BENEFICIAL MICROBES AND OTHER SOIL AMENDMENTS FOR IMPROVING CITRUS: AN UPDATE

Sarah Strauss, PhD

Assistant Professor, Soil Microbiology

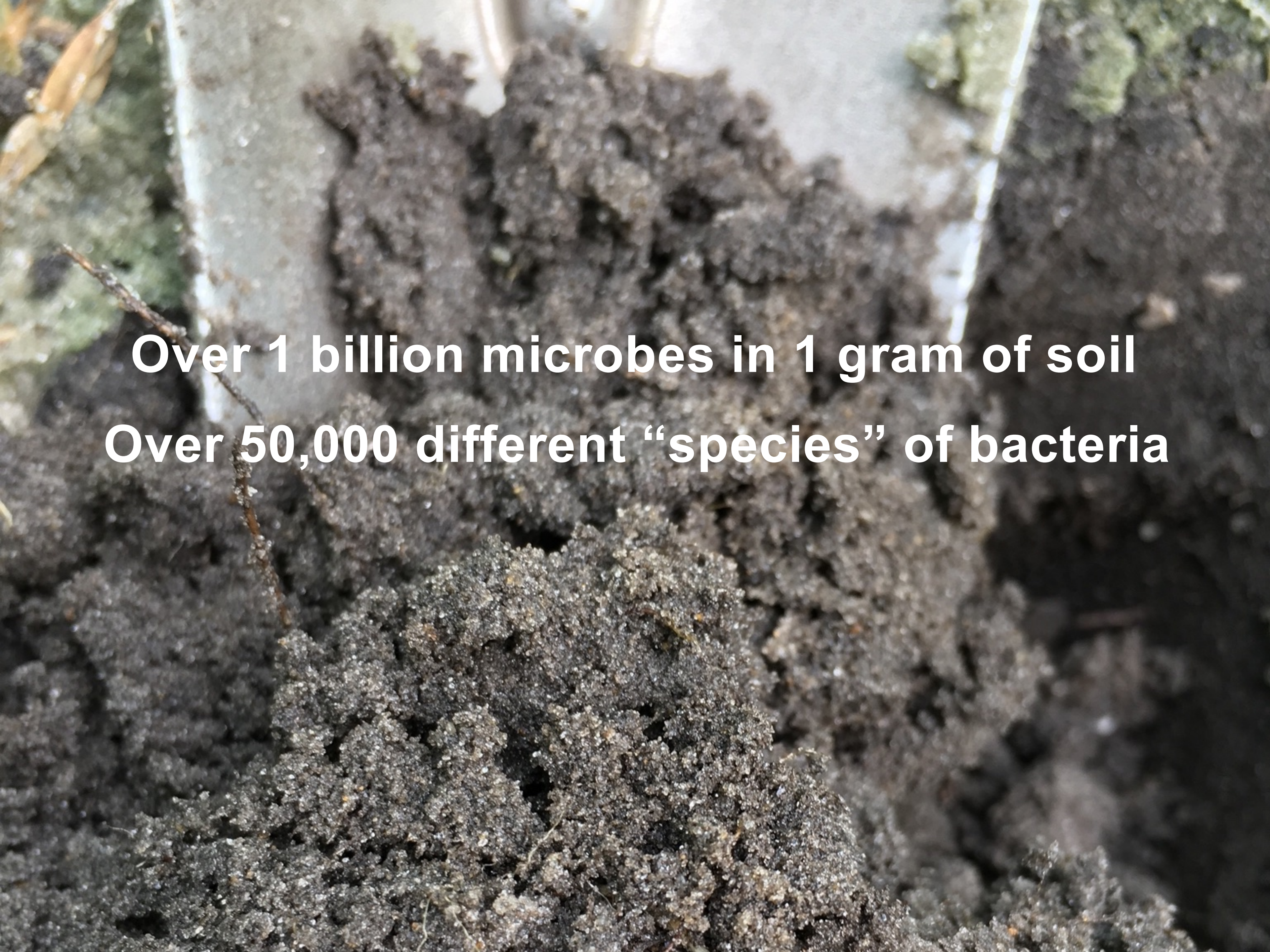
strauss@ufl.edu

@SoilMicroSarah

Soil & Water Sciences

UF | IFAS

UNIVERSITY of FLORIDA


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
phosphate
water
Organic matter
carbon
pH
fungi
arthropods
Soil texture
temperature
plant diversity
Soil stability
nitrate
salinity
nematodes
archaea
Plant age
Exudates
micronutrients

How can we use soil microbiology to help citrus 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

