

MICROBIOME E MICROBIOTA

Marco Chiapello

2020-11-24

<https://bit.ly/39colbU>



Last lesson recap

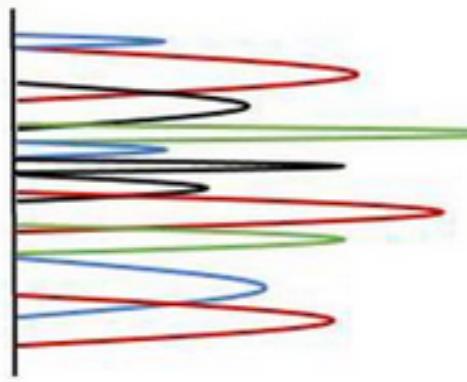
1. DNA Metabarcoding
2. Several techniques can be employed to decipher the microbiota functions
3. System biology is the discipline that integrates the -omics techniques to formulate models that describe the structure of the system

Last lesson recap

CTGACGGTACT

1. DNA Metabarcoding
2. Several techniques can be employed to decipher the microbiota functions

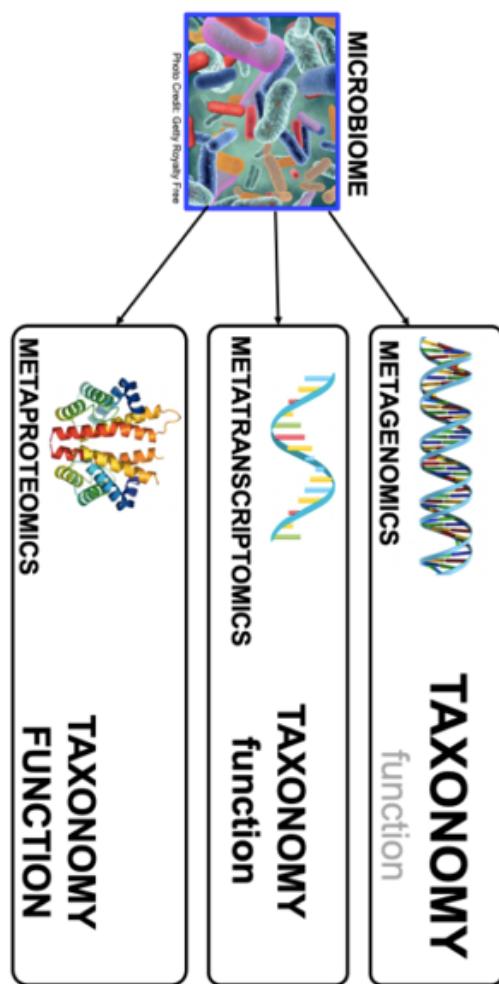
Sequencing of DNA barcode



3. System biology is the discipline that integrates the -omics techniques to formulate models that describe the structure of the system

Last lesson recap

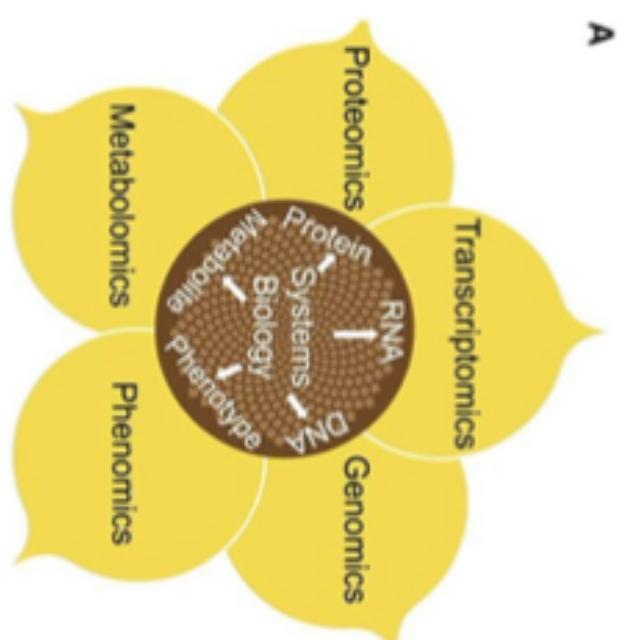
1. DNA Metabarcoding
2. Several techniques can be employed to decipher the microbiota functions



3. System biology is the discipline that integrates the -omics techniques to formulate models that describe the structure of the system

Last lesson recap

1. DNA Metabarcoding
2. Several techniques can be employed to decipher the microbiota functions
3. System biology is the discipline that integrates the -omics techniques to formulate models that describe the structure of the system



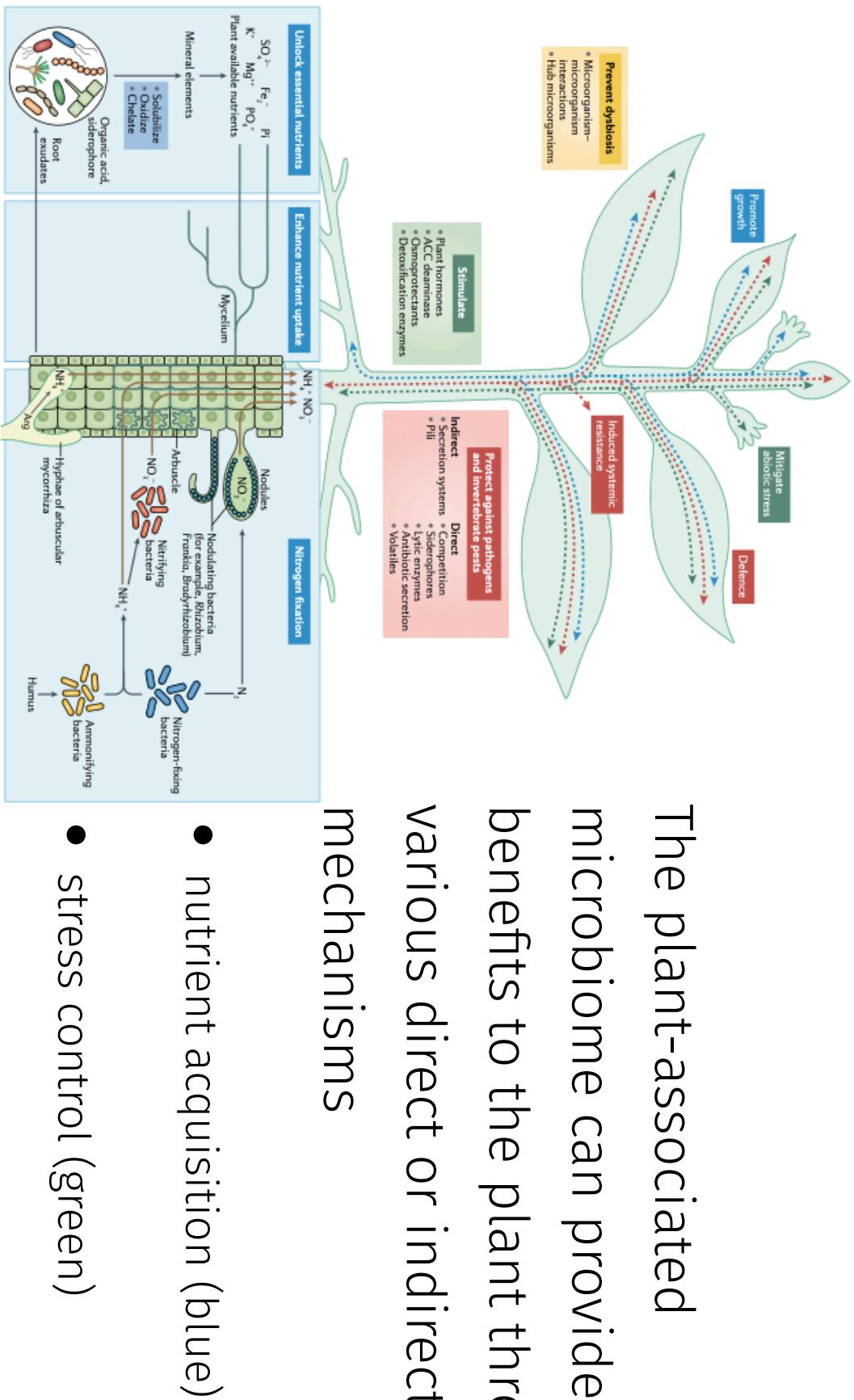
Agenda

- Functions of plant-associated microbiomes
- Can the plant modify the composition of the associated microbiota?
- Can we exploit the microbiota?

Functions of plant-associated microbiomes

Functions of plant-associated microbiomes

The plant-associated microbiome can provide benefits to the plant through various direct or indirect mechanisms

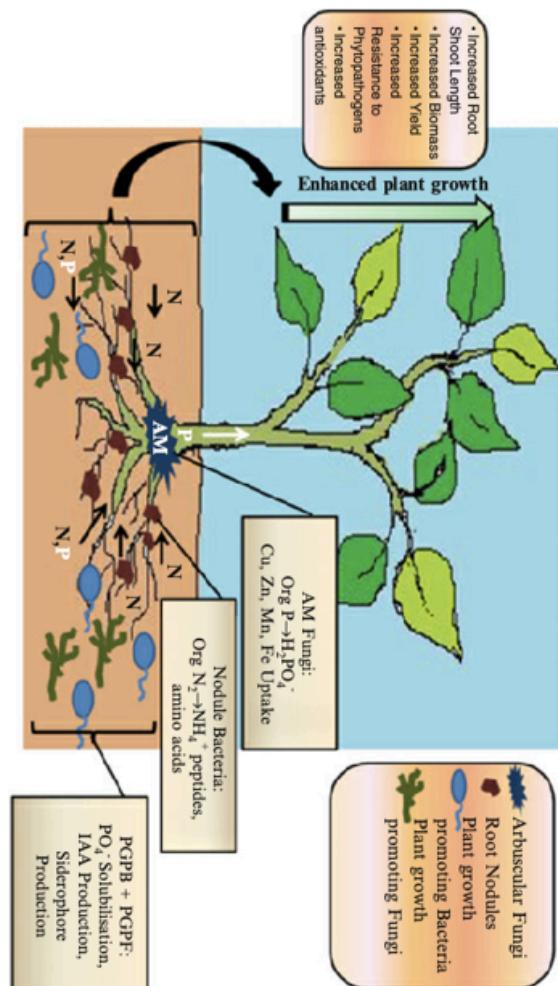


- nutrient acquisition (blue)
- stress control (green)
- defence against pathogens and

Nutrient acquisition

Nutrient acquisition

Plant microbiota has essential functions in improving plant nutrition



- The molecular mechanisms driving nutrient acquisition have been thoroughly studied for plant symbioses with arbuscular mycorrhizal fungi (AMF) and Rhizobium bacteria
- Non-symbiotic plant-growth-promoting bacteria can either enhance the bioavailability of insoluble minerals or improve the root system architecture of host plants, thus increasing the exploratory capacity of the root for water

Nutrient acquisition



ARTICLE

<https://doi.org/10.1038/s42003-019-0481-8>

OPEN

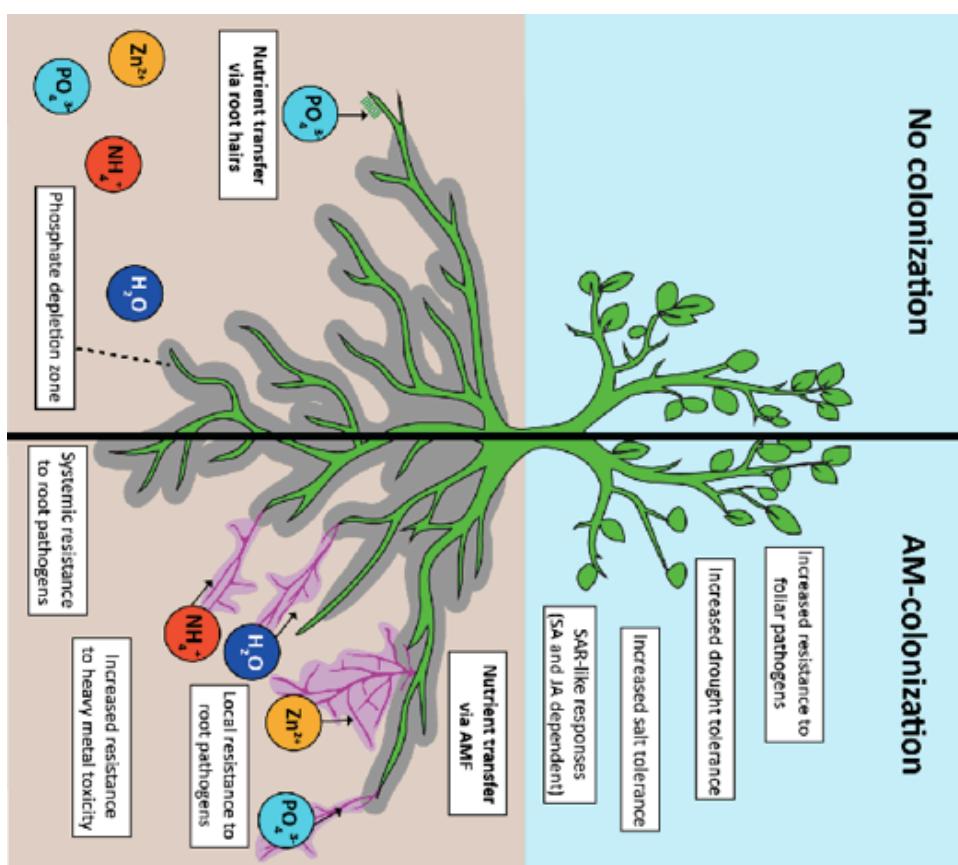
Synergies between mycorrhizal fungi and soil microbial communities increase plant nitrogen acquisition

