UNDERSTANDING AND MANIPULATING SOIL MICROBIAL COMMUNITIES IN FLORIDA VEGETABLE PRODUCTION

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Soil & Water SCIENCES

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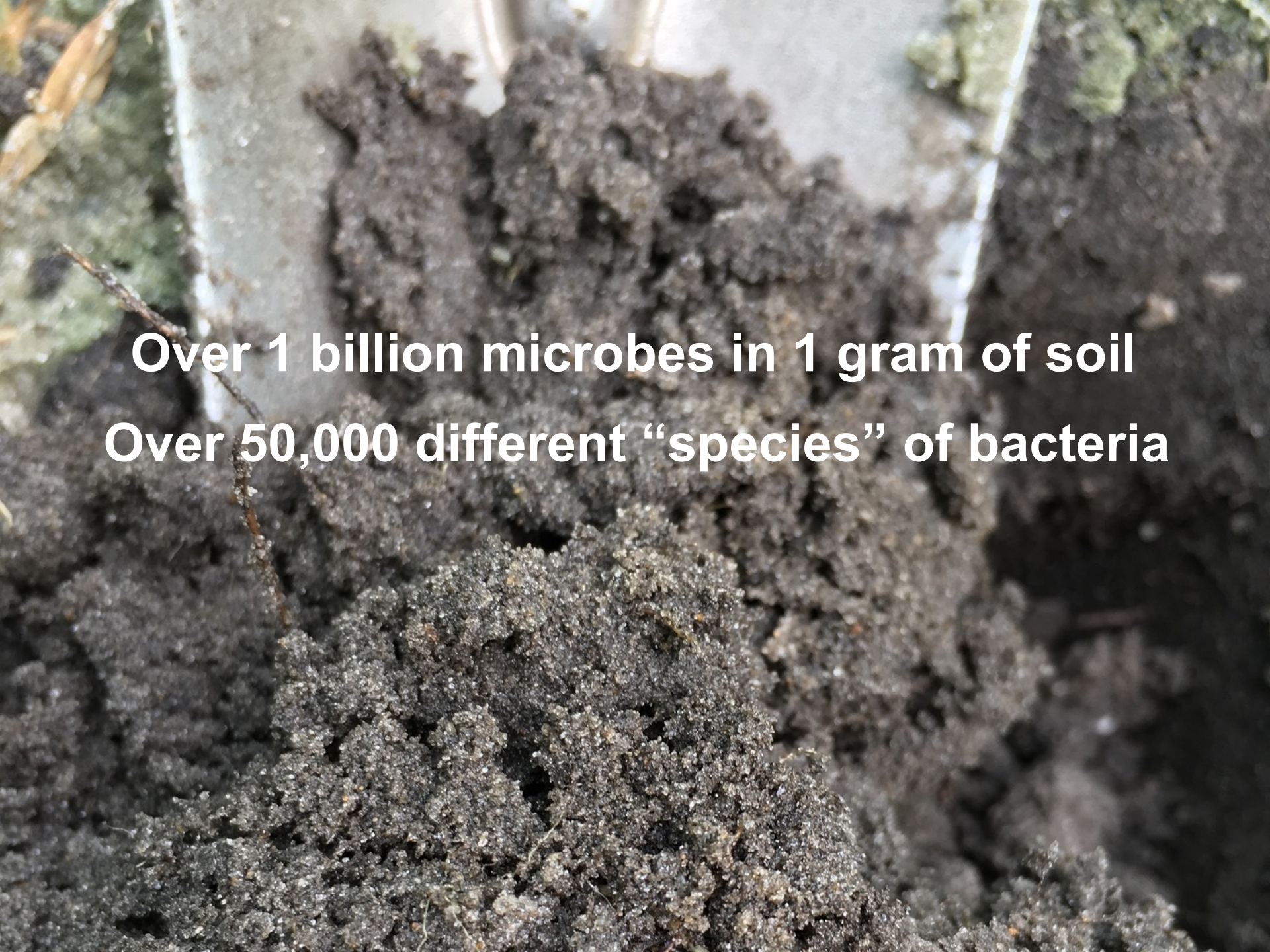
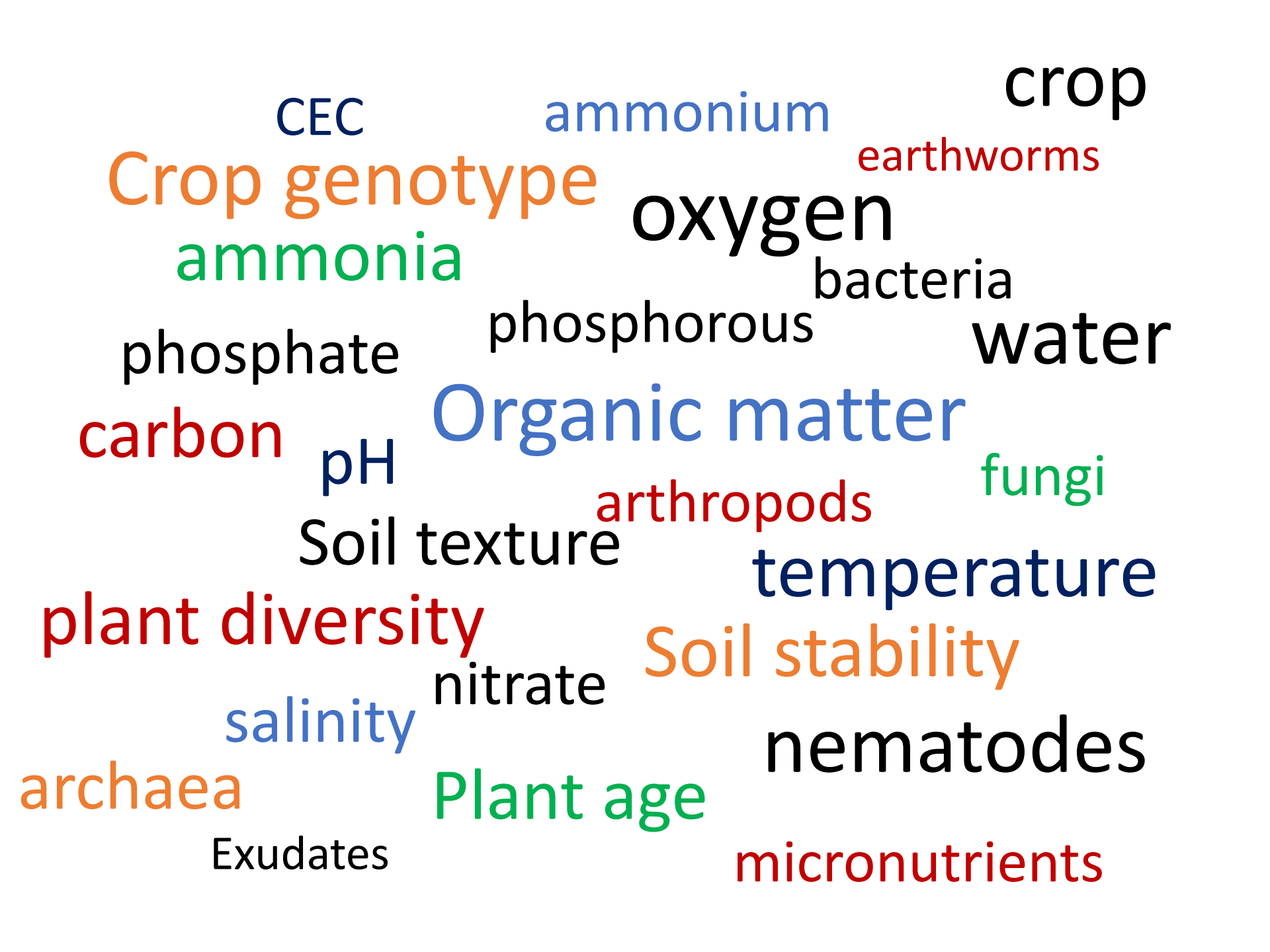
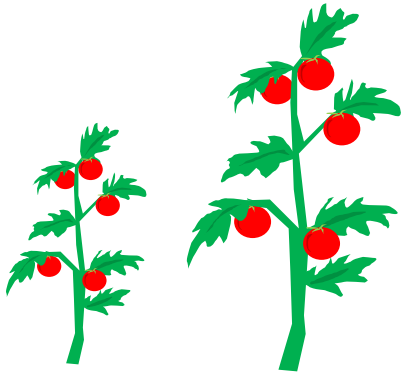
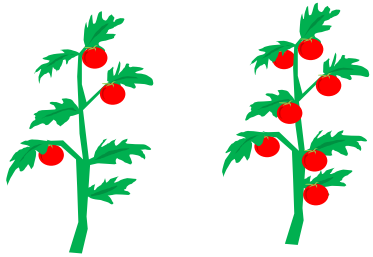