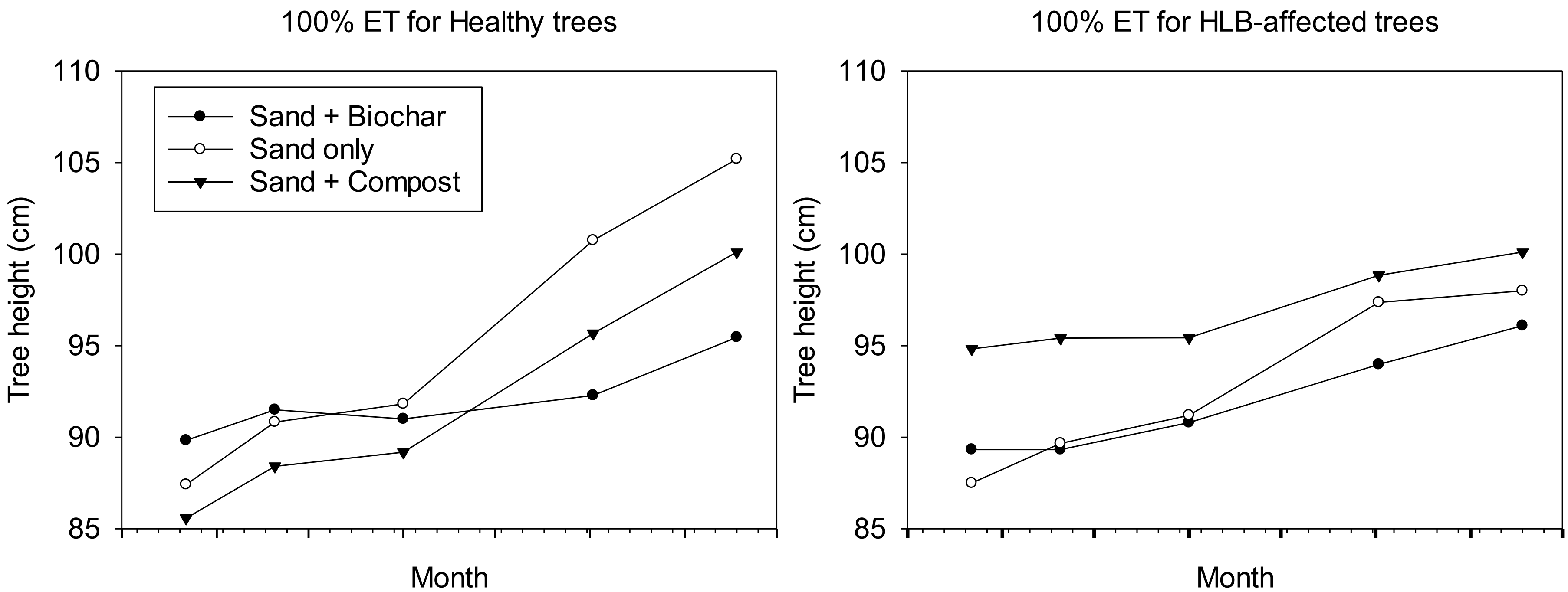
- Soil organic matter (SOM) is very low in Florida
- Increasing SOM takes TIME – results may not occur after only 1 year
- Native soil microbial community not well characterized – and likely unique for each location

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

- Greenhouse trial of HLB-affected and non-affected trees
- 3 soil amendments:
  - Field soil
  - Field soil + compost (5% v/v)
  - Field soil + biochar (3% v/v)
- 2 irrigation rates:
  - 100% evapotranspiration (ET)
  - 75% ET
- 1.5 year experiment