Rachel Hestrin¹, Edith C. Hammer², Carsten W. Mueller¹ ³ & Johannes Lehmann¹ ^{1,4,5}

Nutrient acquisition

Introduction

- Nitrogen (N) is a limiting nutrient in many natural and managed ecosystems
-  Arbuscular mycorrhizal (AM) fungi can substantially enhance plant N acquisition from soil, thereby potentially alleviating plant N limitation and playing an important role in plant productivity and soil nutrient cycling
-  Other soil biota with decomposer capabilities are key players in AM fungal N acquisition and transfer to plants
-  Authors show that multipartite synergies between AM fungi and soil microbial communities substantially enhance plant and fungal N acquisition from organic matter and microbial acquisition of plant photosynthates



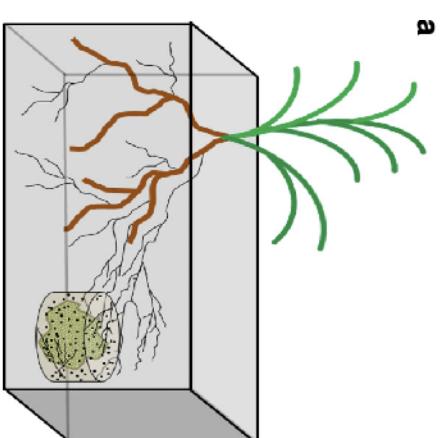
Nutrient acquisition

Experimental design

-  The experimental design allowed to assess the individual and combined contributions of AM fungi and the rest of the soil microbial community to plant N acquisition from organic matter
- The 6 mesocosm treatments included

Plot	Fungi inocula	soil inocula	soil fertilization
control	-	-	none
microbes (N0)	-	+	0 kg N / ha per year
AM fungi	+	-	none
AM fungi + microbes (N196)	+	+	196 kg N / ha per year

Mesocosm design

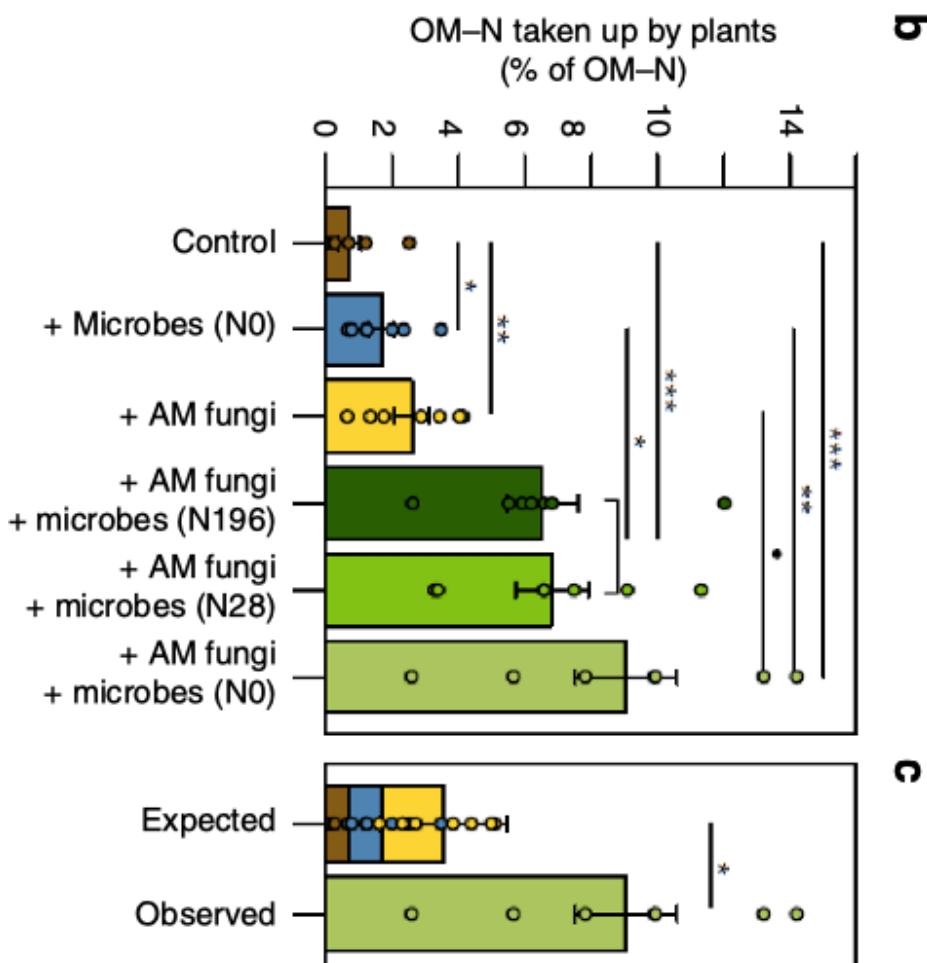


- Terrestrial ecosystems experience substantial N enrichment due to atmospheric deposition and fertilizer applications
- Long-term N enrichment of grassland soils results in substantial changes in microbial community structure and functional gene representation
- The particular mechanisms through which long-term N

Nutrient acquisition

Plant N acquisition from organic matter

- Synergies emerging from these interactions far exceeded an additive effect on plant N acquisition
- Plants grown with either soil microbes or AM fungi acquired twofold and threefold more N from the organic matter than control plants, respectively
- Plants grown with both soil microbes and AM fungi acquired ten to twelvefold more N from the organic matter than control plants
- This ten to twelvefold increase in plant N acquisition is more than double the expected increase in plant N acquisition based on the sum of N taken up by plants grown with free-living soil microbes or AM fungi alone



Stress control

Stress control

Plant-associated

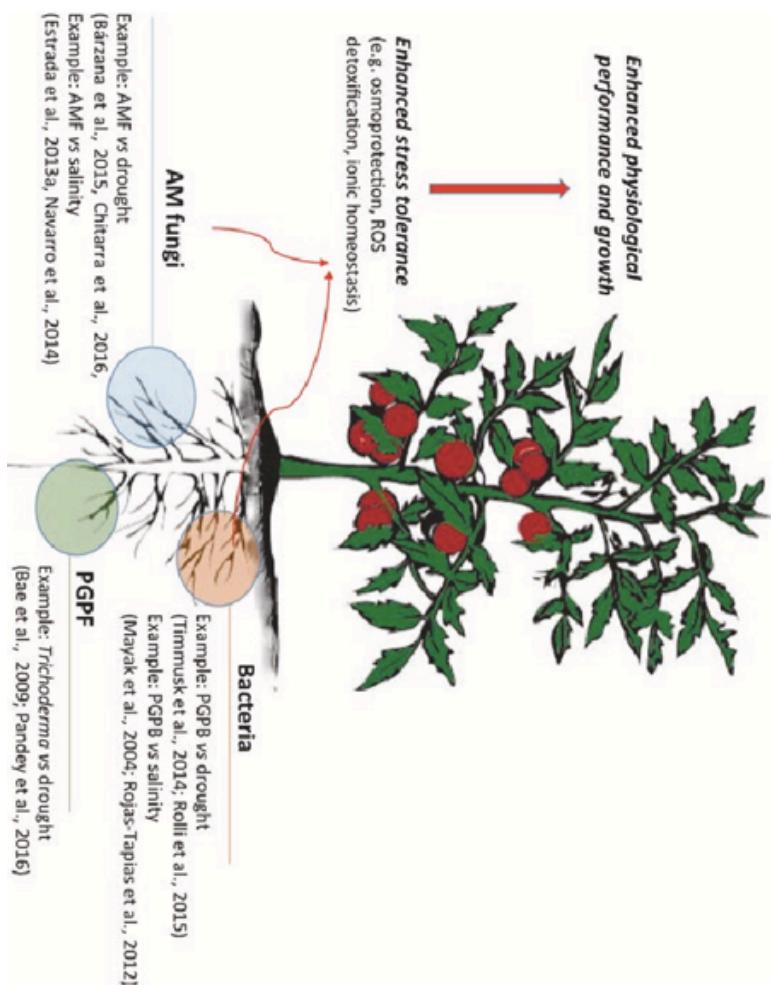
microorganisms could modify

plant evolutionary responses

to environmental stress in at

least three non-mutually-

exclusive pathways



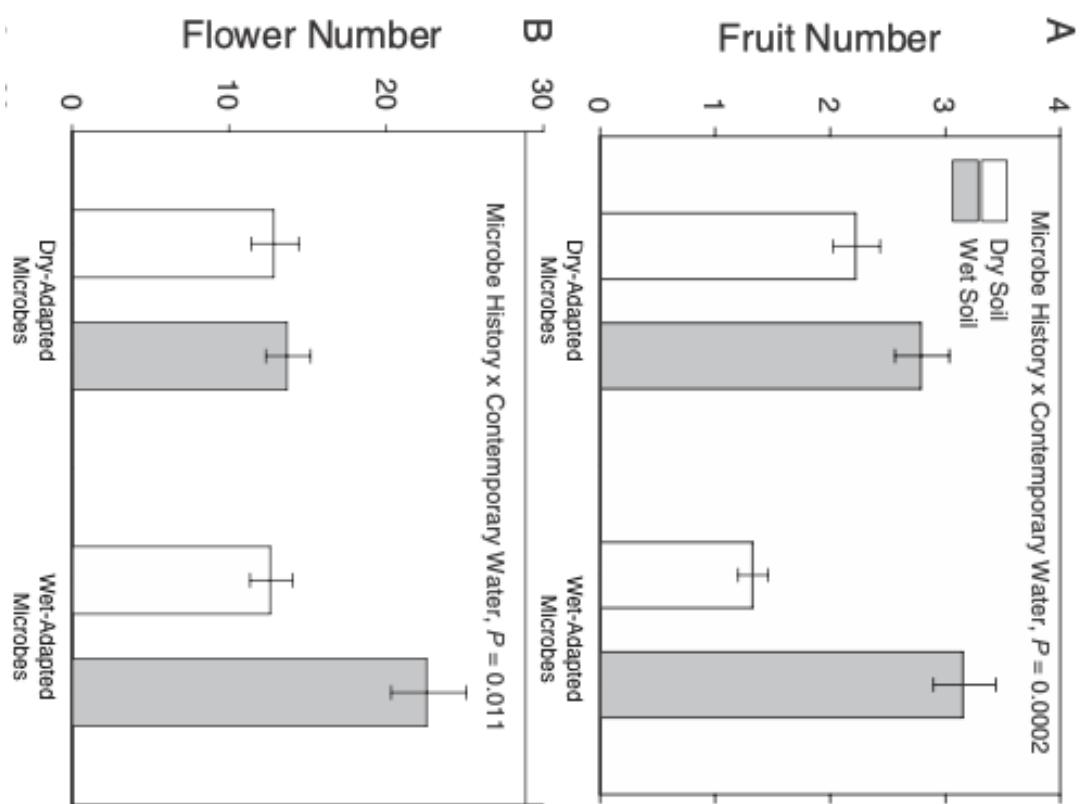
- by altering the fitness of individual plant genotypes
- by altering the expression of plant traits related to fitness

- by altering the strength or direction of natural selection occurring within populations that experience environmental stress

Stress control

Responses to drought

- Experiment examines plant adaptation to drought stress in a multigeneration experiment that manipulated aboveground-belowground feedbacks between plants and soil microbial communities
- Plant fitness in both drought and nondrought environments was linked strongly to the rapid responses of soil microbial community structure to moisture manipulations
- Plants were most fit when their contemporary environmental conditions (wet vs. dry soil) matched the historical environmental conditions (wet vs. dry soil) of their associated microbial community
- Plants may not be limited to "adapt or migrate" strategies
- Plants may benefit from association with interacting species, especially diverse soil microbial communities, that respond rapidly to environmental change



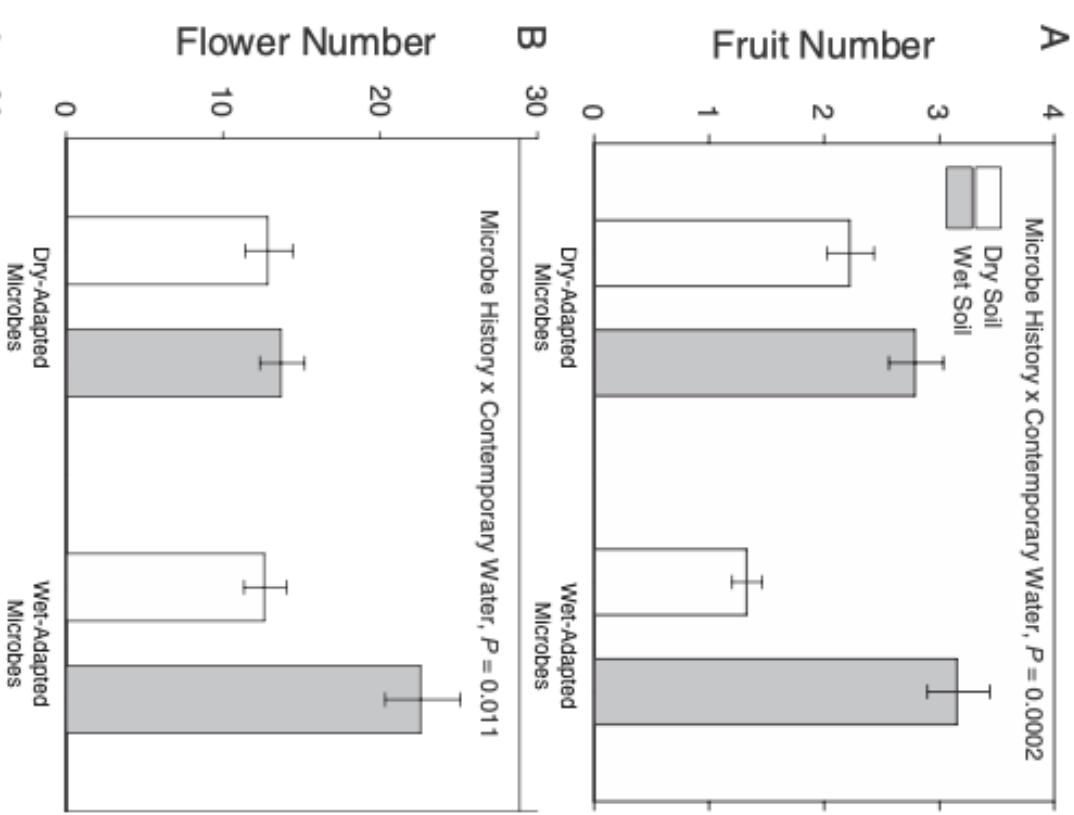
(Lau and Lennon, 2012)

Stress control

Responses to drought

- How belowground microbial communities do affect plant fitness responses to drought stress?

