

# Gene by Environment Interactions between Hosts and their Microbiomes



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**Plant & Animal Genome 32**  
**14 January 2025**



**UNIVERSITY OF  
GEORGIA**

# Different microbiomes matter

## Obesity

*Ridaura et al 2013  
Science 341 (6150)*



## GHG emissions

*Smith et al 2022, Front Microbiol*



## Stress tolerance

*Xu et al 2018, PNAS 115 (18)*



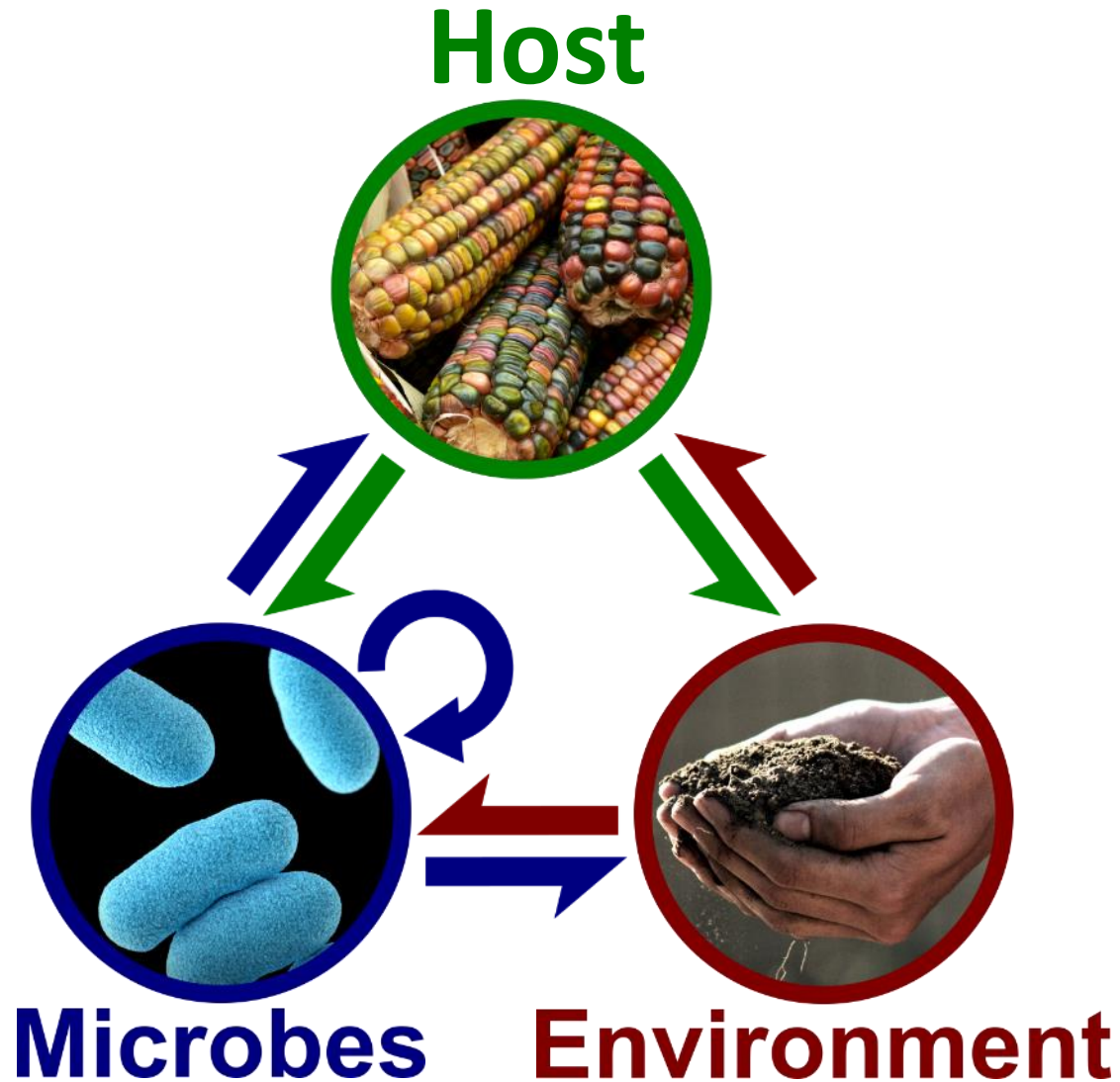
## Resilience

*Osburn et al. 2023  
ISME Comm 3(66)*



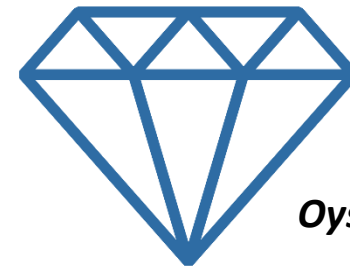
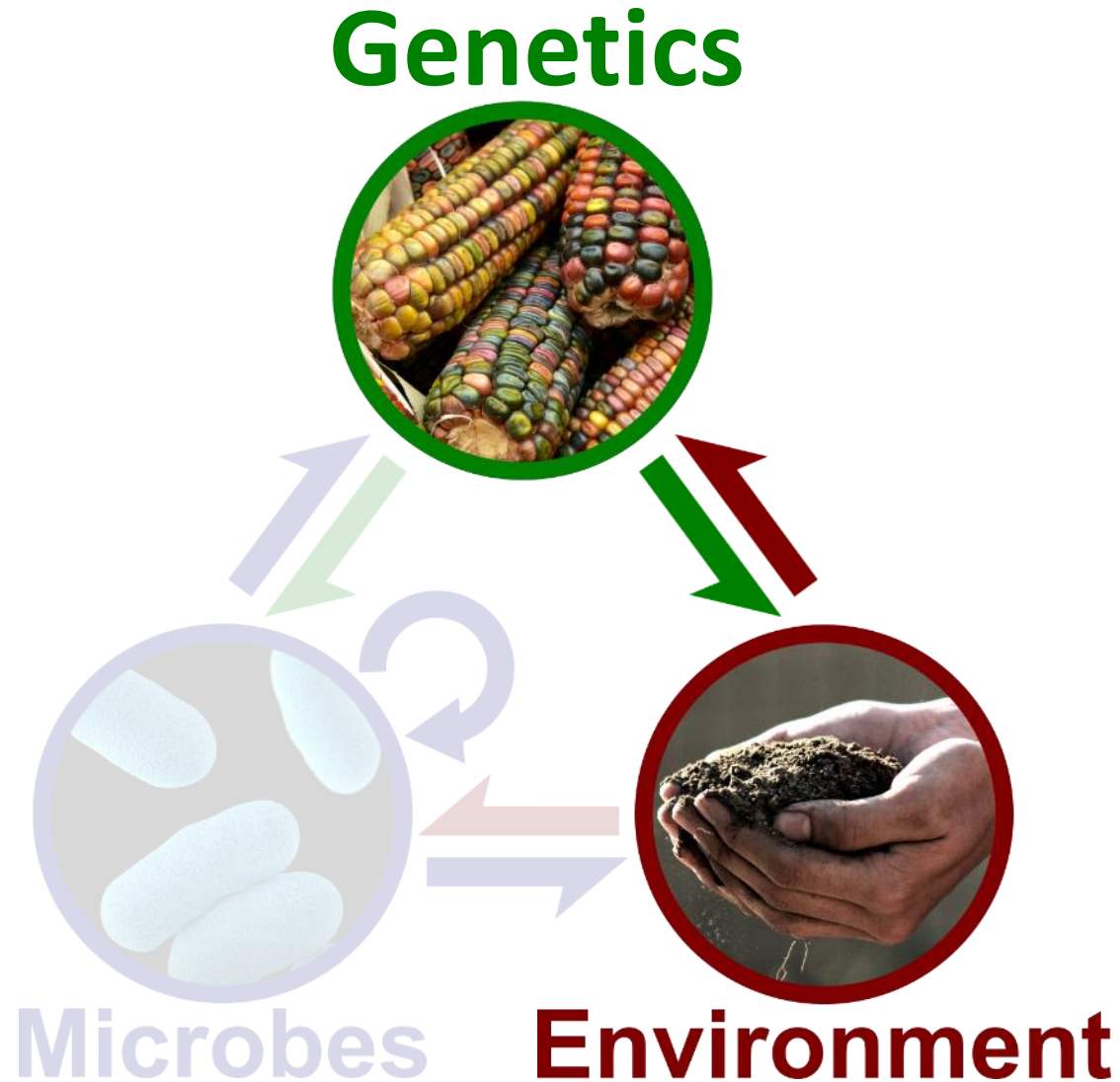


