A decorative graphic on the left side of the slide showing several thin, curved lines representing plant roots or stems, with a grey arrow pointing to the right.

# Opportunities to advance rhizosphere microbiome research with functionally and spatially explicit root sampling

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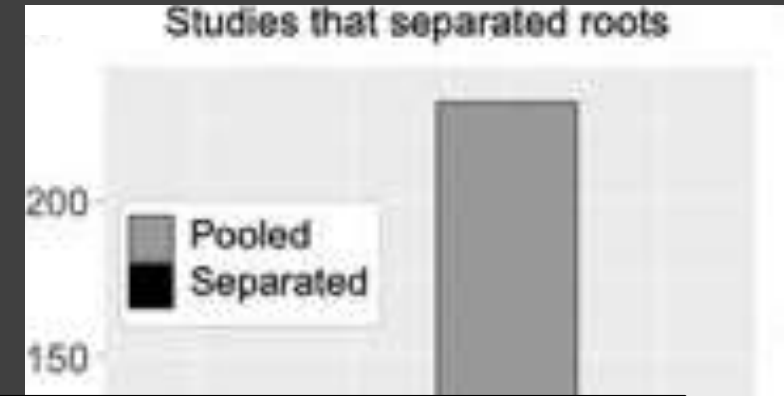
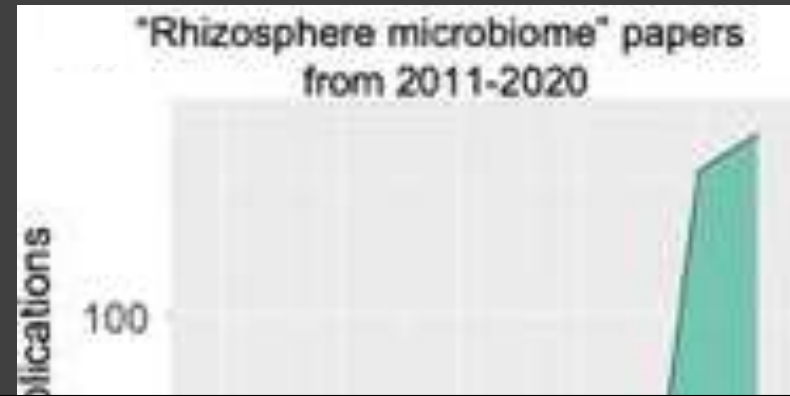
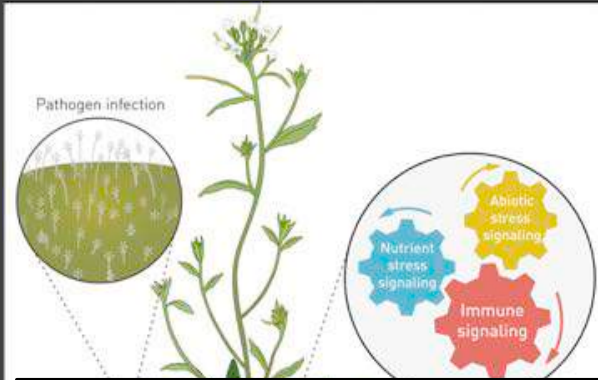


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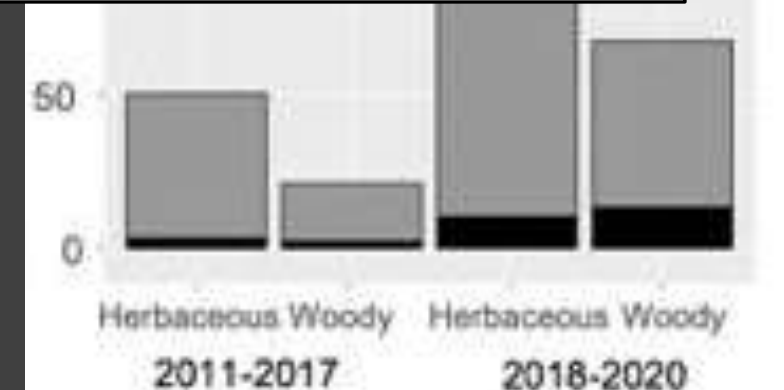
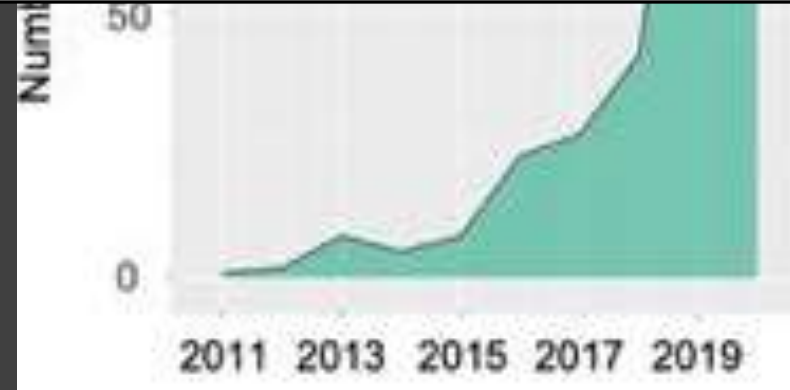
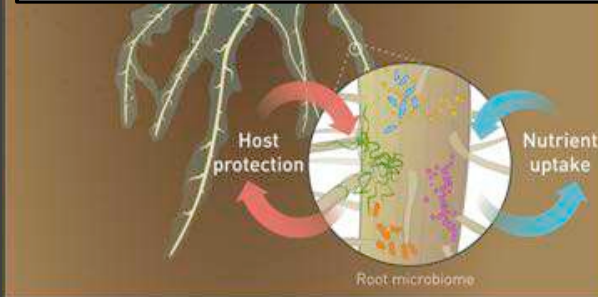


