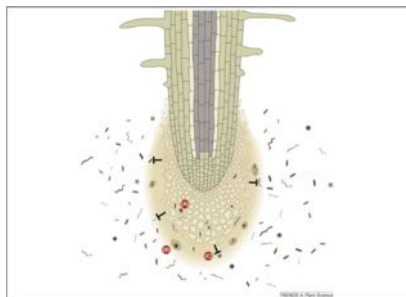
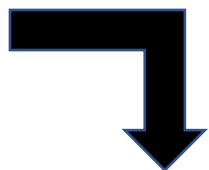
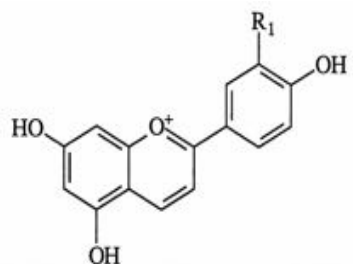


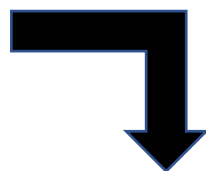
# Rhizosphere Microbial Communities of *Sorghum bicolor* Cultivars with Contrasting Flavonoid Production Patterns

Mara Cloutier, Iffa Gaffoor, Dinakaran Elango, Jin Cui, Debamalya Chatterjee, Mary Ann Bruns, Surinder Chopra

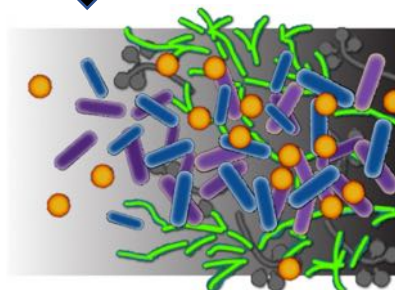
## Flavonoids



## Rhizosphere



## Microbes



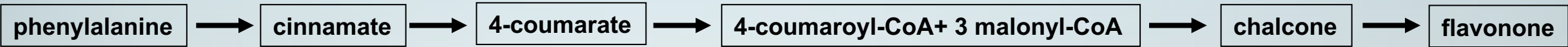
[muc345@psu.edu](mailto:muc345@psu.edu)  
@MaraCloutier



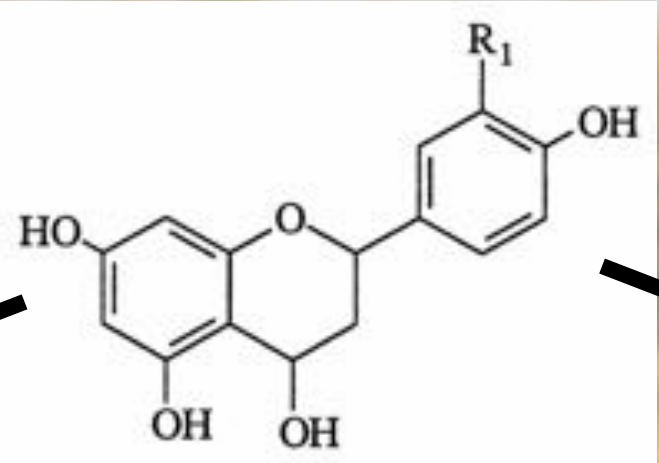
# What Do We Know About *Sorghum bicolor*?