# Host-microbiome interactions are complex



**Everything affects  
everything else**

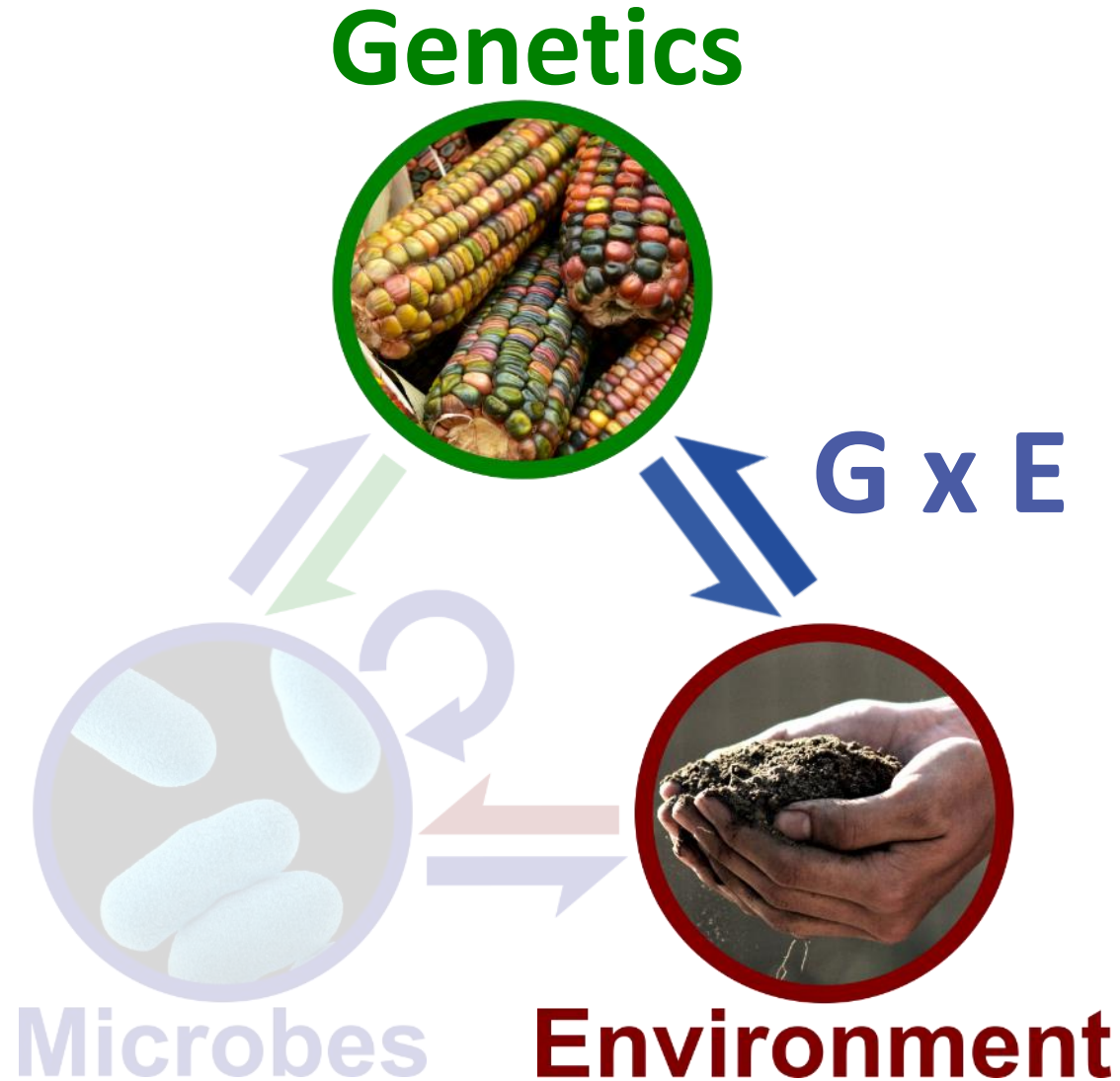
# Host-microbiome interactions are complex



**GEM Model**

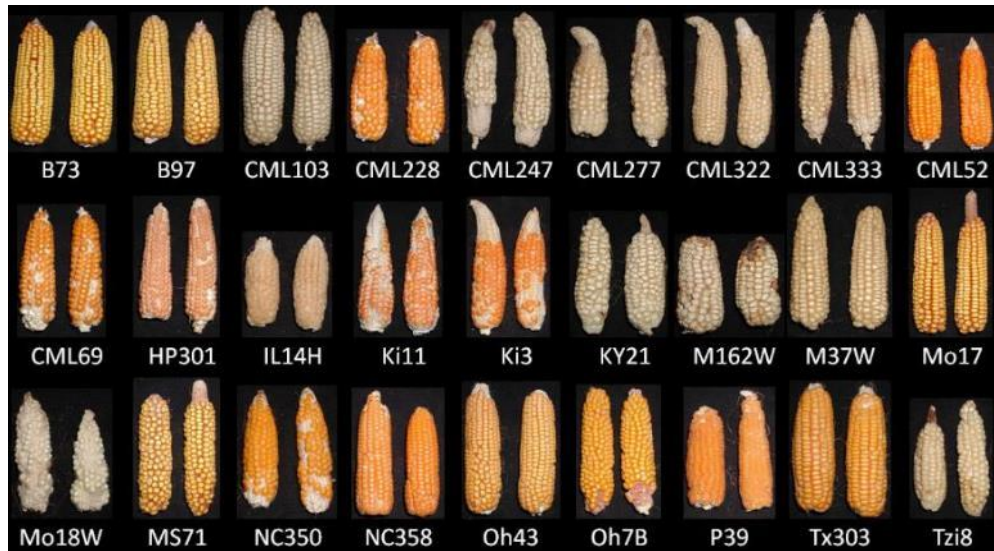
*Oyserman et al. 2021, Front Microbiol 11*

# Host-microbiome interactions are complex

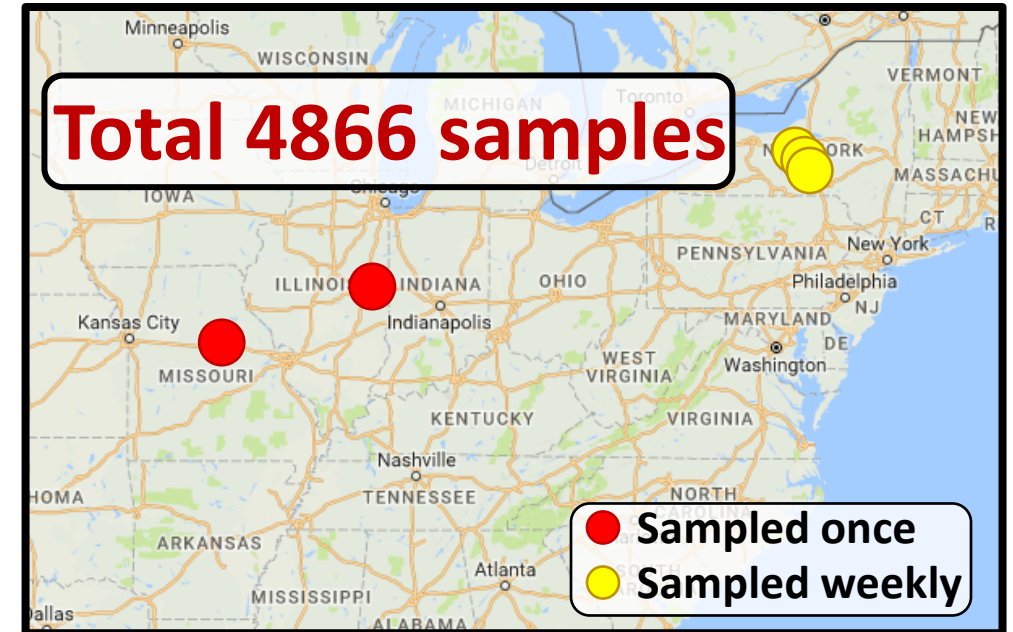
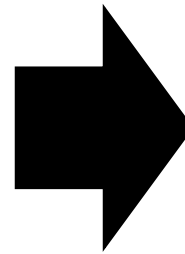


**How important  
are each of  
these?**

# Dissecting the maize rhizosphere



**Diverse Maize Collection**

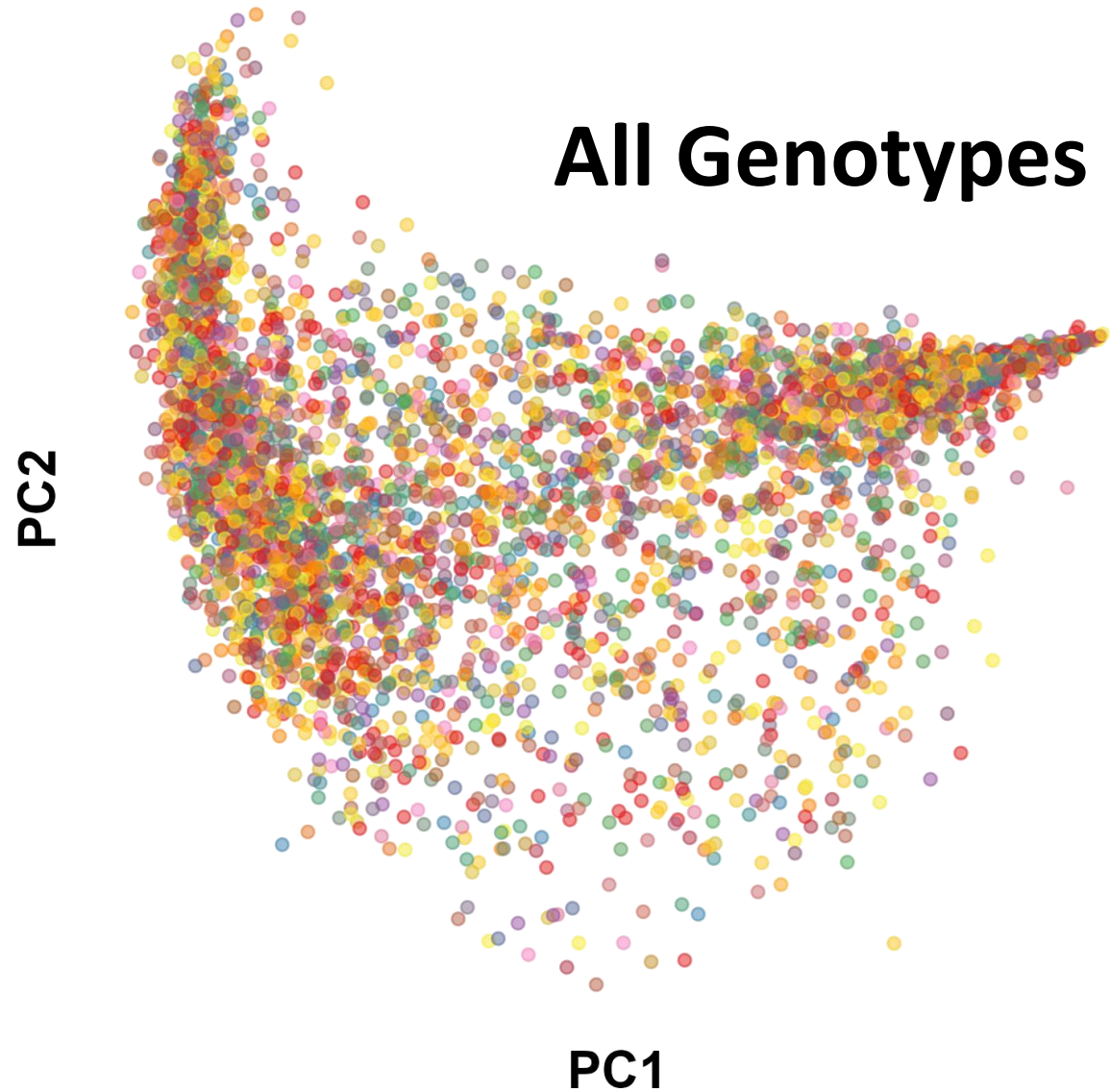


*Experimental design, sampling, and initial analyses by Ruth Ley, Aymé Spor, Jason Peiffer, & Tony Walters*

