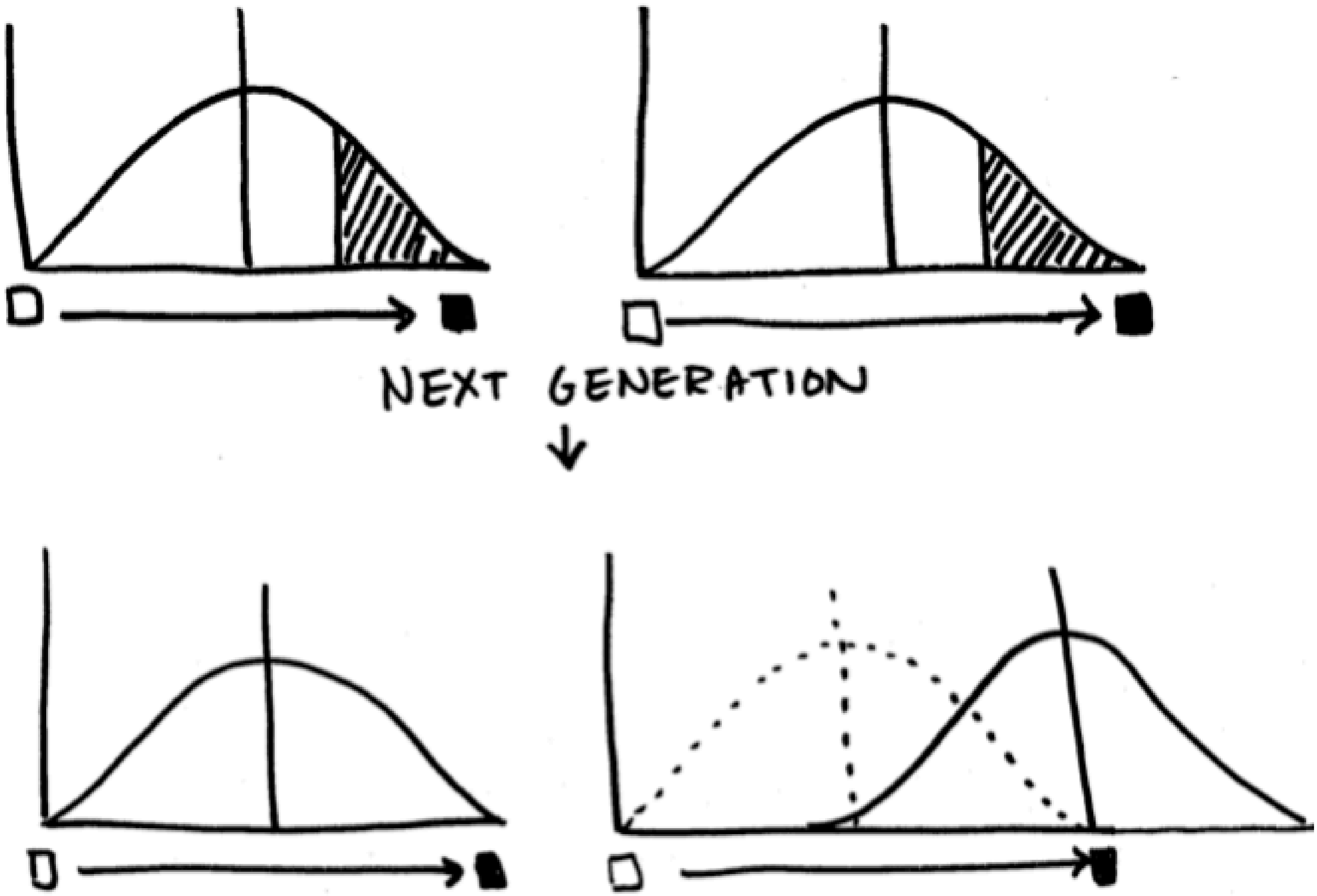


$$V_P = V_A + V_D + V_I + V_E$$



$V_P = V_A + V_I + V_E$

$V_P = V_A + V_D + V_I + V_E$




CCLONES rep map, HEF
Saucier MS
1
2
5
3
4
5
6
7
8
6
1
2
8
9
10
4
3
7
12

$$V_G = V_A + V_D + V_I$$

$$V_P = V_A + V_D + V_I + V_E$$

$V_D$ -> interaction among alleles at a single locus

$V_I$ -> interaction among genes at different loci (epistasis)

---

$V_A$ -> represents the cumulative effect of individual loci; the overall mean is equal to the summed contribution of these loci

- **resemblance between relatives is caused primarily by additive variation**
- **most important for sexually reproducing species**

$$V_P = V_G + V_E$$

$$V_P = V_A + V_D + V_I + V_E$$

---

## Heritability

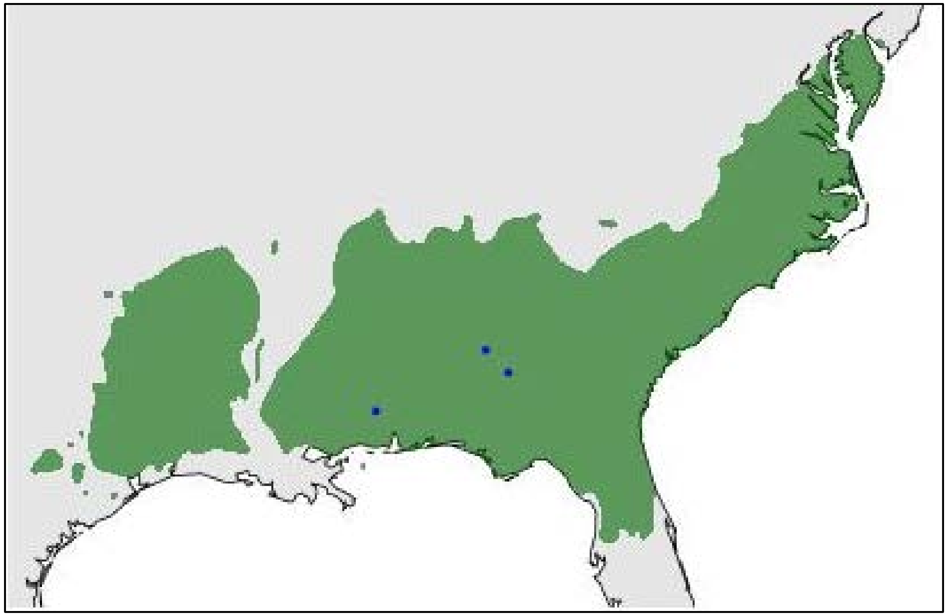
$H^2 = V_G / V_P$ (broad sense)

$h^2 = V_A / V_P$ (narrow sense)