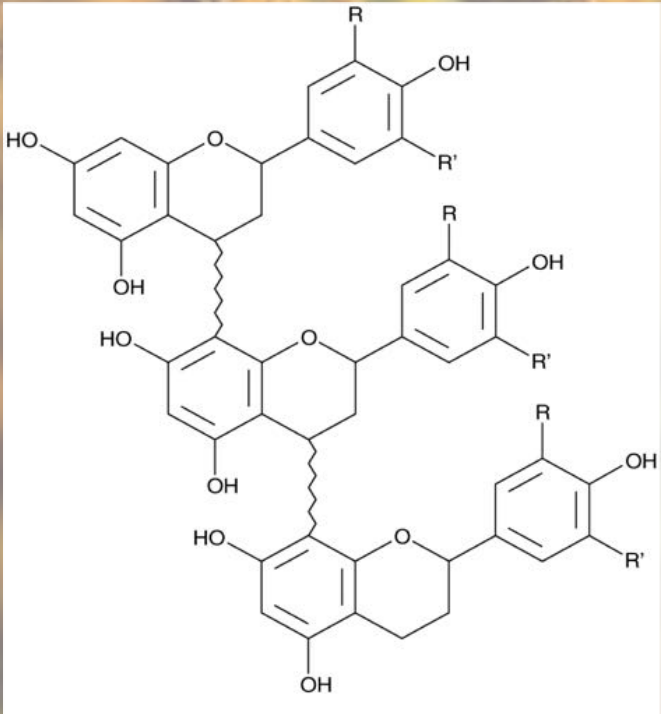




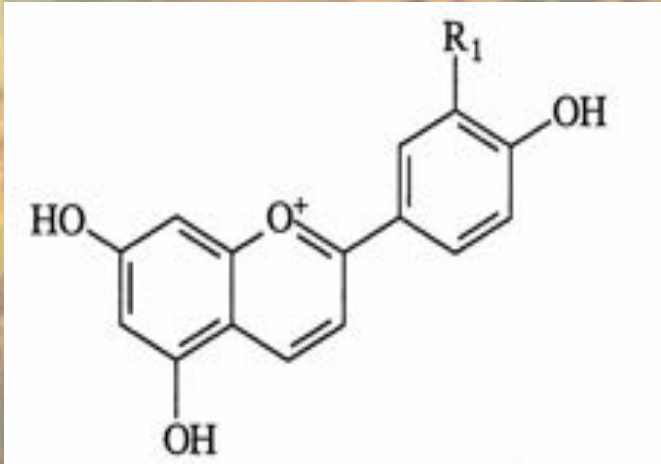
flavan-4-ols



Phlobaphenes

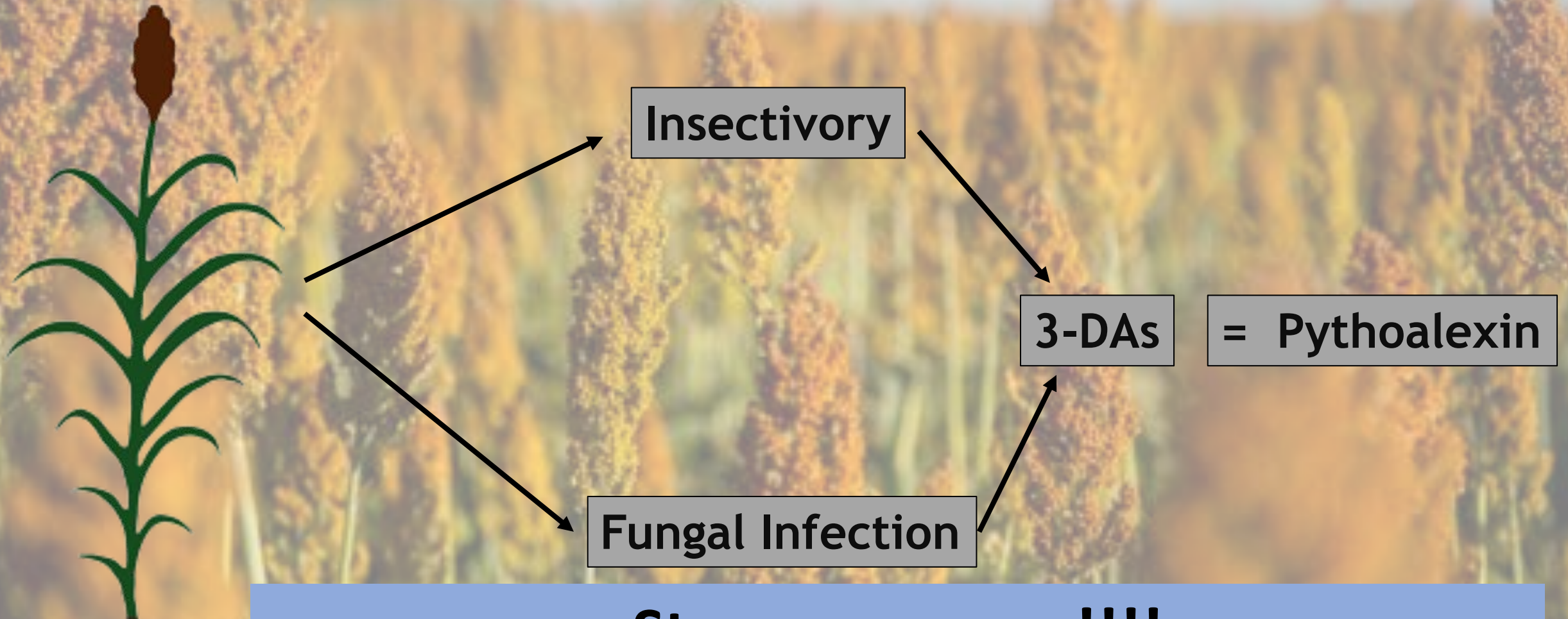


3-Deoxyanthocyanidins (3-DAs)



???

# When are 3-DAs produced?



**Stress response!!!!**



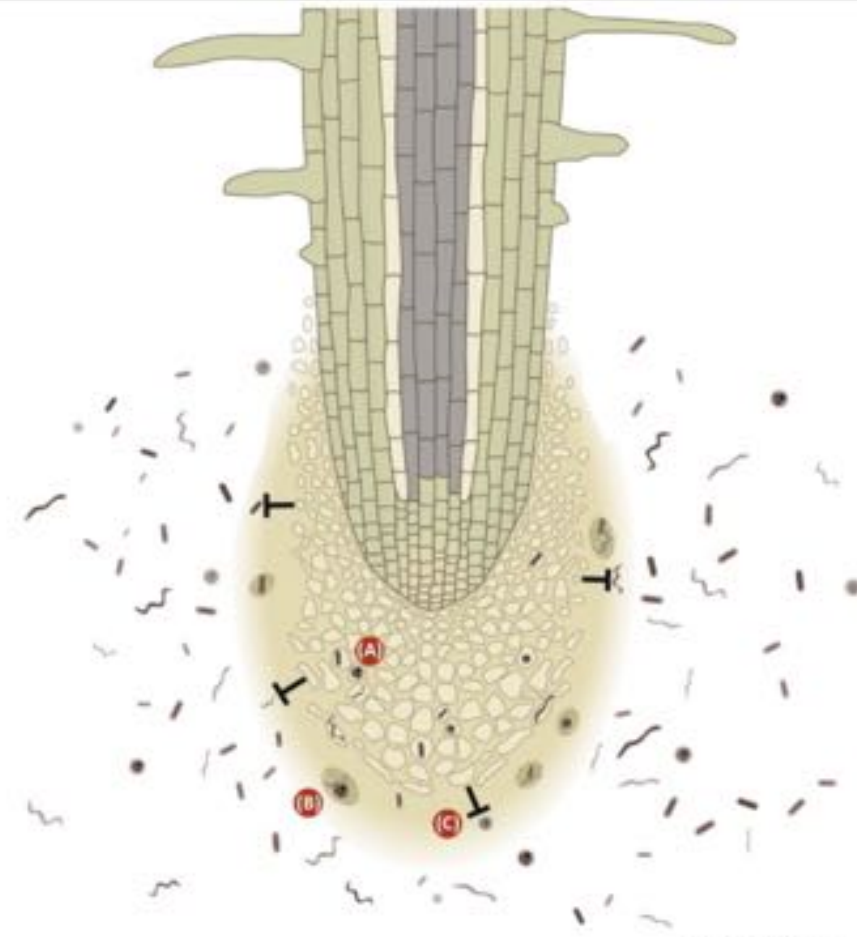
# What About Below Ground?