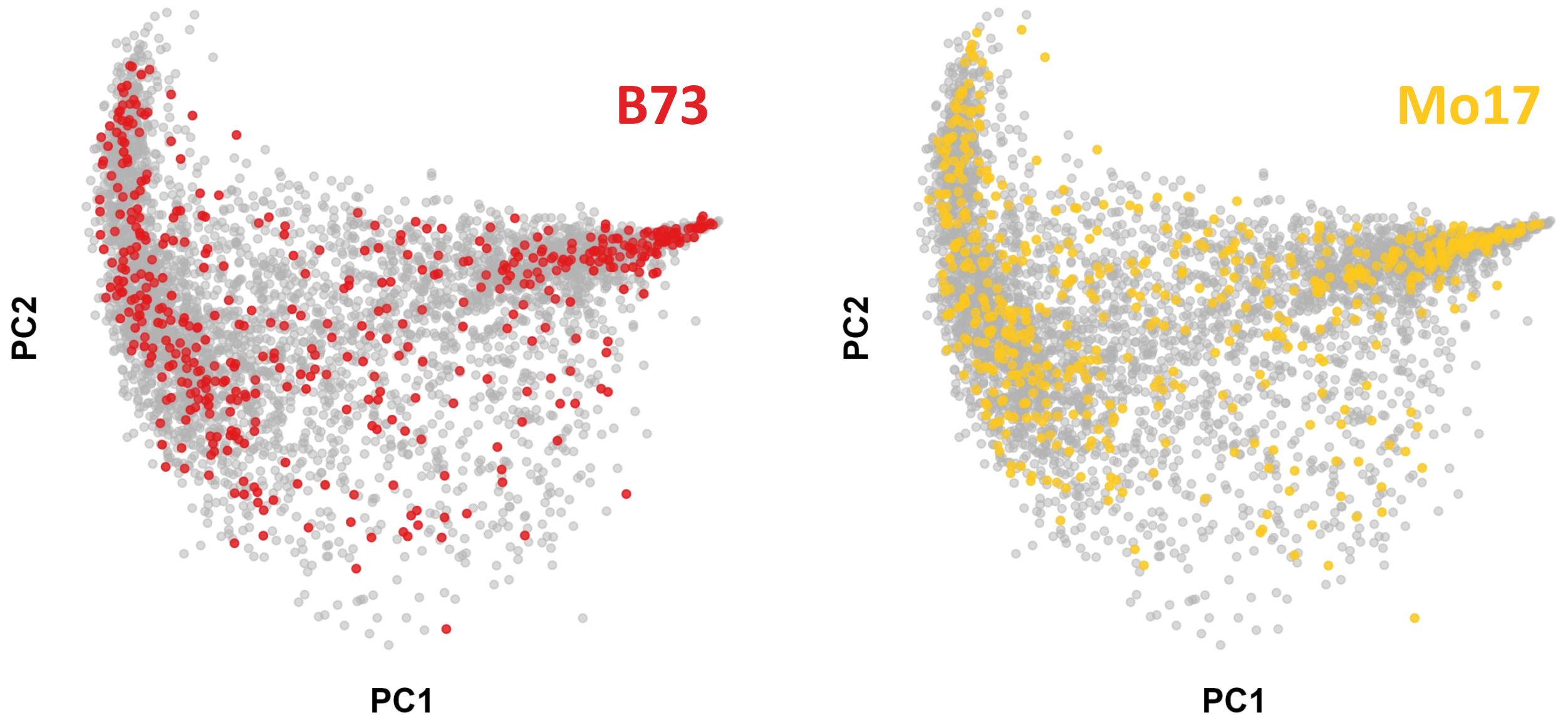




# Genetics has little effect on the rhizosphere



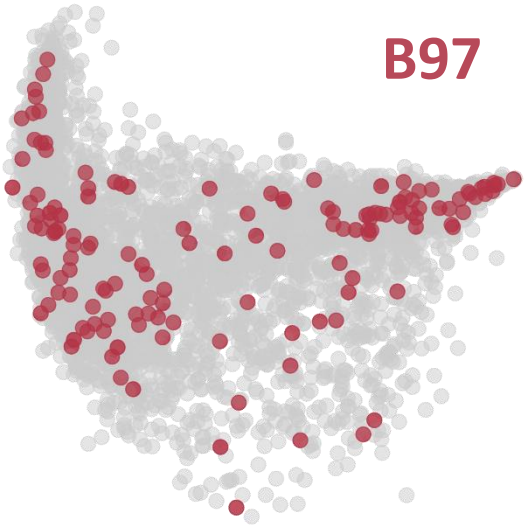
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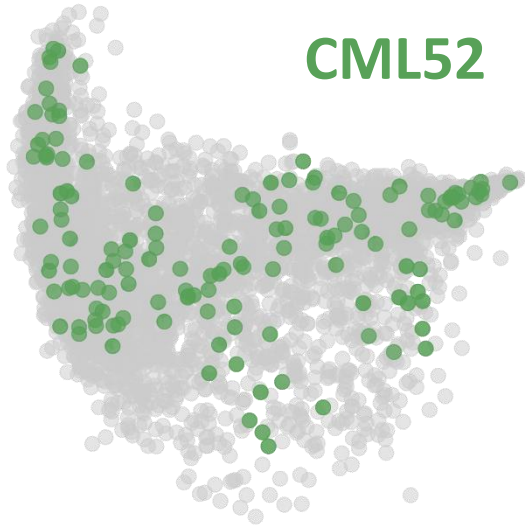


# Genetics has little effect on the rhizosphere

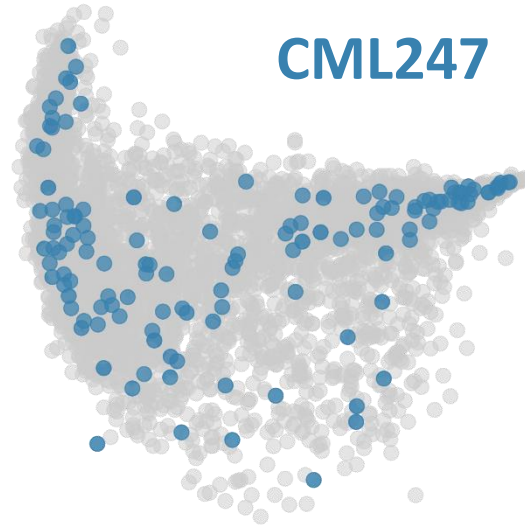
B97



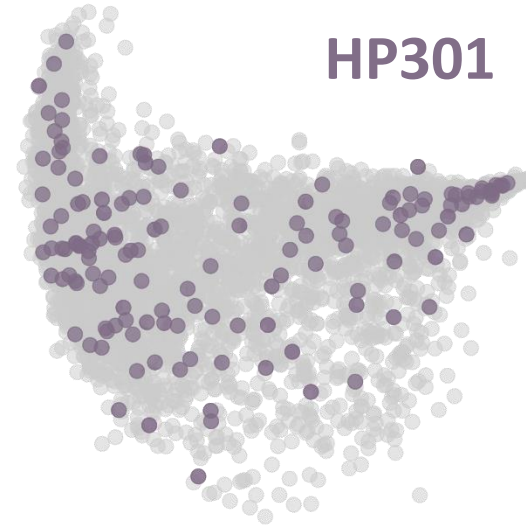
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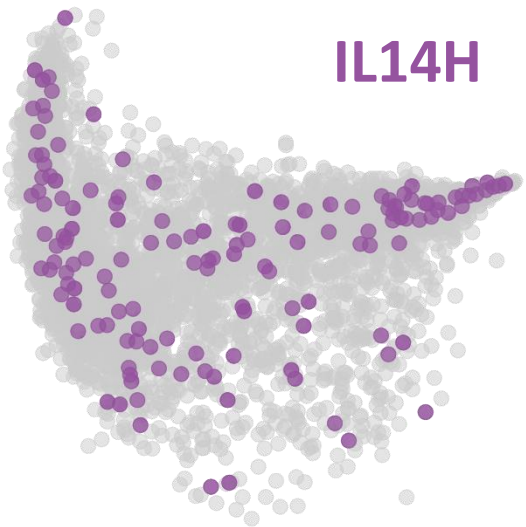
CML247