**Calculating narrow-sense heritability is important for predicting how a trait will respond to selection**

# Estimating additive genetic variation in loblolly pine

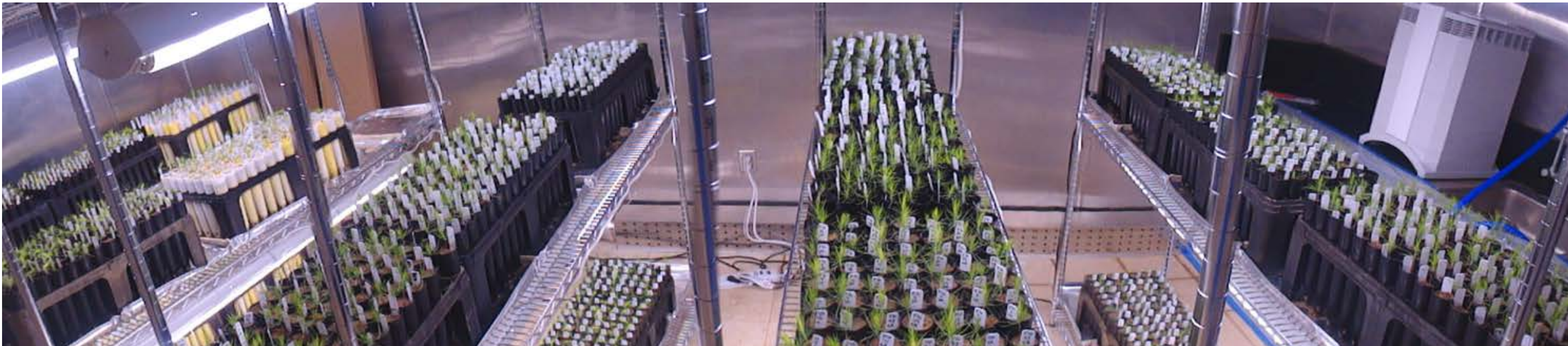
Loblolly Pine, *Pinus taeda*




**1)** 30.615068, -89.059742, **2)** 30.615105, -89.058320, **3)** 30.614052, -89.059983, **4)** 30.614108, -89.058599, **5)** 30.615354, -89.058229, **6)** 30.614858, -89.057139, **7)** 30.614726, -89.058235, **8)** 30.614593, -89.057934, **9)** 30.614368, -89.057131, **10)** 30.614241, -89.056849, **11)** 30.614057, -89.057929, **12)** 30.613595, -89.056867

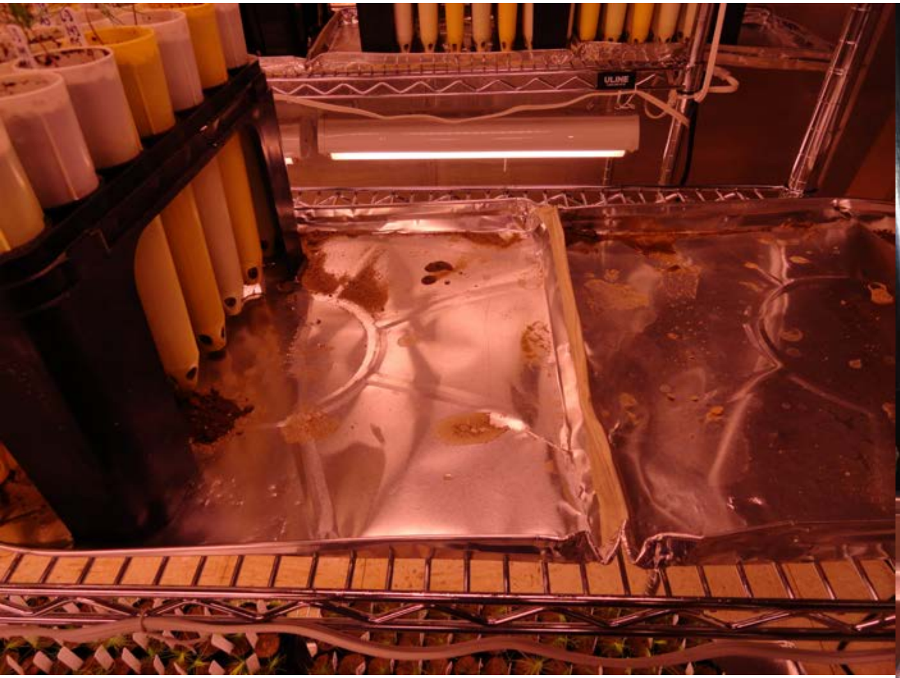
# Chapter 1: Genetically determined pathogen resistance interacts with geographic variation to influence mycorrzhizal community

Bridget J. Piculell, Lori G. Eckhardt, and Jason D. Hoeksema



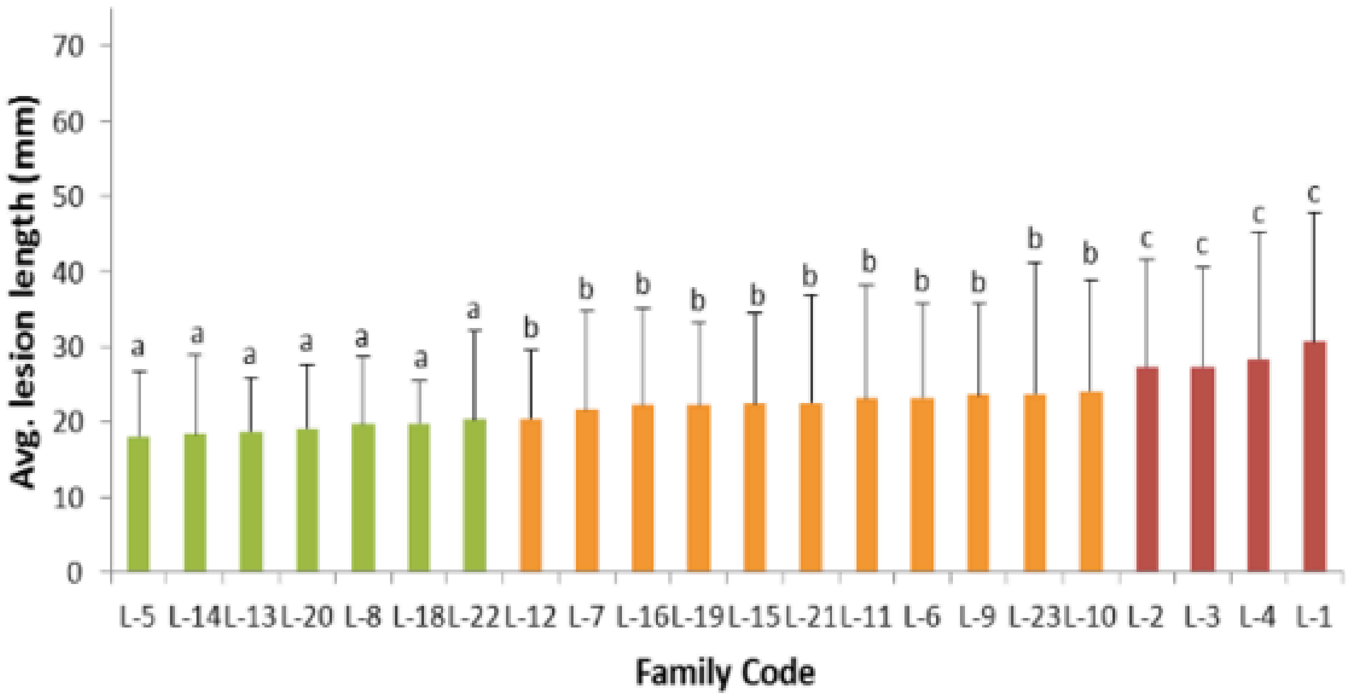
THE UNIVERSITY OF MISSISSIPPI

AUBURN UNIVERSITY


ULINE

Fusiform rust: *Cronartium*
Pine decline: *Leptographium* and *Grosmannia*
(Singh *et al.,* 2014; Lori Eckhardt, pers comm)