# Root Exudates Can Have Huge Impacts on Microbes

**Facilitate  
plant-microbe  
communication**

**Carbon source for  
heterotrophs**



**Attract  
symbiotic  
microbes**

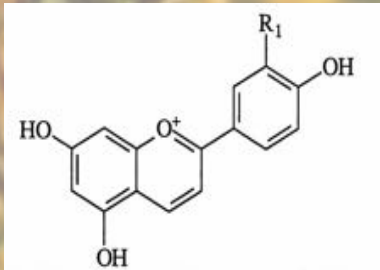
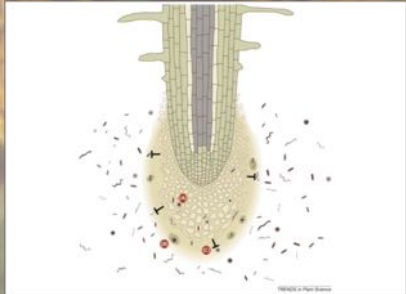
**Repel  
pathogenic  
microbes**

TRENDS in Plant Science



# Hypotheses:

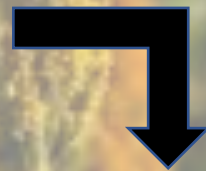
Rhizosphere



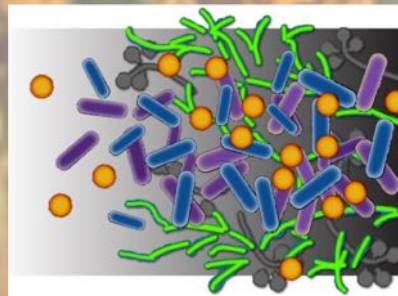
Flavonoids

H1: 3-DA production in sorghum *rhizospheres* will change the bacterial community structure

H2: Specific microbes will be differentially abundant between the flavonoid production patterns



Microbes



# Methodology:

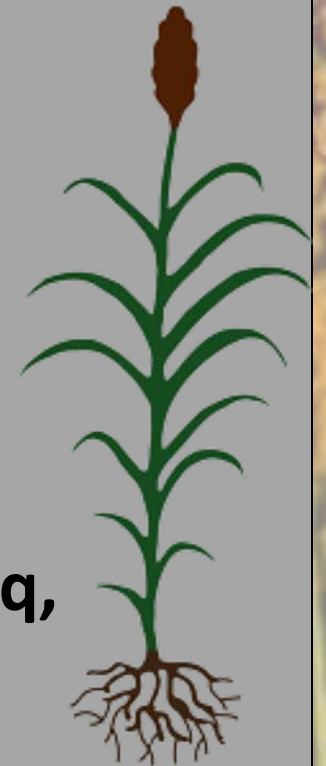
- **5 *Sorghum bicolor* cultivars grown in the field**
  - Randomized complete block design
- **3 sorghum plants excavated per plot**
- **Excess soil removed from roots**
- **Roots washed with water to remove rhizosphere soil**
- **16S Sequencing using Illumina Amplicon Sequencing**





# Methodology:

- **Dada2 used for sequence processing**
  - Machine-learning to determine error rates specific for each set of sequences
- **Sequences were grouped based on 100% sequence similarity**
  - Exact sequence variants (ESVs)
- **Taxonomy assigned with Silva**
- **Statistics performed in R using the following packages: Phyloseq, microbiome, microbiomeSeq, DeSeq2, and vegan**



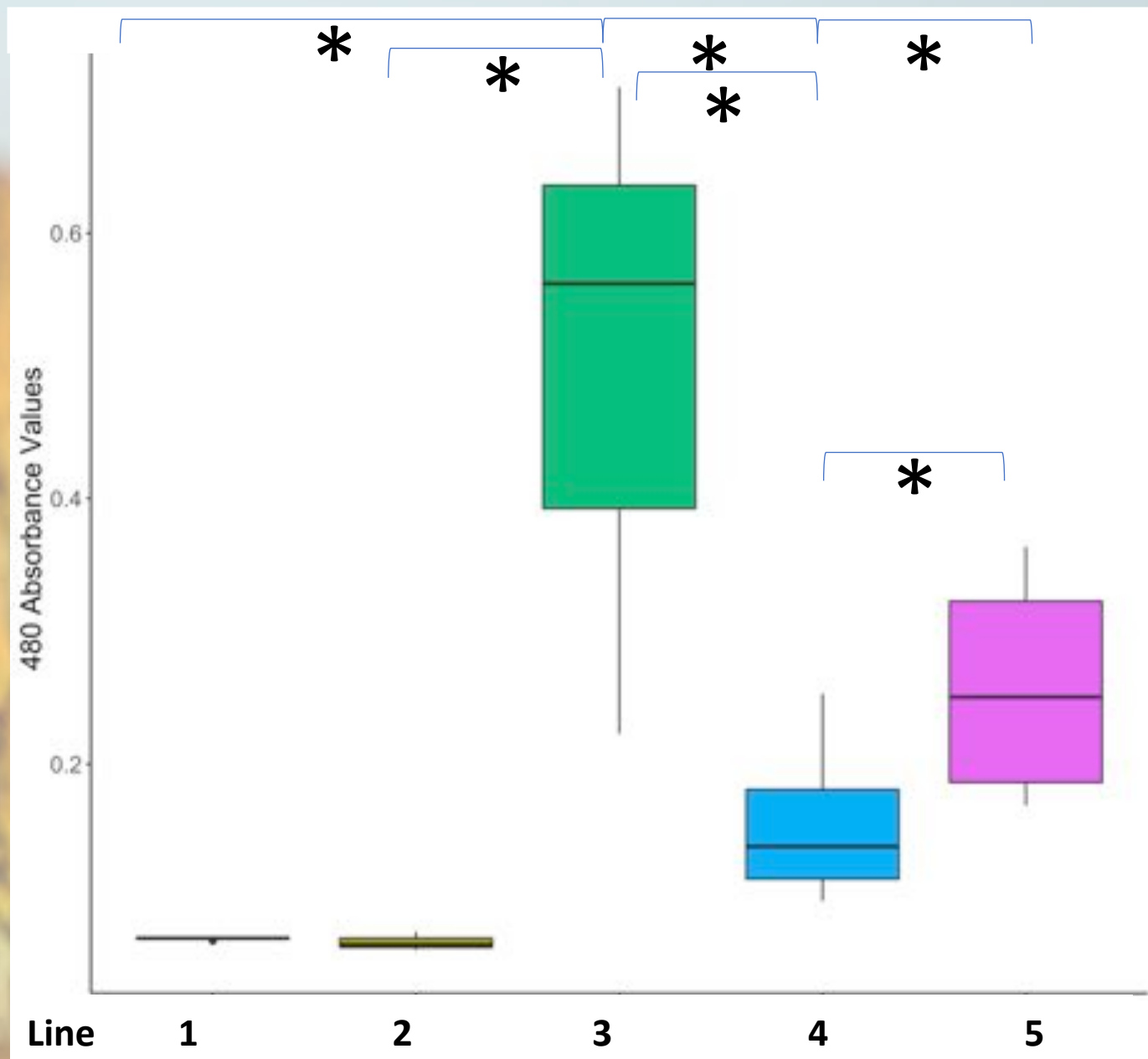
A photograph of a sorghum field with golden-brown seed heads. A semi-transparent grey box is overlaid in the center, containing the text "Results:". 