Dr. Jing Guo  
Visiting scholar

# Many plant functions are microbially-mediated



But not all roots are functionally equal



Bakker et al. 2018, Trends in Plant Science

Fleishman et al. 2021, *In Review*

# How does the underlying functional and spatial heterogeneity of roots impact microbial composition?



Absorptive  
vs.  
Transportive



Developmental  
stage



Spatial  
location



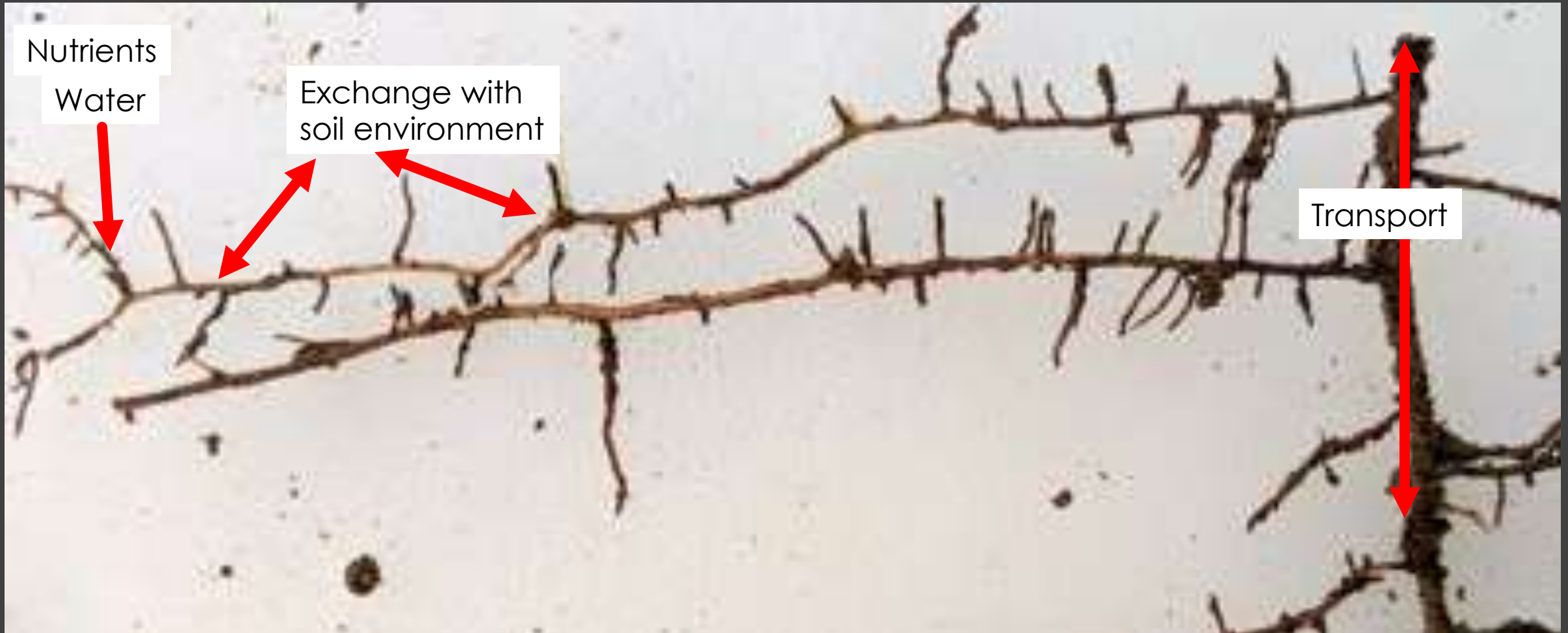
Root systems are heterogeneous environments