Over 1 billion microbes in 1 gram of soil
Over 50,000 different “species” of bacteria


crop
CEC
ammonium
earthworms
Crop genotype
oxygen
ammonia
bacteria
phosphorous
water
phosphate
Organic matter
carbon
pH
fungi
arthropods
Soil texture
temperature
plant diversity
Soil stability
nitrate
salinity
nematodes
archaea
Plant age
Exudates
micronutrients

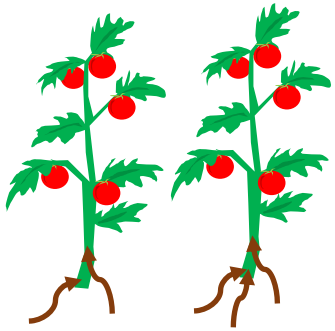
Increase plant growth



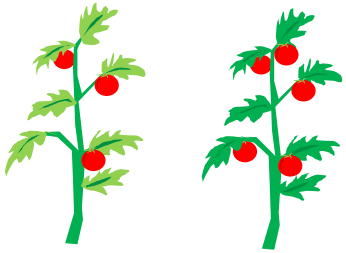
Increase yield



Increase plant nutrient uptake



Reduce disease



How can we use soil microbiology to help vegetable crops?

1. Indirect method: change the **environment**

2. Direct method: change the **community**

1. Indirect method: change the **environment**

- Add a ”food” source for microbes: carbon
  - Compost
  - Plant material - cover crops
  - Develop soil organic matter (SOM)
- Disturb the soil less often
- Keep roots within the soil

1. Indirect method: change the **environment**

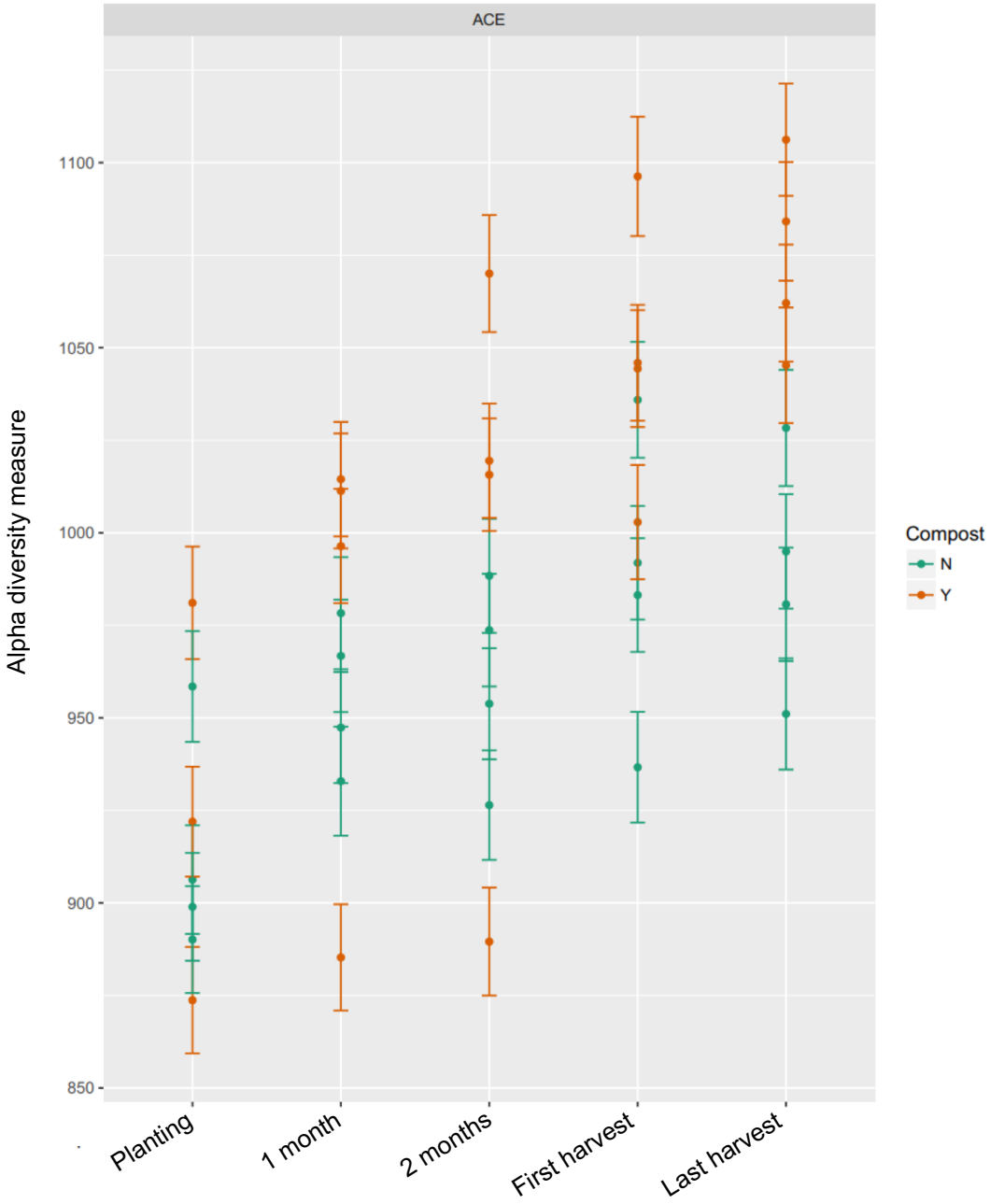
Benefits

- Encourage native microbes to grow – likely beneficial microbes already in soil!
- Increase soil microbial diversity
  - Increase nutrient cycling
  - More competition for resources

