

# MICROBIOMA E MICROBIOTA

Marco Chiapello

2021-10-06

 Slack (<https://bit.ly/3upNjCt>) -  marco.chiapello@unito.it

# About the teacher

- Marco Chiapello, PhD
- Plant Biologist 
- Bioinformatician 
- R addicted 
- Deeply in love with teaching 

# General Introduction



- Learning
- Concept maps
- Feedbacks
- Silly questions

# Course overview - Lecture

- Plant Microbiota (5 hours) 
- Ecological Significance of Viruses (2 hours) 
- Reproducible research (1 hour) 
- Elements of Bioinformatics (2 hours) 

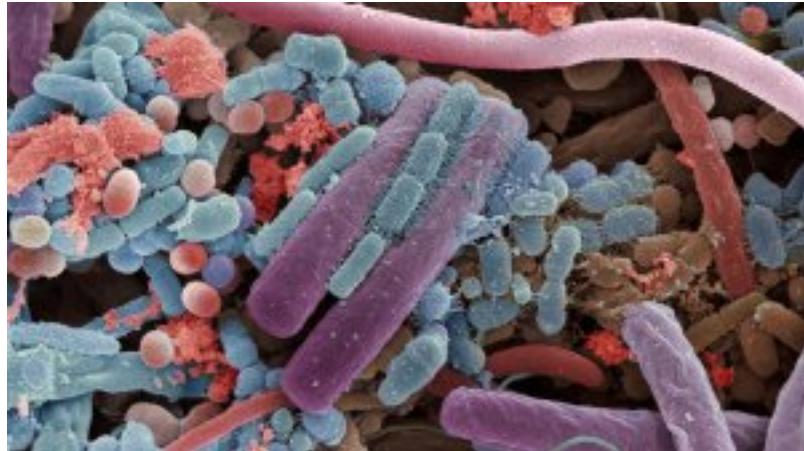
# Course overview - Practical

- Wet lab: How to perform a PCR (3 hours) 
- Dry lab: How to perform alignments/blast/phylogenetic trees (1.5 hours) 
- Dry lab: How to perform microbiota analysis (1.5 hours) 

# Agenda

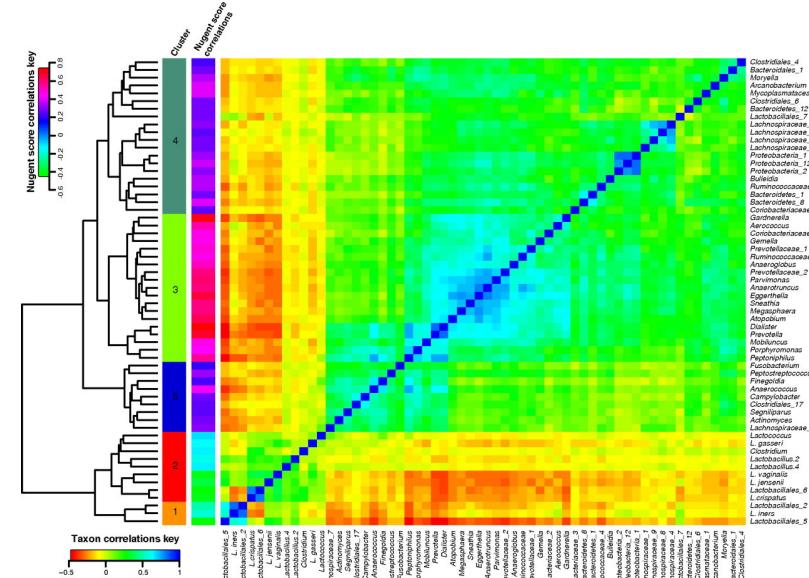
- Introduzione
  - Il microbiota umano
- Il microbiota delle piante
  - Da chi è composto
  - Che funzioni ha
  - Come prende forma

# microBIOTA



si riferisce a una popolazione di microrganismi che colonizza un determinato luogo