Results:

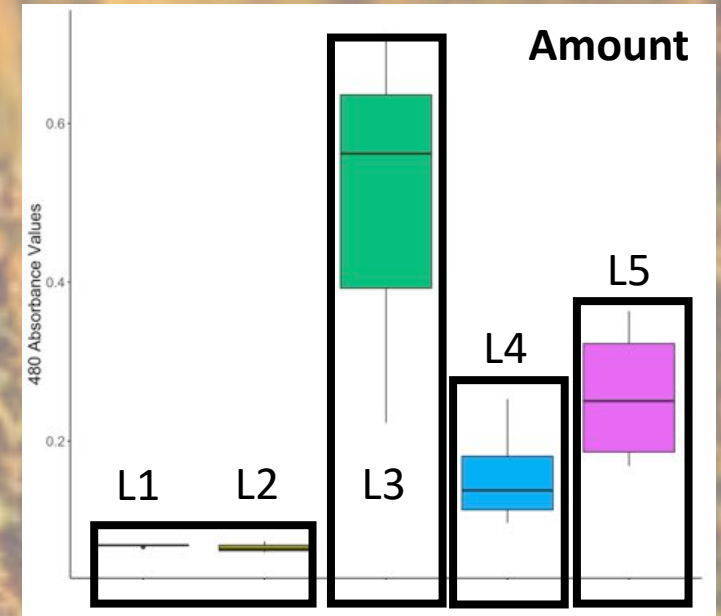
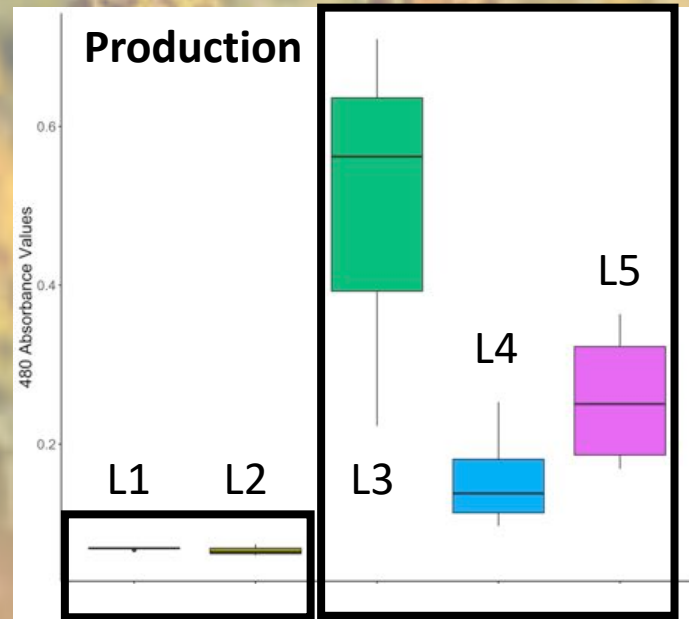
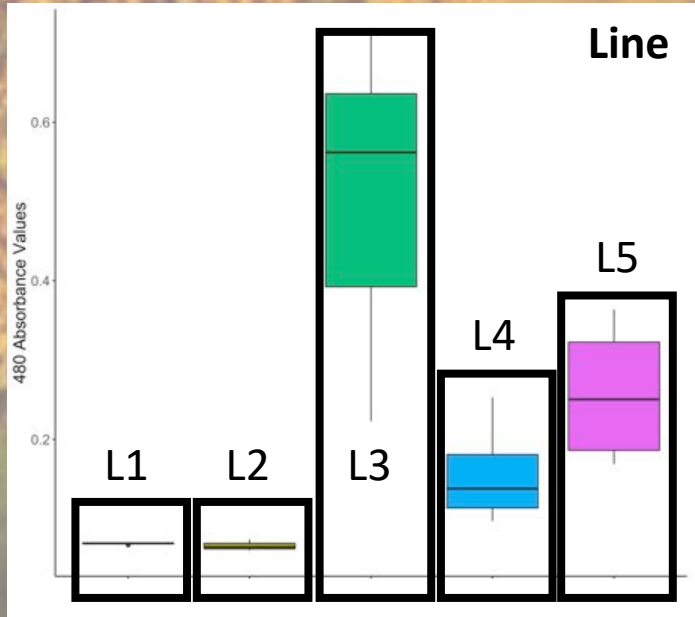