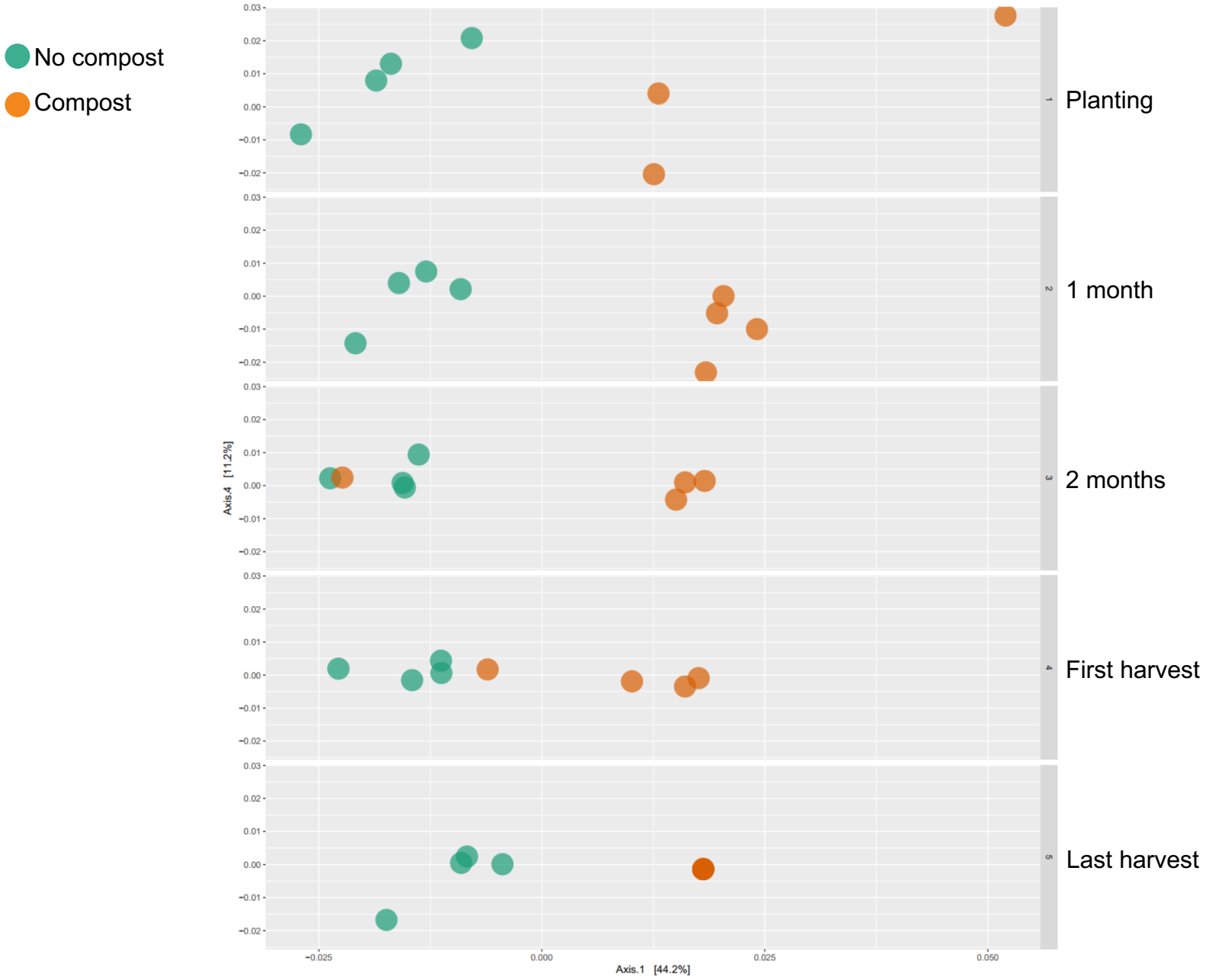
Difficulties

- Soil organic matter (SOM) is very low in Florida
- Increasing SOM takes TIME – results may not occur after only 1 year
- Native soil microbial community not well characterized – and likely unique for each location

Compost addition increased bacterial diversity



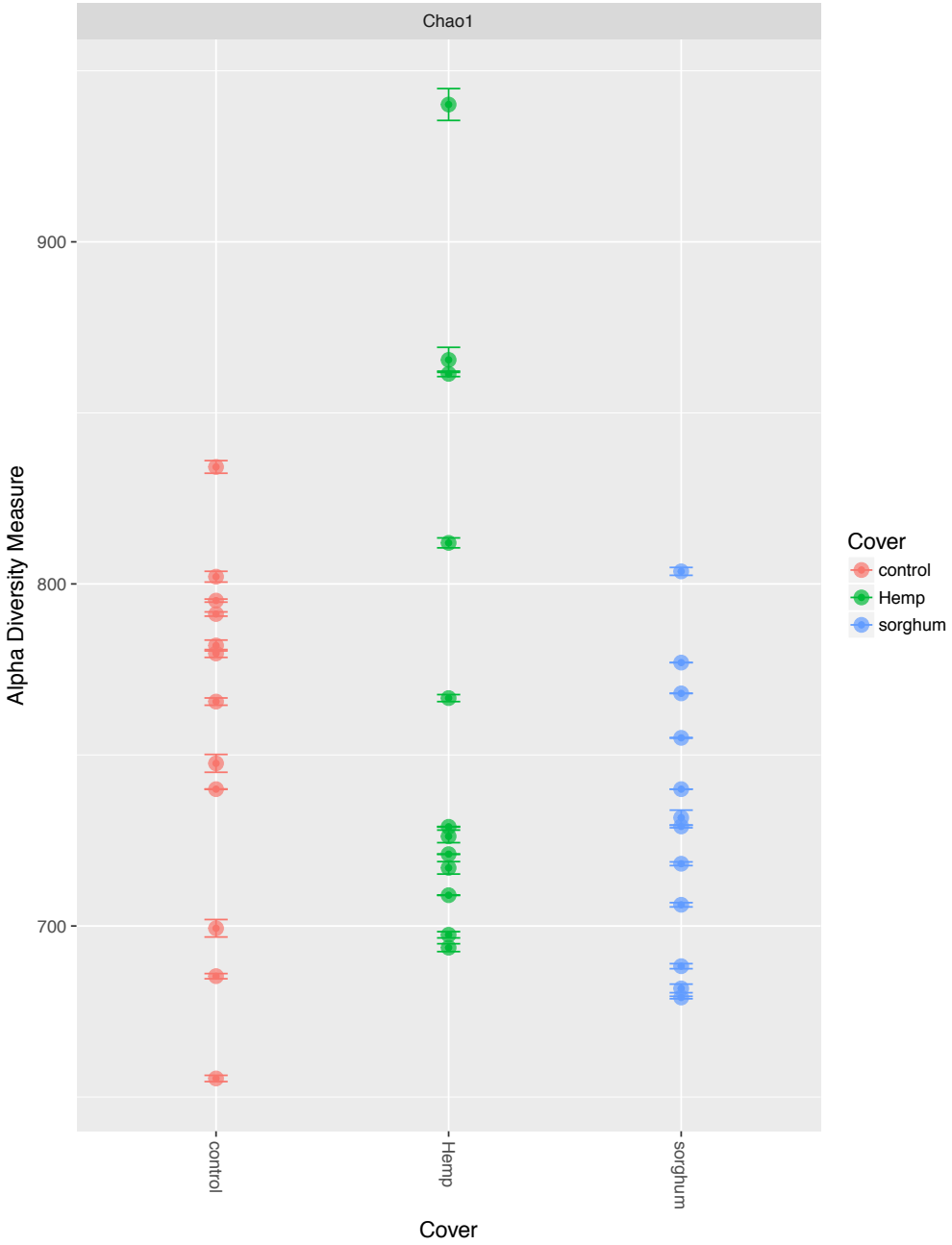
Compost addition impacted bacterial community composition