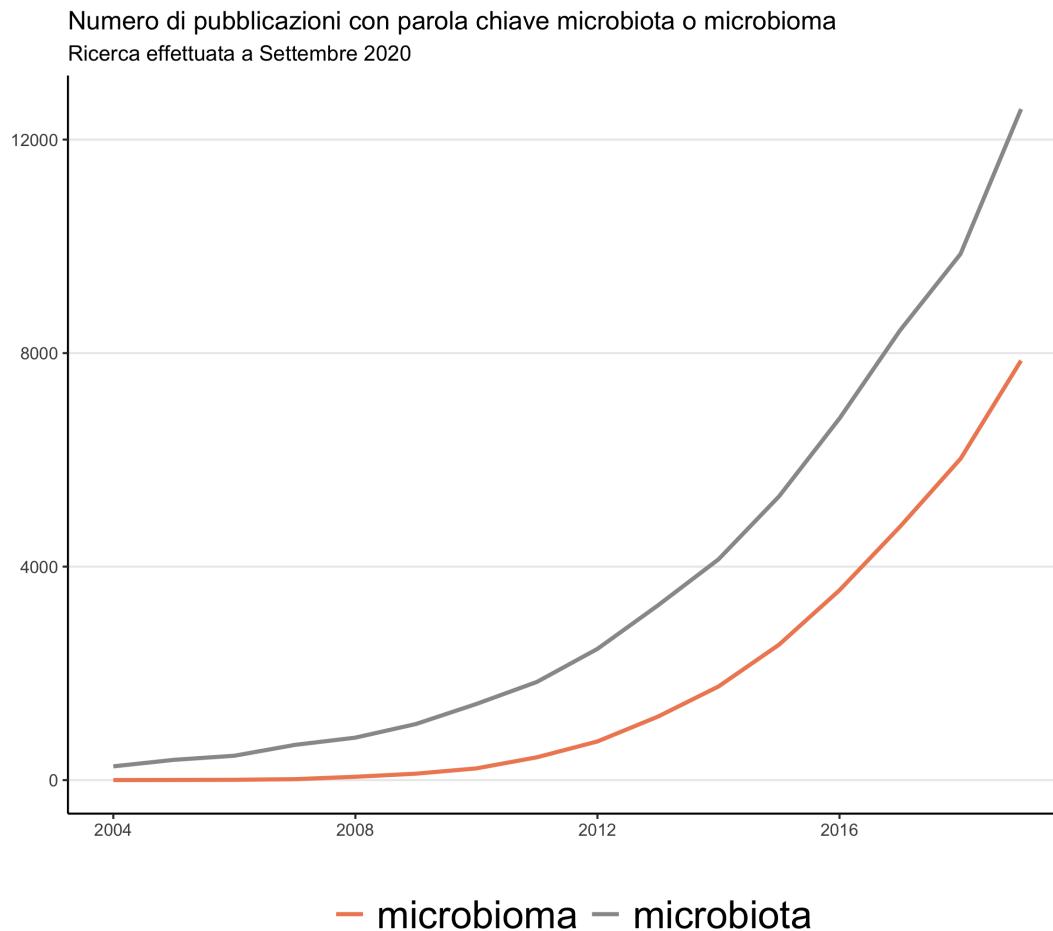
# microBIOMA



indica la totalità del patrimonio genetico posseduto dal microbiota, cioè i geni che quest'ultimo è in grado di esprimere