# Overall Family Ranking

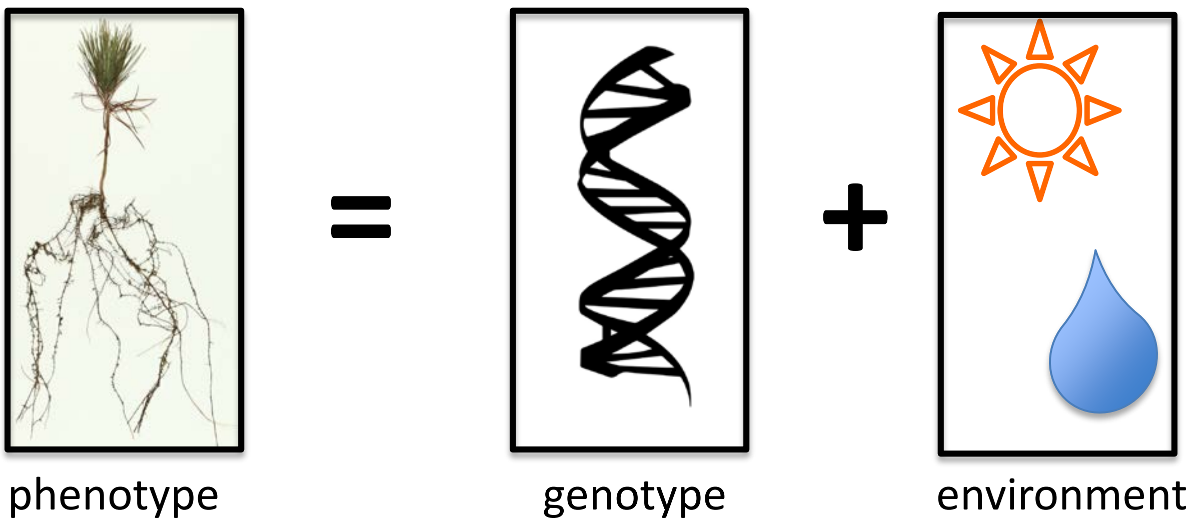


# 1: Heritability and genetic correlations of above and below ground traits in loblolly pine

THE UNIVERSITY OF MISSISSIPPI

FOREST SERVICE U S DEPARTMENT OF AGRICULTURE

# Partitioning variance between genetic and environmental effects



# Partitioning variance between genetic and environmental effects

Phenotype = Genotype + Environment

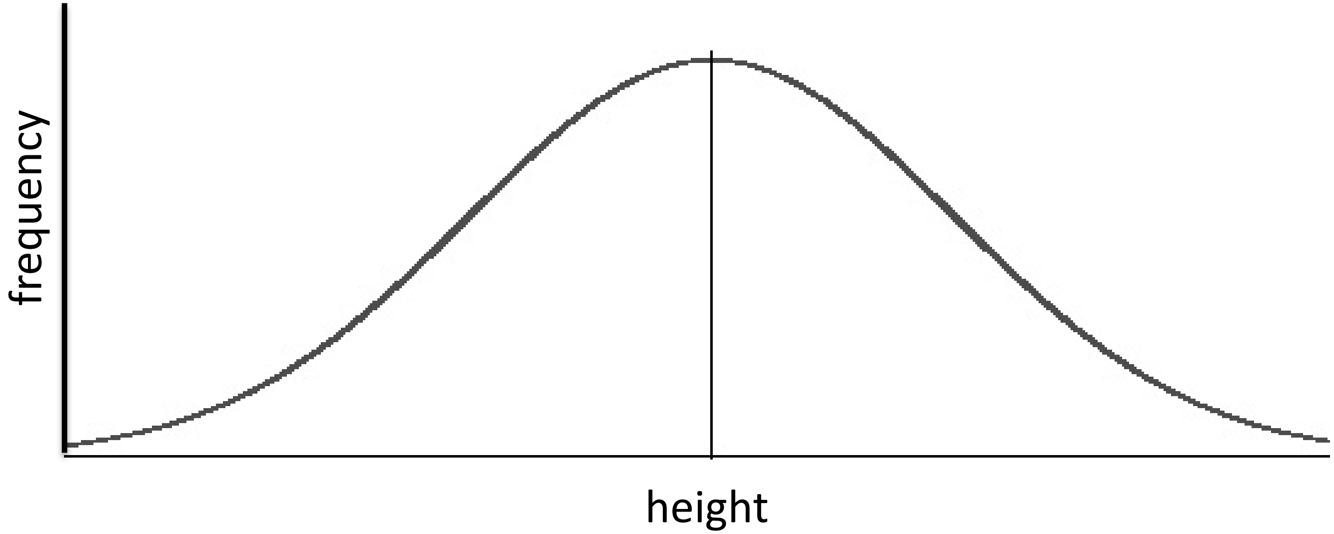
P = G + E (individual)

## Partitioning variance between genetic and environmental effects

Phenotype = Genotype + Environment

$P = G + E$ (individual)

$V_P = V_G + V_E$ (population)




## Partitioning variance between genetic and environmental effects

$$V_P = V_G + V_E$$

additive non additive

$$V_P = \left[ V_A + V_I \right] + V_E$$

$V_A$ represents the cumulative effect of individual loci

$V_I$ interaction among alleles at a single locus
interaction among genes at different loci

**Partitioning variance between genetic and environmental effects**

$$V_P = V_G + V_E$$

additive non additive

$$V_P = \left[ V_A + V_I \right] + V_E$$

- narrow-sense heritability, $h^2 = V_A / V_P$
- broad-sense heritability, $H^2 = V_G / V_P$
- additive genetic correlations

# Heritability and genetic correlations of above and below ground traits in loblolly pine

Q1: How much of the phenotypic variation in a suite of loblolly pine traits is genetically determined?

Q2: Are there additive genetic correlations between mycorrhizal traits of loblolly pine and other traits?

# Harrison Experimental Forest (HEF), Southern Institute of Forest Genetics (USDA), Saucier MS

# Loblolly pine pedigreed population

Sampling scheme

480 trees

160 genotypes (x3)

30 families

Phenotypic traits measured

Fungal colonization (tips/cm)

Fusiform rust infection

Pine tip moth

Height

# Heritability and genetic correlations of above and below ground traits in loblolly pine

Q1: How much of the phenotypic variation in a suite of loblolly pine traits is genetically determined?

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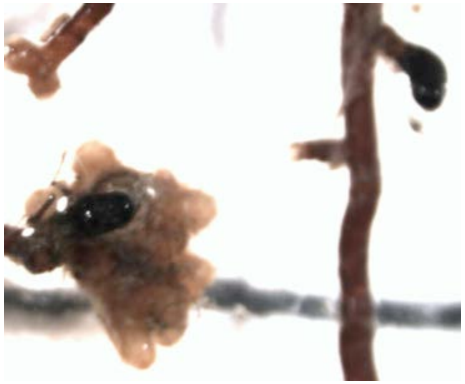


# Heritability estimates for selective traits of loblolly pine

| | $H^2$ | $h^2$ |
|---|---|---|
| **Height** | 0.179 | 0.179 |
| **Rust** | 0.0292 | 0.0292 |
| **Tip Moth** | 0.0791 | 0.0297 |

Broad sense heritability, $H^2 = V_A + V_I / V_P$
Narrow sense heritability, $h^2 = V_A / V_P$

# Heritability estimates for mycorrhizal traits of loblolly pine

| | $H^2$ | $h^2$ |
|---|---|---|
| **Athelioid** | 0.0119 | < 0.001 |
| **Tylospora** | 0.0143 | 0.0132 |
| **Cenococcum** | 0.00378 | 0.00378 |
| **Thelephora** | 0.0197 | 0.0197 |
| **Thelephora2** | 0.109 | < 0.001 |
| **Rhizopogon** | < 0.001 | < 0.001 |
| **Tomentella** | < 0.001 | < 0.001 |
| **Lactarius** | < 0.001 | < 0.001 |
| **Russula** | < 0.001 | < 0.001 |
| **Amphinema** | < 0.001 | < 0.001 |
| **Coltricia** | < 0.001 | < 0.001 |
| **Rhizopogon2** | < 0.001 | < 0.001 |
| **Rhizopogon3** | < 0.001 | < 0.001 |
| **Rhizopogon4** | < 0.001 | < 0.001 |
| **Tot. tips/cm root** | < 0.001 | < 0.001 |

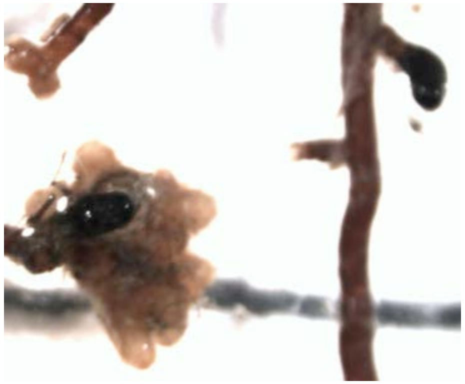
Broad sense heritability, $H^2 = V_A + V_I / V_P$