- ⓘ Shifts in microbial community composition and bacterial diversity could be linked to changes in biogeochemical processes that influence the availability of resources, such as nitrogen (N), that commonly limit plant growth and fitness.



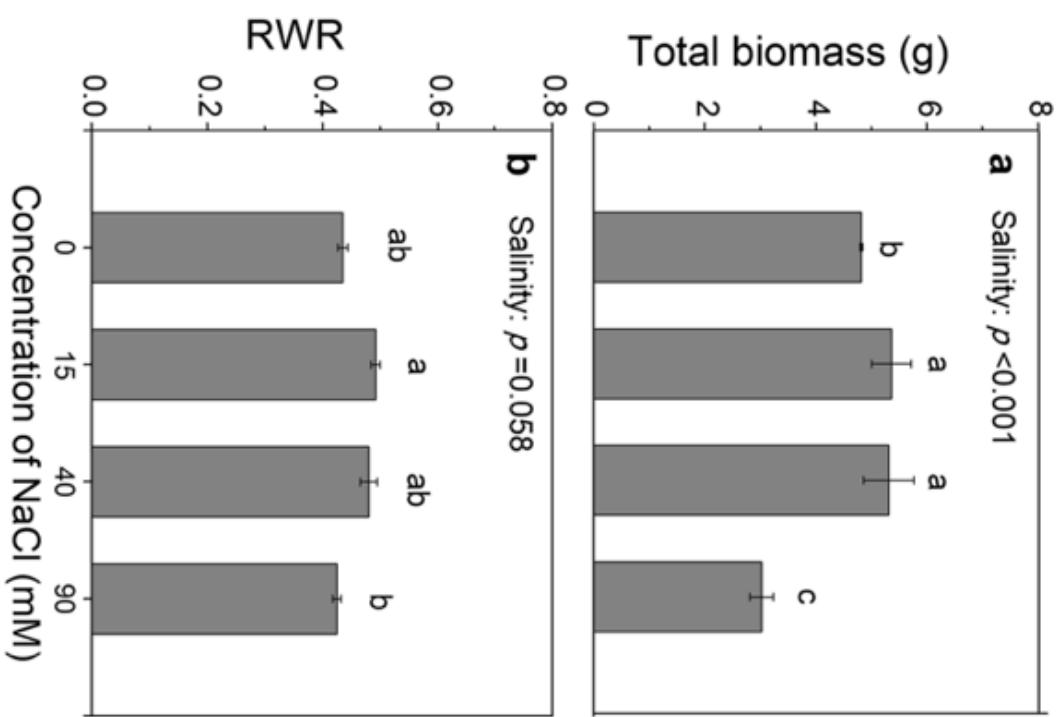
(Lau and Lennon, 2012)

Stress control

Responses to salinity

- Experiments aim to assess whether soil salinity changes the microbial community in the rhizosphere of *Hibiscus hamabo*, and whether these changes in the microbiome feedback on the growth of the plant

- *H. hamabo* was grown in pots with a sand-soil mixture at different salt concentrations (0, 15, 40 and 90 mM NaCl). **Authors tested the effects of the salinity on the plants**
- The salinity treatment significantly affected the total biomass of *H. hamabo*. While root weight ratio was slightly affected

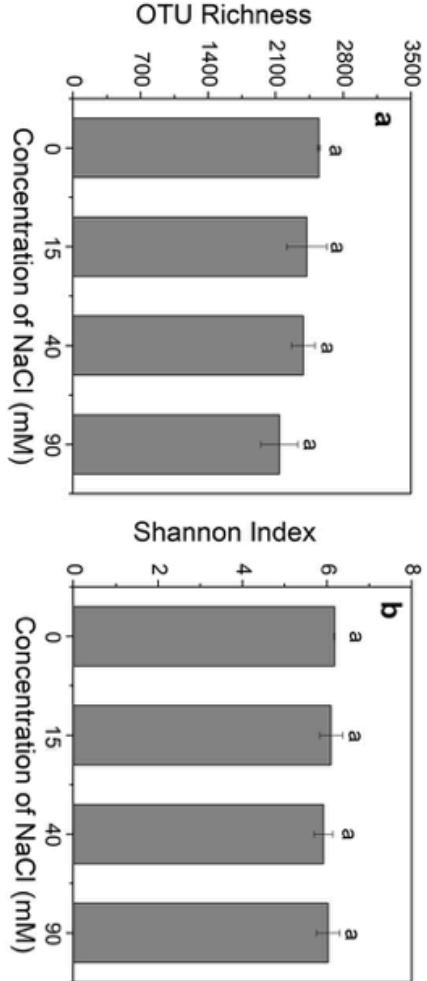


(Yuan, Brunel, van Kleunen, Li, and Jin, 2019)

Stress control

Responses to salinity

- ⚪ Experiments aim to assess whether soil salinity changes the microbial community in the rhizosphere of *Hibiscus hamabo*, and whether these changes in the microbiome feedback on the growth of the plant



- ⚪ *H. hamabo* was grown in pots with a sand-soil mixture at different salt concentrations (0, 15, 40 and 90 mM NaCl). **Authors tested the effects of the salinity on the microbiotas**

- ⓘ There was a slight trend that **bacterial** (a-b) OTU richness and the Shannon indice decreased with increasing salinity (these effects were not significant)

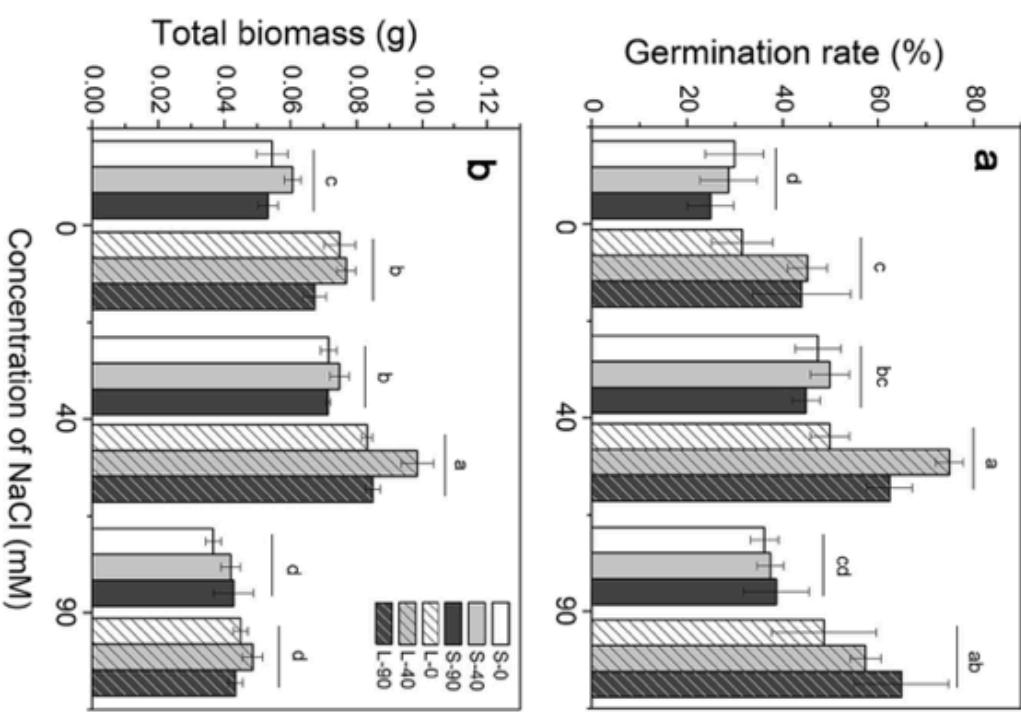
(Yuan Brunel, et al., 2019)

- ⓘ The overall effects of the salinity treatments on **fungal** (d-e) OTU richness and the Shannon indice

Stress control

Responses to salinity

- Experiments aim to assess whether soil salinity changes the microbial community in the rhizosphere of *Hibiscus hamabo*, and whether these changes in the microbiome feedback on the growth of the plant
- *H. hamabo* was grown in pots with root-inoculum addition from previously treated soils (i.e. control with sterilized root inoculum vs the treatments with root inoculum)
- The addition of a live inoculum significantly increased **germination rate**
- The addition of a live inoculum significantly **increased biomass**, effect was stronger at salinities of 0 and 40 mM than at a salinity of 90 mM



(Yuan Brunel, et al., 2019)

Disease resistance

Disease resistance

- **Disease-suppressive soils** are exceptional ecosystems in which crop plants suffer less from specific soil-borne pathogens than expected owing to the activities of other soil microorganisms

Disease resistance

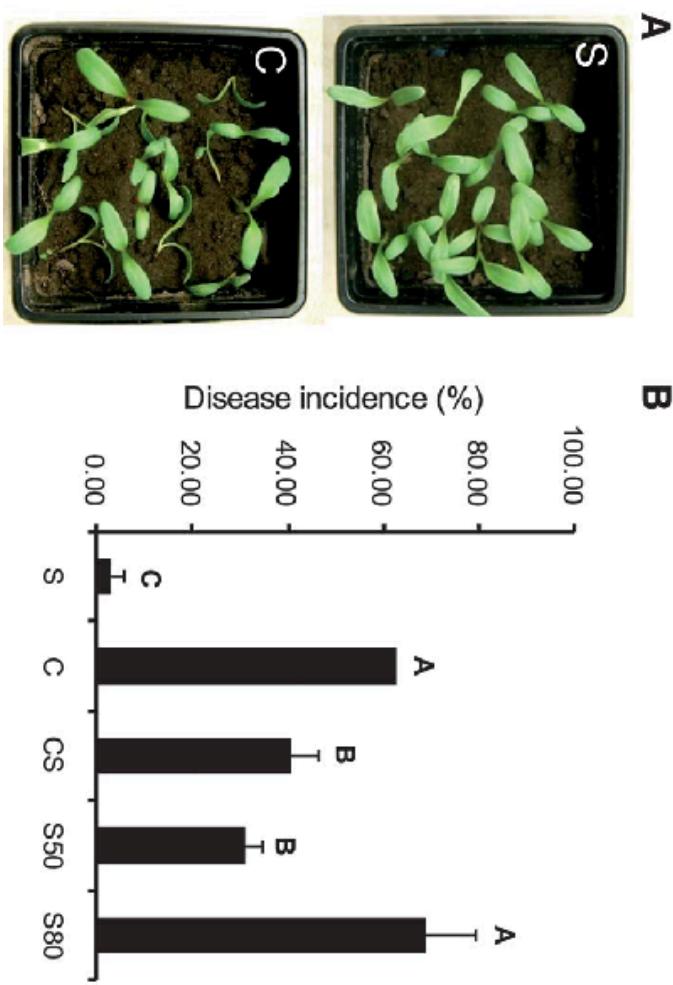
Disease resistance

- The aim of the study was to decipher the rhizosphere microbiome to identify such disease-suppressive microbes and to unravel the mechanisms by which they protect plants against root diseases.