# microBIOTA

# microBIOMA

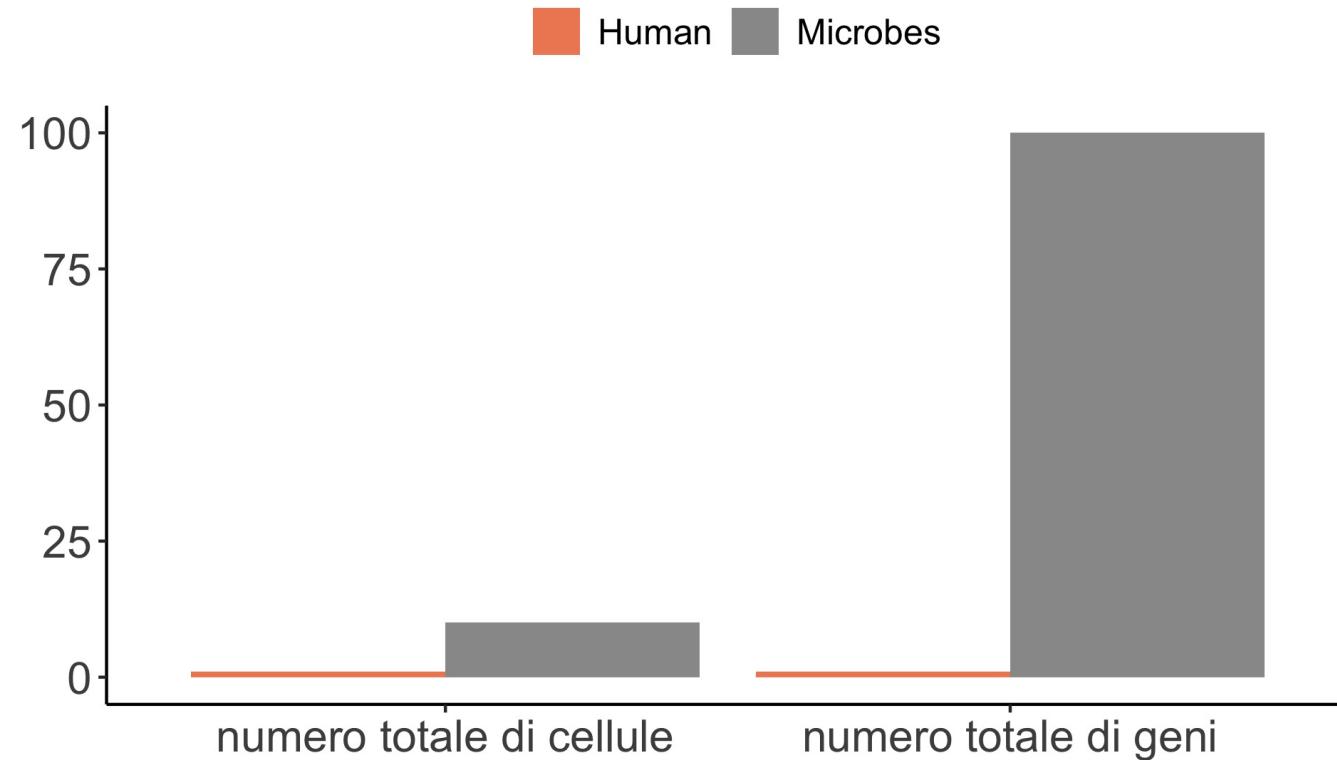


Source: ISI Web of Science

# HMP

Human Microbiome Project

**Il progetto microbioma umano** è una iniziativa dei National Institutes of Health statunitensi con il fine di **identificare e caratterizzare i microrganismi ed il loro rapporto con lo stato di salute e di malattia dell'uomo.**