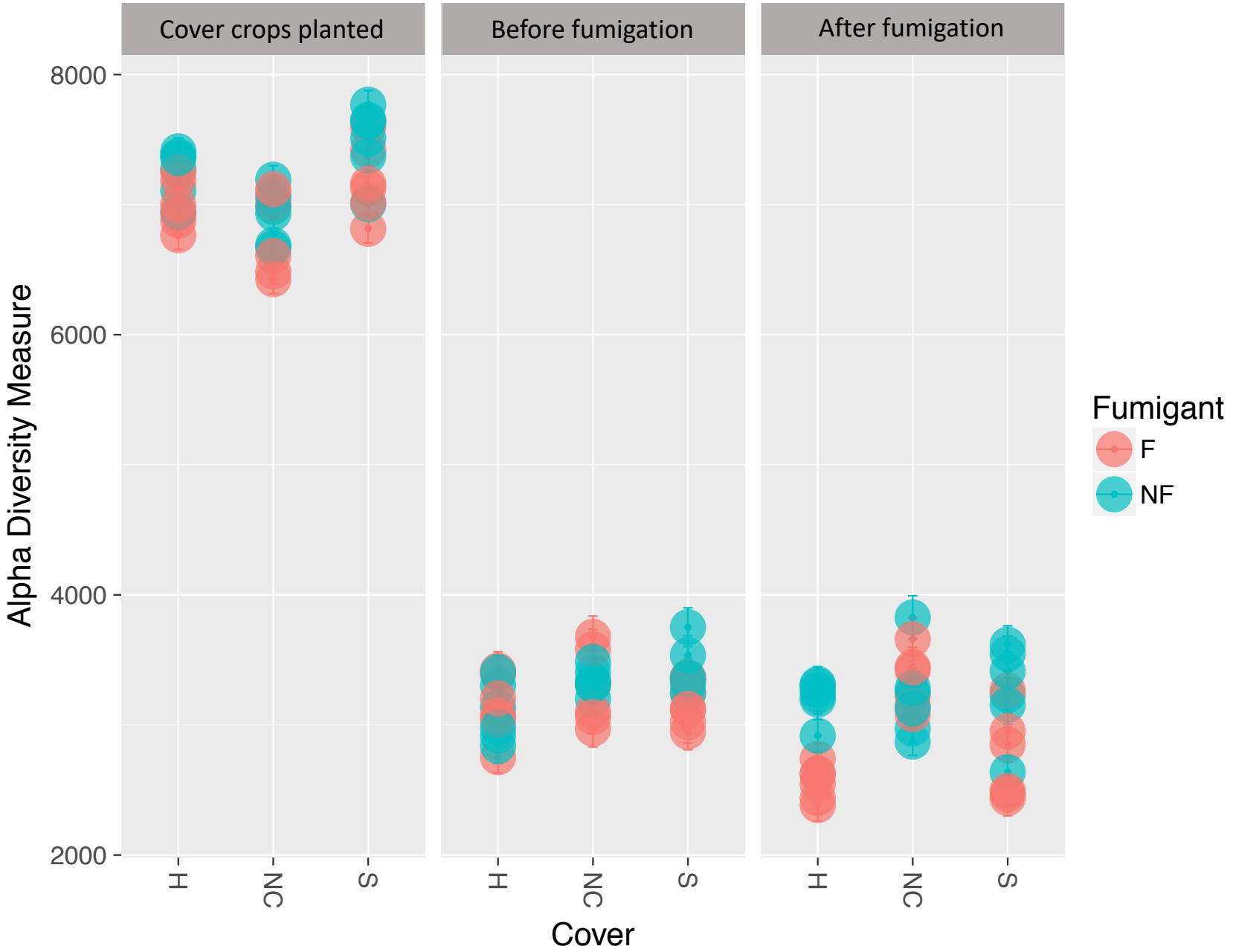
1. Indirect method: change the **environment: cover crops**

- Two cover crops planted: sunn hemp and sorghum
- Compared to a field without cover crops