# Root systems are heterogeneous environments

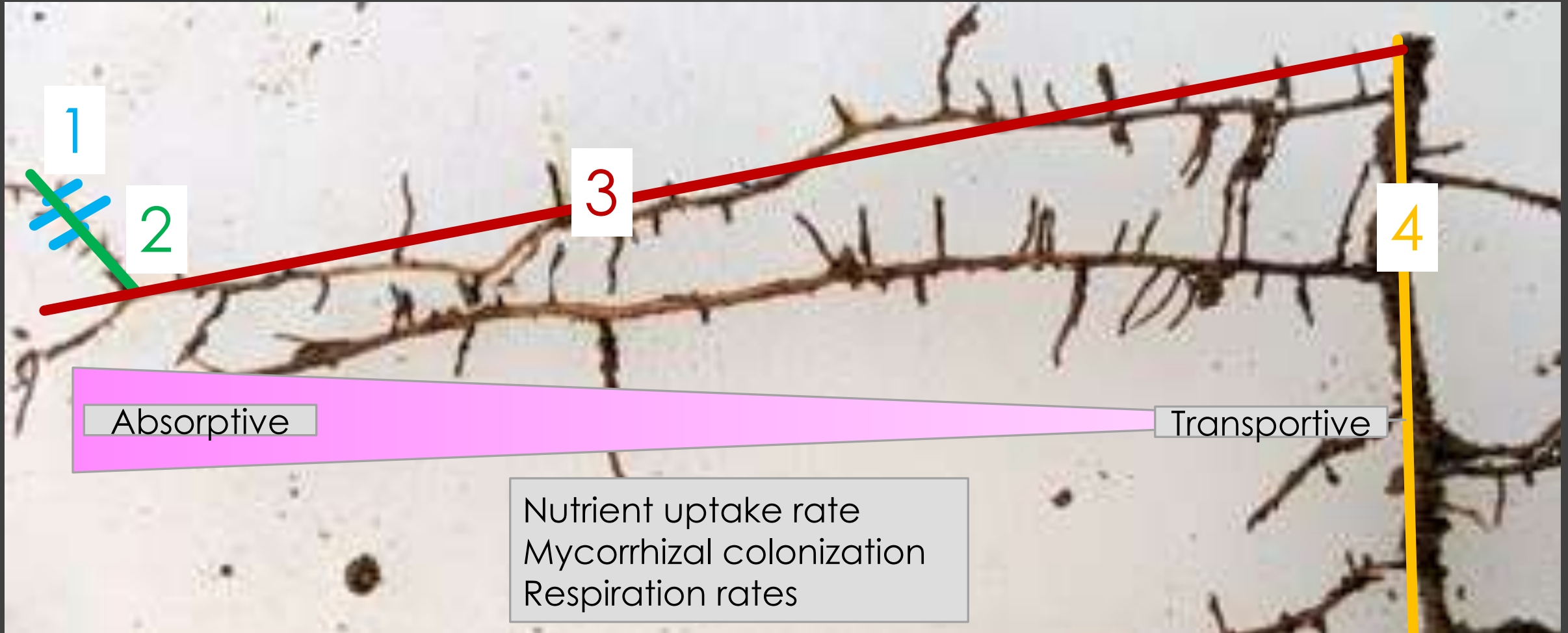


# Absorptive vs. transportive roots





# Root function can be classified by branching order



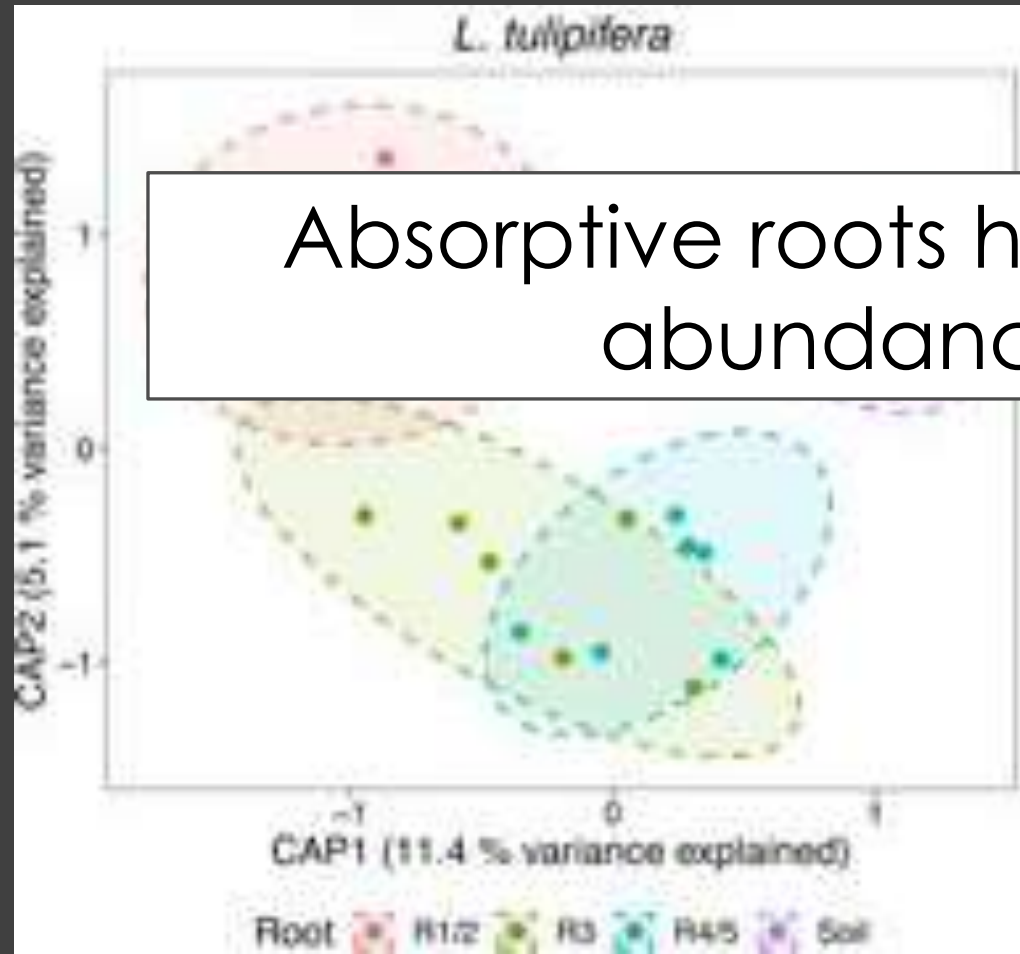


# Do rhizosphere microbiomes vary with root branching order?

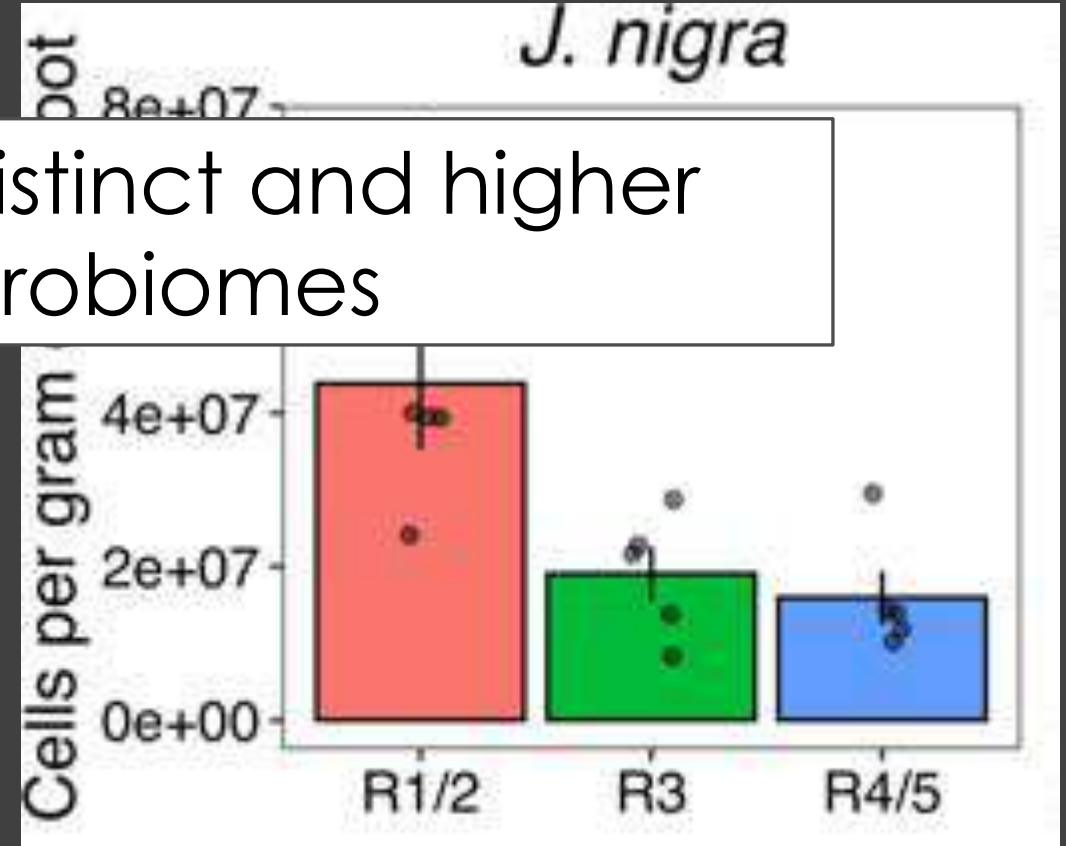
## Common garden



# Root branching order determines composition

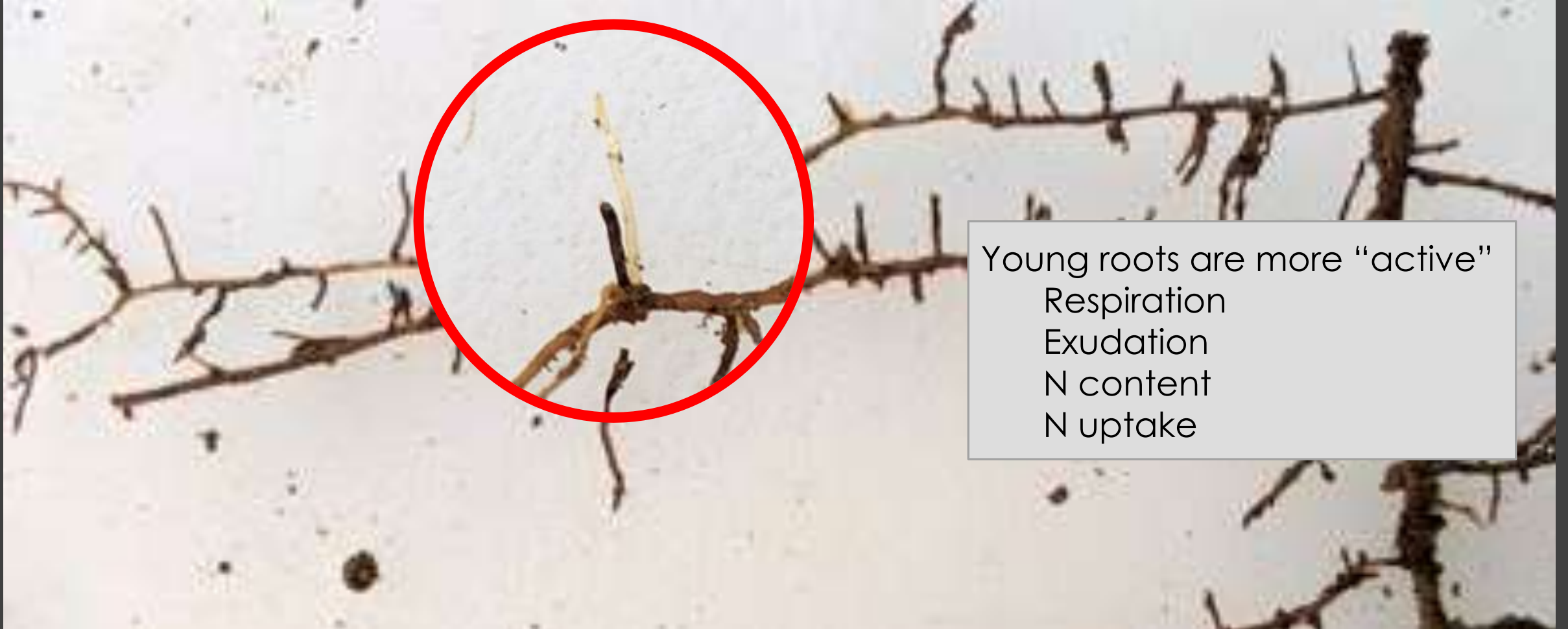