Collaboration with Dr. Davie Kadyampakeni and Dr. Arnold Schumann, UF/IFAS CREC

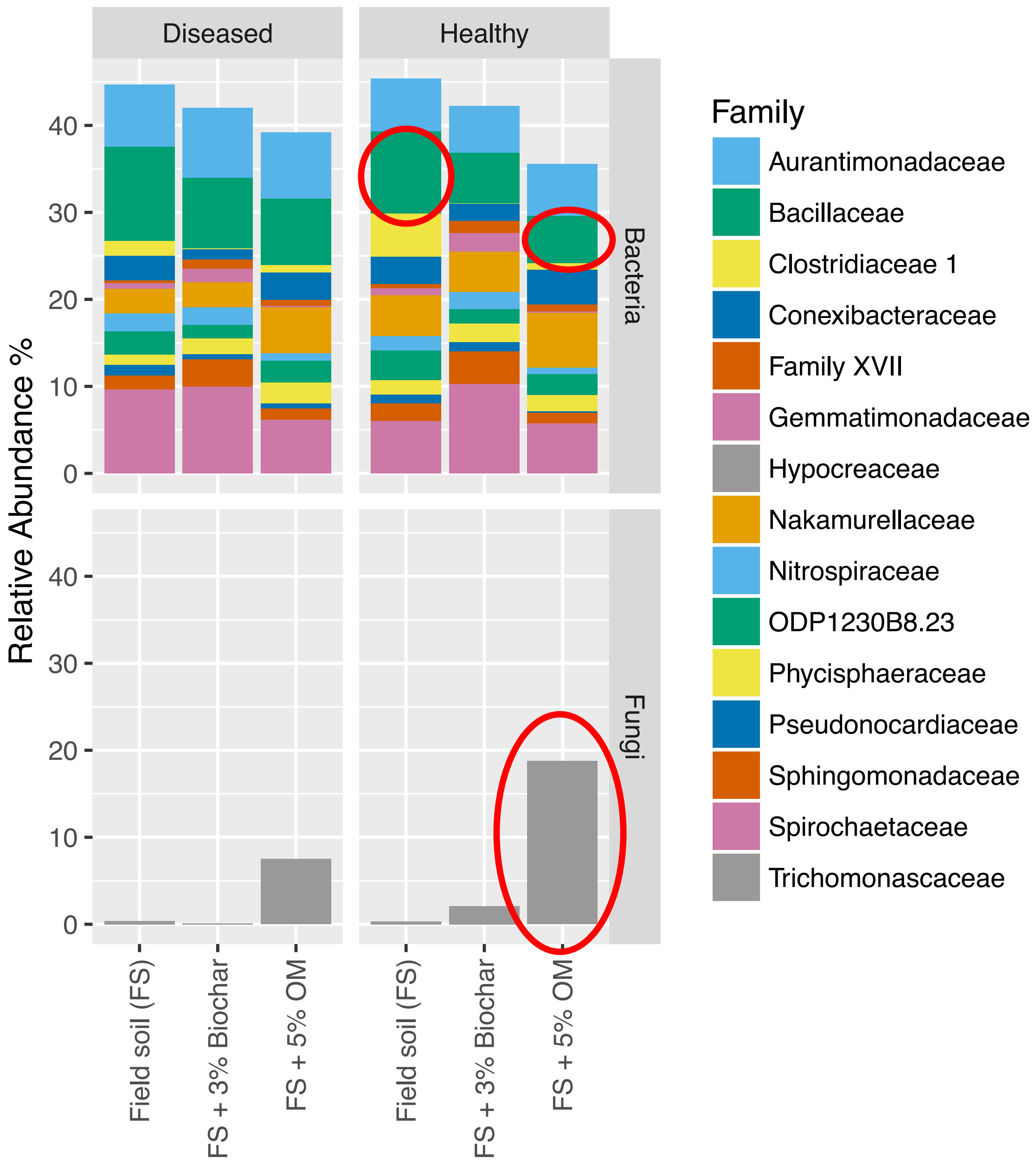
Tree height impacted by soil amendments



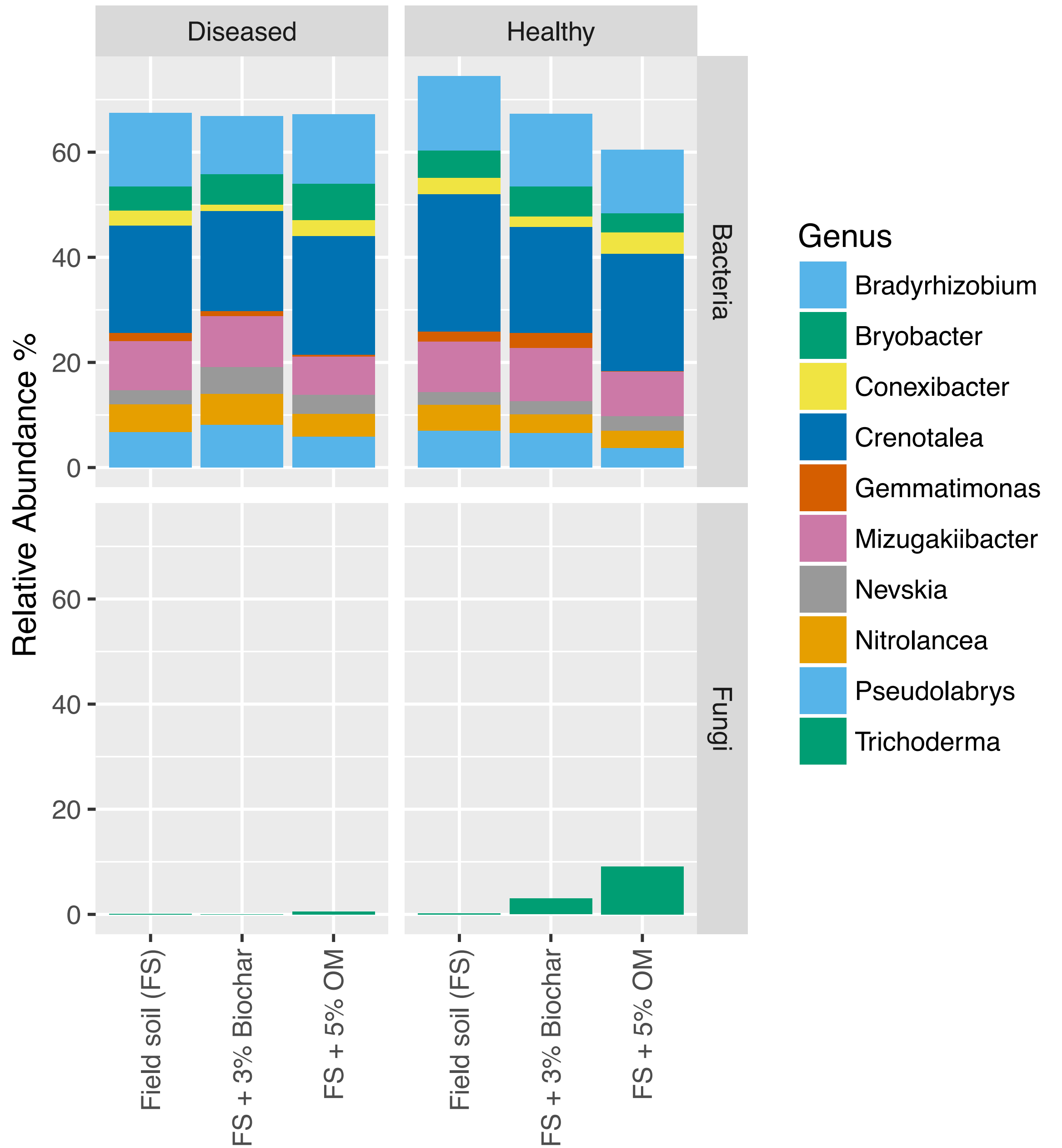
- Root length density was significantly impacted by soil amendments