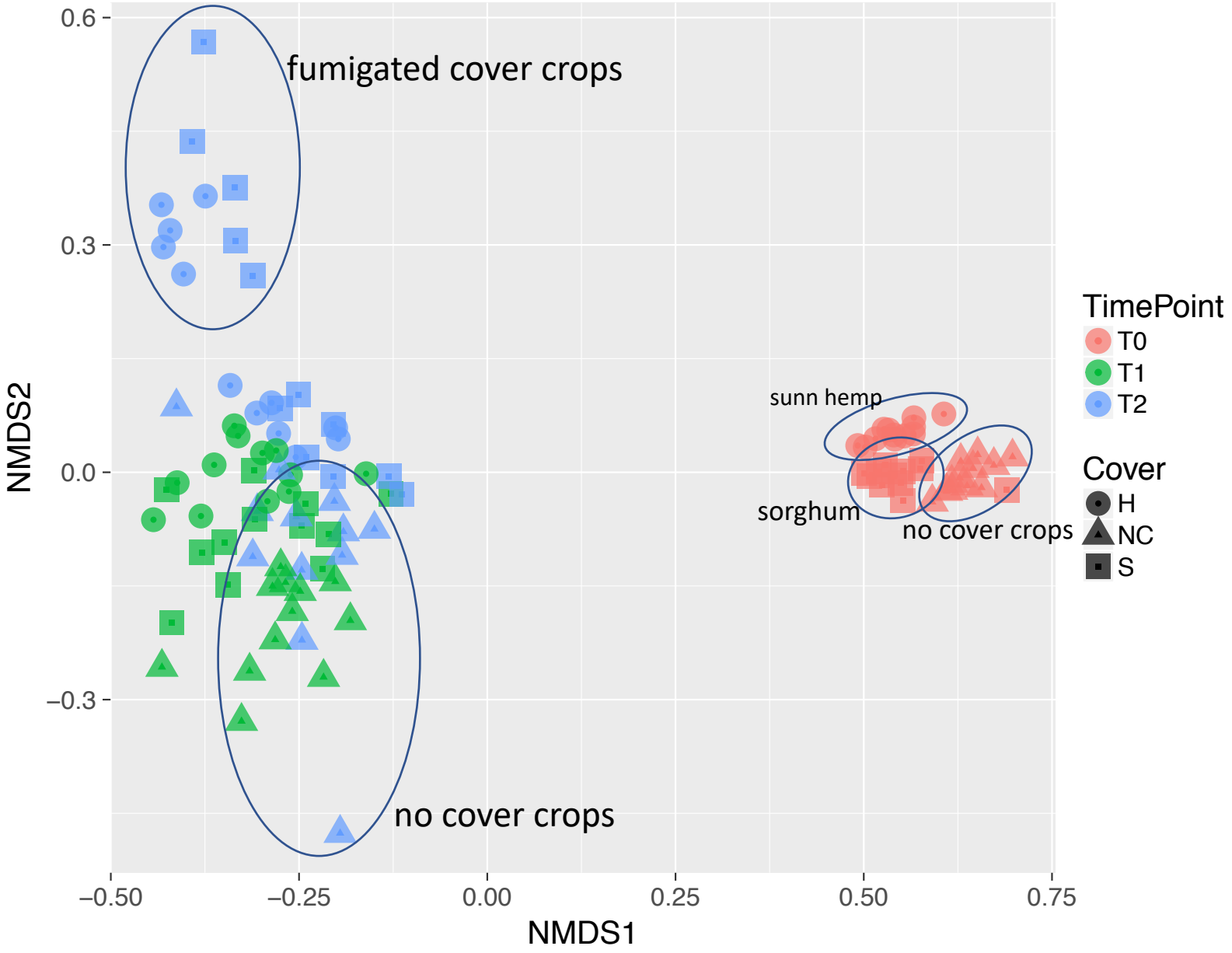
Cover crops had little influence on soil bacterial diversity



Fumigation had little impact on soil bacterial diversity



Cover crops and fumigation do impact soil bacterial community



2. Direct method: change the **community**

- Add specific microbes to the soil
- “Probiotic” approach

MICROBIOME

The Placenta Harbors a Unique Microbiome

Kjersti Aagaard,[1,2,3]* Jun Ma,[1,2] Kathleen M. Antony,[1] Radhika Ganu,[1] Joseph Petrosino,[4] James Versalovic[5]

Humans and their microbiomes have coevolved as a physiologic community composed of distinct body site niches with metabolic and antigenic diversity. The placental microbiome has not been robustly interrogated, despite recent demonstrations of intracellular bacteria with diverse metabolic and immune regulatory functions.

Americangut.org

Inflammatory Bowel Disease as a Model for Translating the Microbiome

Curtis Huttenhower,[1,2,3,*] Aleksandar D. Kostic,[1,2,4] and Ramnik J. Xavier[1,3,4,5,*]
[1]Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA
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http://dx.doi.org/10.1016/j.immuni.2014.05.013

The inflammatory bowel diseases (IBDs) are among the most closely studied chronic inflammatory disorders that involve environmental, host genetic, and commensal microbial factors. This combination of features has made IBD both an appropriate and a high-priority platform for translatable research in host-microbiome

The Dynamics of the Human Infant Gut Microbiome in Development and in Progression toward Type 1 Diabetes

Aleksandar D. Kostic,[1,2,3] Dirk Gevers,[1] Heli Siljander,[4,5] Tommi Vatanen,[1,6] Tuulia Hyötyläinen,[7,11] Anu-Maaria Hämäläinen,[9] Aleksandr Peet,[10] Vallo Tillmann,[10] Päivi Pöhö,[8,11] Ismo Mattila,[7,11] Harri Lähdesmäki,[6] Eric A. Franzosa,[3] Outi Vaarala,[5] Marcus de Goffau,[12] Hermie Harmsen,[12] Jorma Ilonen,[13,14] Suvi M. Virtanen,[15,16,17] Clary B. Clish,[1] Matej Orešič,[7,11] Curtis Huttenhower,[1,3] Mikael Knip,[4,5,18,19,23] on behalf of the DIABIMMUNE Study Group,[22] and Ramnik J. Xavier[1,2,20,21,23,*]
[1]Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA
[2]Center for Computational and Integrative Biology, Massachusetts General Hospital and Harvard Medical School, Boston, MA 02114, USA
[3]Department of Biostatistics, Harvard School of Public Health, Boston, MA 02115, USA

2. Direct method: change the **community**

Benefits

- Potentially target specific microbial function
  - Example: specific bacteria to control soilborne disease
  - Specific Bacillus sp. may increase plant growth

Difficulties

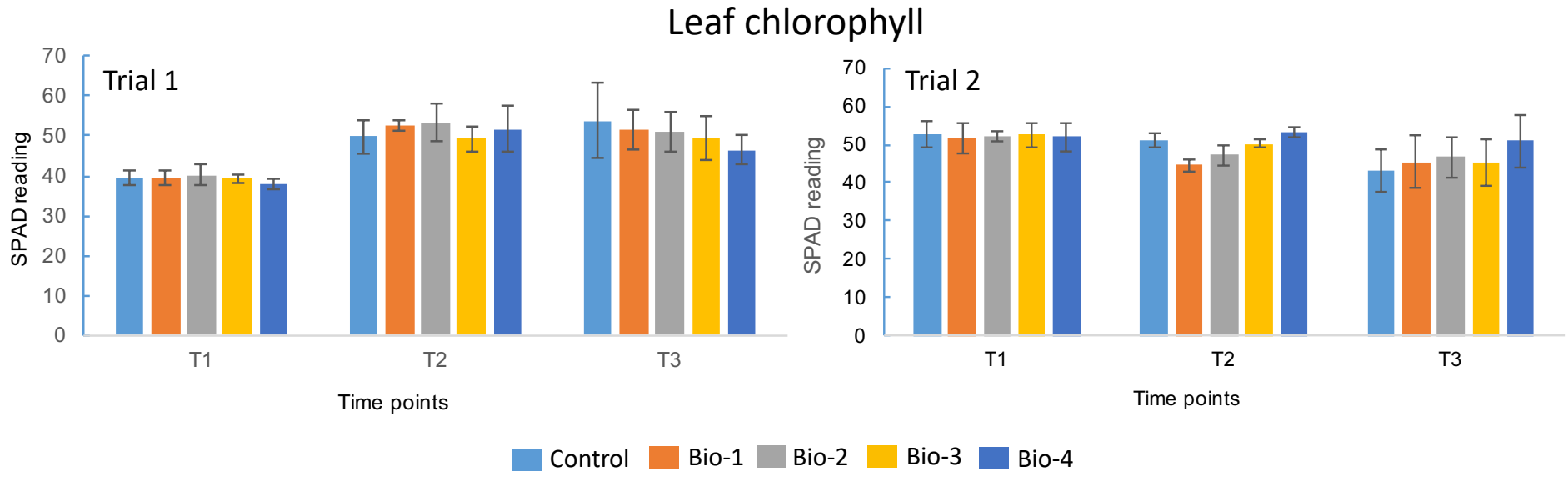
- Beneficial taxa can be very crop and/or environment specific
- Unknown how introduced organisms will interact with native organisms
- Unknown what conditions are necessary to keep introduced organisms alive and increasing in number