Absorptive roots have distinct and higher abundance microbiomes



\* Pattern existed across all 6 tree species

# Absorptive roots differ in developmental stage



Young roots are more “active”  
Respiration  
Exudation  
N content  
N uptake



# Monitoring root age in the field



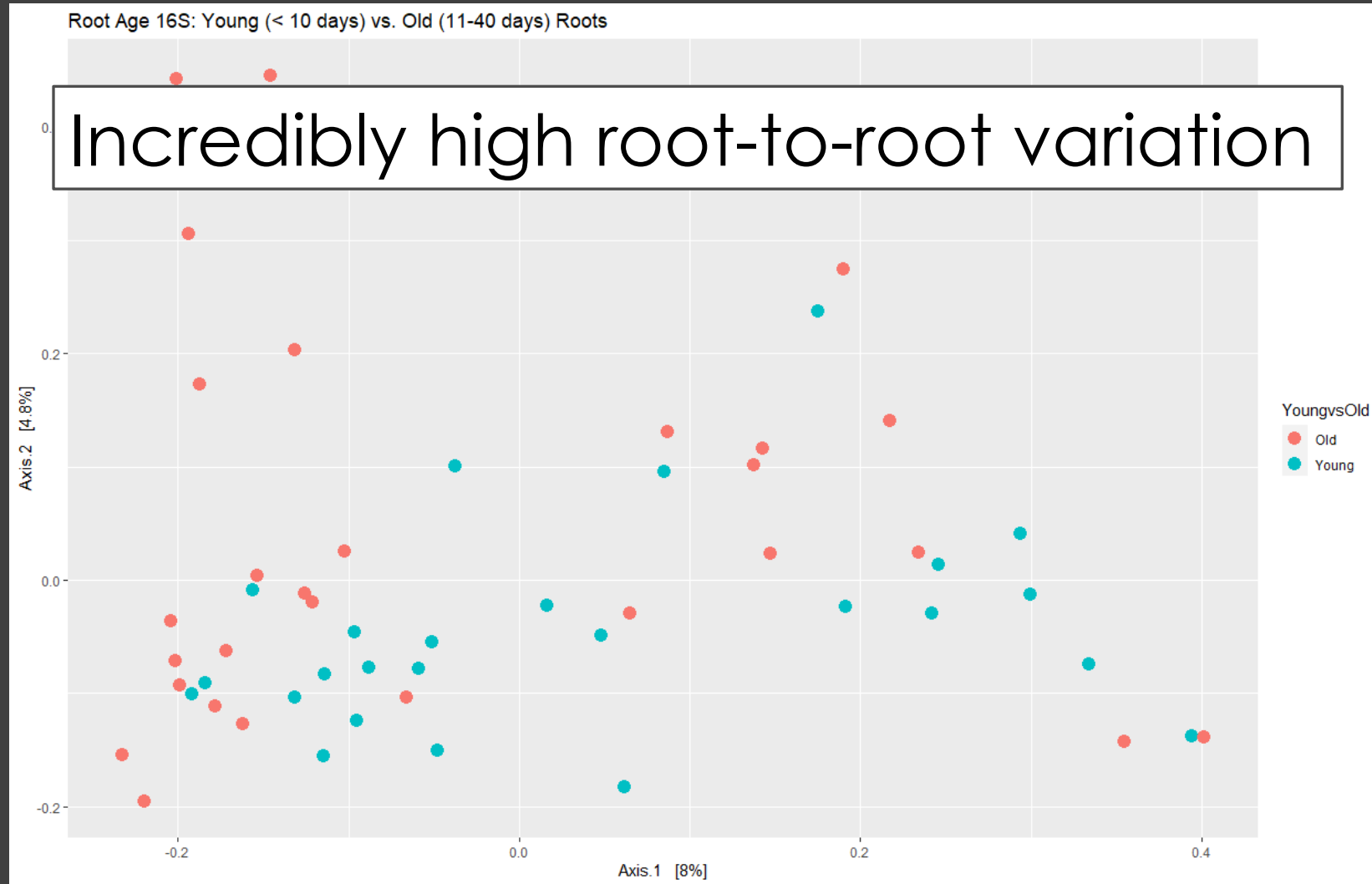


# Monitoring root age in the field

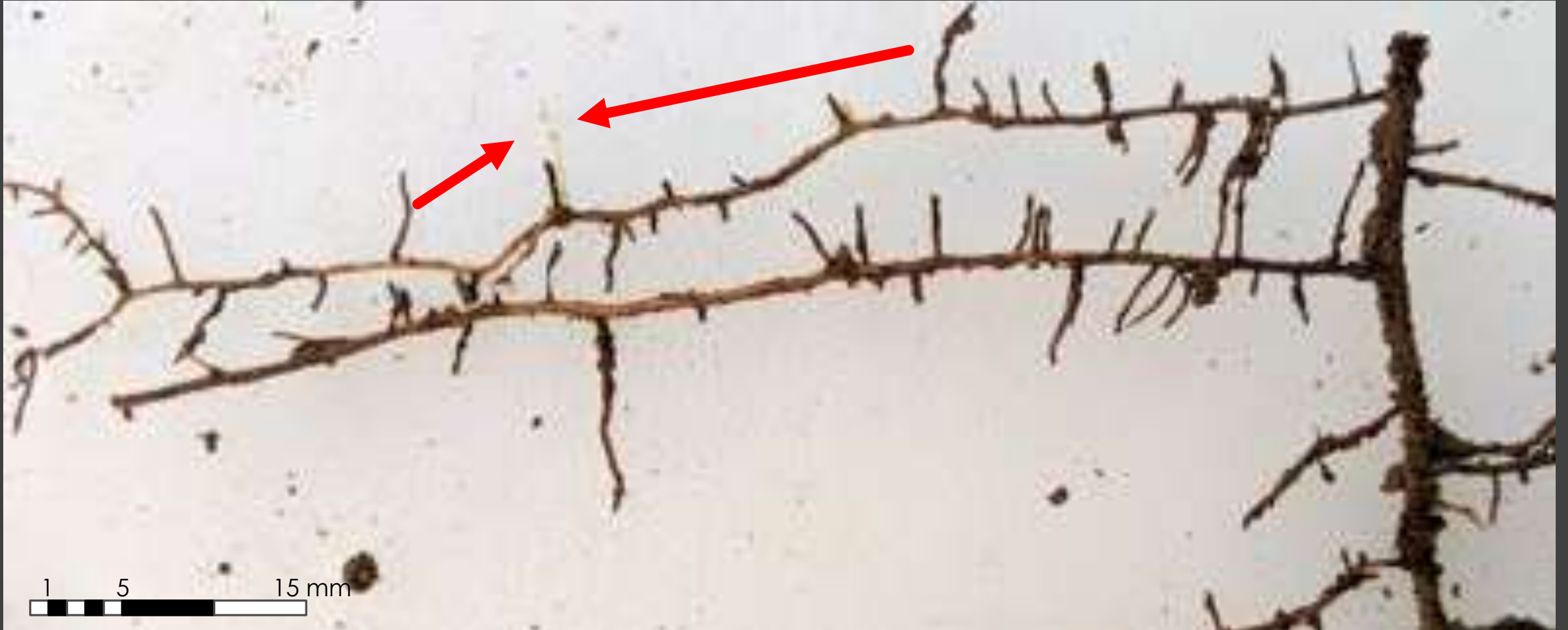


7 vines  
98 individual roots  
Age: 0.5 – 40 days

# Microbial composition differs with root age



# Does root location explain microbial variation?



# Mapping a root system



## Variation Partitioning Analysis (VPA)

- Based on constrained ordinations (RDA) to model microbiome response
- Allows for  $R^2$  generation for multivariate explanatory categories
- Allows for comparison of the relative importance of each category