# 3-DA Production in the Field

\*  $p < 0.05$

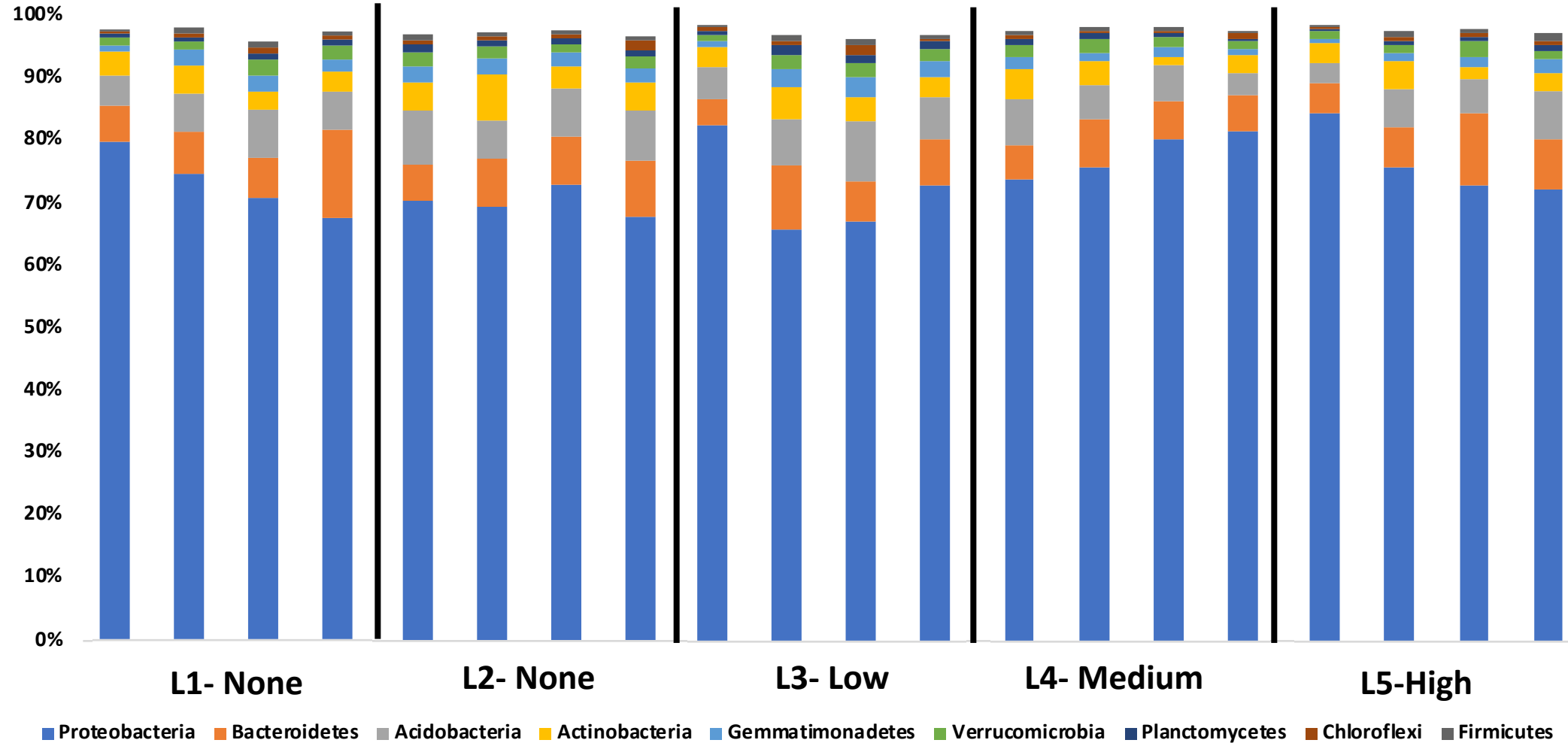


# What Groups Are We Assessing?





# No Patterns in Phylum-Level Distributions

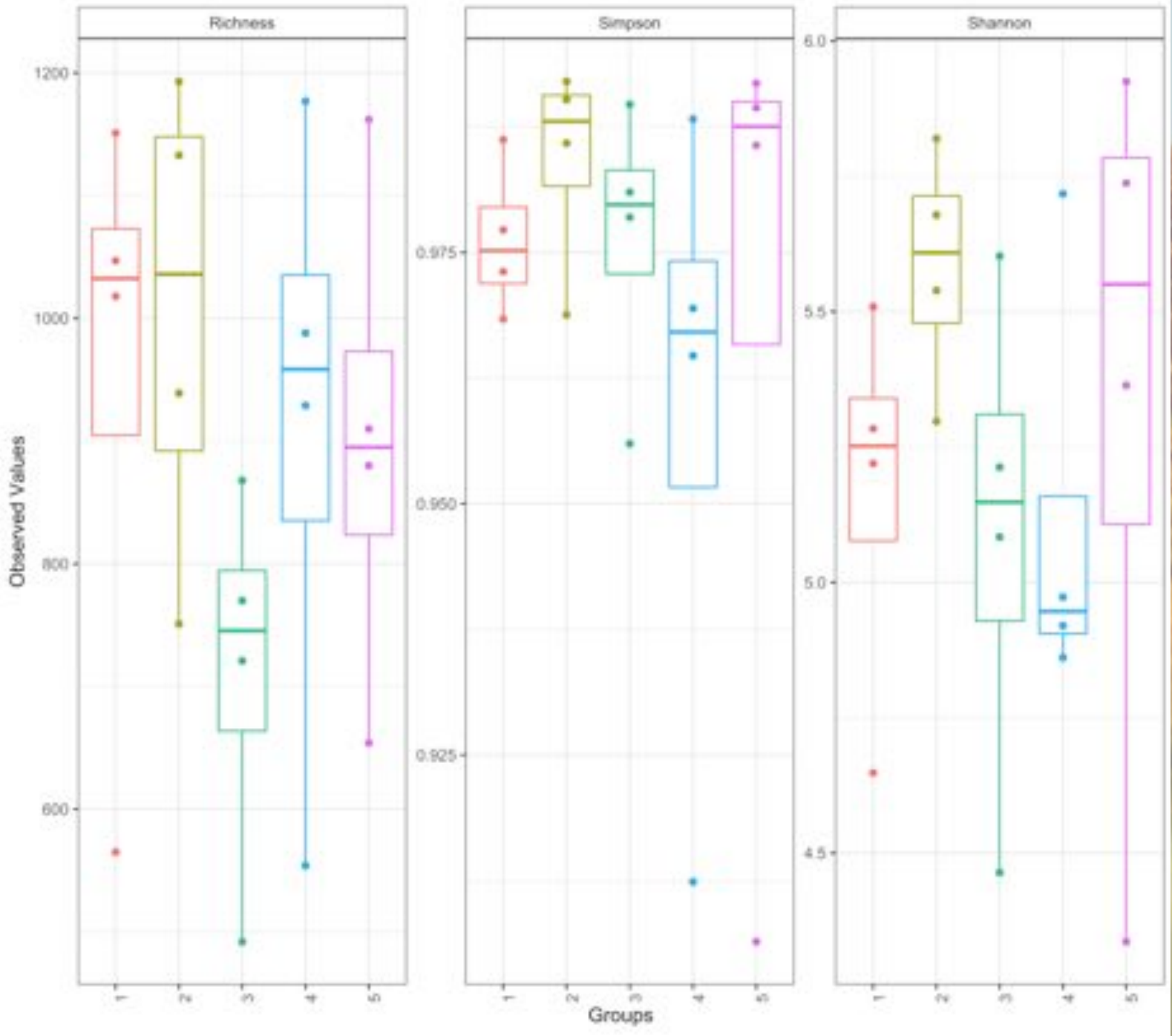


A photograph of a field of sorghum plants with golden-brown seed heads. The plants are in focus in the foreground, with a blurred background of more plants and a clear sky.