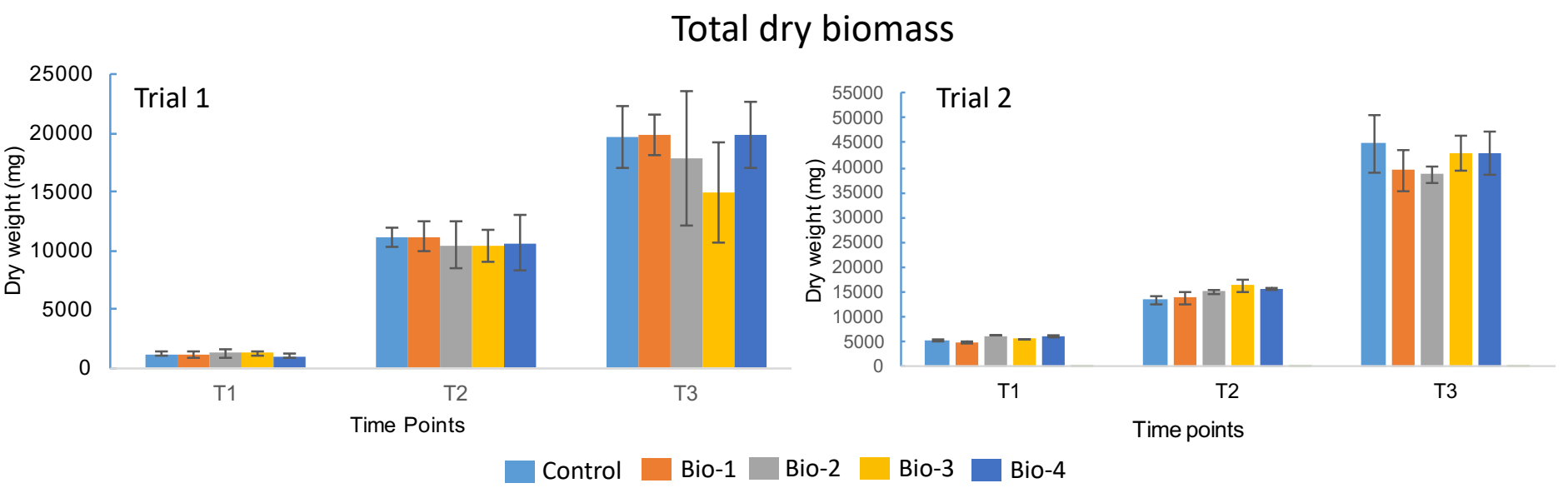
2. Direct method: change the **community**

- Greenhouse trial with tomato

- Four treatments:
  - Bio-1: Mychorrhizae
  - Bio-2: Azospirillum sp., Bacillus sp., Pseudomonas sp., Tricoderma sp.
  - Bio-3: Lactobacillus sp., yeasts
  - Bio-4: Bacillus sp.
- Applied at recommended rates
- Planted in Florida field soil
- Repeated twice