- The investigated soil is suppressive to *Rhizoctonia solani*, an economically important fungal pathogen of many crops

- suppressive soil (S)
- conducive soil (C)
- conducive soil amended with 10% (w/w) of suppressive soil (CS)

- suppressive soil heat-treated at 50°C (S50)
- suppressive soil heat-treated at 80°C (S80)

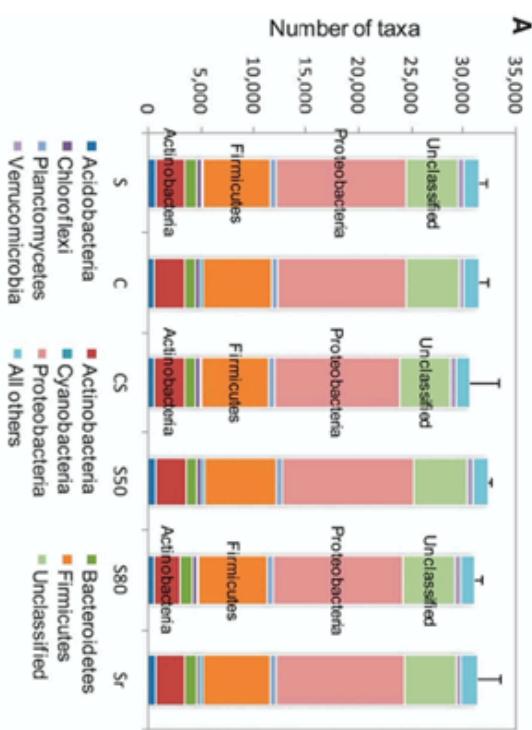


(Mendes, Kruijt, de Brujin, Dekkers, van der Voort, Schneider, Piceno, DeSantis, Andersen, Bakker, and Raaijmakers, 2011)

Disease resistance

Disease resistance

- A total of 33,346 bacterial and archaeal OTUs were detected in the rhizosphere microbiome
- - When comparing the six soil treatments with different levels of disease suppressiveness, no significant differences were found in the number of detected bacterial taxa
- + When the abundance of the detected taxa was taken into account, six clusters of samples that corresponded to the six soil treatments were found

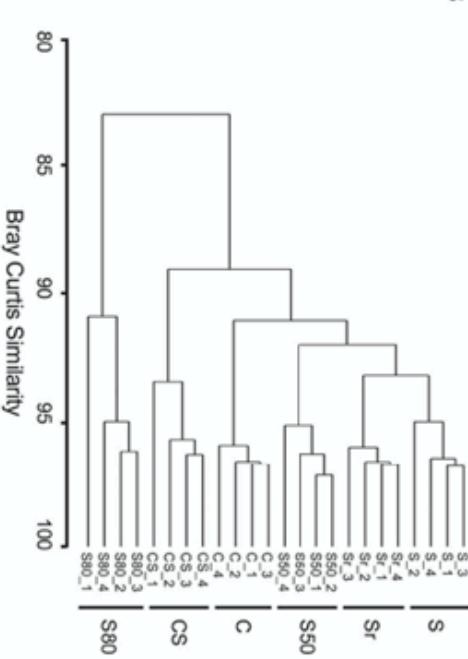


These results suggest that

the relative abundance of several bacterial taxa

is a **more important** indicator of disease

suppression



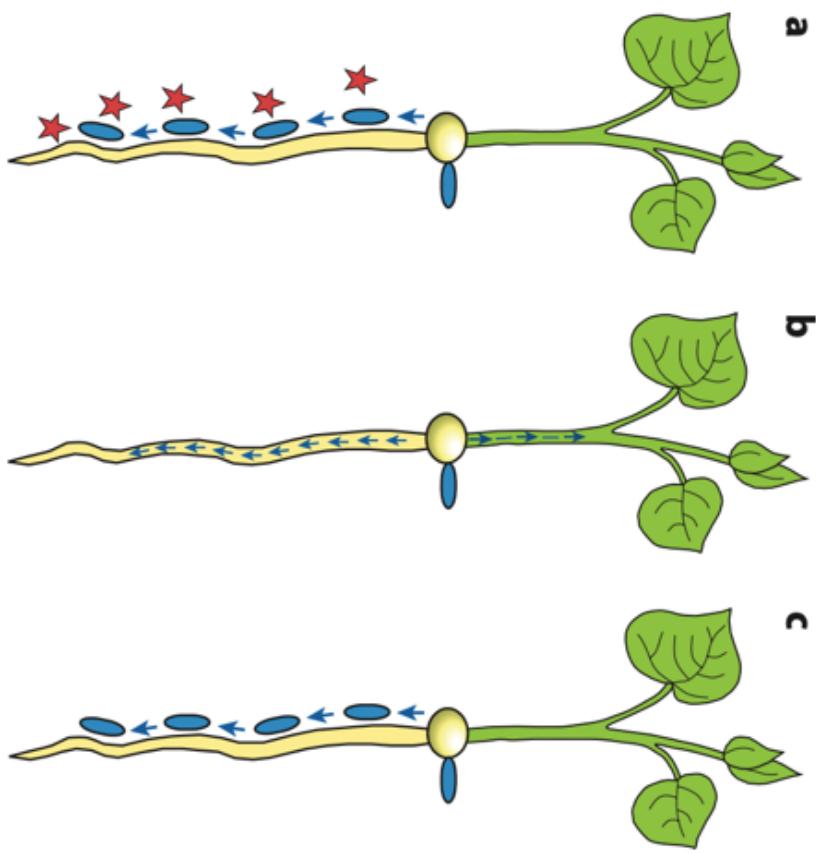
(Mendes Kruijt, et al., 2011)

Disease resistance

How soil-born microbes control the plant disease?

Disease resistance

- (a) **Antibiosis:** The bacterium colonizes the growing root system and delivers antibiotic molecules around the root, thereby harming pathogens that approach the root
- (b) **Induced systemic resistance (ISR):** many bacterial products induce systemic signaling, which can result in protection of the whole plant against diseases caused by different organisms
- (c) **Competition for nutrients and niches:**
Biocontrol bacteria acting through this mechanism excel in fast chemotactic movement along the growing root in their efficient hunt for root exudate components, thereby outcompeting the pathogen in scavenging nutrients and in occupying niches on the root

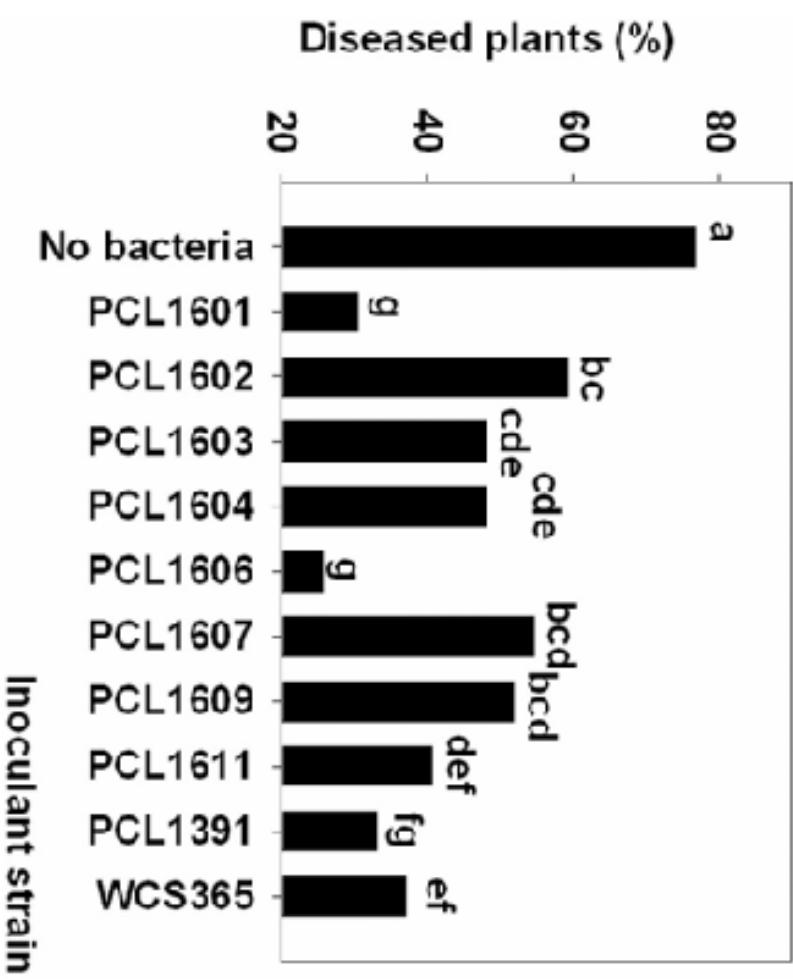


(Lugtenberg and Kamilova, 2009)

Disease resistance

Antibiosis

- *Dematophora necatrix* is the cause of avocado Dematophthora root rot (also called white root rot)
- A set of eight bacterial strains was selected on the basis of growth inhibitory activity against *D. necatrix*. Upon testing the biocontrol ability of these strains in a newly developed avocado test system and in a tomato test system, it became apparent that PCL1606 exhibited the highest biocontrol ability
- This compound was purified and subsequently identified as 2-hexyl 5-propyl resorcinol (HPR).



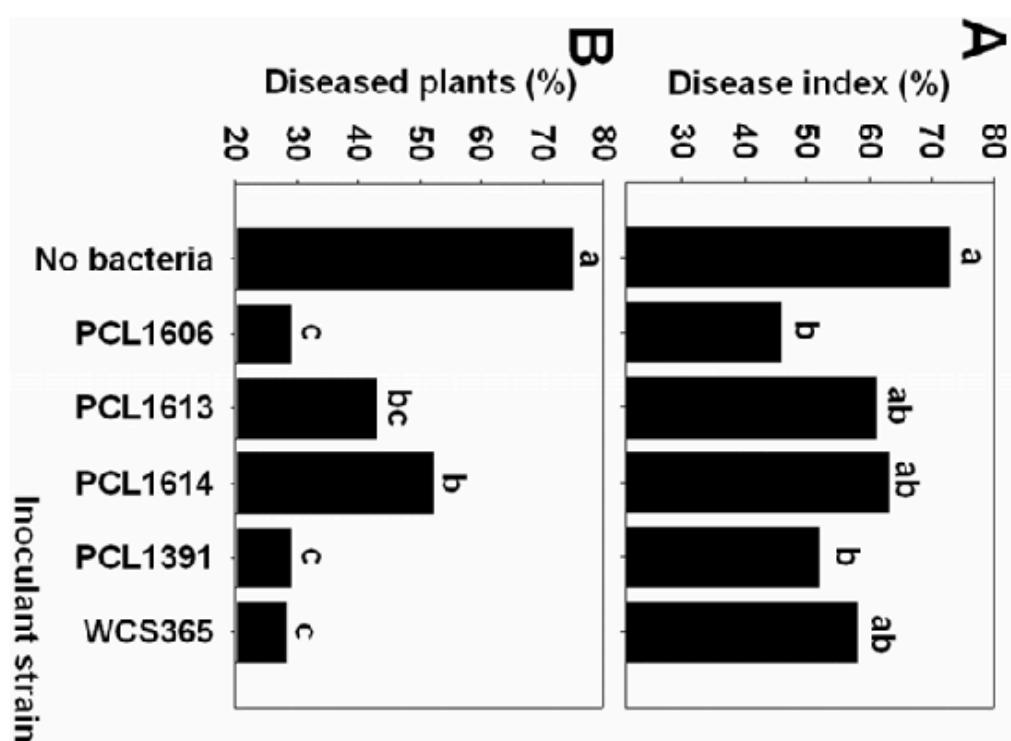
(Cazorla, Duckett, Bergström, Noreen, Odijk, Lugtenberg, Thomas-

Oates, and Bloomberg, 2006)

Disease resistance

Antibiosis

- *Dematophora necatrix* is the cause of avocado Dematophora root rot (also called white root rot)
- A set of eight bacterial strains was selected on the basis of growth inhibitory activity against *D. necatrix*. Upon testing the biocontrol ability of these strains in a newly developed avocado test system and in a tomato test system, it became apparent that PCL1606 exhibited the highest biocontrol ability
- This compound was purified and subsequently identified as 2-hexyl 5-propyl resorcinol (HPR).
- To study the role of HPR in biocontrol activity, two mutants of PCL1606 impaired in antagonistic activity were selected



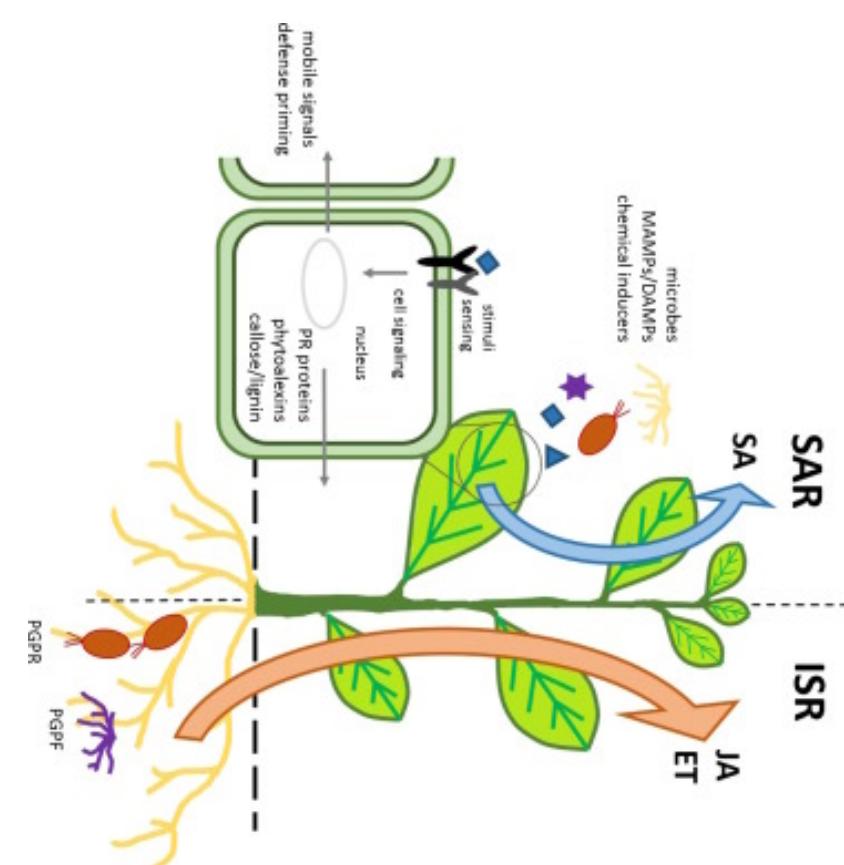
(Cazorla Duckett, et al., 2006)