**L'essere umano va concepito come  
composto da cellule umane e microbiche**

# Temporal human microbiota

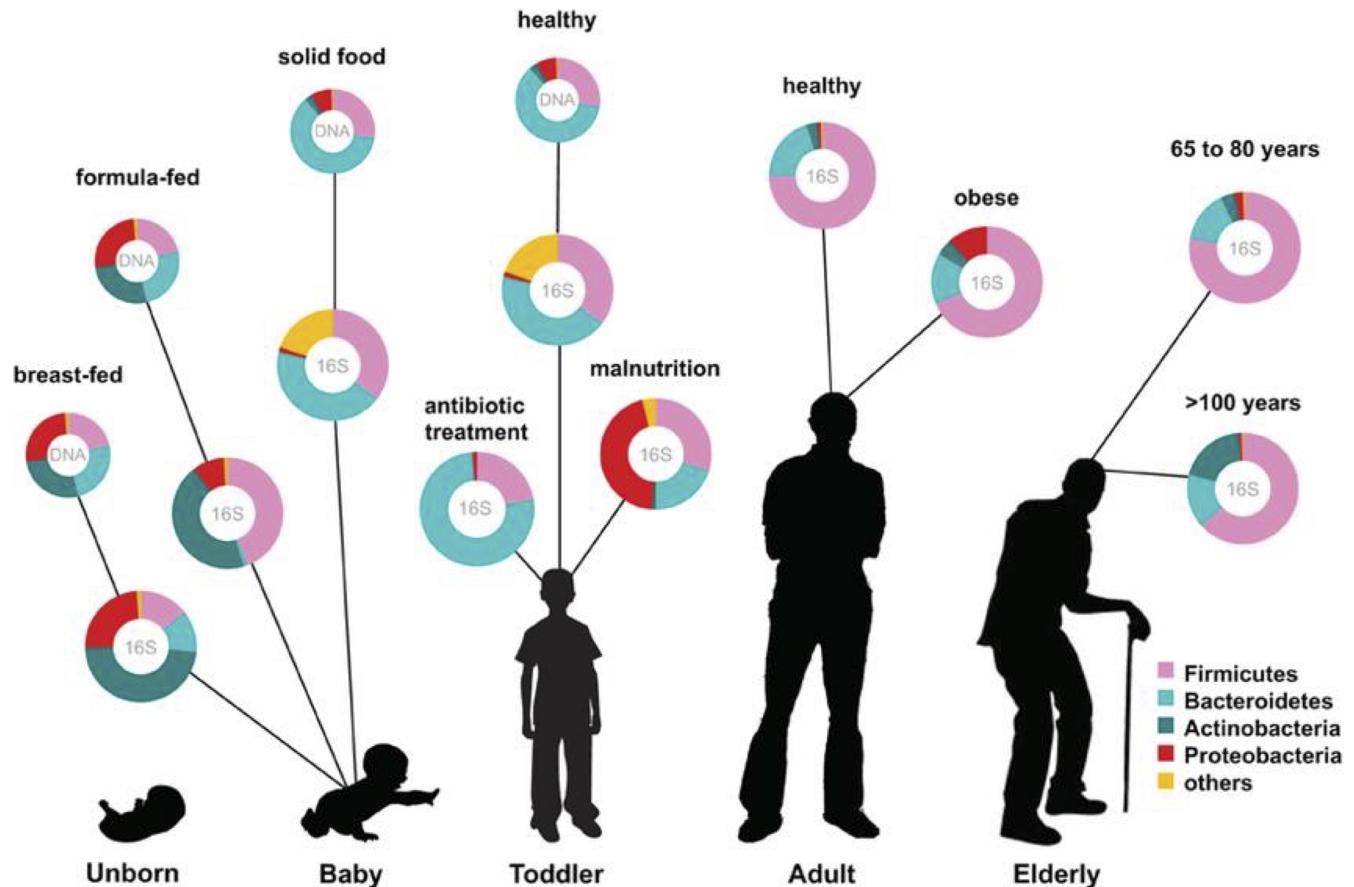
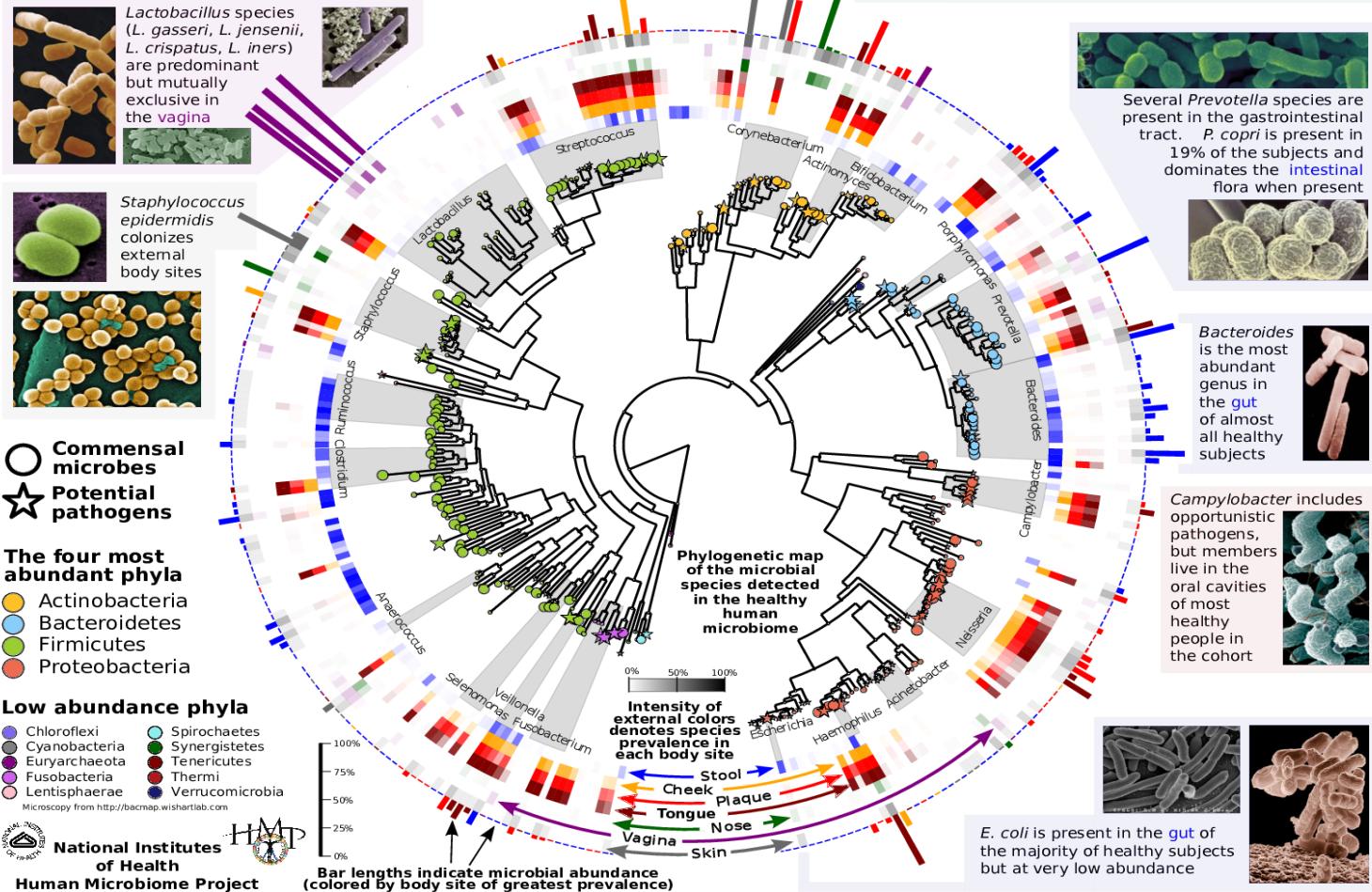