- Compost amendment reduced water-stress in HLB-affected and healthy trees

- Soil and tree nutrient data still being analyzed

Soil amendments impacted soil microbial community composition



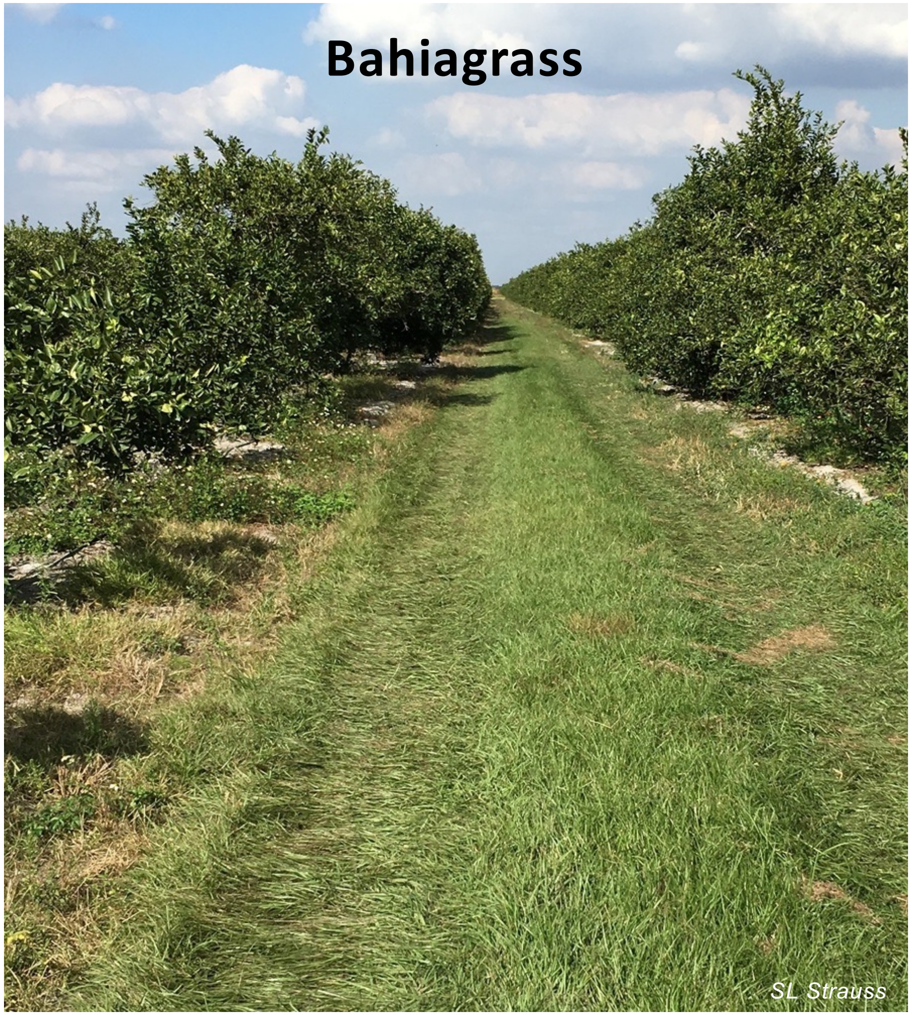
Irrigation level impacted soil microbial community composition