Disease resistance

Induced systemic resistance

• **Sistemic Acquired Resistance**

(SAR) corresponds to a plant "vaccination" against a broad range of pathogens. Induced by local contact with MAMPs, PAMPs or effectors. SAR is mainly mediated and dependent on Salicylic Acid



• **Induced Systemic Resistance**

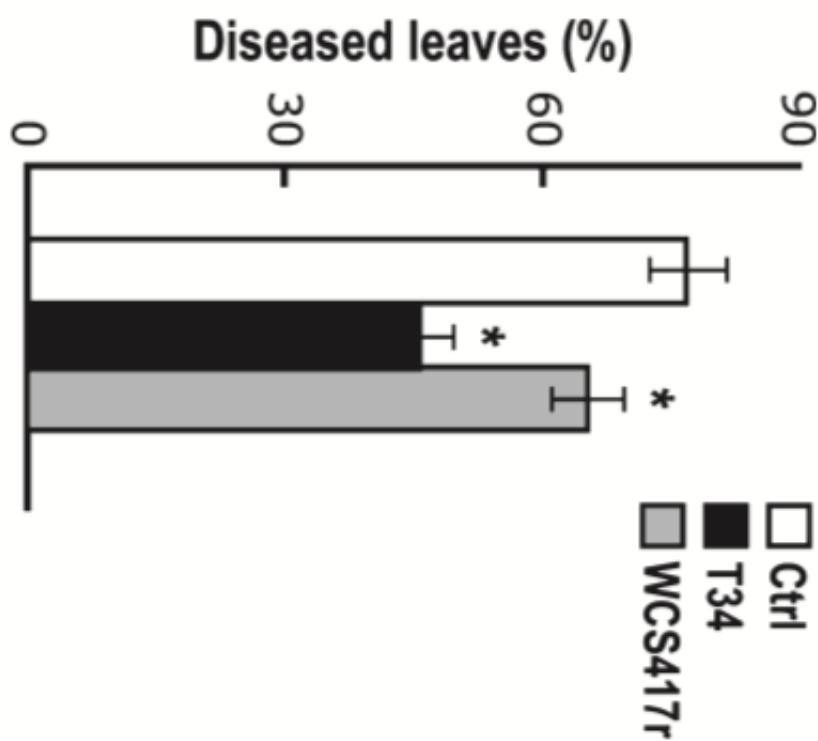
(ISR) is initiated in roots by plant-growth-promoting microbes (PGPM) and leads to resistance priming in distant parts of the plant ISR is mainly mediated and dependent by Jasmonic Acid (JA)

(Burketova, Trda, Ott, and Valentova, 2015)

Disease resistance

Induced systemic resistance

- Determine whether root colonisation by *Trichoderma asperellum* isolate T34 (T34) can enhance resistance in *Arabidopsis* against foliar pathogens
- The severity of bacterial speck disease inflicted by *Pseudomonas syringae* was quantified for control, T34-treated plants and *Pseudomonas fluorescens* WCS417r bacteria (non-pathogenic)



(Segarra, der Ent, Trillas, and Pieterse, 2009)

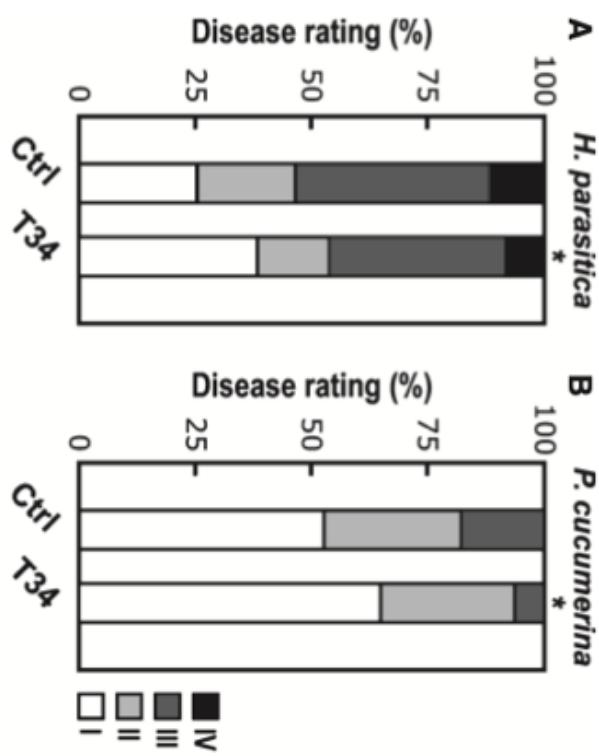
Disease resistance

Induced systemic resistance

- WCS417r is known to be effective against a broad range of pathogens, including obligate biotrophs and necrotrophic fungi

- ⓘ To investigate whether T34-ISR is similarly effective against these types of pathogens

- ⓘ The level of T34-induced protection against the biotrophic oomycete *Hyaloperonospora parasitica* and the necrotrophic fungus *Plectosphaerella cucumerina* was assessed.



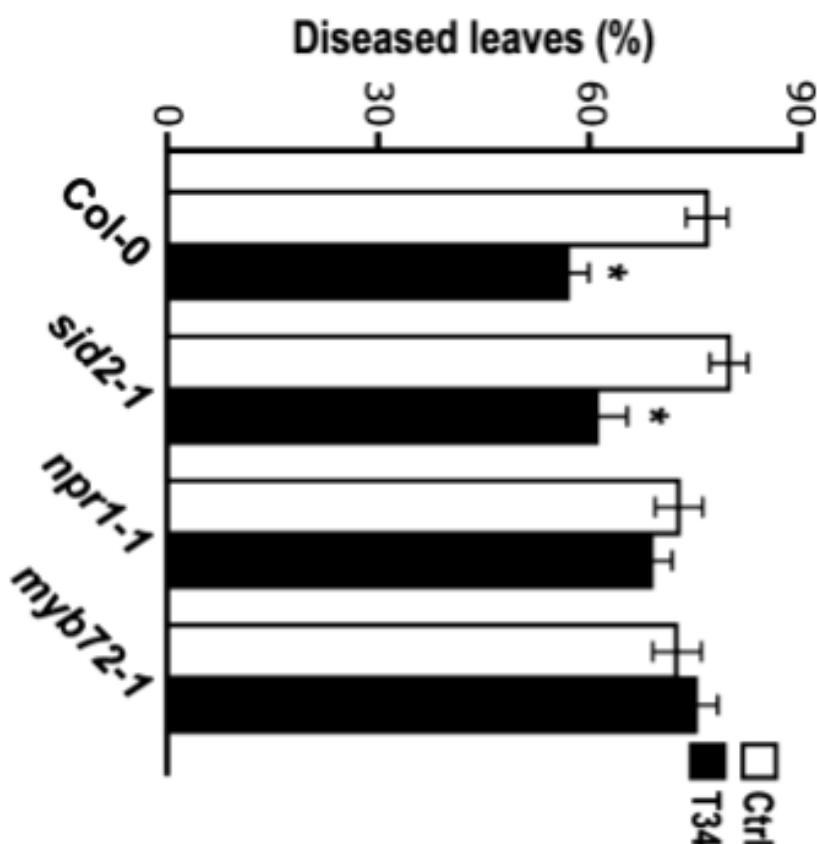
- These results demonstrate that colonisation of *Arabidopsis* roots by T34 triggers a systemic resistance response that is effective against different types of foliar

- Class I: no sporulation
- Class II: trailing necrosis
- Class III: <50% of the leaf area covered with sporangia
- Class IV: >50% of the leaf area covered with sporangia, with additional chlorosis and leaf collapse
- Class I: no symptom
- Class II: lesion diameter <2 mm
- Class III: lesion diameter >2 mm

Disease resistance

Induced systemic resistance

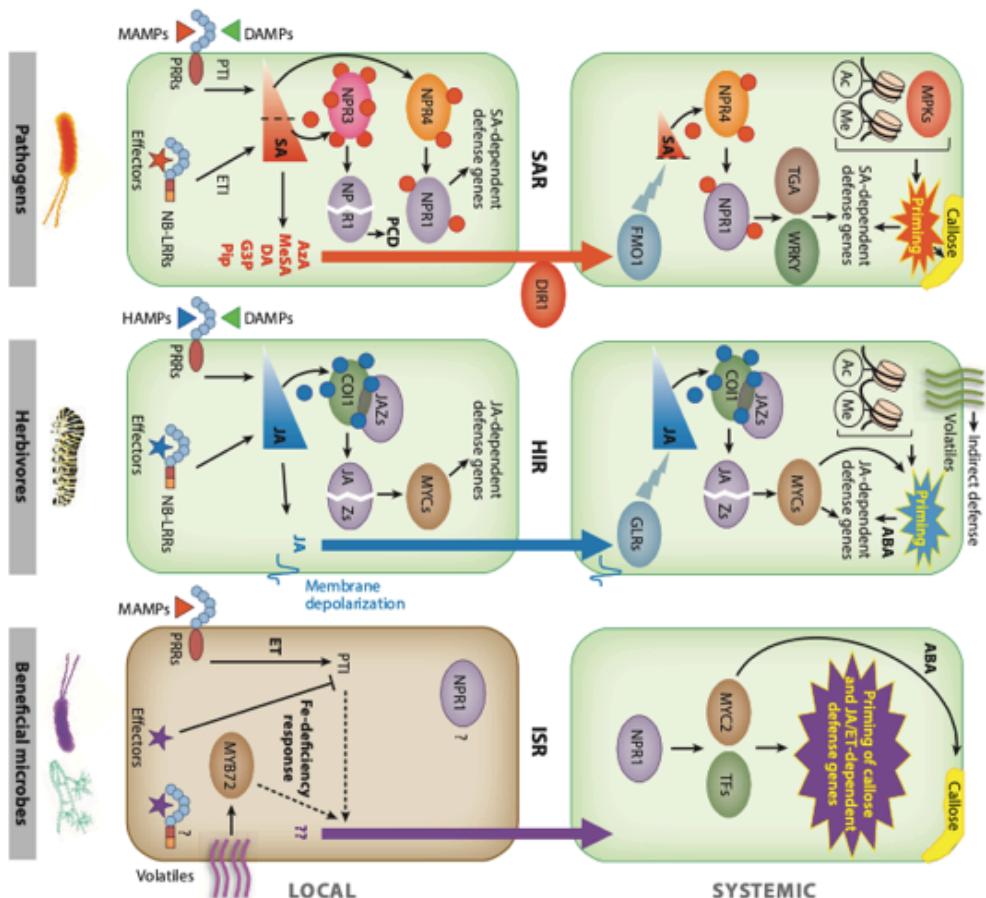
- ◎ How T34 activates ISR response in *Arabidopsis*?
- 💡 Assessed T34-induced resistance in:
 - *sid2-1*: salicylic acid impaired mutant (**SAR**)
 - *npr1-1*: disrupted both **SAR** and **ISR** response
 - *myb72-1*: specifically affected in early steps of **ISR** signalling, but not in component required for general ET or JA signalling
- + *sid2-1* developed a similar level of resistance as wildtype indicating that T34-ISR functions independently of SA
- + *npr1-1* is blocked in its ability to mount ISR, indicating that the regulatory protein NPR1 is required for expression of this type of



(Segarra der Ent, et al., 2009)

Disease resistance

Priming: sensitization of the whole plant for enhanced defense; characterized by a faster and stronger activation of cellular defenses upon invasion



Disease resistance

Competition for nutrients and niches

- ⓘ To study tomato foot and root rot, a plant disease caused by

the fungus *Fusarium oxysporum f.sp. radicis-lycopersici*, and the disease control through the mechanism "competition for

nutrients and niches"

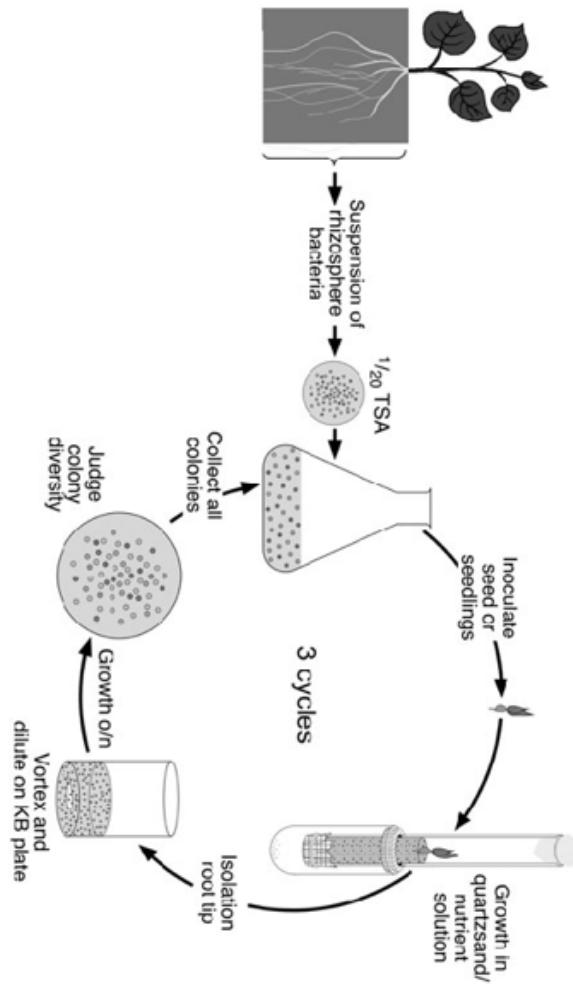
- ⓘ Microbes were isolated from the rhizospheres of tomato plants. Grown briefly in liquid and used to inoculate sterile germinated seedlings. After those microbes had reached the 1-cm-long root tip were shaken off the root tip, plated on KB agar, judged for colony diversity, and the cells from the combined colonies were used for another enrichment cycle.