Figure 1: Human microbiota: onset and shaping through life stages and perturbations. The graph provides a global overview of the relative abundance of key phyla of the human microbiota composition in different stages of life. Measured by either 16S RNA or metagenomic approaches (DNA). Data arriving from: Babies breast- and formula-fed (Schwartz et al., 2012), baby solid food (Koenig et al., 2011), toddler antibiotic treatment (Koenig et al., 2011), toddler healthy or malnourished (Monira et al., 2011), adult, elderly, and centenarian healthy (Biagi et al., 2010), and adult obese (Zhang et al., 2009).ti

# Spatial human microbiota

## A map of diversity in the human microbiome



# Human microbiota functions (Kho and Lal, 2018)

Disease categories	Specific diseases	Associated dysbiotic features	Reference
Immune-mediated/autoimmune diseases	inflammatory bowel disease (IBD)	<ul style="list-style-type: none"> <li>• Increase in virulent gut microbes (<i>Enterobacteriaceae</i> species, <i>Bacteroides fragilis</i>) and mucolytic <i>Ruminococcus</i> sp.</li> <li>• Decrease in butyrate-producing <i>Firmicutes</i> (such as <i>Faecalibacterium prausnitzii</i>, <i>Roseburia hominis</i>)</li> </ul>	Sokol et al., 2008; Png et al., 2010; Willing et al., 2010; Machiels et al., 2014
	Irritable bowel syndrome (IBS)	<ul style="list-style-type: none"> <li>• Increase in <i>Escherichia coli</i></li> <li>• Decrease in <i>Clostridium leptum</i> group of bacteria and <i>Bifidobacterium</i>.</li> <li>• Decrease in bile acid biotransformation</li> </ul>	Duboc et al., 2012
	Celiac disease	<ul style="list-style-type: none"> <li>• Increase in <i>Bacteroides–Prevotella</i> group</li> <li>• Decrease in <i>Bifidobacterium</i></li> <li>• Varying observation (decrease or no change) in <i>Clostridium histolyticum</i>, <i>C. lituseburense</i>, and <i>Faecalibacterium prausnitzii</i></li> <li>• Alteration in SCFAs composition, but overall increase in total SCFA</li> </ul>	Tjellström et al., 2005; Nadal et al., 2007; De Palma et al., 2010
	Systemic lupus erythematosus (SLE)	<ul style="list-style-type: none"> <li>• Increase in <i>Blautia</i> sp. and Gram-negative bacteria such as <i>Proteobacteria</i>.</li> <li>• Decrease in gut microbiota diversity, <i>Odonbacter</i> sp., <i>Alistipes</i> sp.</li> <li>• Increase in serum endotoxin</li> </ul>	Shi et al., 2014; Luo et al., 2018
	Type-1 diabetes	<ul style="list-style-type: none"> <li>• Increase in <i>Bacteroidetes</i></li> <li>• Decrease in <i>Actinobacteria</i>, <i>Firmicutes</i>, and <i>Firmicutes/Bacteroidetes</i> ratio</li> </ul>	Murri et al., 2013
	Rheumatoid arthritis (RA)	<ul style="list-style-type: none"> <li>• Increase in <i>Prevotella copri</i> and decrease in <i>Bacteroides</i> sp. In new-onset RA</li> <li>• Increase in microbiota diversity of <i>Lactobacillus</i> genus in early RA</li> <li>• Increase in fecal burden of <i>Clostridium difficile</i>, and <i>C. difficile/Bifidobacteria</i> ratio</li> </ul>	Liu et al., 2013; Scher et al., 2013
	Atopic disease (E.g., childhood allergic asthma)		Kalliomäki et al., 2001