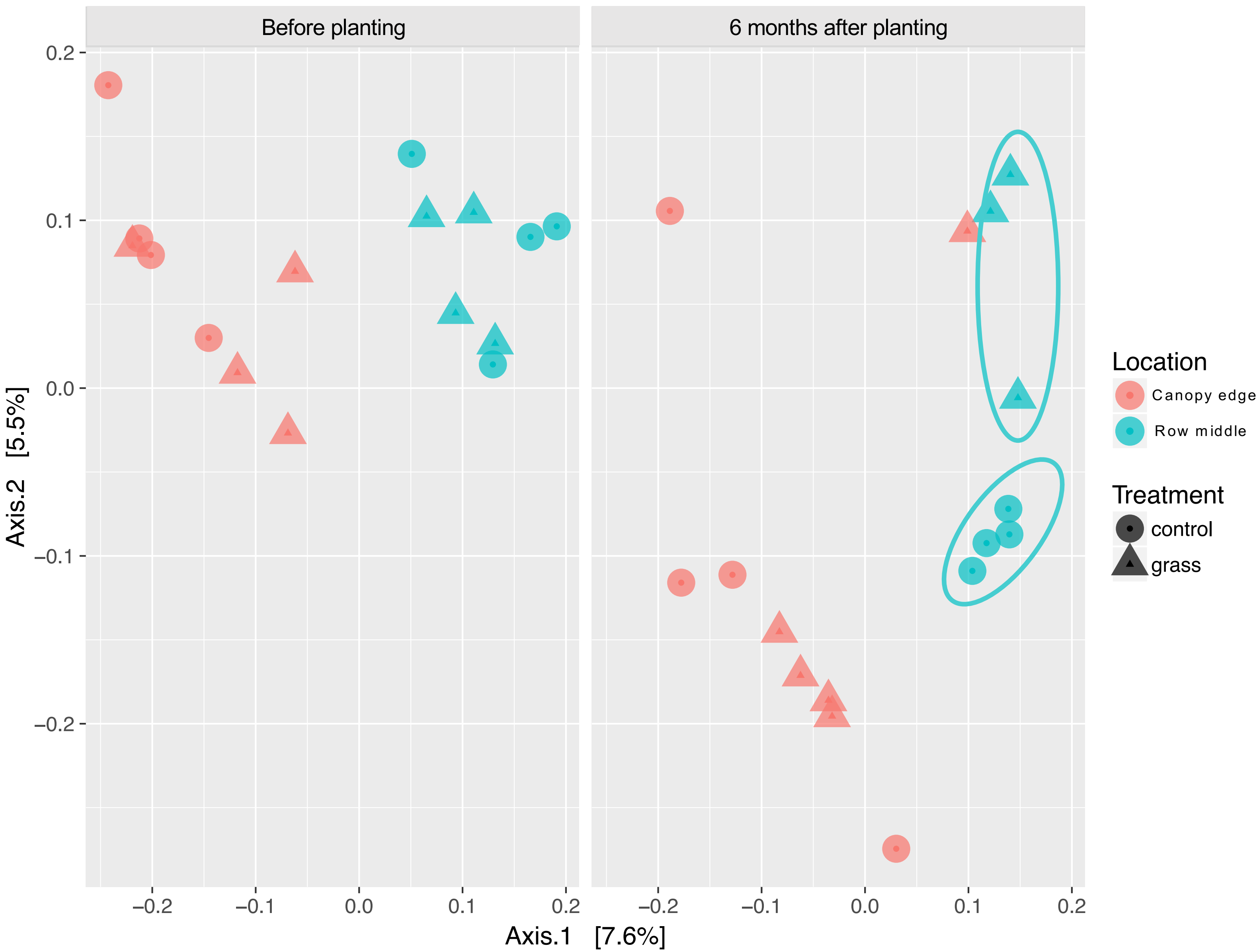
1. Indirect method: change the **environment**