After a total of three cycles the bacteria were selected for competitive root colonization experiments.

- ⓘ The observation that bacteria selected by the enrichment

method grow much better on exudate than random

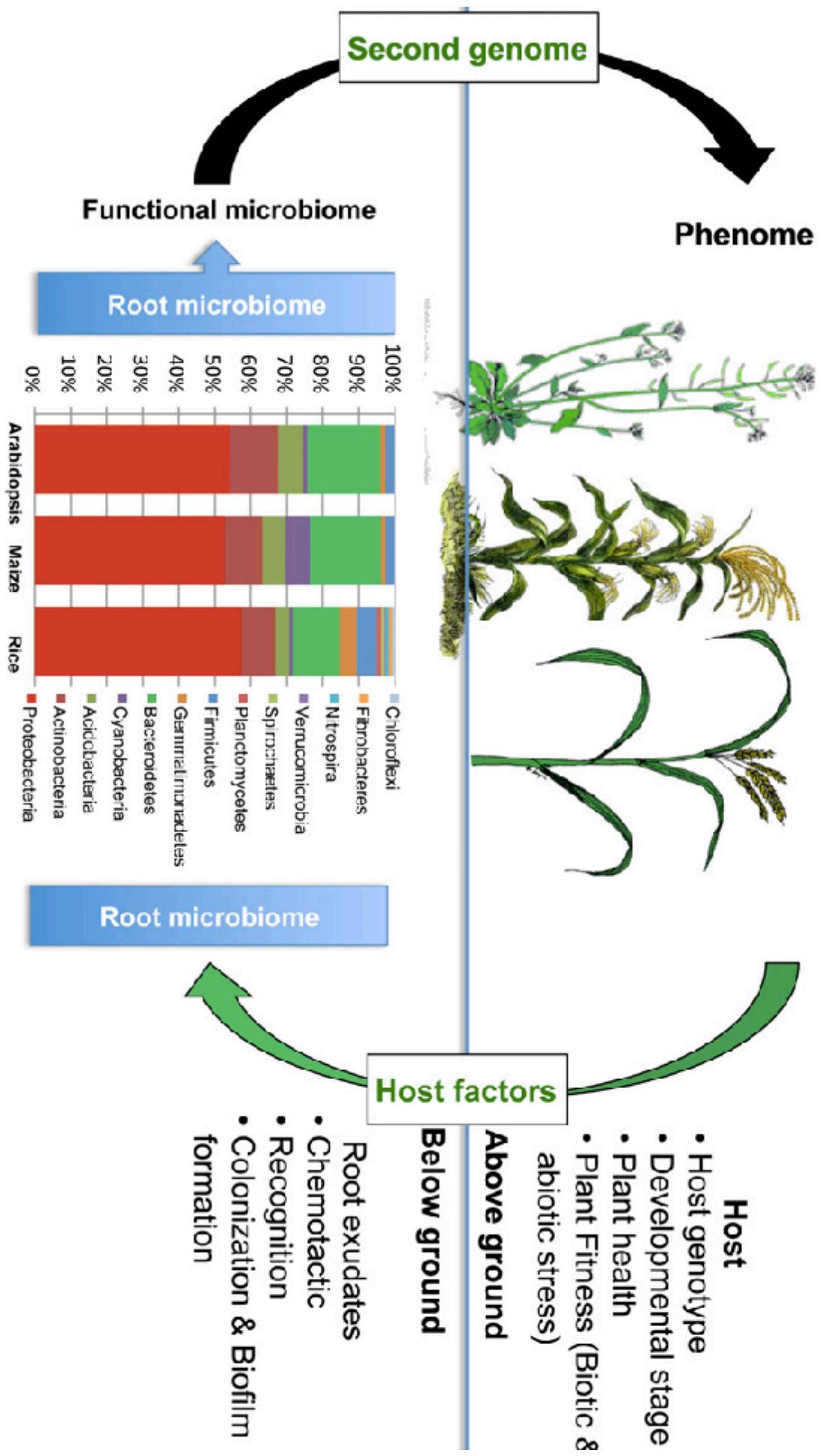
rhizobacteria shows that these strains utilize exudates



(Kamilova, Validov, Azarova, Mulders, and Lugtenberg, 2005)

Can the plant modify the composition of the
associated microbiota?

Plants modify the composition of microbiota

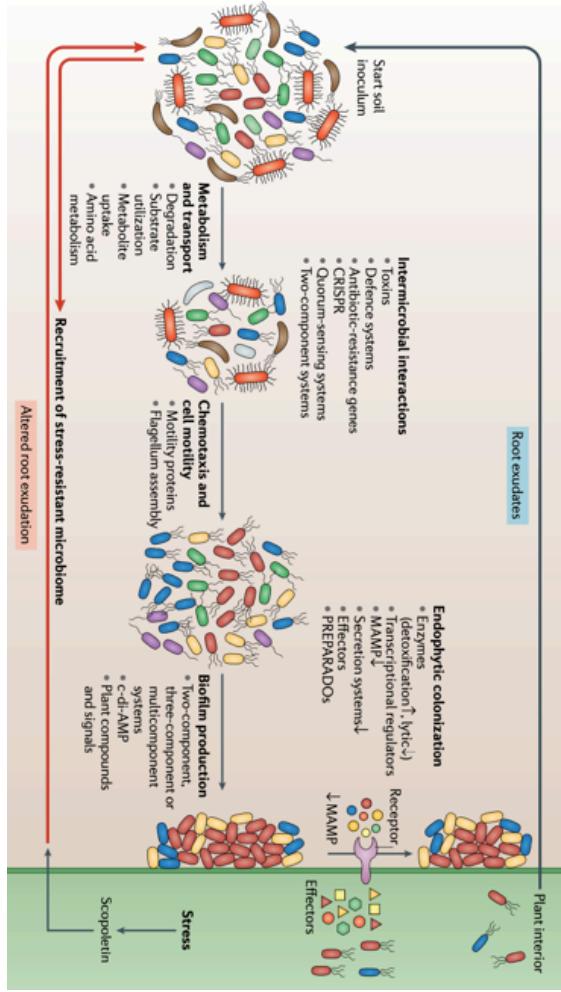


(Lakshmanan, Selvaraj, and Bais, 2014)

Plants modify the composition of microbiota

Plant sensing and the initiation of colonization

1. Plants release exudates
 - **Plant exudates:** complex mixtures of soluble organic substances that are secreted by living plants
2. Plant-associated microorganisms use **chemotaxis** to sense and respond to plant-derived signals
3. Once a signal is perceived, **microorganisms move towards the plant** with the use of flagella
4. Microorganisms attach to the root surface and form a **biofilm**
5. Genes that encode proteins involved in bacterial chemotaxis, flagella assembly, bacterial motility and biofilm formation are **highly abundant in the rhizosphere compared with the bulk soil**

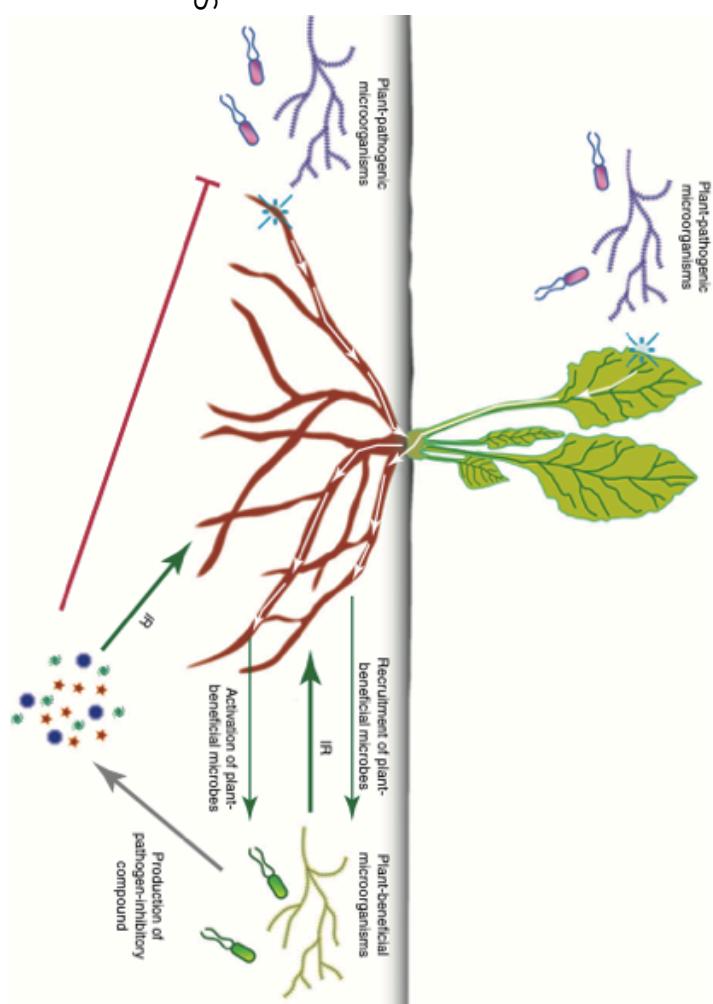


(Trivedi, Leach, Tringe, Sa, and Singh, 2020)

Plants modify the composition of microbiota

How plant can recruit beneficial microbes

- 💡 The plant-associated **microbiota is shaped** by complex interactions among the plant, microorganisms and the environment
- 💡 Metabolic diversification of root exudates within the plant kingdom may provide a basis for communication and recognition that directs the **assembly and maintenance** of a distinct microbiota tailored to the needs of the host
- Plant in response to local environments can **recruit distinct plant-associated microbial communities**

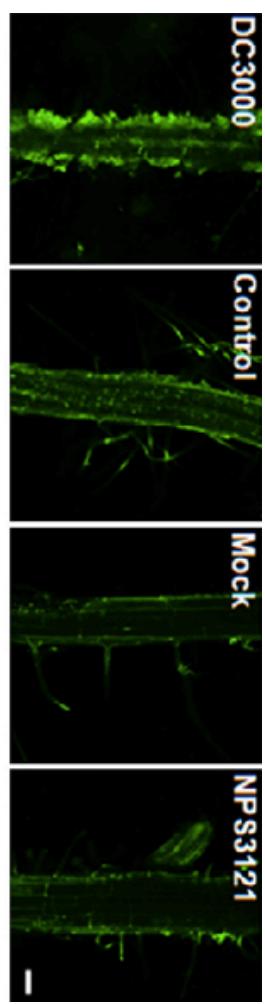


(Berendsen Pieterse, et al., 2012)

Plants modify the composition of microbiota

How plant can recruit beneficial microbes

- Demonstration that roots selectively secrete Malic acid and effectively signal beneficial rhizobacteria establishes a regulatory role of root metabolites in recruitment of beneficial microbes
- Aerial infection with *Pseudomonas syringae* strains Pst DC3000 **correlate with changes in root symbiont colonization** (*Bacillus subtilis* strain FB17) implicated root exudate involvement in the beneficial microbe recruitment



(Rudrappa, Czermmek, Paré, and Bais, 2008)

Plants modify the composition of microbiota

How plant can recruit beneficial microbes

- ⓘ Can leaf infection trigger changes in the composition of root metabolites?