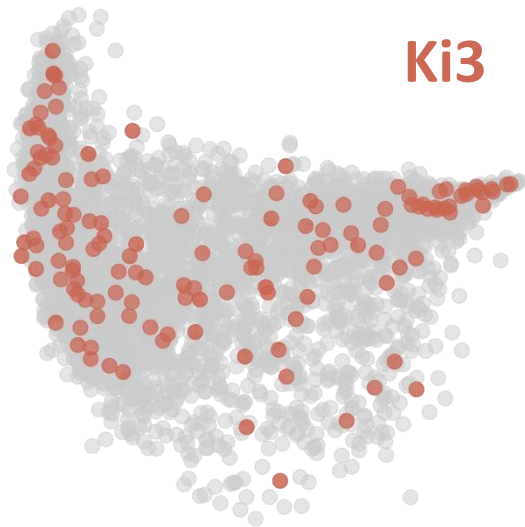
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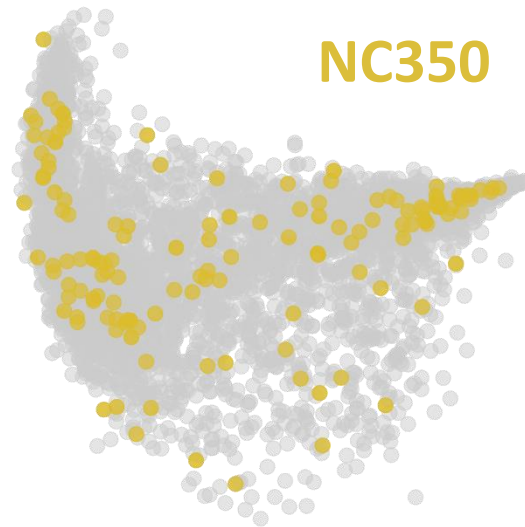
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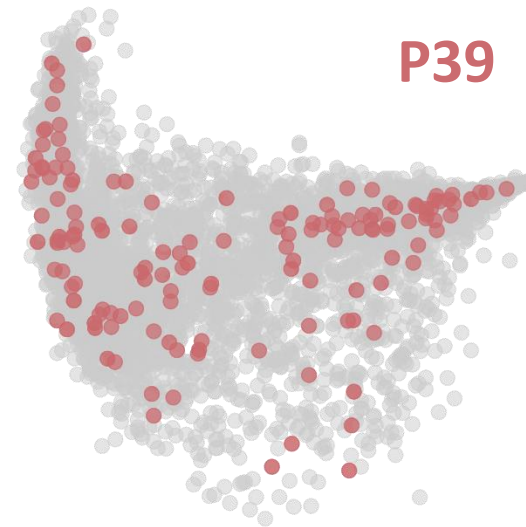
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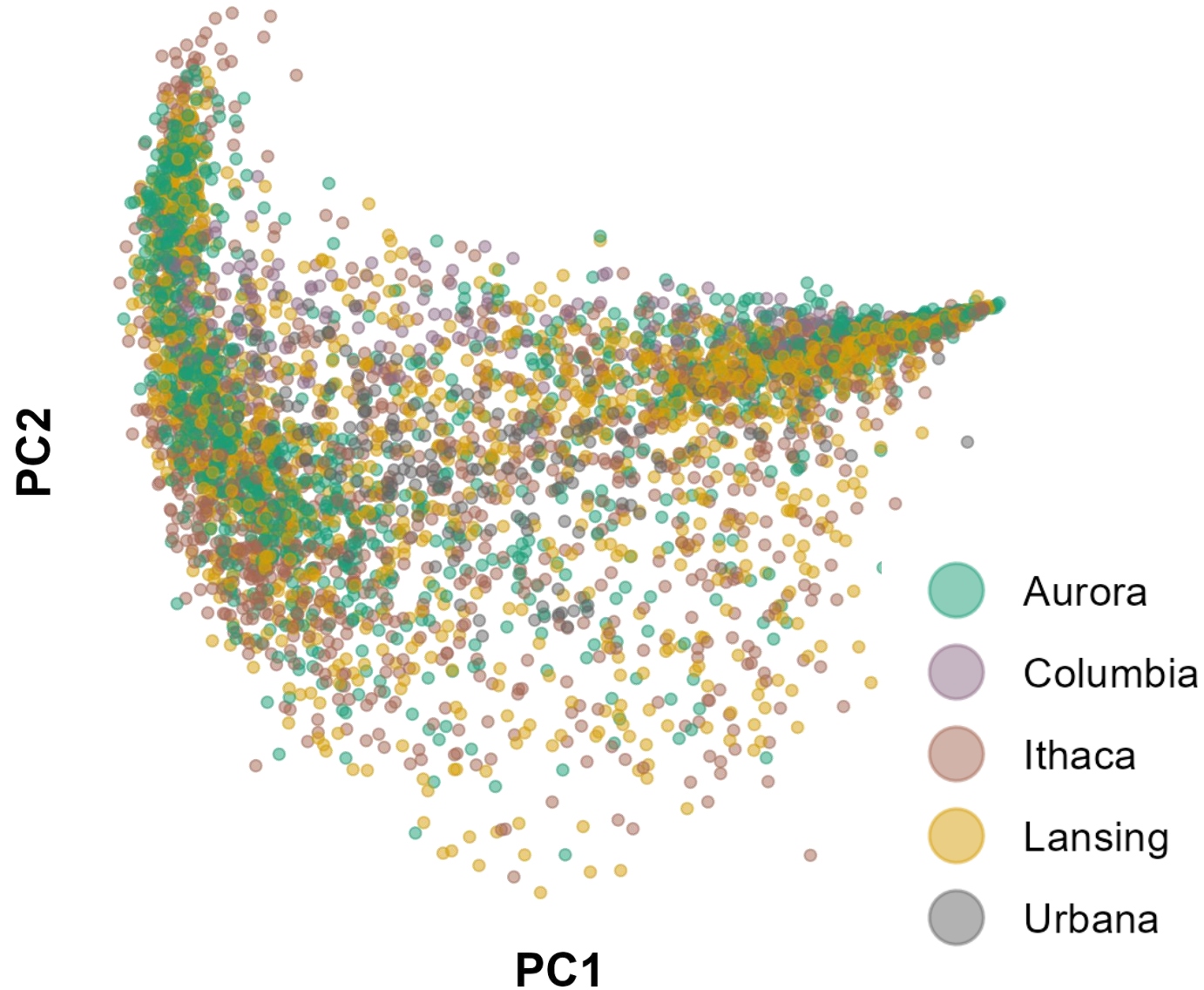
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P39