- Bahiagrass planted in row middles of established commercial grove

Collaboration with Dr. Ramdas Kanissery, UF/IFAS SWFREC



Cover crop can influence soil microbial community



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

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

RESEARCH ARTICLE

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
[2]Department of Biostatistics, Harvard School of Public Health, Boston, MA 02115, USA
[3]Center for the Study of Inflammatory Bowel Disease, Massachusetts General Hospital and Harvard Medical School, Boston, MA 02114, USA
[4]Center for Computational and Integrative Biology, Massachusetts General Hospital and Harvard Medical School, Boston, MA 02114, USA
[5]Gastrointestinal Unit, Massachusetts General Hospital and Harvard Medical School, Boston, MA 02114, USA
*Correspondence: chuttenh@hsph.harvard.edu (C.H.), xavier@molbio.mgh.harvard.edu (R.J.X.)
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

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**

- Apply biostimulants to mature trees in two commercial groves:
  - High-input management (> $2,000/acre)
  - Low-input management (± $1,000/acre)
    - Same rootstock, similar tree age, all affected by HLB

Collaboration with Dr. Ute Albrecht, UF/IFAS SWFREC

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

- Treatments:
  - Pure liquid seaweed (*Ascophyllum nodosum*)
  - Soluble fluvic acids (69%)
  - Beneficial microbes (*Bacillus* spp. plus *Trichoderma*)
  - Seaweed + microbes
  - Fulvic acids + microbes
  - No-treatment control
- Complete randomized design with 6 replications (5 trees/replicate)
- Monthly applications (soil drench) begun in November 2016

Six-month evaluation: Low input management

Treatment	TRL (m)	SRL (m/g)	REL	TTC (µM)	DI
Control	51.0	20.3	0.30	26.9 b	2.6
Fulvic acid (FA)	41.5	20.5	0.32	33.8 ab	2.6
Seaweed (SW)	42.0	24.1	0.22	47.9 a	2.7
Microbes (MB)	52.3	19.7	0.22	38.7 ab	2.4
FA + MB	41.5	19.7	0.36	26.6 b	2.5
SW + MV	66.0	22.8	0.23	47.7 a	2.4
	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P = 0.0133$	$P > 0.05$

TRL = Total root length; SRL = Specific root length; REL = Root electrolyte leakage
TTC = Method to determine root metabolic activity
DI = HLB disease index (0 = no symptoms, 5 = > 75% of canopy with symptoms

Six-month evaluation: High input management

Treatment	TRL (m)	SRL (m/g)	REL	TTC (µM)	DI
Control	38.3	16.4	0.23	44.1	2.5
Fulvic acid (FA)	39.8	15.0	0.28	37.1	2.5
Seaweed (SW)	60.4	15.9	0.17	43.1	2.0
Microbes (MB)	31.9	16.8	0.29	46.5	2.2
FA + MB	61.6	14.7	0.19	46.9	2.2
SW + MV	59.7	18.9	0.23	45.5	2.2
	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P > 0.05$