Spurious correlation

Plants modify the composition of microbiota

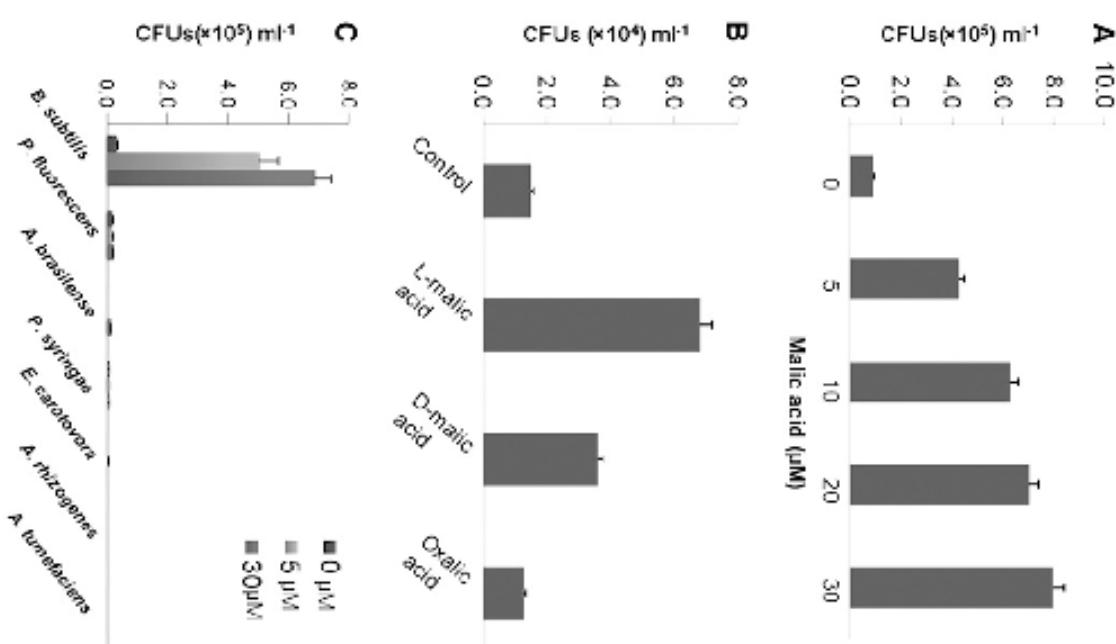
How plant can recruit beneficial microbes

- **?** Can leaf infection trigger changes in the composition of root metabolites?
- **¶** Root secretions from plants subjected to different aerial bacterial infection treatments were collected and chemically analyzed by HPLC
- **¶** The peak was characterized by liquid chromatography-mass spectrometry and determined to be **malic acid**

Plants modify the composition of microbiota

How plant can recruit beneficial microbes

- **?** Is the malic acid able to selectively recruit the symbiont colonization (*Bacillus subtilis* strain FB17)?
- *B. subtilis* exhibits positive chemotaxis towards Malic Acid
- L-MA specifically chemoattracts FB17
- None of the tested bacteria shows any significant motility toward L-MA compared to *B. subtilis*



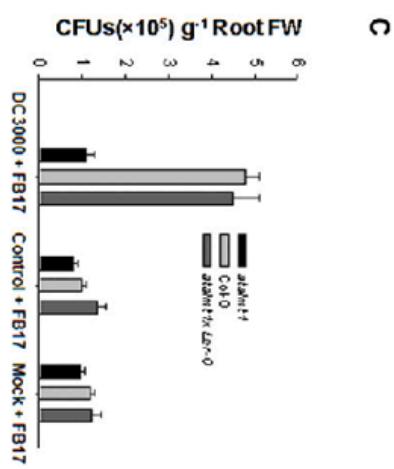
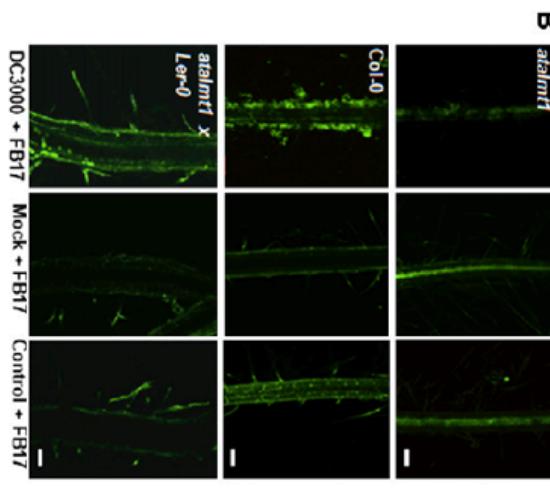
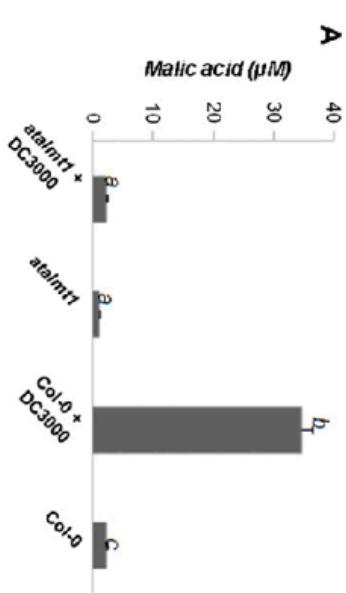
Plants modify the composition of microbiota

How plant can recruit beneficial microbes

- **?** Does MA transporter mutant fails to recruit *B. subtilis* onto the root surface?

- **?** *Arabidopsis* knockout mutant *Atalmt1* **deficient in root MA secretion** was assayed to confirm the role of MA secretions in recruiting FB17

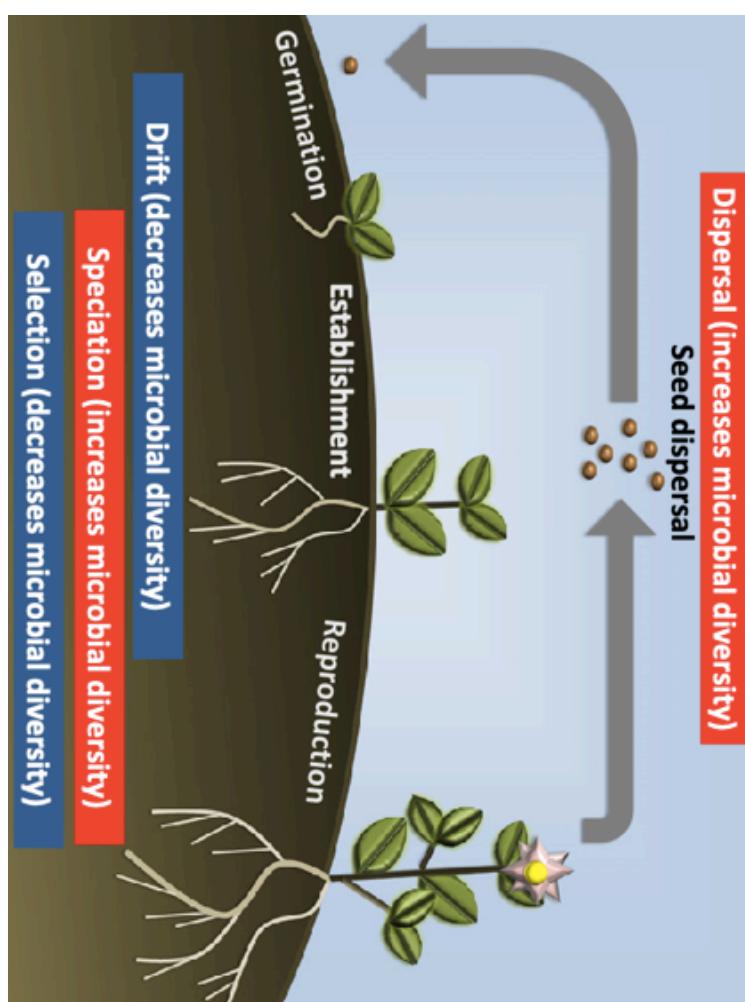
- **?** *Atalmt1* x *Ler-0* line **restored wild-type Col-0 phenotype** under *Pst* DC3000 infection



Plants modify the composition of microbiota

Dynamics of the plant-associated microbiome

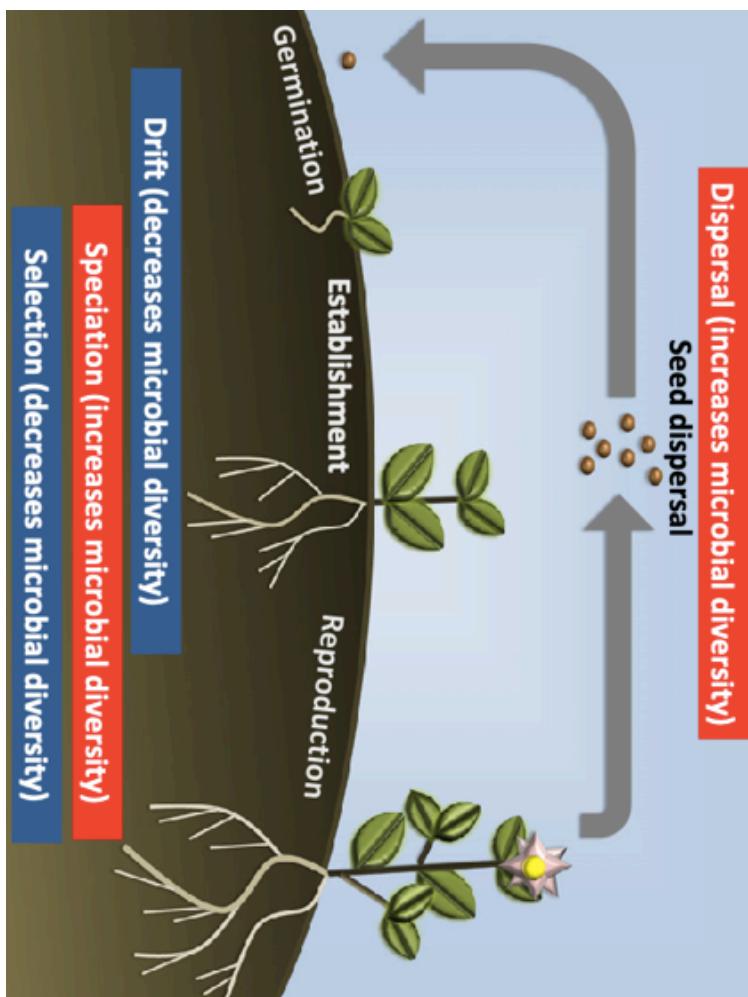
- ⚡ The assembly of a plant-associated microbiome is a **successional, multistep process** that is determined by dispersal, species interactions, the environment and the host
- **Early colonizers** could be **transmitted vertically ↑**, via the parents, through seed transmission pathways
- Once **seeds germinate**, microbiome assembly is likely to be driven by **horizontal transfer ↔:**
 - seed-borne microorganisms preferentially become associated with aboveground plant tissues



Plants modify the composition of microbiota

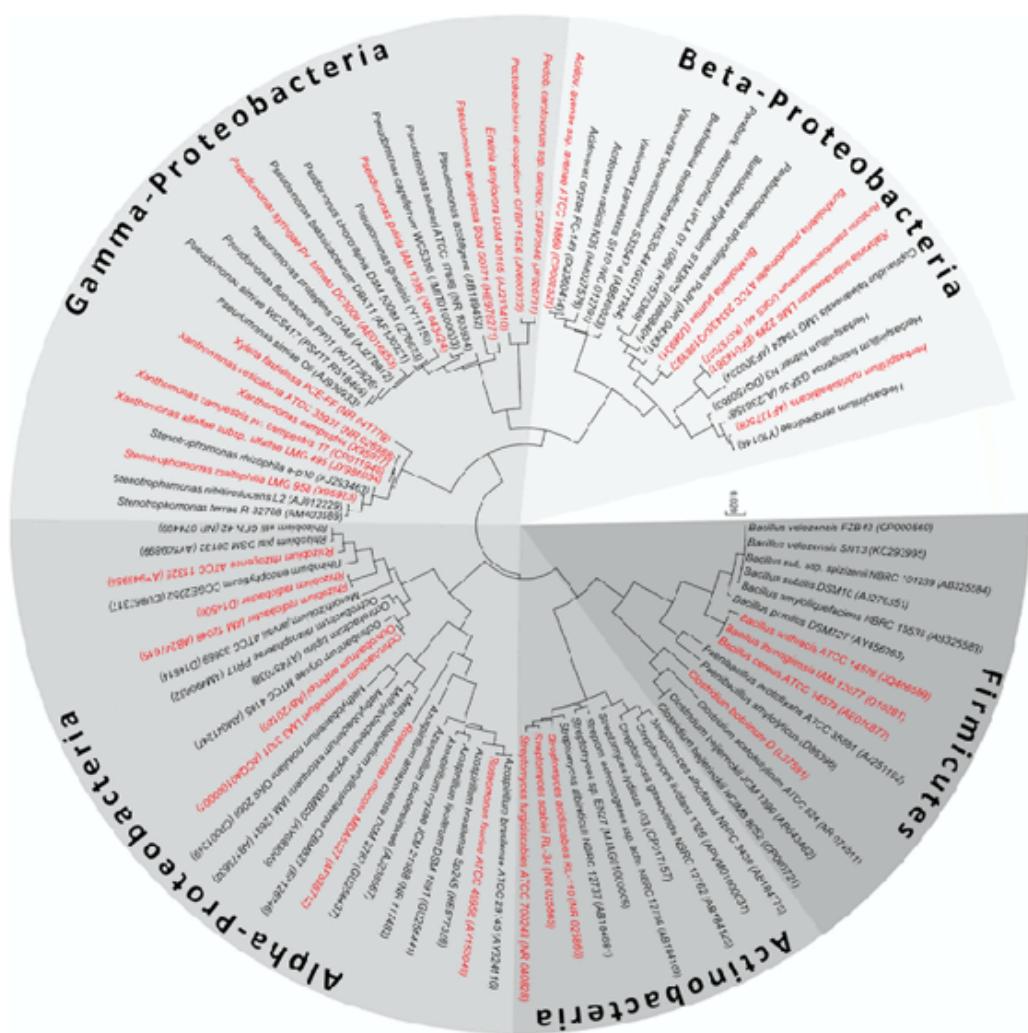
Dynamics of the plant-associated microbiome

- Microbiomes is **highly dynamic** in the early vegetative phase 🌱, begins to **converge** throughout vegetative growth 🌸 and **stabilizes** during the reproductive phase 🌸
- A small fraction of microbial taxa belonging to the **core microbiota** are consistently maintained throughout plant development
- Specific traits (drought tolerance, disease resistance) that are conferred by associations with a particular microbial group can be **passed from mother plants to offspring** ↗



Plants modify the composition of microbiota

Evolutionary Relationship of PGPB and Pathogenic Bacteria



Can we exploit the microbiota?