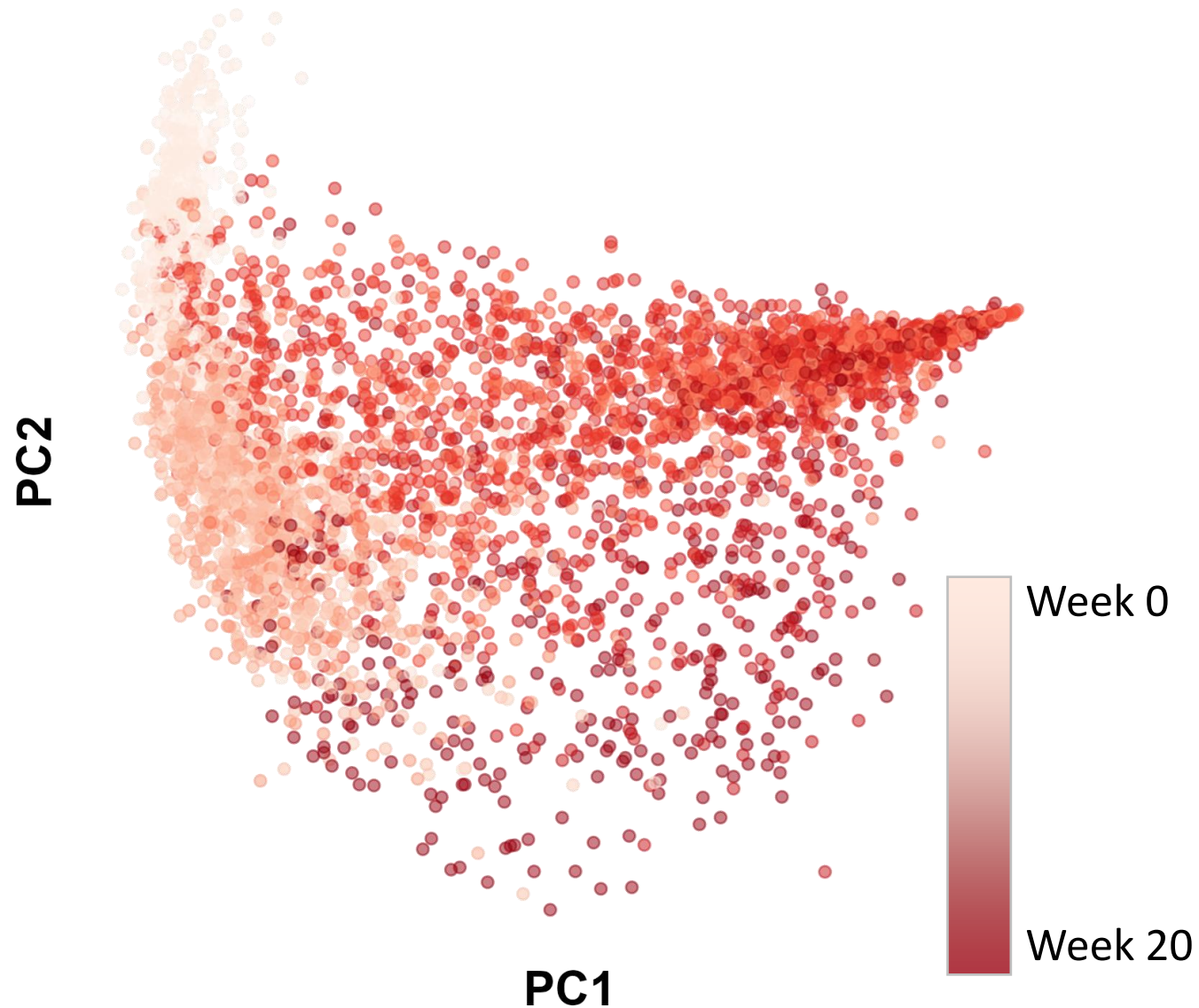


# Location has little effect on the rhizosphere



- No obvious patterns by location either

# Time effects dominate the maize rhizosphere

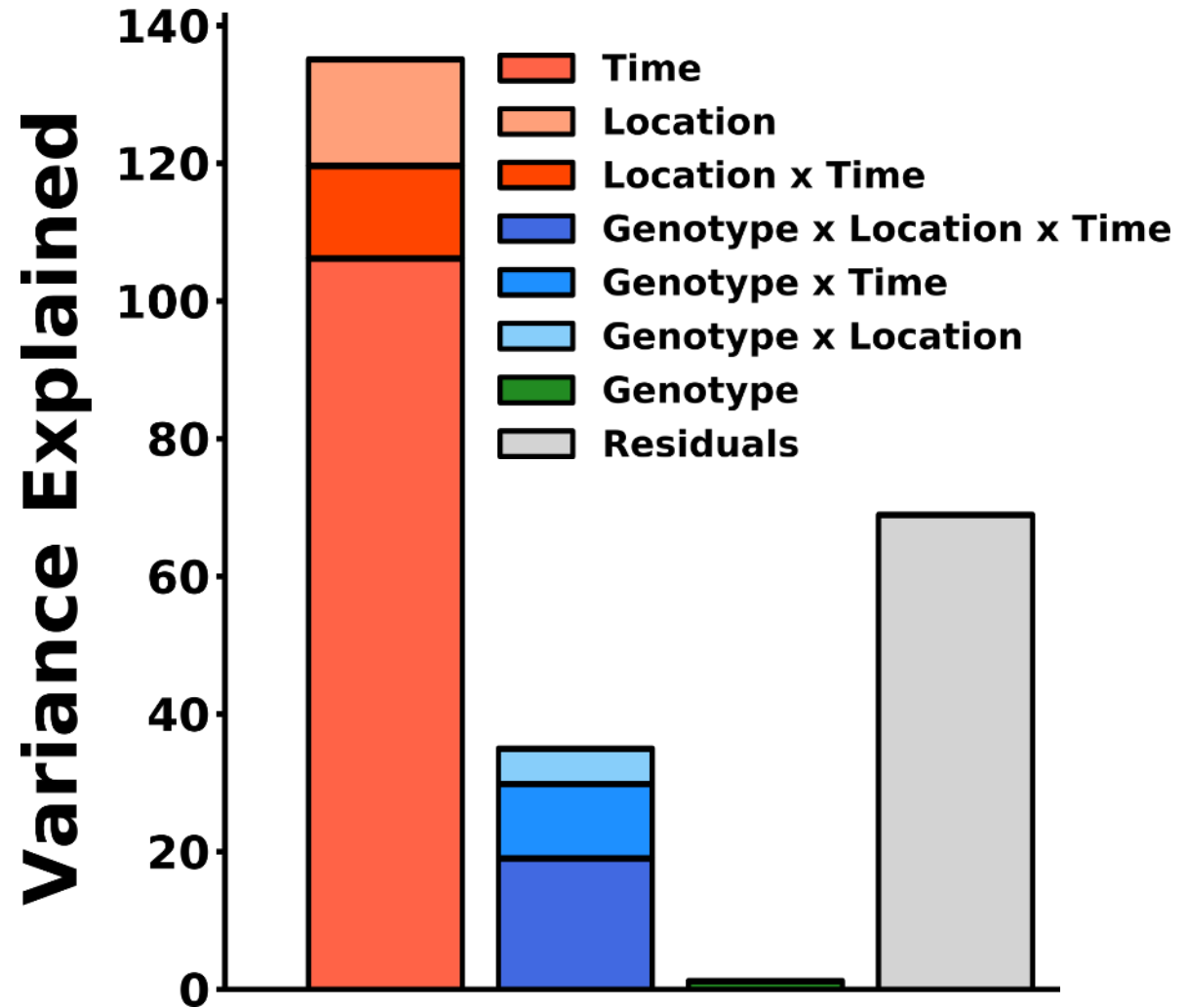


- No obvious patterns by location
- Time very significant



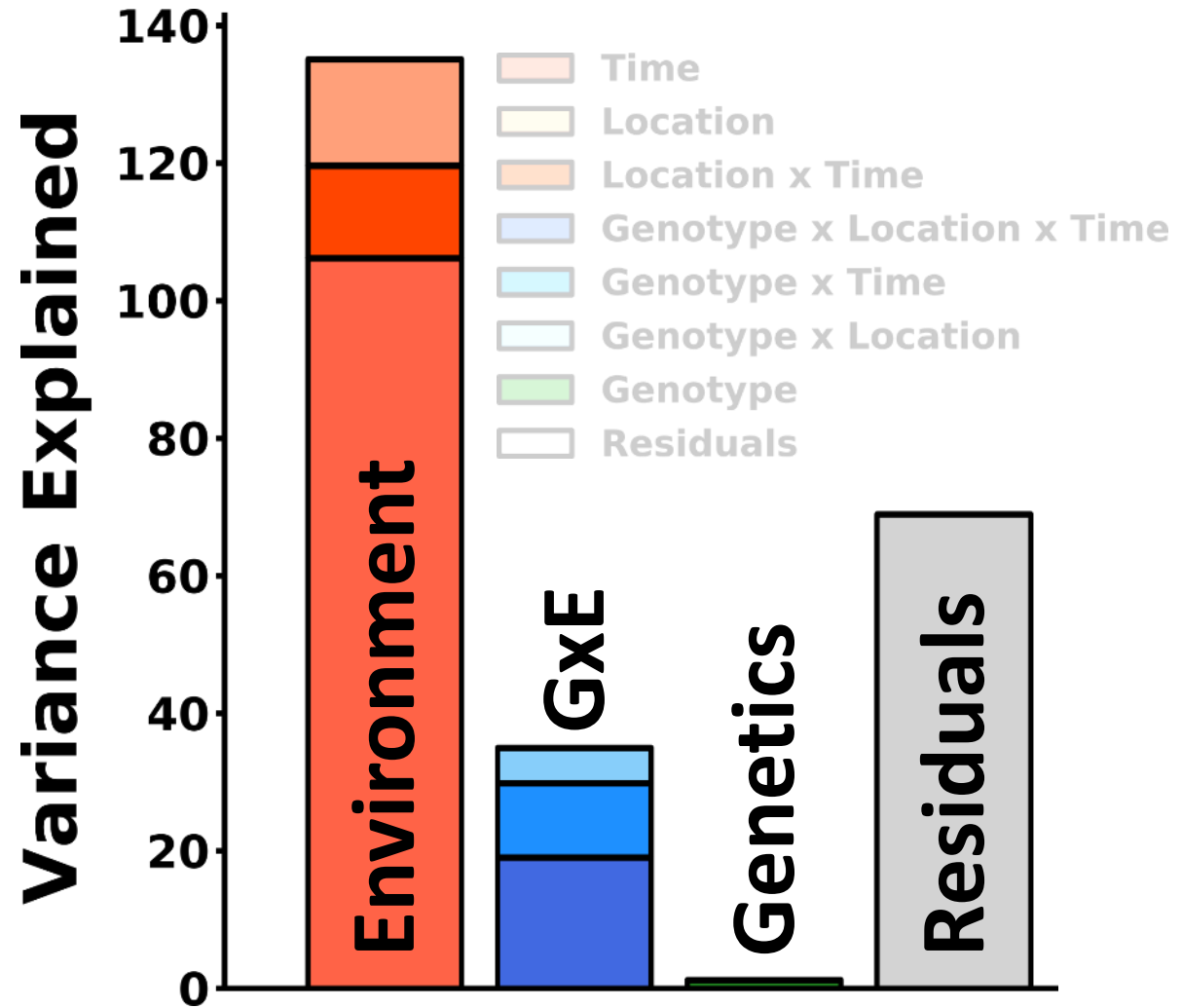
# Maize genetics plays a minor role in the rhizosphere