Narrow sense heritability, $h^2 = V_A / V_P$

# Heritability and genetic correlations of above and below ground traits in loblolly pine

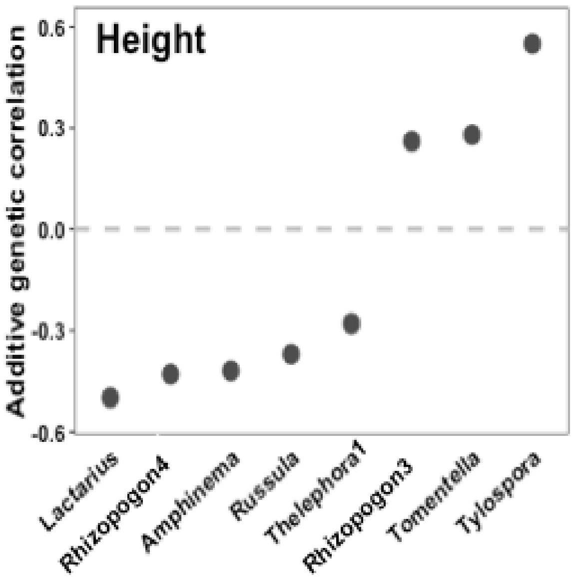
Q1: How much of the phenotypic variation in a suite of loblolly pine traits is genetically determined and how much of the genetic variation is due to either additive genetic variation or interactive genetic effects such as dominance and epistasis?

Q2: Are there additive genetic correlations between mycorrhizal traits of loblolly pine and other traits?



# Genetic correlations between traits in loblolly pine

Pearson's r shown for all significant correlations ($p < 0.05$)



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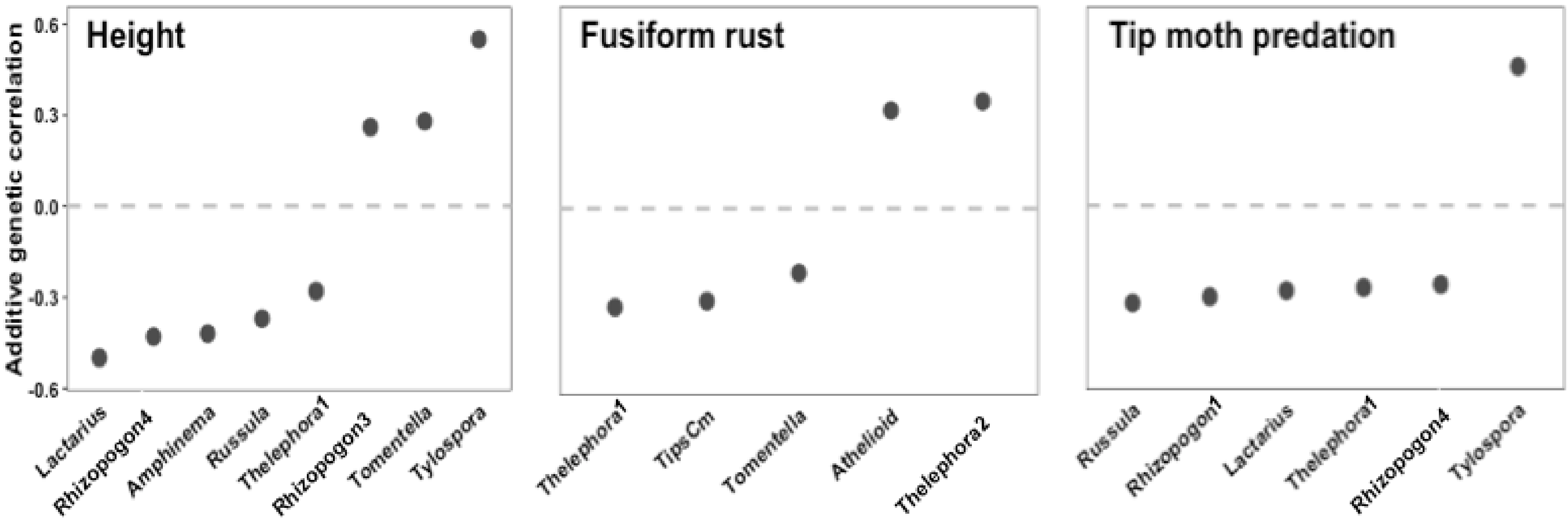
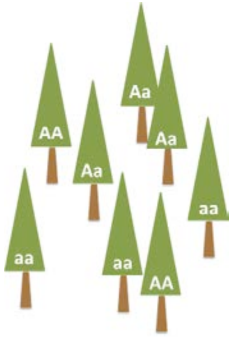
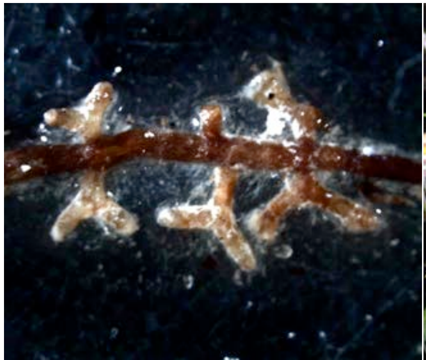


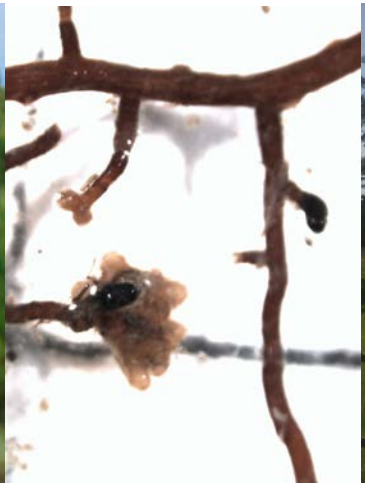
# Conclusions

- environmental variation has more influence on mycorrhizal community than genetic variation
- genetic correlations between mycorrhizal traits and other traits




# 2: Association mapping of ectomycorrhizal traits in loblolly pine



# Harrison Experimental Forest (HEF), Southern Institute of Forest Genetics (USDA), Saucier MS

# SNP Associations with loblolly traits

Illumina Infinium SNP chip

**2923 SNPs (1420 informative)**

**160 genotypes (152 successful)**

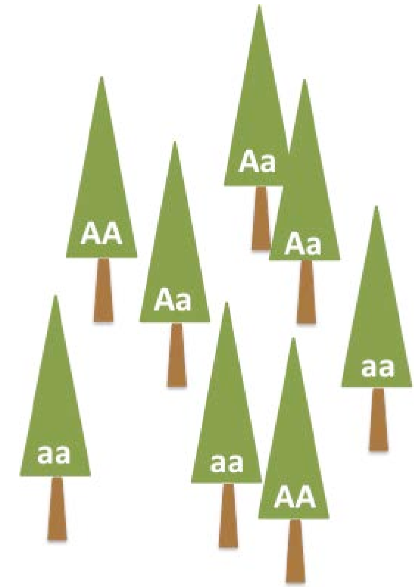
20 loblolly pine traits:

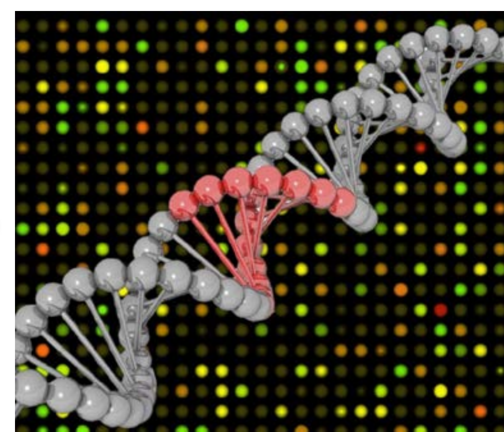
Height

Rust

Tip moth

Fungal colonization traits



| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 74517 | A:G | A:G | G:G | A:A | A:A | G:G | C:C | A:G | G:G |
| 74519 | A:A | G:G | A:G | A:C | A:C | A:G | C:C | A:G | G:G |
| 74521 | A:A | G:G | A:G | A:C | A:C | A:G | A:C | A:G | A:G |
| 74522 | A:A | G:G | A:G | A:C | A:C | G:G | C:C | A:A | G:G |
| 74612 | A:G | A:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |
| 74618 | A:A | G:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |
| 74623 | A:G | A:G | G:G | A:A | A:A | G:G | C:C | A:A | G:G |
| 74628 | A:A | G:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |
| 74711 | A:A | G:G | G:G | A:A | A:C | G:G | C:C | A:G | G:G |
| 74716 | A:G | A:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |

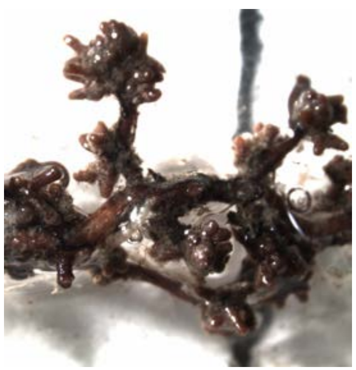
# Association mapping of ectomycorrhizal traits in loblolly pine

Q1: What can we say about the number and effect of genes involved in mycorrhizal traits in loblolly pine?

Q2: Can we determine a genetic basis for the correlations detected in the quantitative genetics study?

Q3: Can we ascribe putative function to any of the relevant SNPs?

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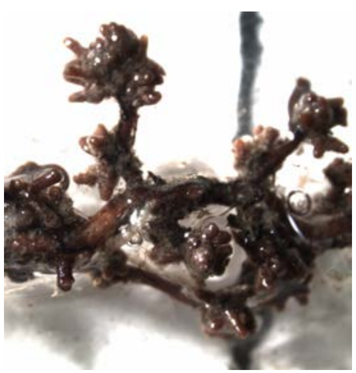
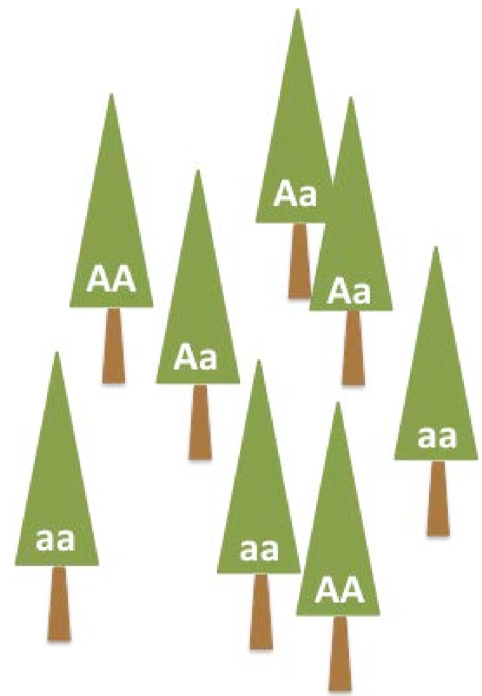



# SNP Associations with loblolly traits

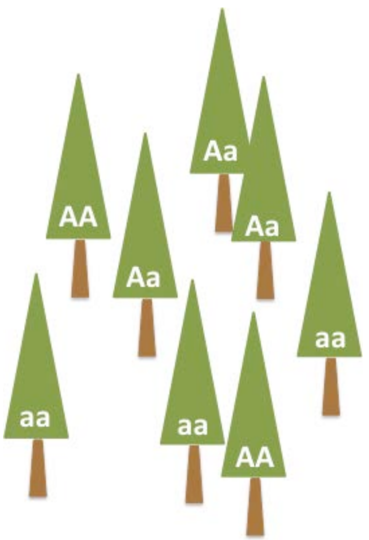
| | |
|---|---|
| **Rhizopogon3** | **9** |
| **Coltricia** | **7** |
| **Cenococcum** | **4** |
| **Rhizopogon4** | **3** |
| **Tomentella** | **3** |
| **Rhizopogon2** | **2** |
| **Thelephora2** | **2** |
| **Tylospora** | **2** |
| **Rust** | **1** |

33 significant associations at $p \leq 3.5 \times 10^{-5}$



# Many genes of small effect or few genes of large effect?

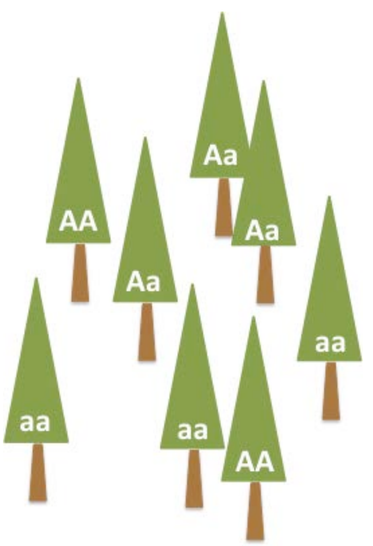
The number of loci controlling a trait can affect the degree and frequency of local adaptation (Nuismer et al., 2007; Savolainen et al., 2013)



# Many genes of small effect or few genes of large effect?

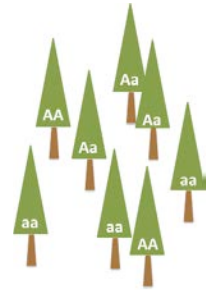
The number of loci controlling a trait can affect the degree and frequency of local adaptation (Nuismer et al., 2007; Savolainen et al., 2013)

Percentage of phenotypic variance in mycorrhizal traits attributed to marker effects ($R^2$) ranged from 13% to 55%



**Quantitative genetic analysis**

- low genetic variation

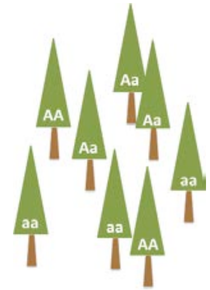



**SNP association analysis**

- high genetic variation

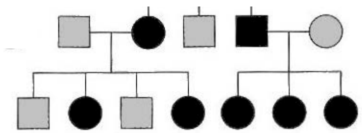
## Quantitative genetic analysis

- low genetic variation




## SNP association analysis

- high genetic variation



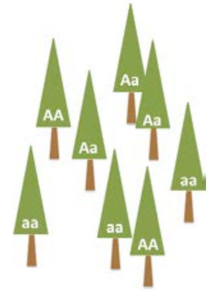
Pedigree

Relationship matrix

| | A | B | C | D | E |
|---|---|---|---|---|---|
| A | 1 | .5 | .25 | 0 | .25 |
| B | | 1 | .5 | .25 | 0 |
| C | | | 1 | 0 | .25 |
| D | | | | 1 | .5 |
| E | | | | | 1 |

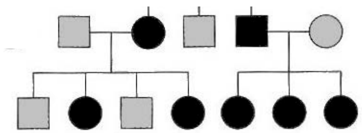
## Quantitative genetic analysis

- low genetic variation




## SNP association analysis

- high genetic variation



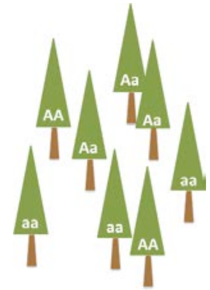
Pedigree

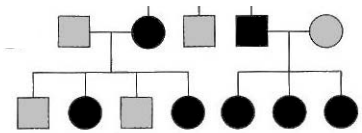
| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 74517 | A:G | A:G | G:G | A:A | A:A | G:G | C:C | A:G | G:G |
| 74519 | A:A | G:G | A:G | A:C | A:C | A:G | C:C | A:G | G:G |
| 74521 | A:A | G:G | A:G | A:C | A:C | A:G | A:C | A:G | A:G |
| 74522 | A:A | G:G | A:G | A:C | A:C | G:G | C:C | A:A | G:G |
| 74612 | A:G | A:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |
| 74618 | A:A | G:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |
| 74623 | A:G | A:G | G:G | A:A | A:A | G:G | C:C | A:A | G:G |
| 74628 | A:A | G:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |
| 74711 | A:A | G:G | G:G | A:A | A:C | G:G | C:C | A:G | G:G |
| 74716 | A:G | A:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |

Relationship matrix

| | A | B | C | D | E |
|---|---|---|---|---|---|
| A | 1 | .5 | .25 | 0 | .25 |
| B | | 1 | .5 | .25 | 0 |
| C | | | 1 | 0 | .25 |
| D | | | | 1 | .5 |
| E | | | | | 1 |

| | A | B | C | D | E |
|---|---|---|---|---|---|
| A | 1 | .72 | .31 | .11 | .21 |
| B | | 1 | .57 | .42 | .08 |
| C | | | 1 | .10 | .22 |
| D | | | | 1 | .47 |
| E | | | | | 1 |

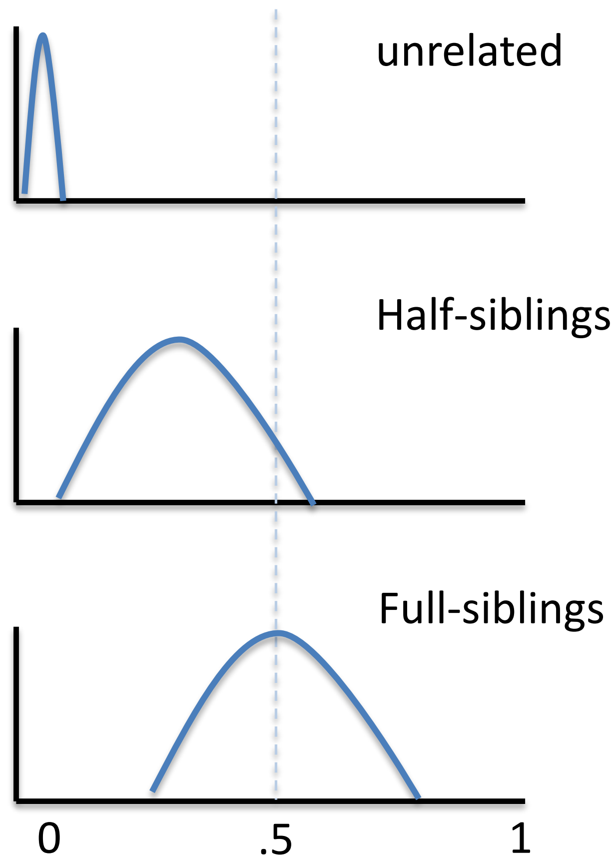


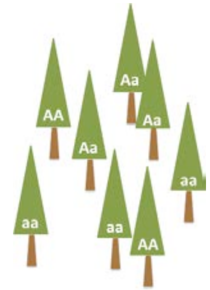



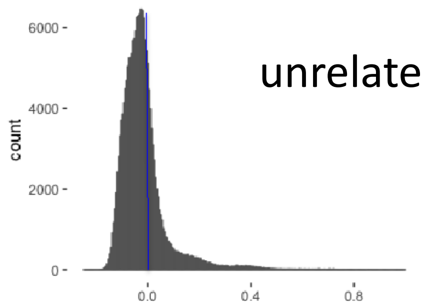
Pedigree

## Relationship matrix

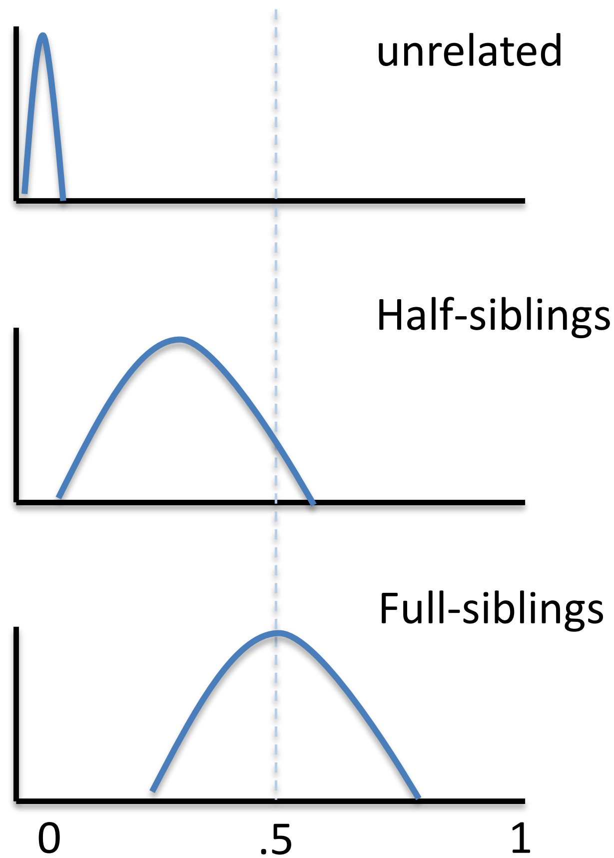
| | A | B | C | D | E |
|---|---|---|---|---|---|
| A | 1 | .5 | .25 | 0 | .25 |
| B | | 1 | .5 | .25 | 0 |
| C | | | 1 | 0 | .25 |
| D | | | | 1 | .5 |
| E | | | | | 1 |