# Mapping a root system



## Variation Partitioning Analysis (VPA)

1. Root traits  
(branching order, age, color)

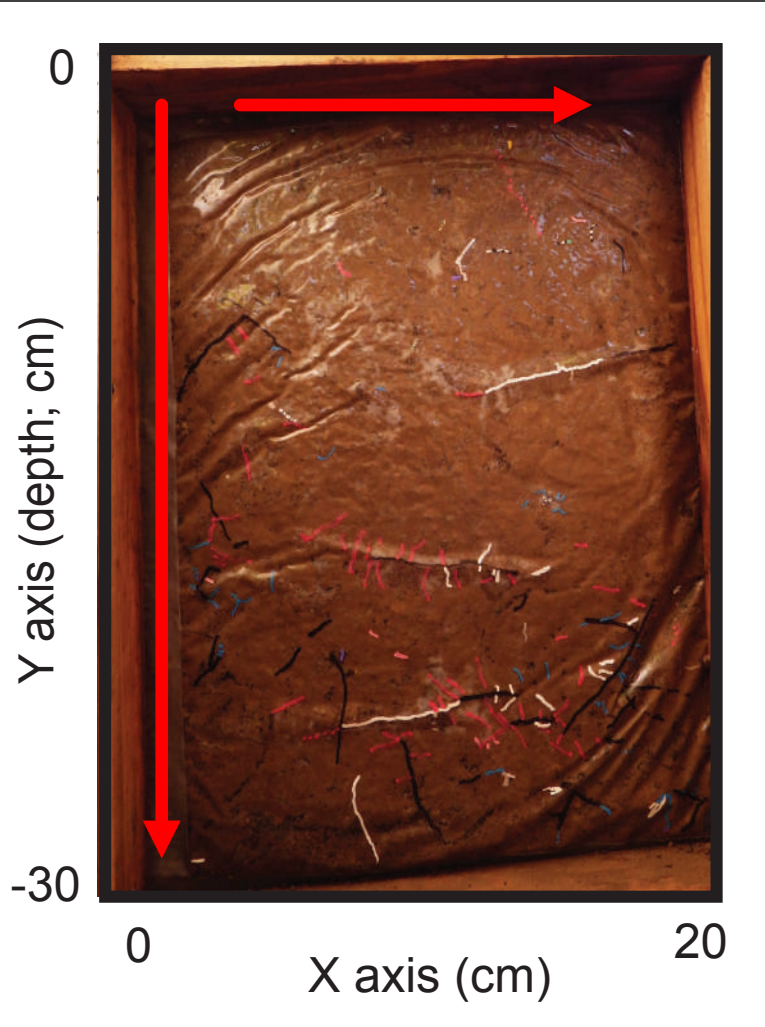
# Mapping a root system



## Variation Partitioning Analysis (VPA)

1. Root traits  
(branching order, age, color)
2. Root cluster