No significant treatment effects

TRL = Total root length; SRL = Specific root length; REL = Root electrolyte leakage
TTC = Method to determine root metabolic activity
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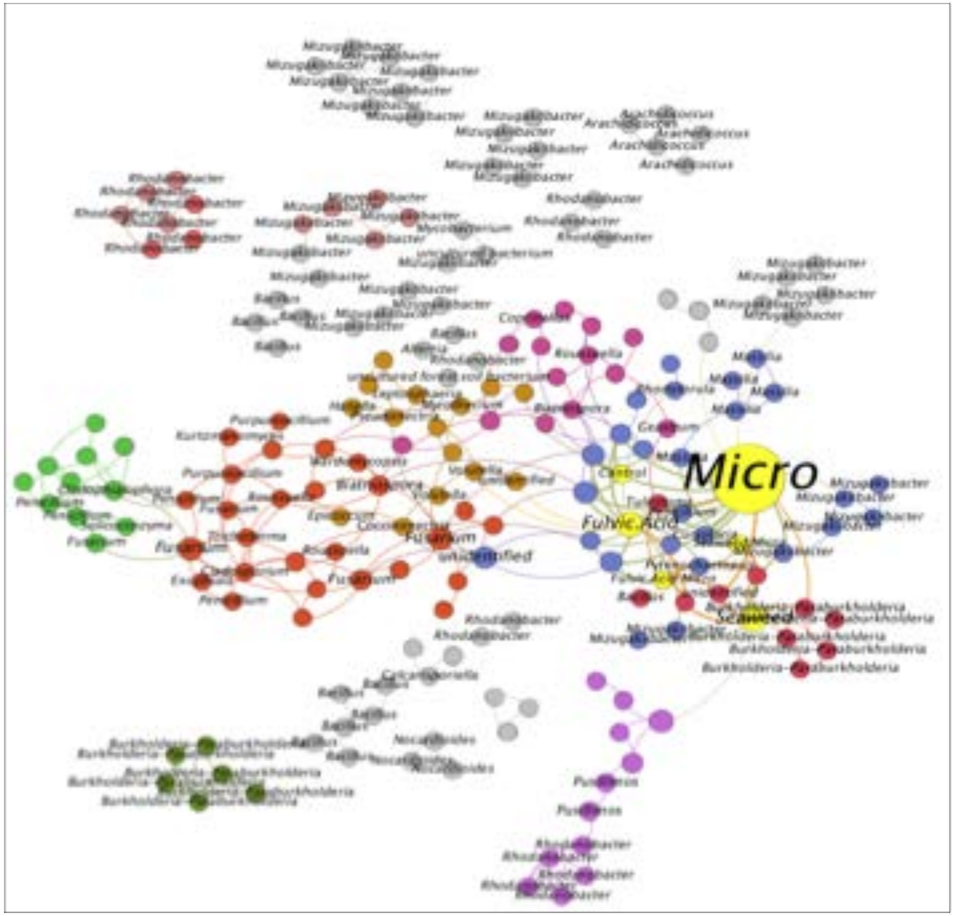
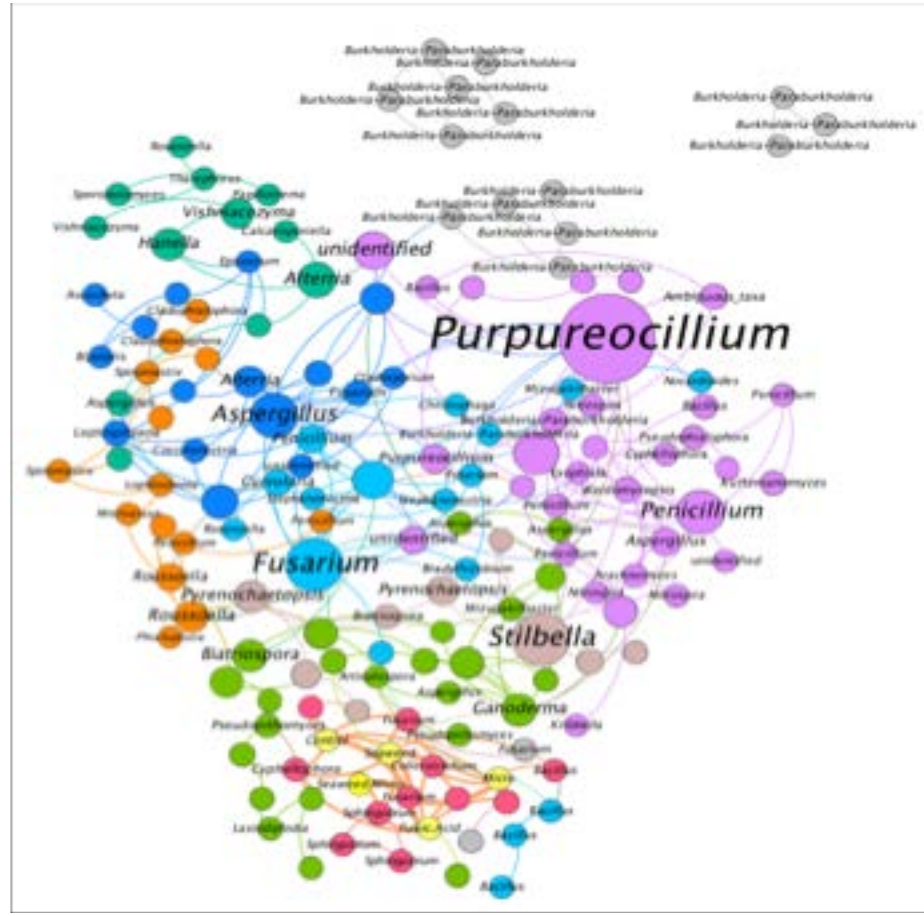
Management impacted soil microbial interactions