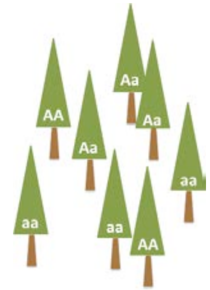


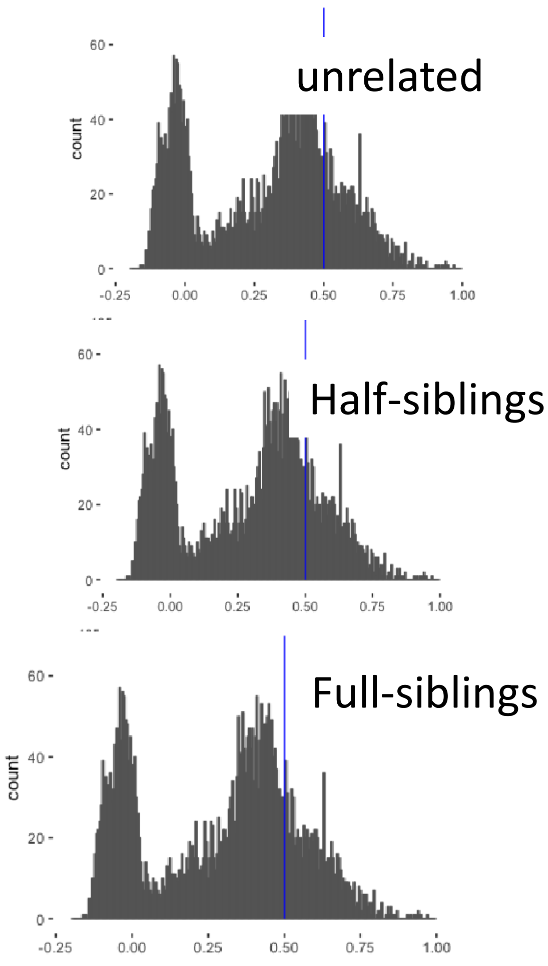

AA
Aa
Aa
Aa
aa
aa
aa
AA

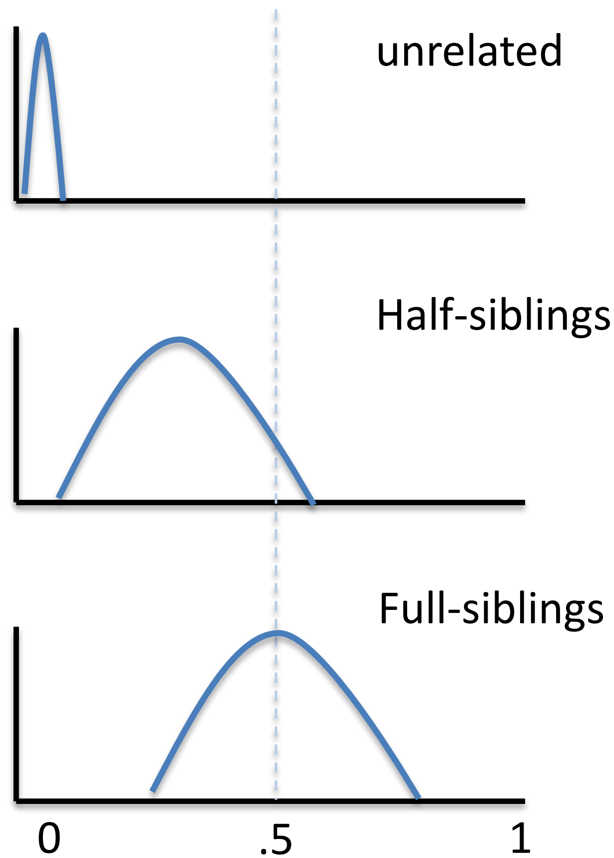

6000
4000
2000
0
count
0.0
0.4
0.8

unrelated


unrelated
Half-siblings
Full-siblings
0
.5
1

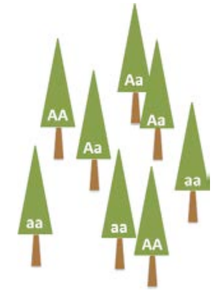

AA
Aa
Aa
Aa
aa
aa
aa
AA


unrelated
Half-siblings
Full-siblings
count
60
40
20
0
-0.25
0.00
0.25
0.50
0.75
1.00


unrelated
Half-siblings
Full-siblings
0
.5
1

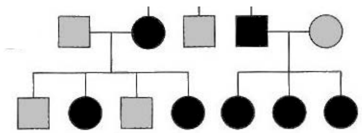
# Quantitative genetic analysis

- low genetic variation




# SNP association analysis

- high genetic variation



Pedigree

Relationship matrix

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|---|---|---|---|---|---|
| A | 1 | .5 | .25 | 0 | .25 |
| B | | 1 | .5 | .25 | 0 |
| C | | | 1 | 0 | .25 |
| D | | | | 1 | .5 |
| E | | | | | 1 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 74517 | A:G | A:G | G:G | A:A | A:A | G:G | C:C | A:G | G:G |
| 74519 | A:A | G:G | A:G | A:C | A:C | A:G | C:C | A:G | G:G |
| 74521 | A:A | G:G | A:G | A:C | A:C | A:G | A:C | A:G | A:G |
| 74522 | A:A | G:G | A:G | A:C | A:C | G:G | C:C | A:A | G:G |
| 74612 | A:G | A:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |
| 74618 | A:A | G:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |
| 74623 | A:G | A:G | G:G | A:A | A:A | G:G | C:C | A:A | G:G |
| 74628 | A:A | G:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |
| 74711 | A:A | G:G | G:G | A:A | A:C | G:G | C:C | A:G | G:G |
| 74716 | A:G | A:G | G:G | A:A | A:C | A:G | C:C | A:A | G:G |

| | A | B | C | D | E |
|---|---|---|---|---|---|
| A | 1 | .72 | .31 | .11 | .21 |
| B | | 1 | .57 | .42 | .08 |
| C | | | 1 | .10 | .22 |
| D | | | | 1 | .47 |
| E | | | | | 1 |

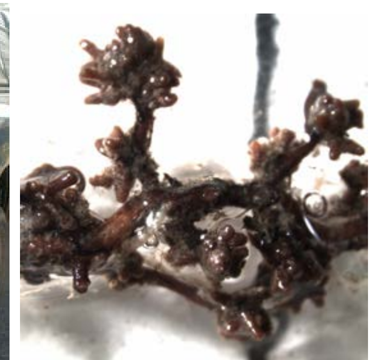
# Chapter 3: Association mapping of ectomycorrhizal traits in loblolly pine

Q1: What can we say about the number and effect of genes involved in mycorrhizal traits in loblolly pine?

Q2: Can we determine a genetic basis for the correlations detected in the quantitative genetics study?

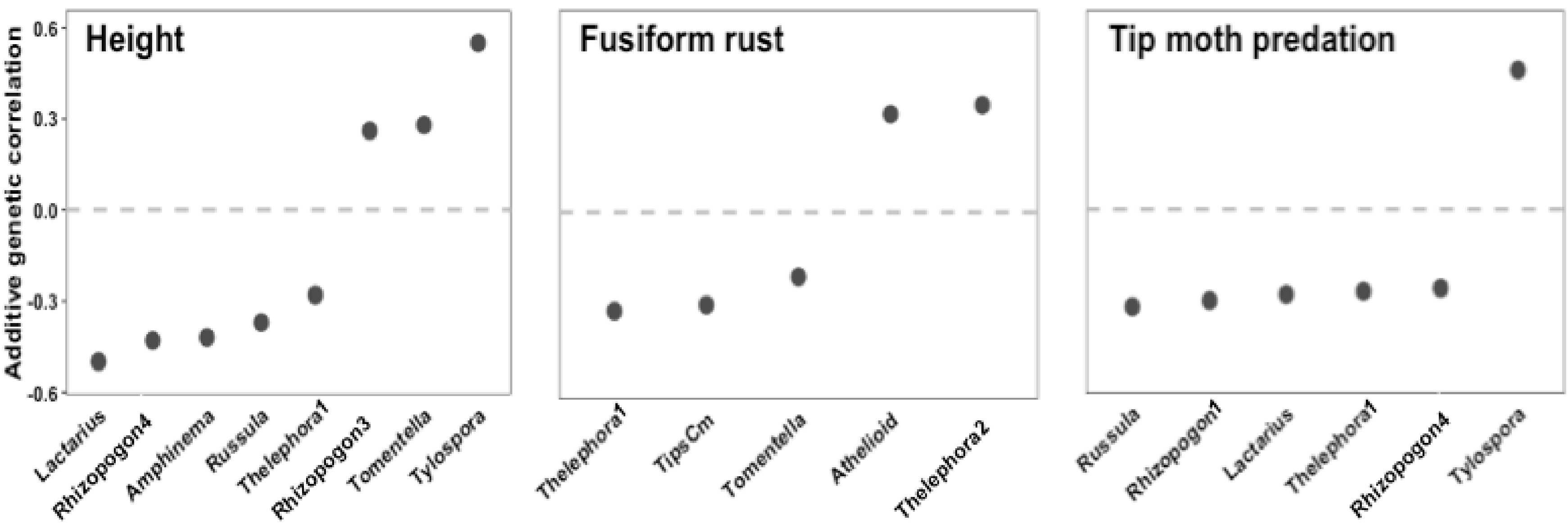
Q3:  Can we ascribe putative function to any of the relevant SNPs?