Can we exploit the microbiota?

Inoculation of microbial consortium

- Microorganisms have long been applied as inoculants for biocontrol or biostimulation

BUT



Can we exploit the microbiota?

Outcomes of inoculation with a microbial consortium

- **Outcomes of inoculating** with a five-member consortium in the presence of a diverse environmental microbial pool
- Three cultivars are depicted growing in **three different regimes**: a normal year, a drought year, and low-input management

- **Genotype effects:**

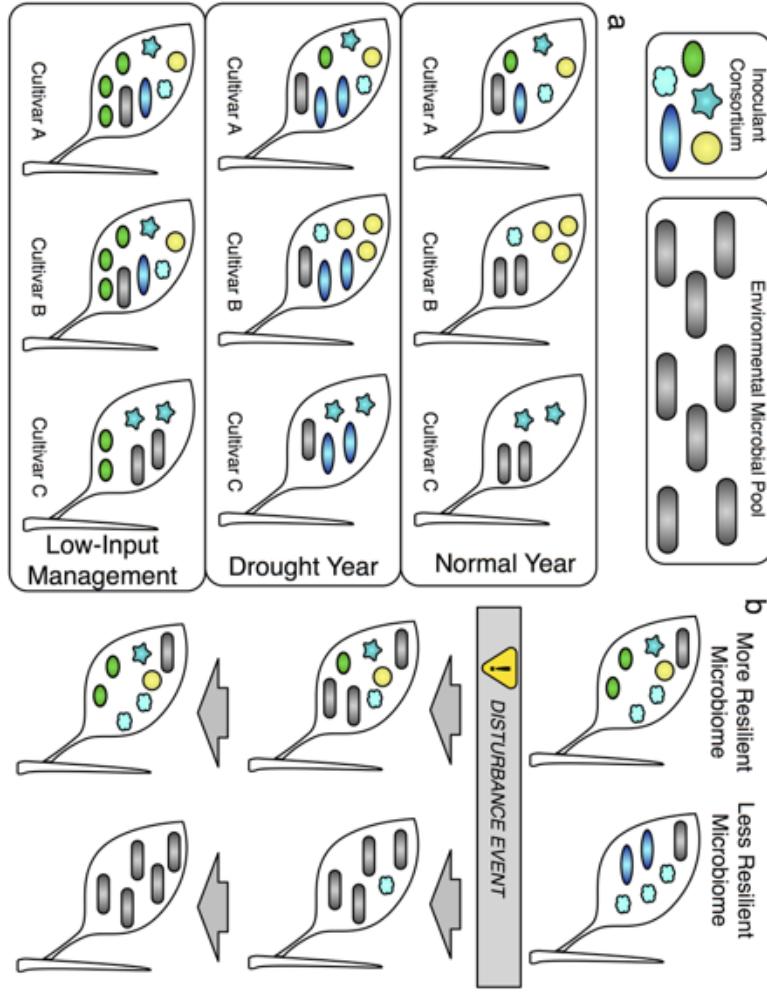
- In a normal year, Cultivar A is colonized by all five members of the inoculant consortium
- Cultivar B is colonized only by yellow spheres
- Cultivar C is colonized only by teal stars

- **Environment/ management effects:**

- The drought year shows higher colonization by blue ovals
- Under low-input management all cultivars show increased colonization by the green spiky ovals

- **Temporal dynamics** of two communities after a disturbance event:

- The more resilient community recovers to its initial state



Can we exploit the microbiota?

Microbiome engineering using synthetic microbial communities

- **⚠ There is NOT a "one size fits all"** microorganism community"
- **💡 Synthetic microbial communities (synComs) of varied complexity have been constructed using bottom-up combinations**
- To build a synCom selection of core functions are more important than taxonomical selection
- synComs with different complexities can be designed through predictive modelling that evaluates trait redundancy, dominance, modularity, interactions and assembly

Companies Examples

Can we exploit the microbiota?



BioConsortia Inc. is devoted to developing solutions through **enhanced crop productivity** and is aware that **microbial products have a major role** to play in future mainstream agricultural crops

<https://bioconsortia.com/>

Can we exploit the microbiota?

Founded in New Zealand in 1994

The company specializes in the discovery and development of natural microbial products

Breakthrough in Advanced Microbial Selection (AMS) process in 2009

Focused on perfecting the innovative R&D platform for AMS

In 2014, the decision was made to globalize

BioConsortia raised \$15 million from Khosla Ventures and Otter Capital, and establishing the headquarters and labs in Davis, CA

Strong R&D Expertise

30 highly experienced experts from industry and academia, including
12 PhDs

Highest level of competency in ultra-high-throughput biological screening

Can we exploit the microbiota?

Can we exploit the microbiota?



At Mycorrhizal Applications, we harness the power and wisdom of natural systems to promote living soils and increase quality, productivity, and health in all industries involving soils, plants, and people

Can we exploit the microbiota?

Founded in USA

Mycorrhizal Applications was established in the Dr. Amaranthuses' garage, with a focus on producing ectomycorrhizal slurries for use in forest restoration

Large-scale production in 2002

The company moved to its first large-scale production and office building

Entered into the agriculture industry in 2004

Its MycoApply® Micronized Endo product being utilized as a seed coat, kick starting the next growth phase for the company

Products for international markets in 2016

New highly-concentrated MycoApply® products for the Agriculture markets and non-Agriculture sectors like Horticulture, Nurseries and Turf Management

Development and launch of new formulations in 2020

New advanced carrier technology for agriculture and for horticulture and turf

Can we exploit the microbiota?



	Endomycorrhizal Fungi			
	<i>Glomus mosseae</i>	<i>Glomus aggregatum</i>	<i>Glomus intraradices</i>	<i>Glomus etunicatum</i>
Plant Nutrition Attributes				
Increased Nitrogen (N) uptake	X	X	X	X
Increased Phosphorus (P) uptake	X	X	X	X
Can access organic forms of N and P			X	
Increases mineral uptake			X	X
Effective root colonization with time-release fertilizers	X	X		
Tolerant of high fertility levels		X		
High levels of enzyme activity benefiting nutrient and micronutrient acquisition	X		X	X
Plant Growth and Establishment				
Improved performance of woody perennials	X		X	X
Increases fruiting and flowering	X		X	X
Improves plant performance in sandy soils		X		
Improves performance of palms and fruit trees		X	X	
Increases crop yields	X		X	X
Improves growth and performance of turf grasses, agricultural crops and nursery stock	X		X	
Very effective in agricultural soils	X		X	X
Improved plant establishment	X		X	X
Well adapted to a wide variety of plants and soil conditions	X		X	
Improved growth of grain crops	X		X	
Increases production of vegetable crops	X		X	
Improved growth of tropical and sub-tropical fruits		X	X	

Can we exploit the microbiota?

Biome Makers

leaders in soil functionality analytics



Global scope

Our goal is to recover the health of our soils and create a more sustainable future.

Advanced Technology

Proprietary technology combining DNA Sequencing, Bioinformatics, and Intelligent computing to enable functional interpretation of microbiome communities.

Rock star team

Highly skilled team in genetics, software engineering, microbiology, agronomy, and data science. Meet them!

<https://biomemakers.com>

Can we exploit the microbiota?

Biome Markers is born in San Francisco, taking action to recover soil health through technology

2015

Tails and market validation for advance soil analysis in vineyard

2016

Launched the operational portal with all the features to be an easy and friendly platform

Community recognition

Many awards for providing the best technology for any crop and soil analysis

2018

Launch BeCrop and Ggeom platforms (even on mobile)

Can we exploit the microbiota?



BeCrop

Smart Agriculture

Farmers & Agronomists

BeCrop is the most advanced technology for functional soil analysis, combining DNA Sequencing and intelligent computing.

Crop specific data-driven insights on what the soil really needs to be healthy for **any crop and any soil**.

Can we exploit the microbiota?

FOUR STEPS,

a complete crop status evaluation



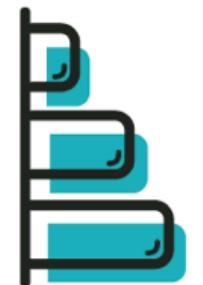
1
Order
BECROP

You will receive your
Soil Collection Kit



2
Collect the
samples

Just three
spoonfuls of soil



3
Get the results
PDF report

Quick
turnaround



4
Optimize
your farming

Get the most out of
your field!

Can we exploit the microbiota?

TRANSLATING DNA

into actionable data

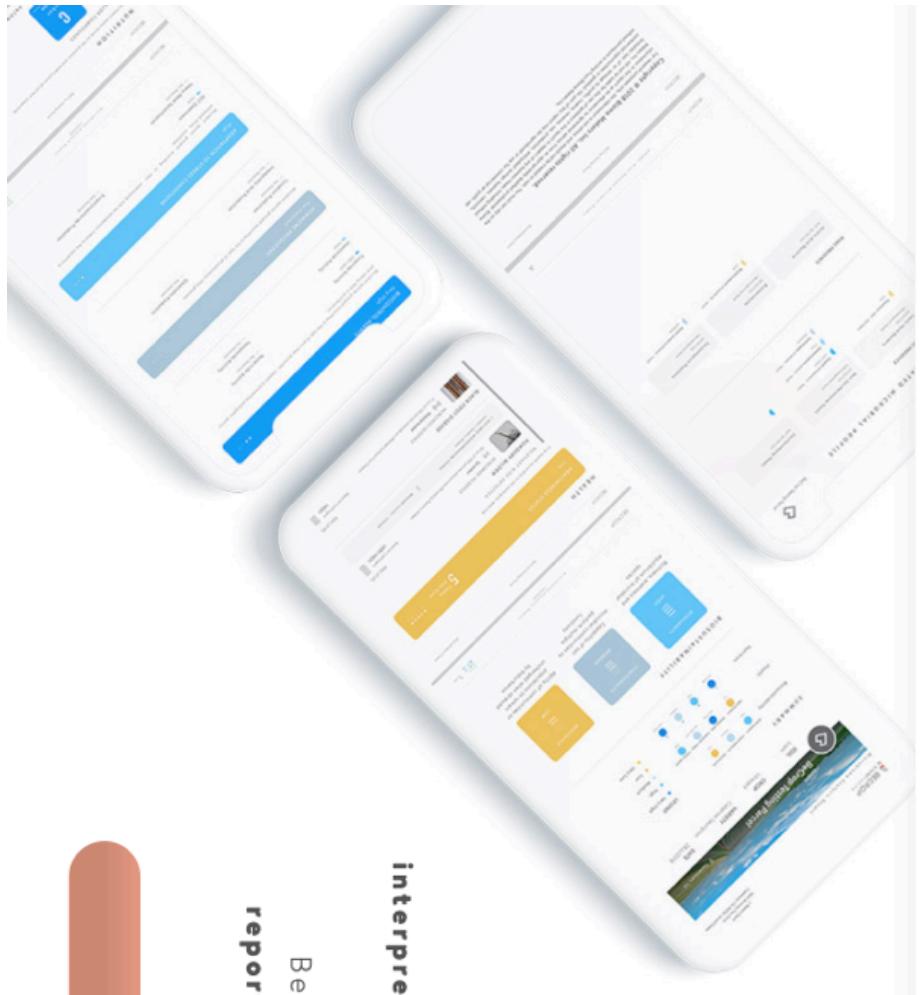
BECROP is a proprietary technology developed in-house by **BIOMEMAKERS**

integrating genomics, AI and AgData to identify the microbial biomarkers

providing a meaningful explanation of soil function in agriculture.

BECROP is a proprietary technology developed in-house by **B I O M E M A K E R S** integrating genomics, AI and AgData to identify the microbial biomarkers providing a meaningful explanation of soil function in agriculture.

Can we exploit the microbiota?



TAKE CONTROL of your crop

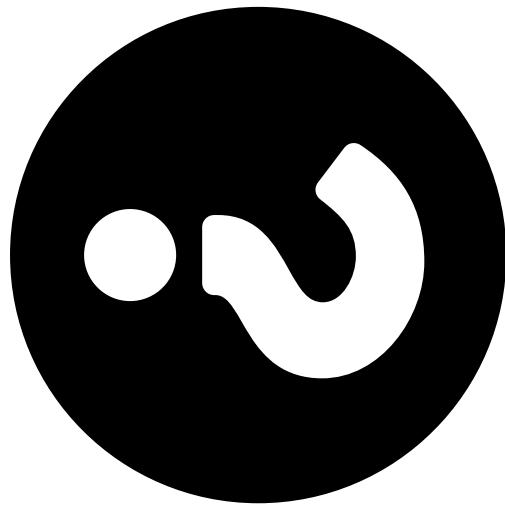
Get the complete microbial analysis and **customized interpretation of your microbiome** based on its biodiversity, vulnerability and nutrition pathways.

BeCrop turns your samples into an **easy-to-understand report** with all the information you need to make the best farming decisions.

 LAUNCH BECROP

Can we exploit the microbiota?

Questions about the lesson



Slack - marco.chiapello@unito.it