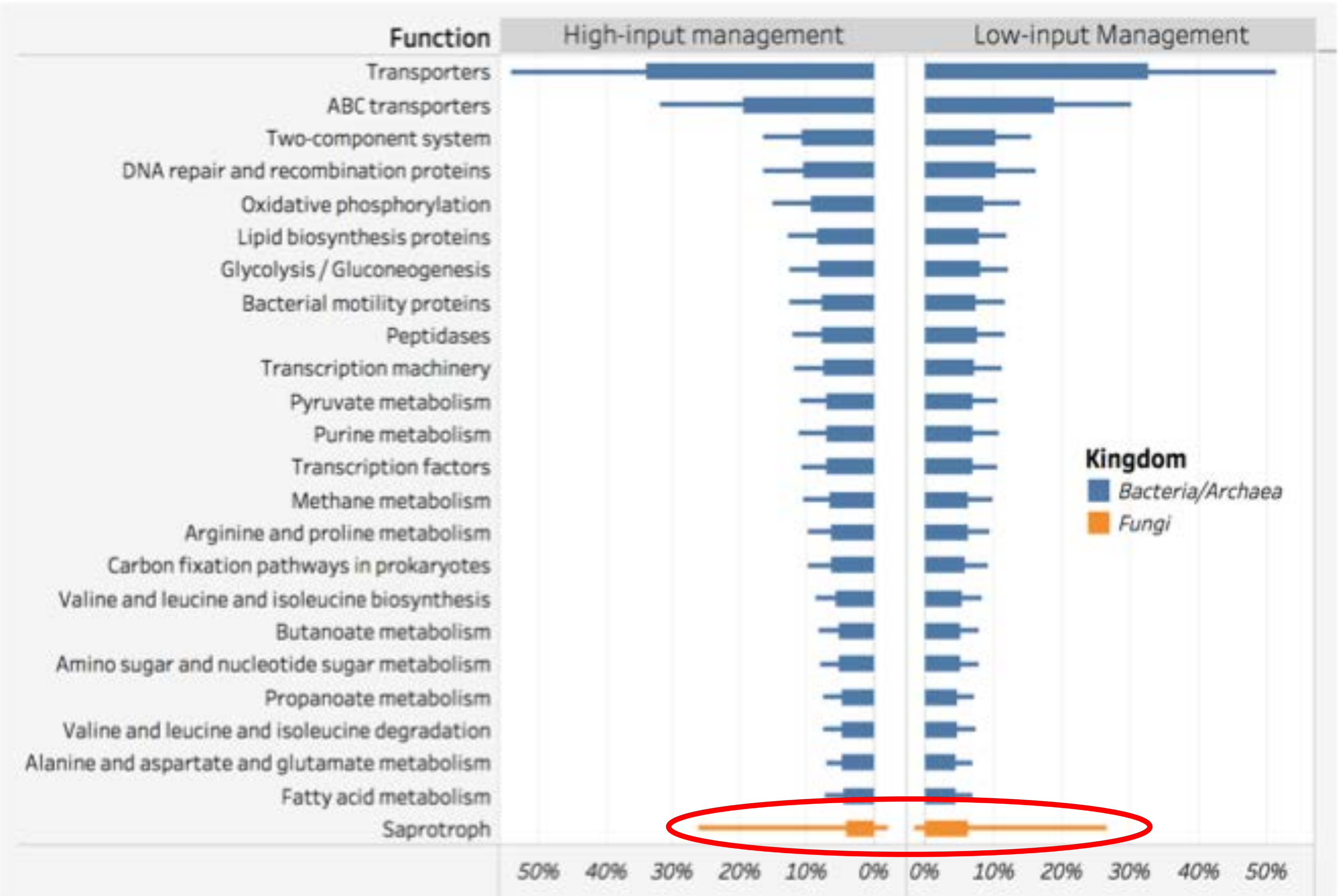
High input management



Low input management



Management may impact soil microbial functions



What's next for soil microbes in citrus?

- Increase understanding of relationship between community composition and function
- Examine methods to assess inoculation and abundance of added organisms
- Optimize methods for adding SOM to Florida soils

Dr. Ute Albrecht
Dr. Davie Kadaymapakeni
Dr. Arnold Shumann

Bryce Meyering
Amanda Gray

Joby Sherrod (Duda & Sons)
John Paul (John Paul Inc.)
Frank Vega (John Paul Inc.)

Strauss Lab:

Dr. Andrea Nuzzo, Postdoctoral Research Associate
Rachel Berner, Biological Scientist
John Santiago, MS student
David Toole, MS student
Kira Sorochkina, PhD student
Clayton Nevins, PhD Student

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Have you seen me?

email: strauss@ufl.edu