- Break effects apart by influence

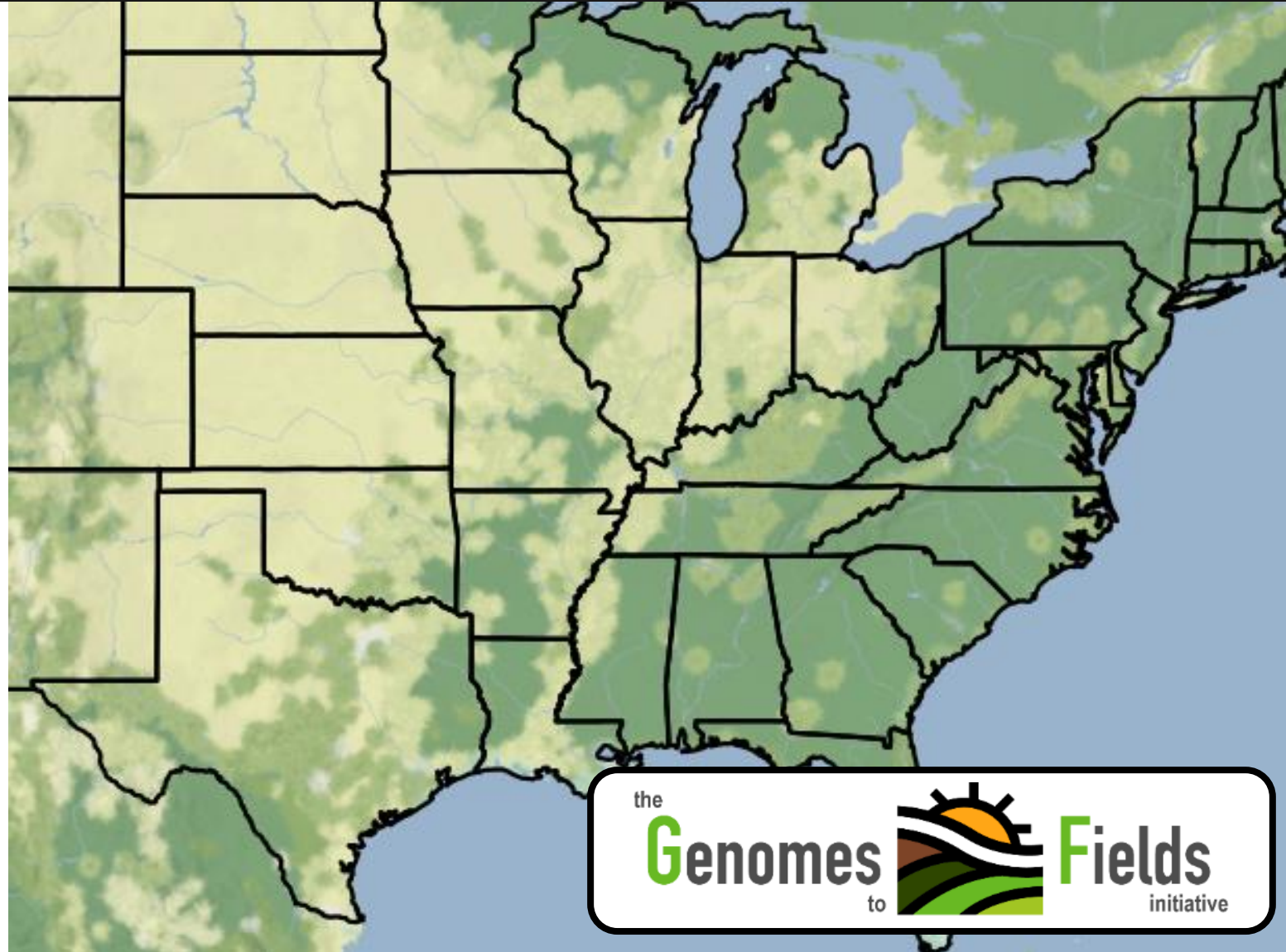


# Maize genetics plays a minor role in the rhizosphere

- Break effects apart by influence
- Environment dominates
- Almost zero genetics
  - But GxE moderately significant



# Sampling the Stalk Microbiome

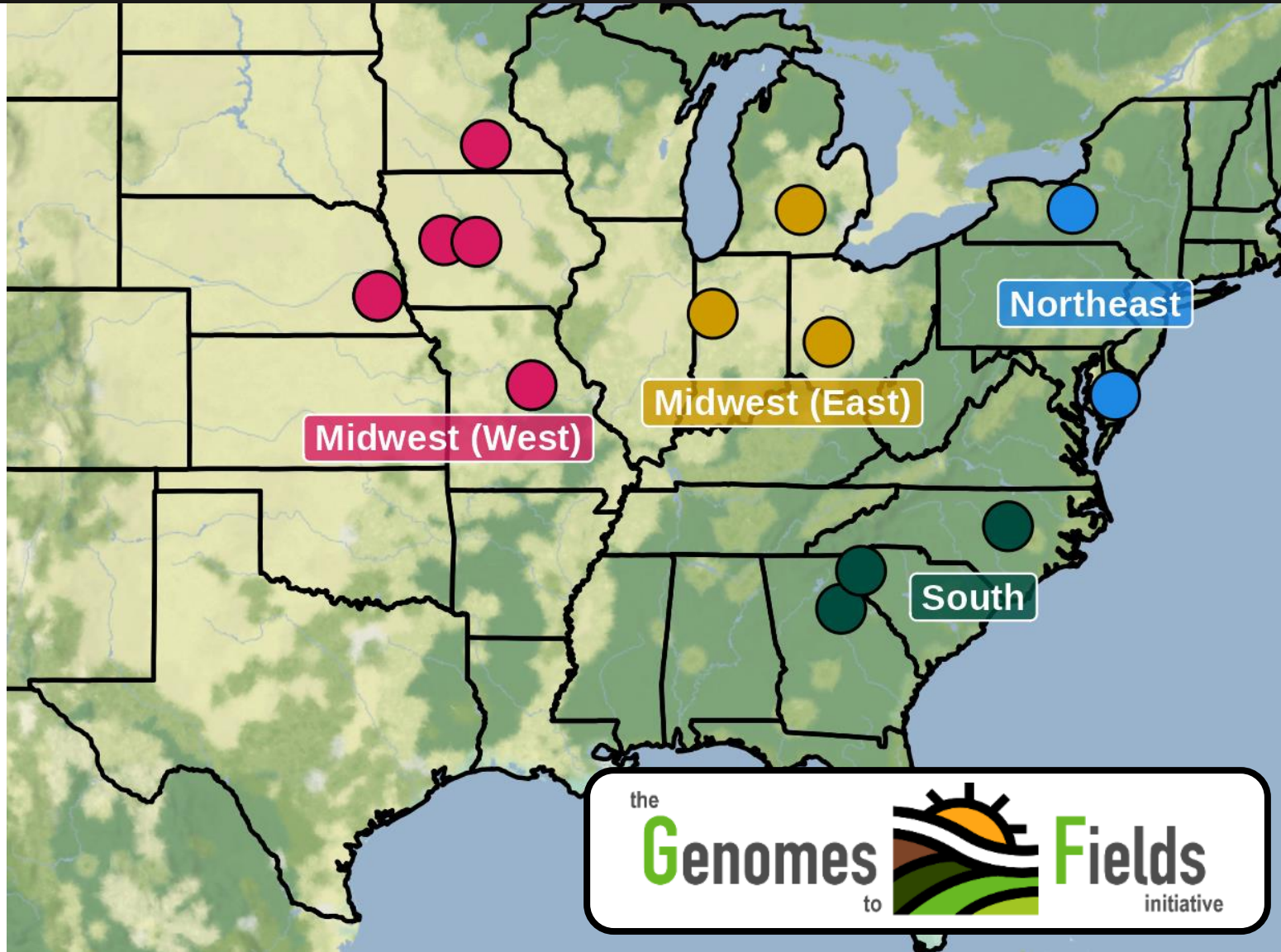




# Sampling the Stalk Microbiome

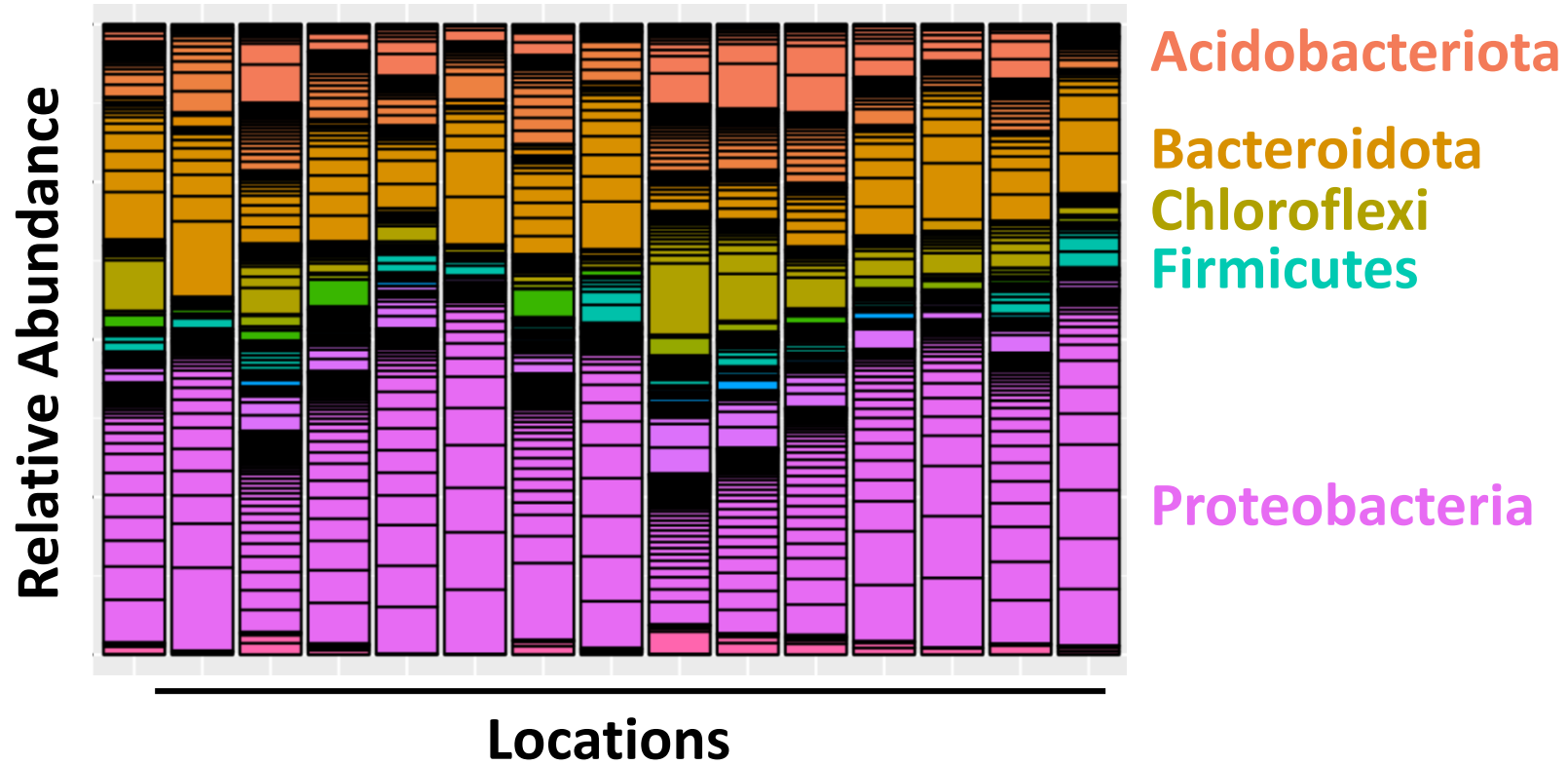


- Replicated genotypes across locations
  - 19 genotypes
  - $\geq 2$  reps in  $\geq 5$  locations