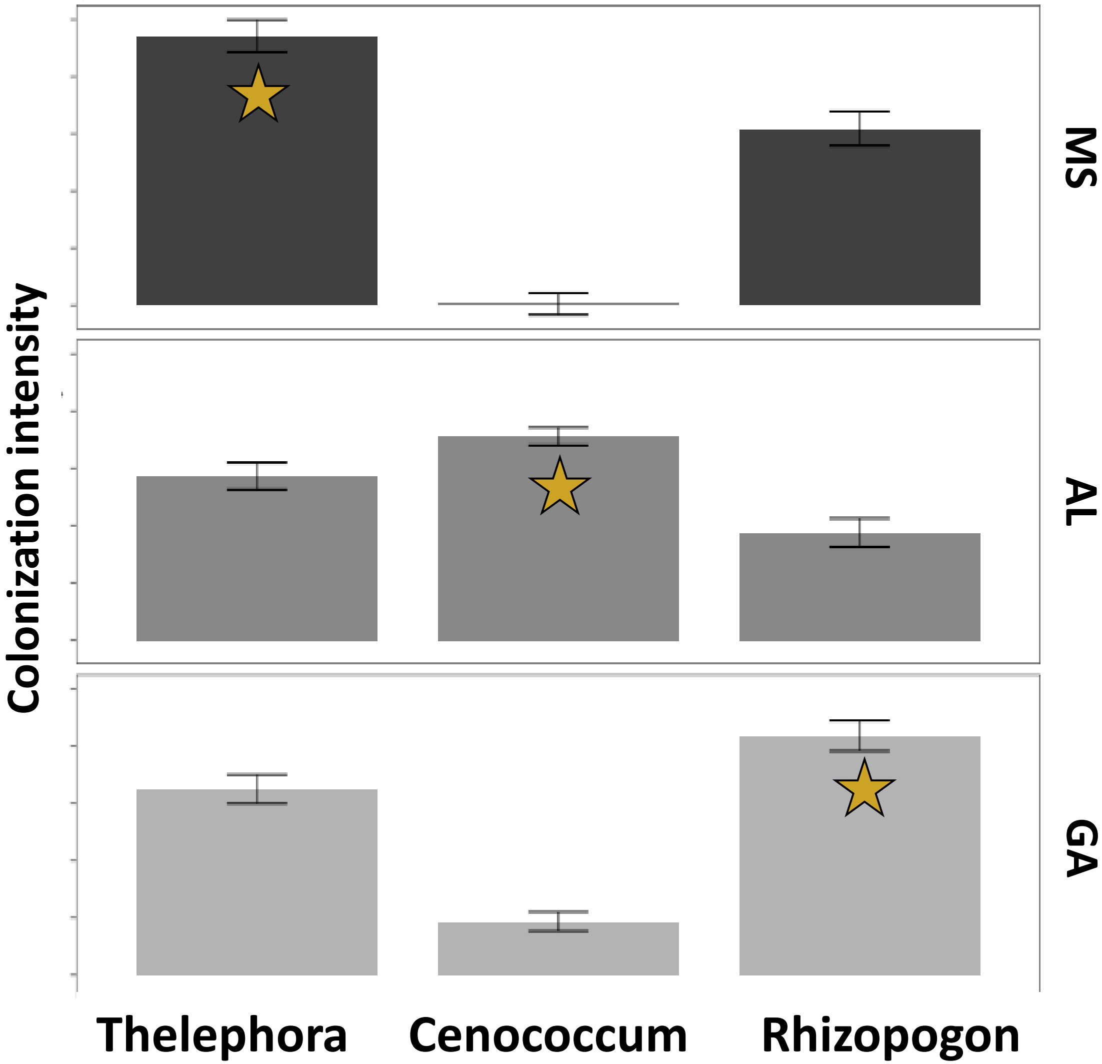

Can we use the SNP data to determine a probably genetic basis for the correlations detected in the quantitative genetics study?

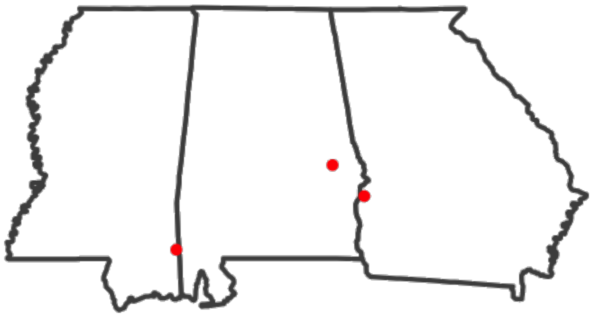
**Sadly, no.**



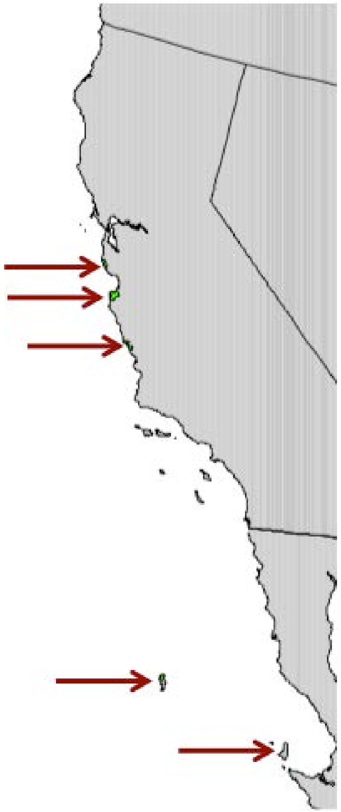
# The abundance of three of the four major fungal colonizers was determined solely by soil inoculation source

*Rhizopogon* ($F_{2,532}$= 19.342, $p$ = 7.787 e-09), *Cenococcum* ($F_{2,532}$= 120.840, $p$ = <2.0 e-16), and *Thelephora* ($F_{2,532}$= 12.5084, $p$ = 4.91e-06)



# Discussion



Monterey Pine

## Comparison with Monterey Pine

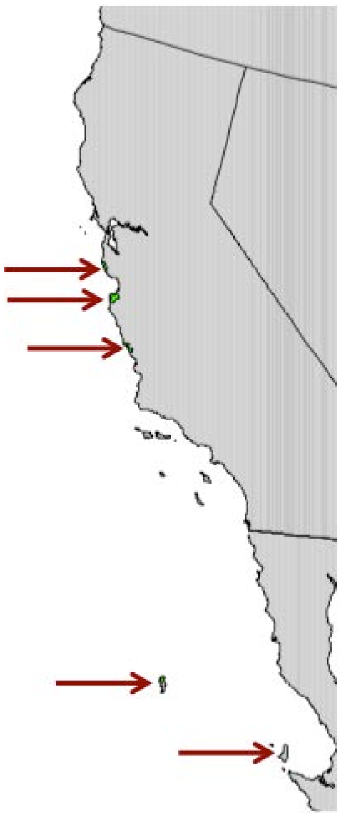
(Hoeksema et al *Ecology* 2012)

- five sampling locations
- few dominant fungal sp
- differed among soil AND plant

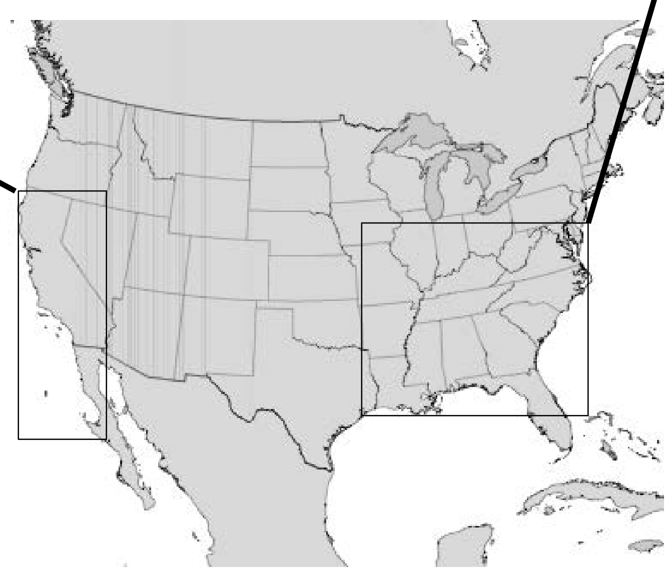
# Discussion

Both show
- variation in soil fungal community

Different population structures



Monterey Pine



Loblolly Pine