Microbial additions did not impact plant growth





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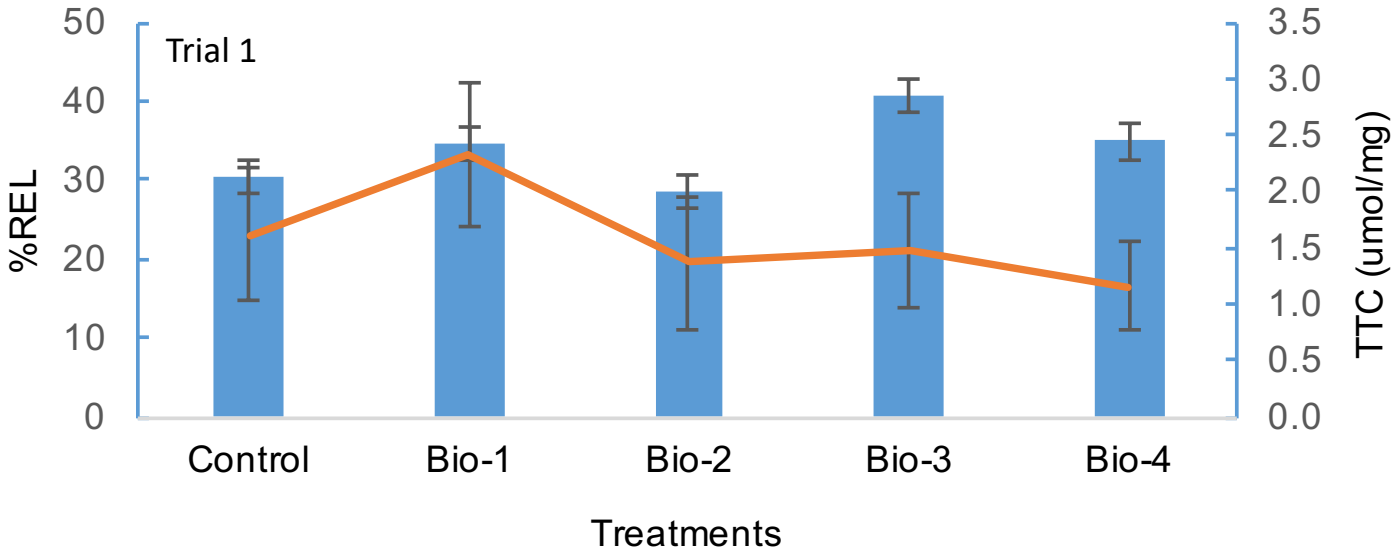
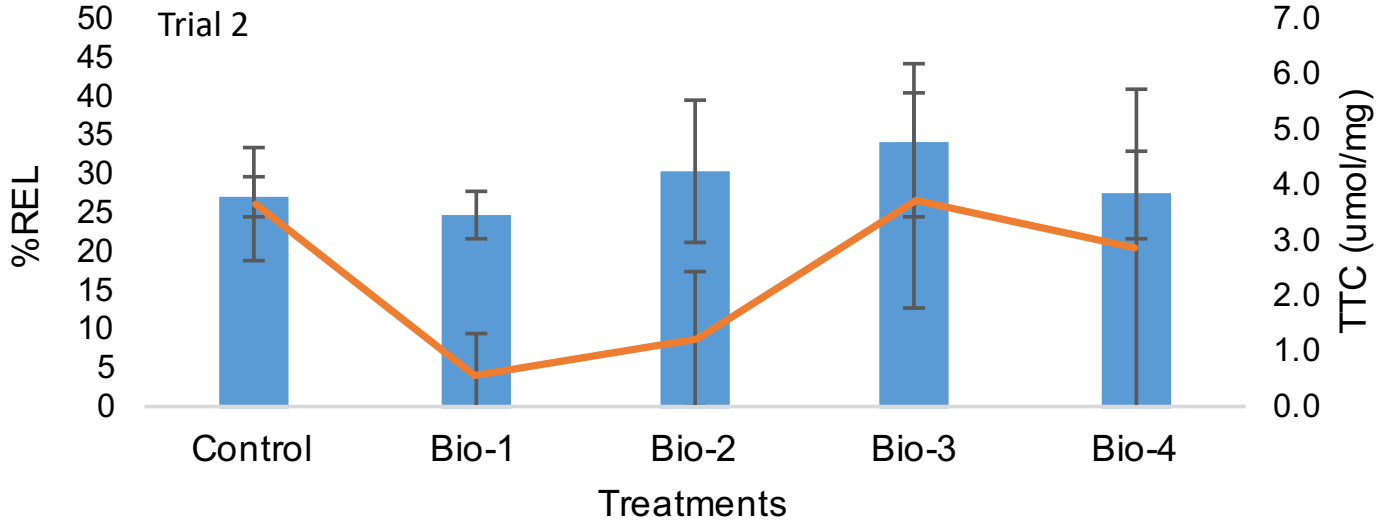
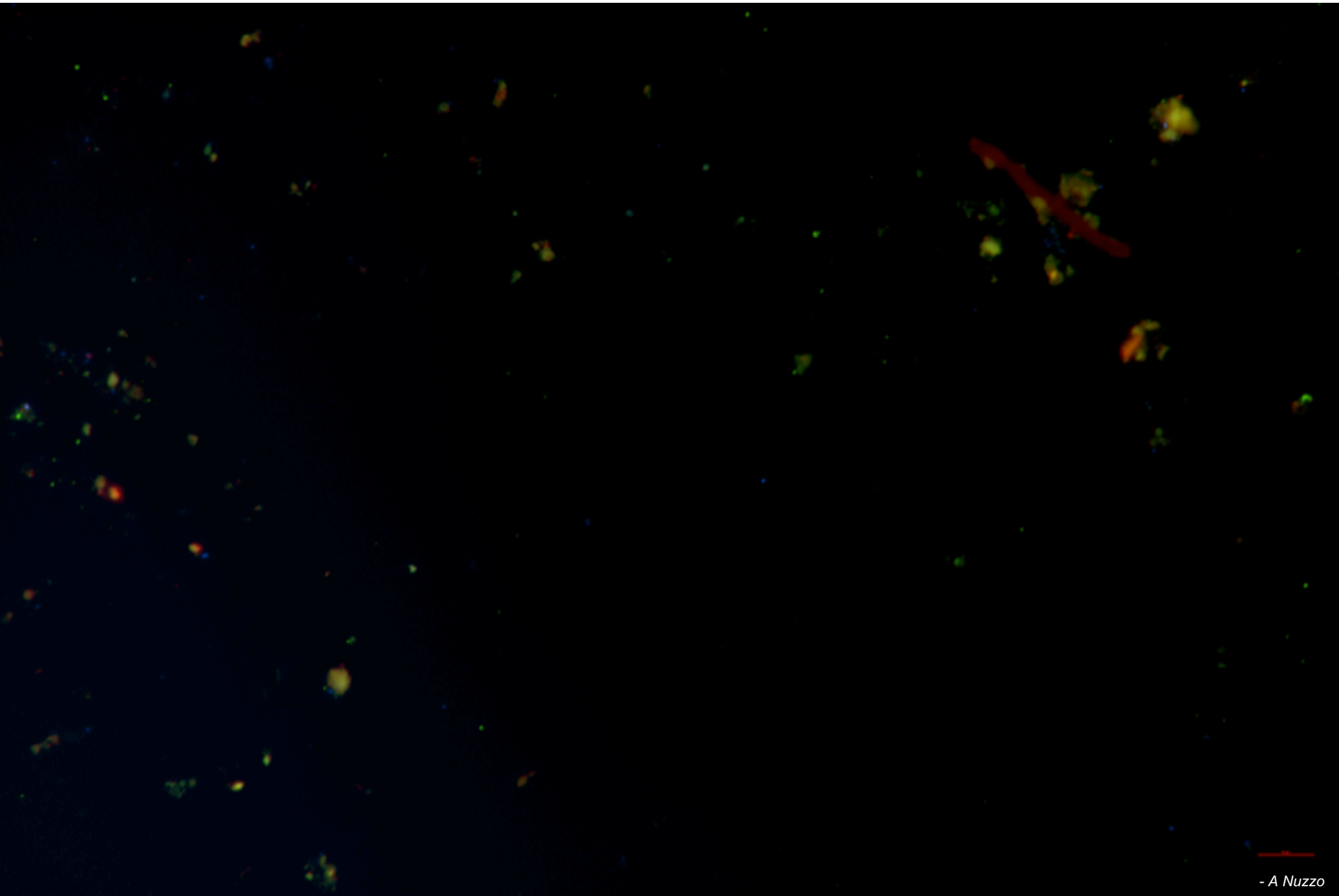