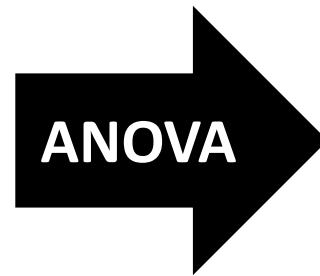
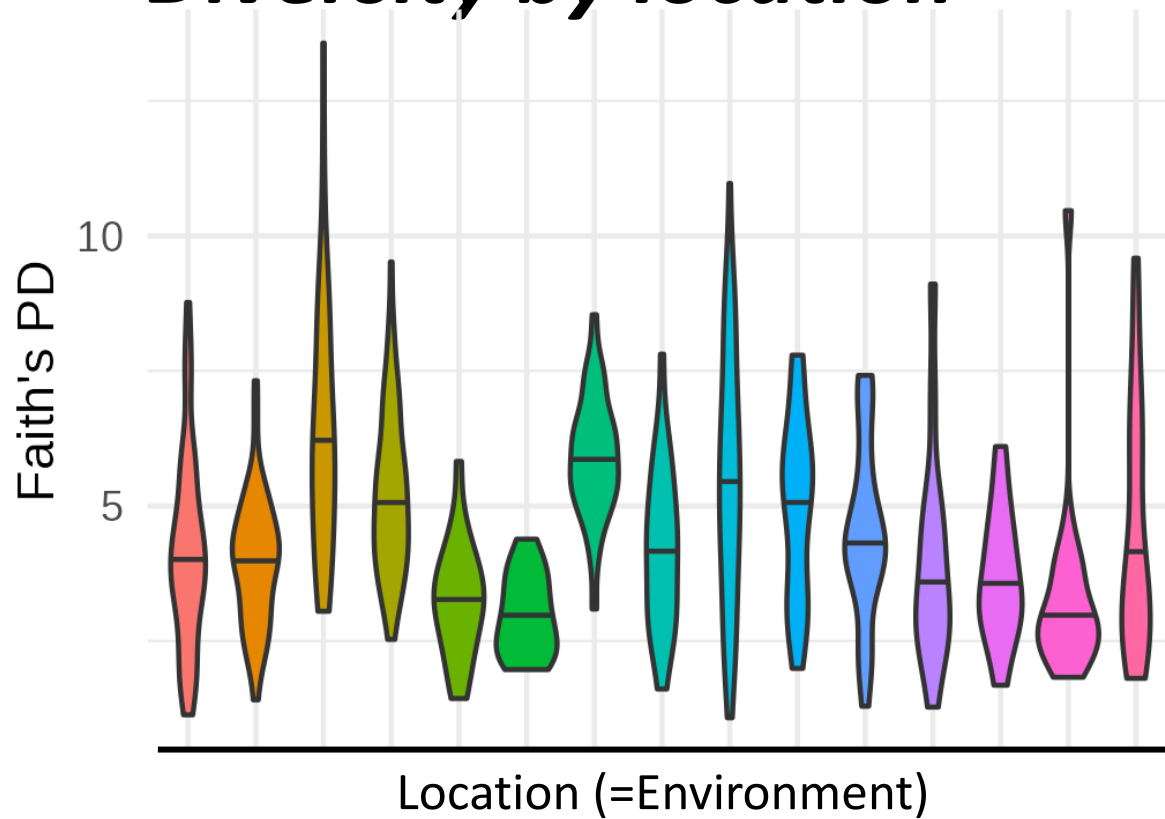
# Diversity varies by location