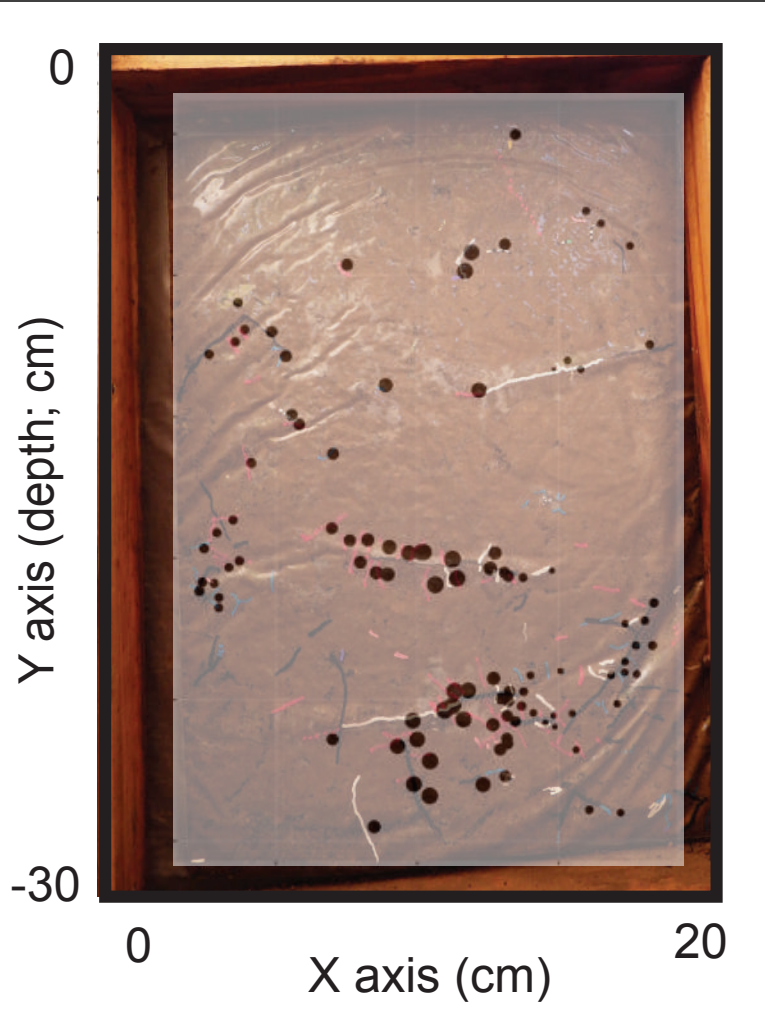
# Mapping a root system



## Variation Partitioning Analysis (VPA)

1. Root traits  
(branching order, age, color)
2. Root cluster
3. Linear spatial trend (X,Y)

# Mapping a root system

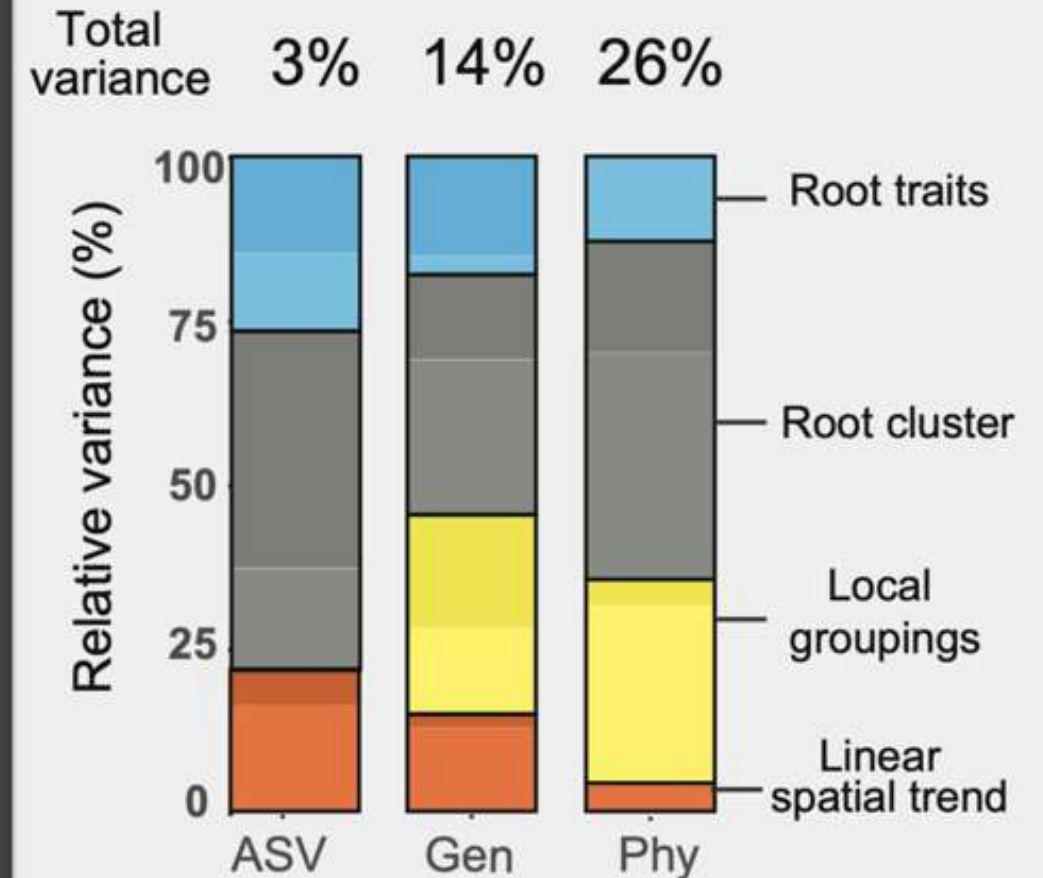
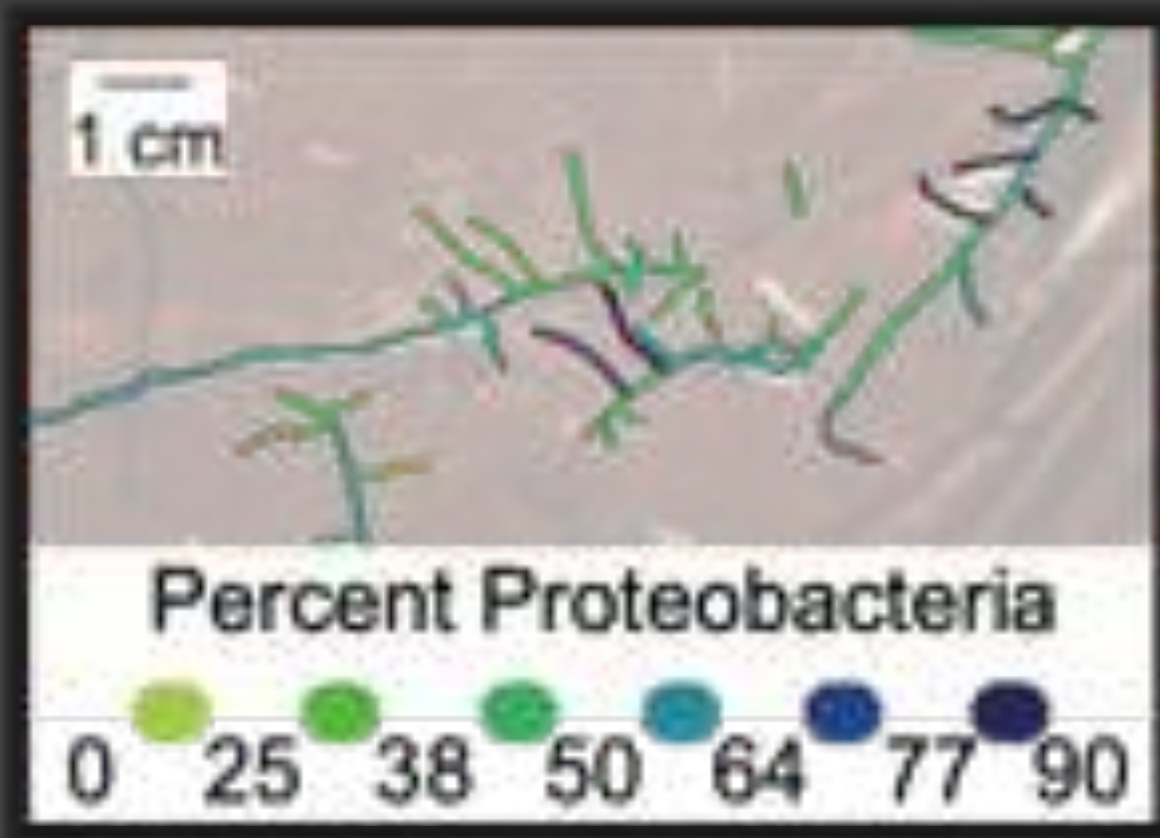