# Alpha-Diversity



# No Differences in Alpha-Diversity



**Flavonoid production:**

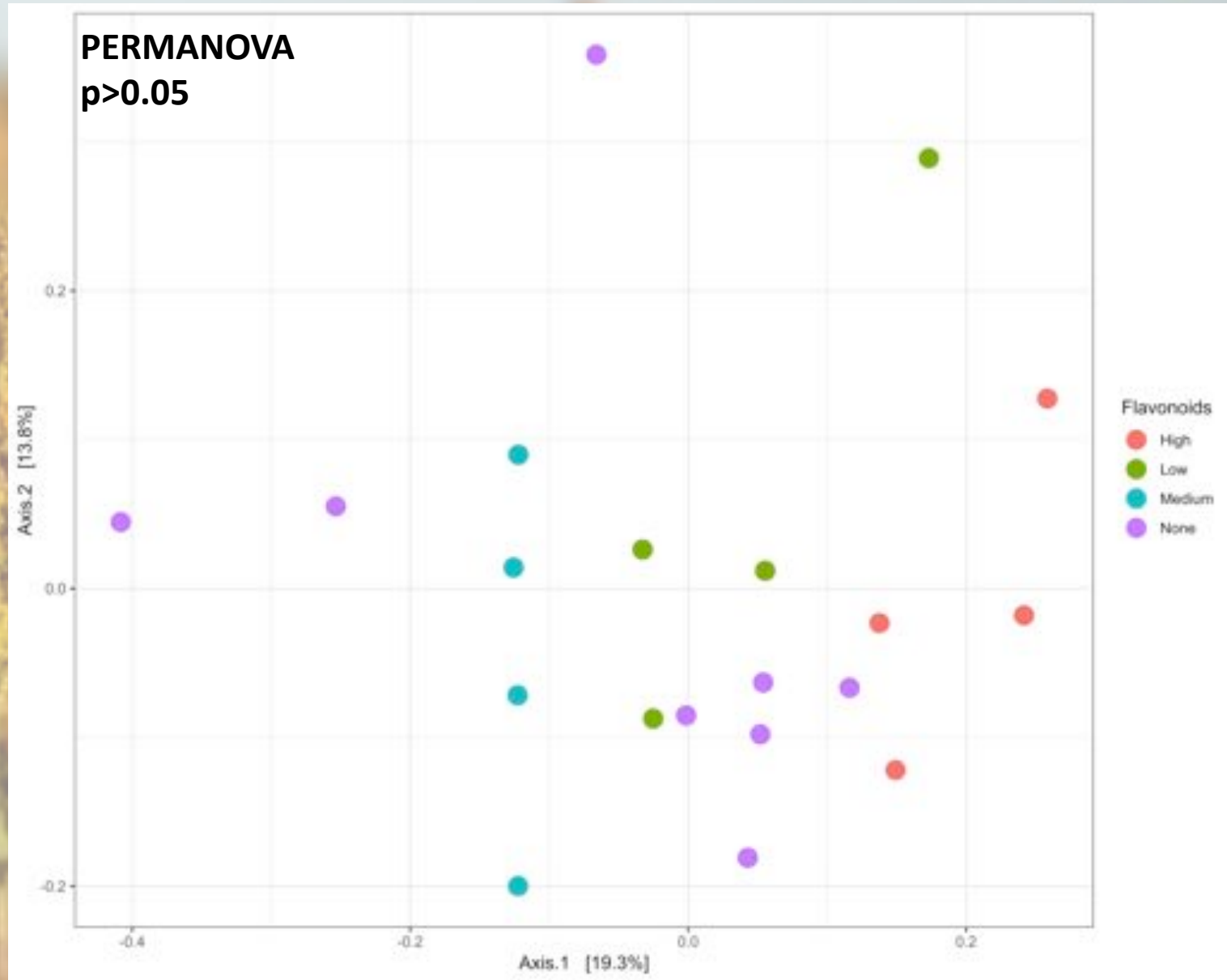
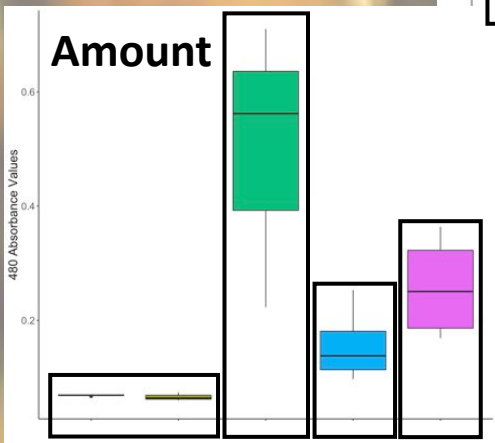
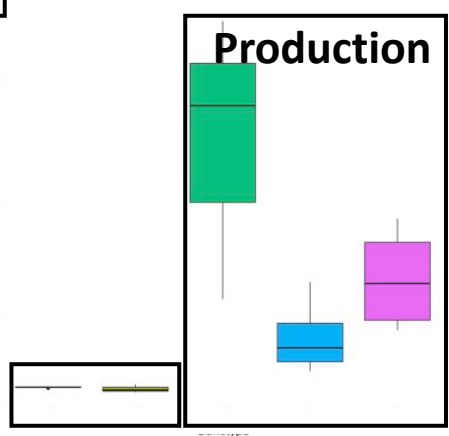
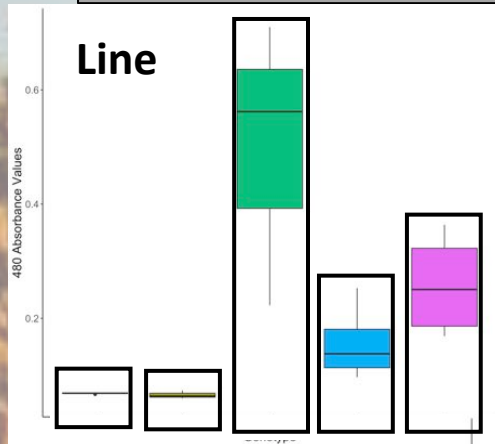
- 1 = Medium
- 2 = None
- 3 = High
- 4 = None
- 5 = Low

A photograph of a field of sorghum plants with golden-brown seed heads. The plants are in focus in the foreground, with a blurred background of more plants and a clear sky.

# Beta-Diversity



# Bacterial Composition and Abundance is Similar



A photograph of a field of sorghum plants with golden-brown seed heads. The plants are in focus in the foreground, with a blurred background of more plants and a clear sky.