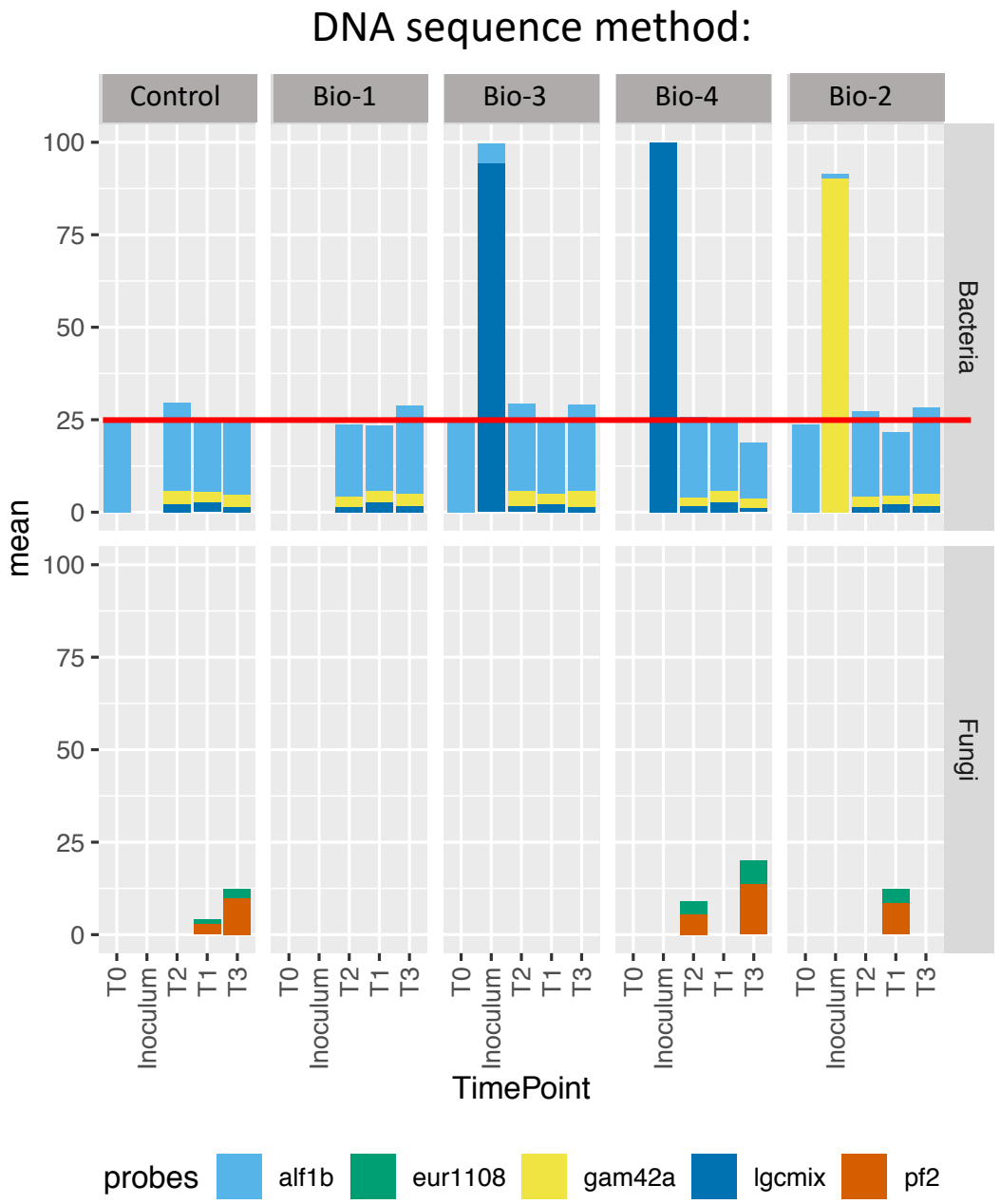


2. Direct method: change the **community**



- A Nuzzo

Microbial additions did not impact microbial community composition



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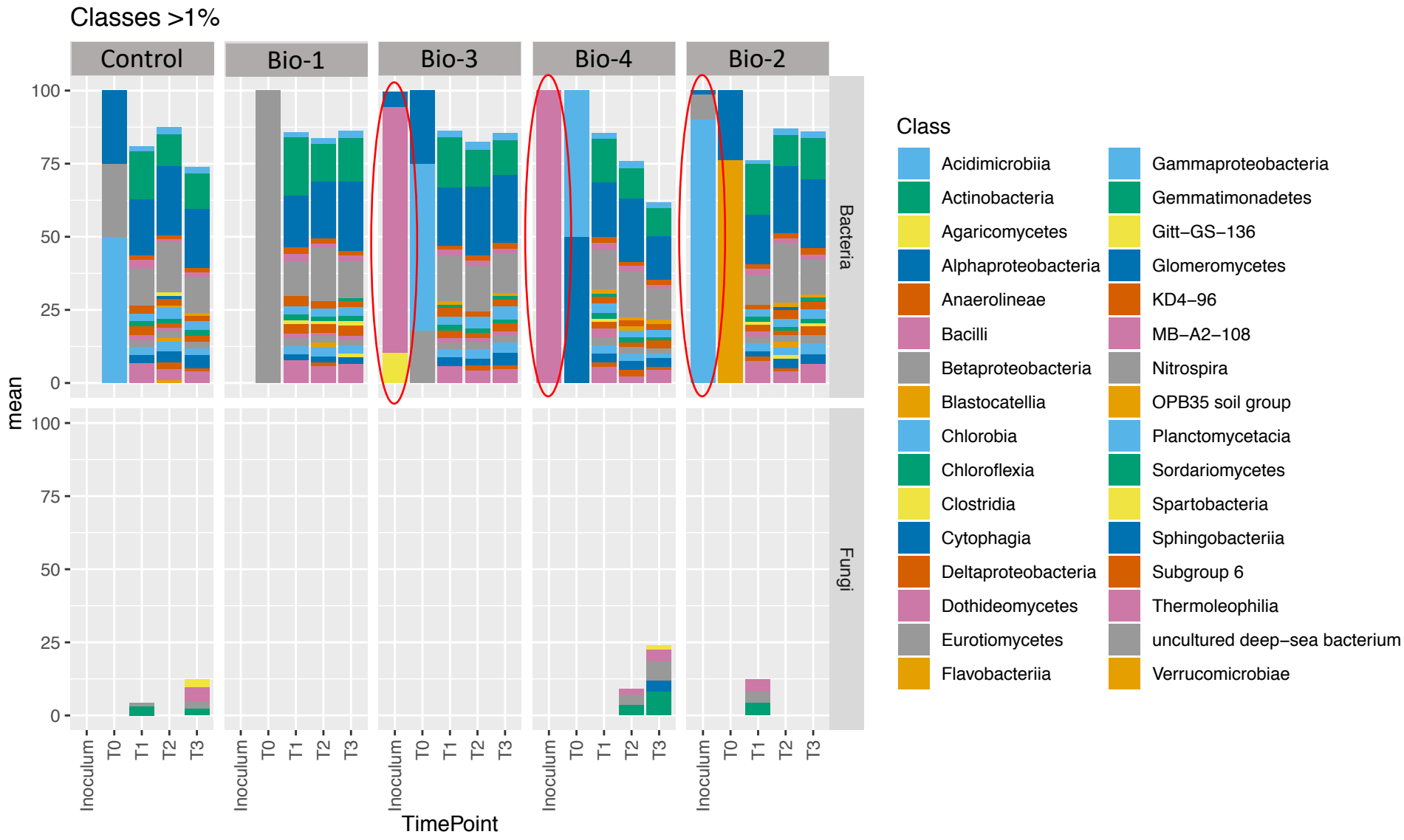

Summary

- Soil microbial communities are complex
  - Many factors involved in determining community composition and interactions with plants

- Great potential for improving plant growth via microbial communities
  - Combination of “indirect” and “direct” methods likely necessary

  - Much more research needed to understand these interactions


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