## Variation Partitioning Analysis (VPA)

1. Root traits  
(branching order, age, color)
2. Root cluster
3. Linear spatial trend (X,Y)
4. Local groupings (MEMs)



# Root traits explain less variation than spatially structured factors



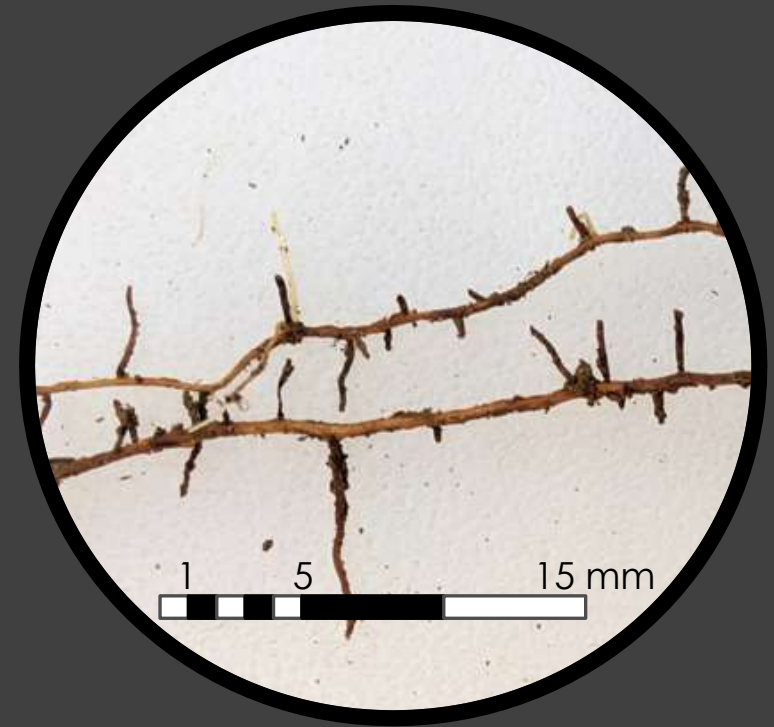
# The underlying functional and spatial heterogeneity of roots impacts microbial composition



Branching  
order



Developmental  
stage



Spatial  
location

# How can functionally explicit sampling advance rhizosphere microbial research?

- Match sampling schemes to research questions
  - *Pooled sampling*: net impacts
  - *Separated sampling*: function-based; variation-minimized
- When considering assembly, cannot ignore spatial structuring



# Acknowledgements

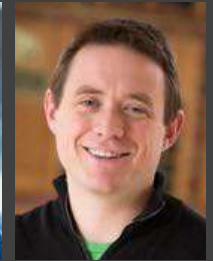
Eissenstat Root Ecology Lab

Centinari Viticulture Lab

Bell Microbiome Manipulation Lab

Don Smith, Jeremy Harper, and Hort Farm Staff

Hayden Bock, Jing Guo, Ryan Trexler





# Penn State Microbiome Center

- Established in 2016
- 80 Research Groups from 10 different colleges and institutes (arts and anthropology to zygotes and zoology; human, animal, plant, environmental health)
- 40 weekly seminars and 2-3 workshops per semester
- Kick Start Program for beginners
- Data Analysis Working Group (DAWG) led by students and postdocs
- Industrial programming and partnerships (contact [CaroleeBull@psu.edu](mailto:CaroleeBull@psu.edu) for information)
- Formal Microbiome Sciences Dual Title being proposed
- NEW SENIOR LEVEL DIRECTOR being recruited
- Visit our website: [microbiome.psu.edu](http://microbiome.psu.edu)
- Follow us on Twitter @PSUmBiome