What About Individual Organisms?



Microbes  
Differentially  
Abundant  
Across  
Genotypes

# Flavonoid production:

- 1 = Medium
- 2 = None
- 3 = High
- 4 = None
- 5 = Low

# Flavonoid production:

- 1 = Medium
- 2 = None
- 3 = High
- 4 = None
- 5 = Low

# Flavonoid production:

- 1 = Medium
- 2 = None
- 3 = High
- 4 = None
- 5 = Low

# Flavonoid production:

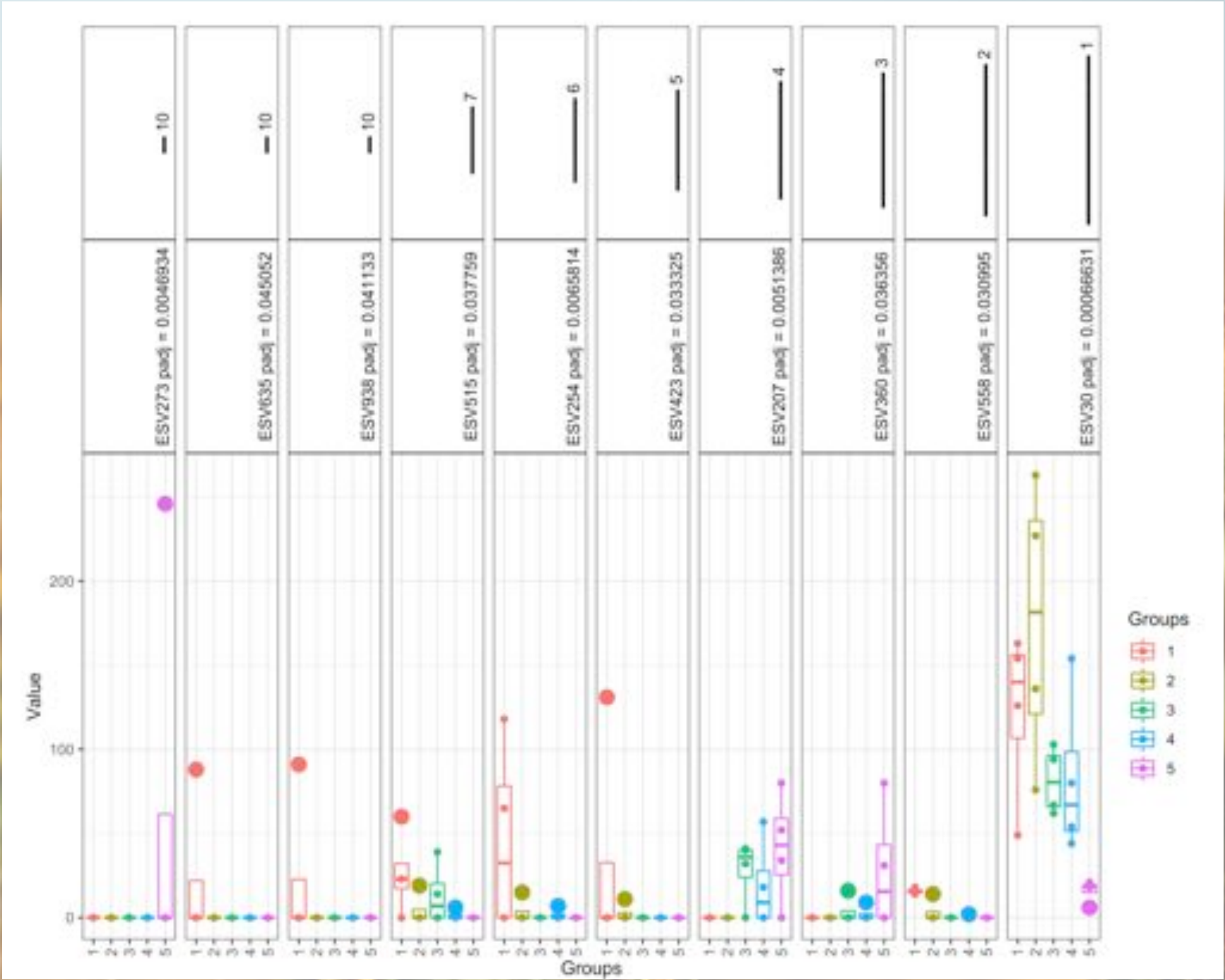
- 1 = Medium
- 2 = None
- 3 = High
- 4 = None
- 5 = Low