## *Bacterial Families*

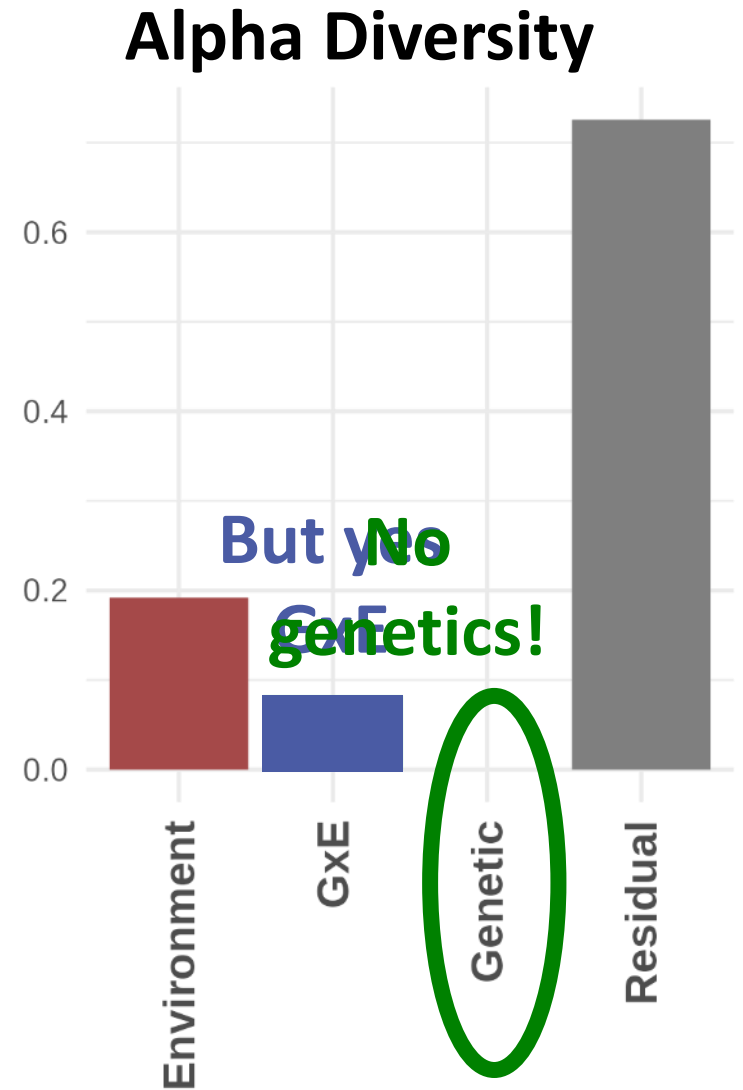


# Effect of plant genetics

## Diversity by location



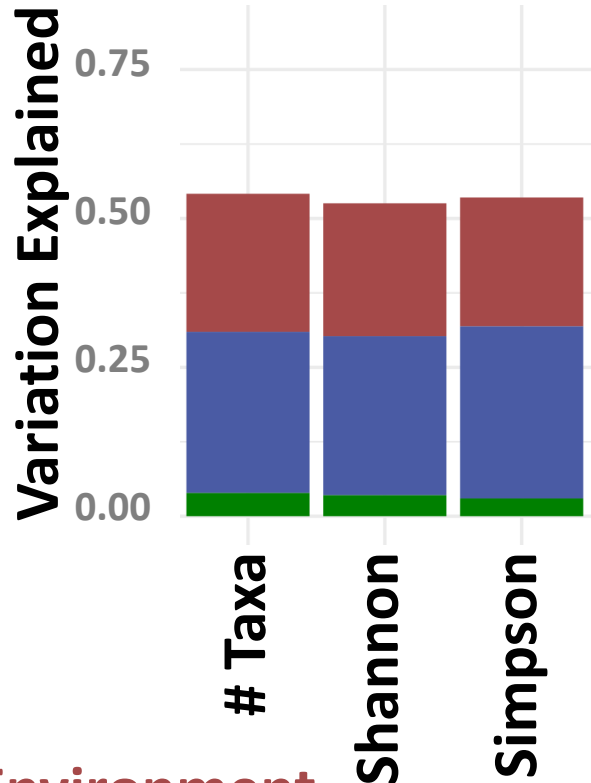
## Variance Explained



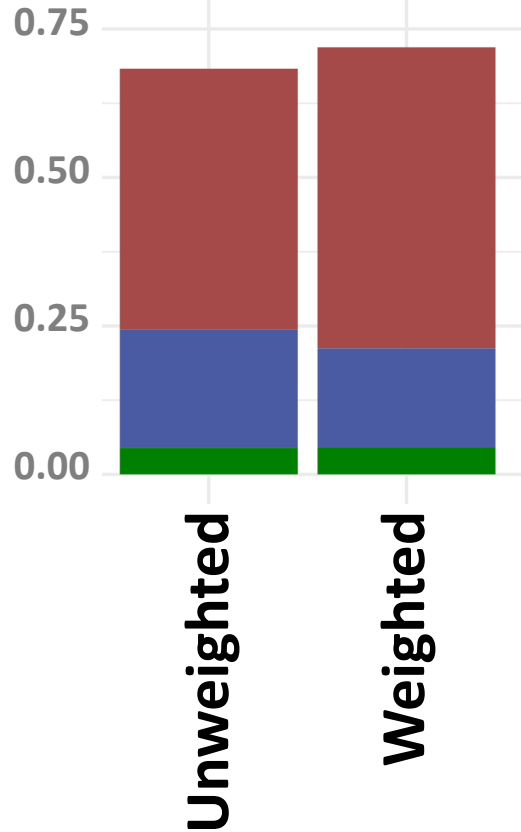


# GxE is consistently significant

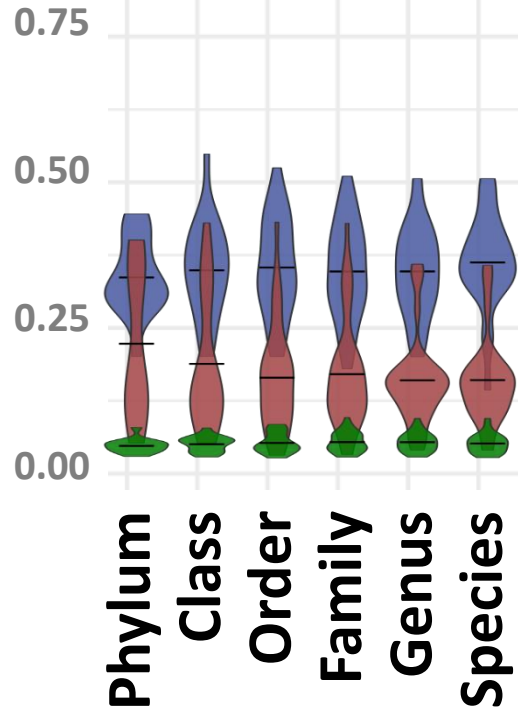
## Alpha Diversity



## Beta Diversity



## Taxonomy



**Genetics is minor**

**Environment explains 20-50%**

**GxE also 20-50%**

Environment  
GxE  
Genetics

# Other examples



*Univ. Wisconsin*

## Switchgrass

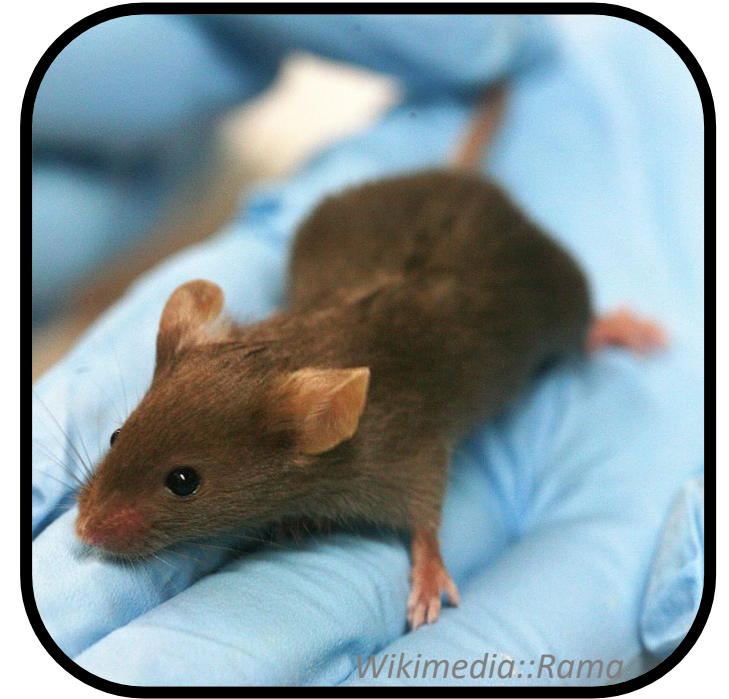
Edwards et al. 2023, Curr Biol 33



*Sanjay Achara*

## Drosophila

Staubach et al. 2013, PLoS ONE 8(8)

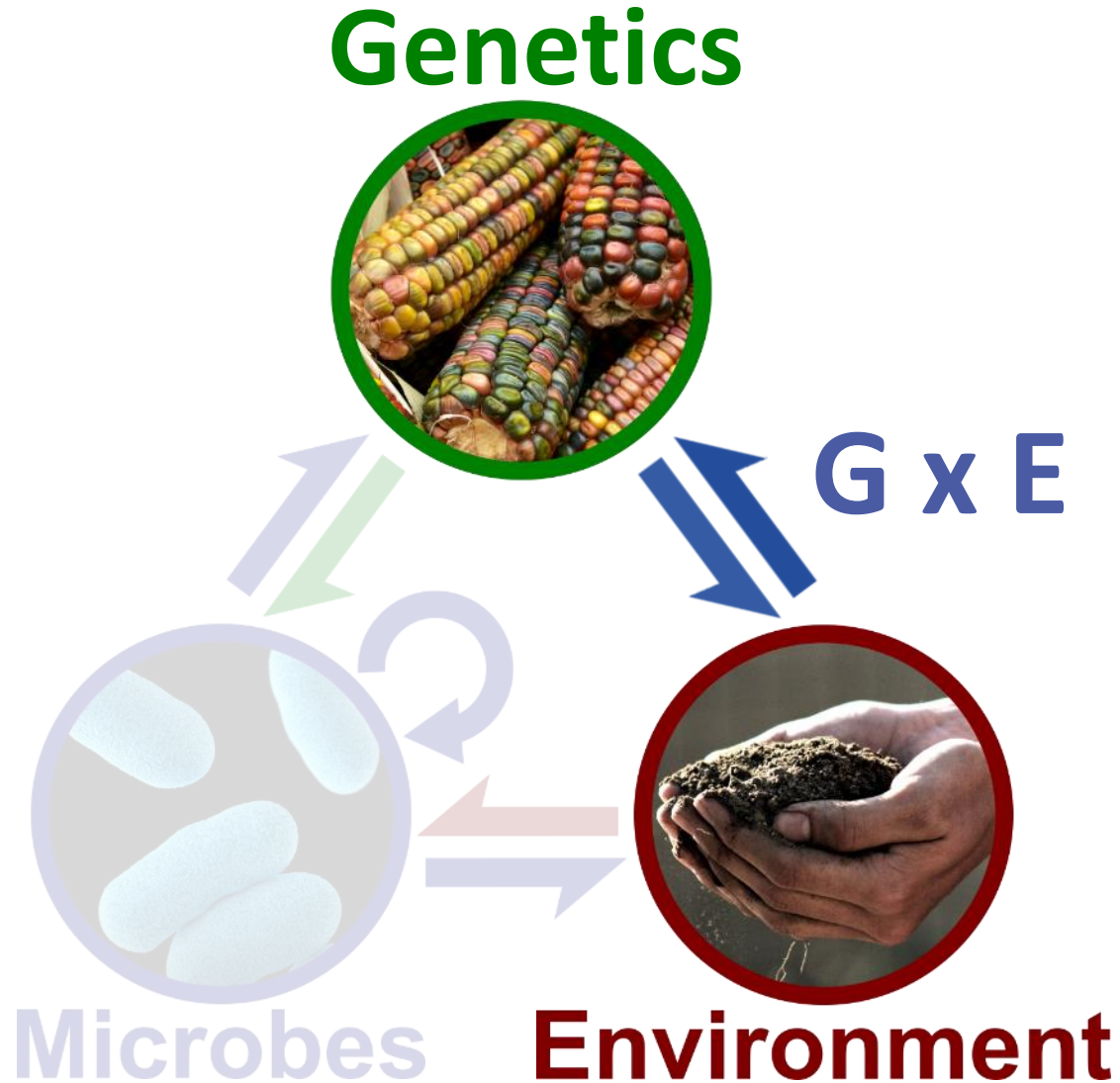


*Wikimedia::Rama*

## Huntington Disease

Gubert et al 2022, iScience 25

# So what does it all mean?



**Inconsistent across  
environments**

*but*

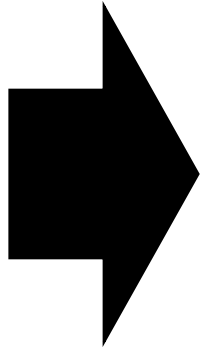
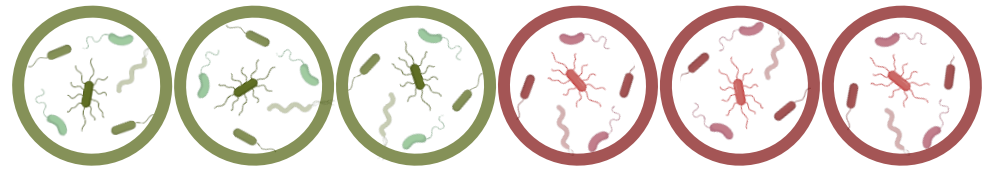
**Consistent within  
environments**

**Significant & consistent**

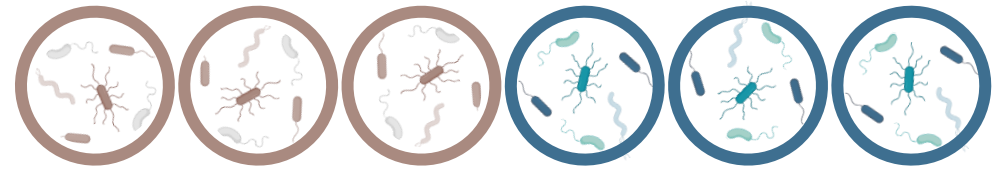


# GxE in practice

## Environment 1



## Environment 2





# Acknowledgements

## The Wallace Lab

- Hanxia Li
- Holly Griffis

## The Genomes to Fields Initiative

## Rhizosphere work

- Ruth E. Ley (Max Planck)
  - Ayme Spor
  - Tony Walters
- Jeff Dangl (UNC Chapel Hill)
- Susannah Tringe (JGI)

## Funding

- The University of Georgia
- The Foundation for Food and Agriculture Research
- DOE Joint Genome Institute
- Genomes to Fields funders
  - The Georgia Agricultural Commodity Commission for Corn
  - Iowa Corn Growers Association
  - And many other state agencies



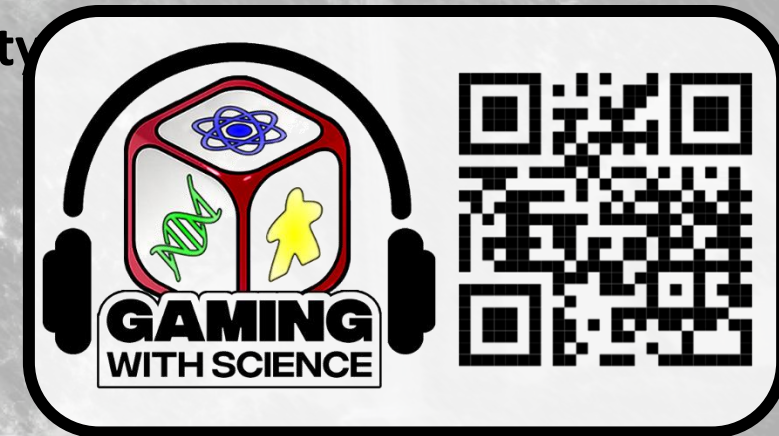
**Renato Santos**

P093: Plant-Microbe  
Coexpression



**Darrian  
Talamantes**

P398: Tall Fescue  
Symbiosis & Stress



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**JGI**



the  
**Genomes**  
to



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initiative



TheWallaceLab