# Flavonoid production:

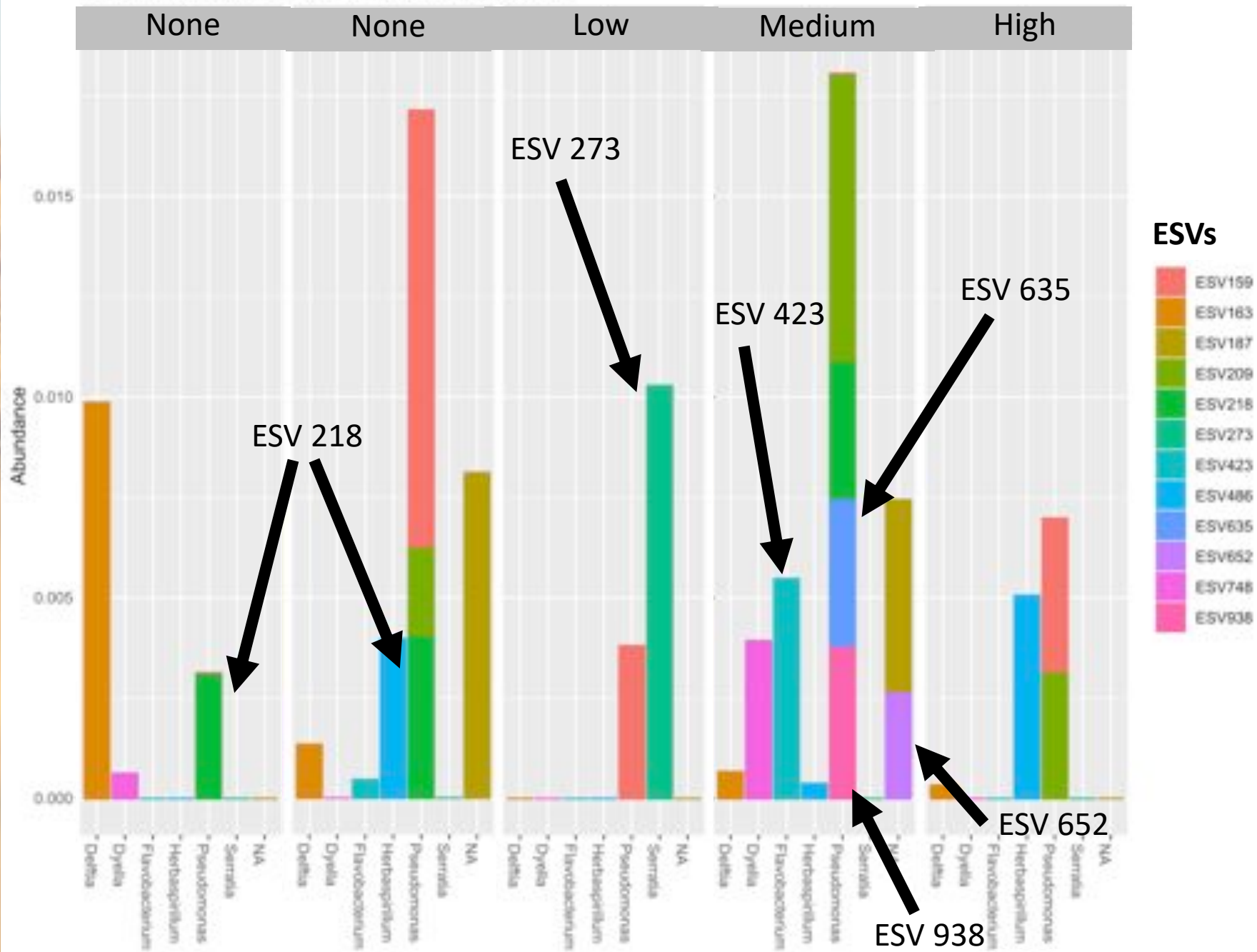
- 1 = Medium
- 2 = None
- 3 = High
- 4 = None
- 5 = Low

# Flavonoid production:

- 1 = Medium
- 2 = None
- 3 = High
- 4 = None
- 5 = Low



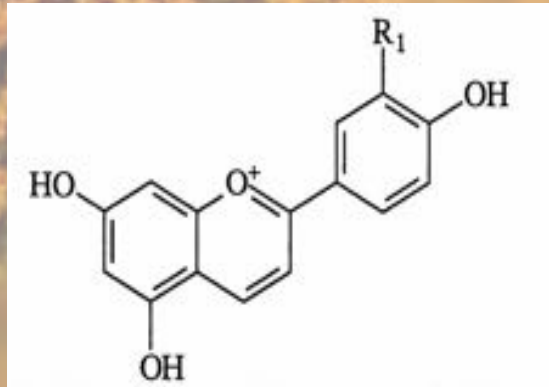
# ESVs Differentially Abundant Across Genotypes



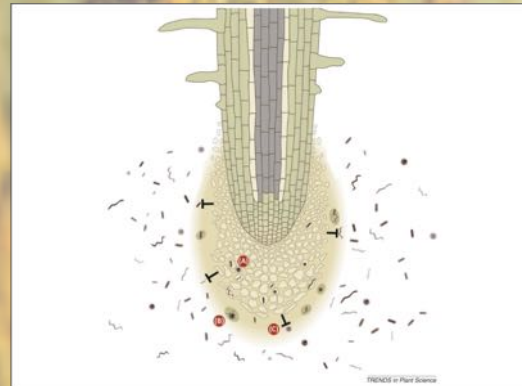


# What Does This Mean?

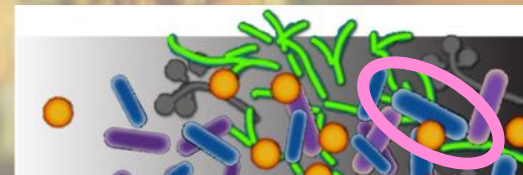
## Flavonoids



## Rhizosphere



## Microbes



**3-DA impacts are organism specific!**

# Next Steps:

- **Analyze fungal communities (ITS sequencing)**
- **Analyze communities post freeze (abiotic stress)**
- **Assess active microbes and metabolisms under sorghum genotypes (meta-transcriptomics)**
- **Isolate and screen rhizosphere microbes against 3-DAs**



# Acknowledgements

## **Coauthors:**

**Dr. Surinder Chopra**

**Dr. Mary Ann Bruns**

**Iffa Gaffoor**

**Dinakaran Elango**

**Jin Cui**

**Debamalya Chatterjee**



**Microbiome Center at Penn State University**

## **Chopra Lab:**

**Kameron Wittmeyer**

**Jillian Smothergill**

**Jeff Prusch**

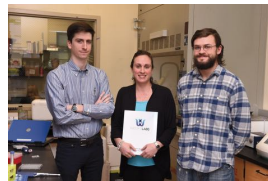
**Cullen Dixon**



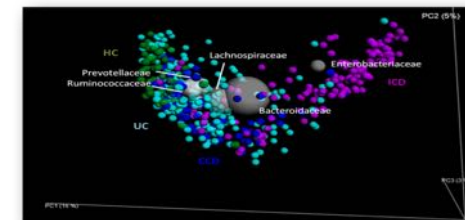
# Wright Labs, LLC

- Biotech startup in Huntingdon, PA that specializes in DNA/RNA sequencing and bioinformatic analysis.
  - 16S rRNA Analysis
  - ITS Analysis
  - Shotgun Metagenomics/Metatranscriptomics
- Cofounded by Dr. Regina Lamendella
  - Ph.D Department of Civil and Environmental Engineering and EPA Trainee, NSF GK-12 Fellow
  - Postdoc: Lawrence Berkeley National Lab (supervisors Janet Jansson and Terry Hazen)
  - Assistant Professor, Juniata College
    - NIH, NSF, DOE-funded labs

[www.wrightlabs.org](http://www.wrightlabs.org)



WRIGHTLABS





*Wright Labs is working with more than 60 different academic, governmental, and private institutions*





A photograph of a sorghum field with golden-brown seed heads. A semi-transparent grey rectangle is centered over the image, containing the text "Questions?".

Questions?