# Human microbiota functions (Kho and Lal, 2018)

Disease categories	Specific diseases	Associated dysbiotic features	Reference
Metabolic disorders/cardiovascular disorders	Obesity	<ul style="list-style-type: none"><li>Increase in <i>Firmicutes</i>, <i>Actinobacter</i></li></ul>	Turnbaugh et al., 2006, 2009a; Koliada et al., 2017
	Type-2 diabetes	<ul style="list-style-type: none"><li>Varying observation (decrease, no change, increase) in <i>Bacteroidetes</i></li><li>Increase in glycoside hydrolase and SCFAs (butyrate and acetate)</li><li>Increase in <i>Lactobacillus</i></li><li>Decrease in <i>Clostridium coccoides</i>, <i>Atopobium</i> cluster, and <i>Prevotella</i></li><li>Decrease in butyrate biosynthesis</li></ul>	Qin et al., 2012; Sato et al., 2014
	Hypertension	<ul style="list-style-type: none"><li>Increase in the Firmicutes/Bacteroidetes ratio, lactate-producer</li><li>Decrease in microbiota diversity, acetate- and butyrate-producers</li></ul>	Yang et al., 2015
	Atherosclerosis	<ul style="list-style-type: none"><li>Increase in metabolites TMAO, endotoxin level (risk factor for early atherosclerosis)</li></ul>	Wiedermann et al., 1999; Koeth et al., 2013
Cancer	Colorectal cancer (CRC)	<ul style="list-style-type: none"><li>Increase in enterotoxigenic <i>Bacteroides fragilis</i>, and pathogens <i>Fusobacterium</i> and <i>Campylobacter</i> sp.</li><li>Decrease in butyrate-producer (<i>Faecalibacterium</i> and <i>Roseburia</i>)</li></ul>	Wang et al., 2012; Wu et al., 2013

# Human microbiota functions (Kho and Lal, 2018)

Disease categories	Specific diseases	Associated dysbiotic features	Reference
Neurological disease	Autism spectrum disorder (ASD)	<ul style="list-style-type: none"><li>• Increase in <i>Clostridium</i> sp., <i>Bacteroidetes</i>, <i>Lactobacillus</i>, <i>Desulfovibrio</i></li><li>• Decrease in <i>Bifidobacteria</i></li></ul>	Song et al., 2004; Adams et al., 2011
	Alzheimer's disease	<ul style="list-style-type: none"><li>• Possible connection between gut microbiota-synthesized amyloids, LPS, <math>\gamma</math>-aminobutyric acid (GABA – major inhibitory neurotransmitter), and the increased permeability of gut barrier and blood brain barrier with age</li></ul>	Pistollato et al., 2016
	Depression	<ul style="list-style-type: none"><li>• Increase in genus <i>Eggerthella</i>, <i>Holdemania</i>, <i>Gelria</i>, <i>Tunicibacter</i>, <i>Paraprevotella</i>, <i>Anaerofilum</i></li><li>• Decrease in gut microbiota diversity, <i>Prevotella</i> and <i>Dialister</i></li></ul>	Kelly et al., 2016
	Parkinson's Disease	<ul style="list-style-type: none"><li>• Increase in anti-inflammatory butyrate-producers from genus <i>Blautia</i>, <i>Coprococcus</i>, and <i>Roseburia</i> in patient fecal sample, pro-inflammatory <i>Proteobacteria</i> in patient mucosa</li><li>• Increased gene expression in LPS biosynthesis and microbial type III secretion system</li></ul>	Keshavarzian et al., 2015
Infectious disease	<i>Clostridium difficile</i> infection (CDI)	<ul style="list-style-type: none"><li>• Increase in <i>Clostridium difficile</i>;</li><li>• Decrease in gut microbiota diversity and secondary bile acids-producing <i>Clostridium scindens</i></li></ul>	Theriot et al., 2014
Uremic disease	Chronic kidney disease	<ul style="list-style-type: none"><li>• Increase in <i>Firmicutes</i>, <i>Proteobacteria</i>, and <i>Actinobacteria</i></li><li>• Decrease in <i>Lactobacilli</i></li></ul>	Vaziri et al., 2013

# Il microbiota delle piante

---

Numero di pubblicazioni con parola chiave microbiota e pianta o microbioma e pianta  
Ricerca effettuata a Settembre 2020



Source: ISI Web of Science

# Composizione del microbiota

---

# Composizione del microbiota

## Glossario

- **Rhizosphere:**

- **Phyllosphere:**

- **Endophytes:**

- **bulk soil:**

# Composizione del microbiota

## Glossario

- **Rhizosphere:** The region of soil in the vicinity of plant roots that is influenced by plant-derived nutrients and oxygen availability; it is not a region of definable size or shape, but instead consists of a gradient in chemical, biological and physical properties that change both radially and longitudinally along the root.
- **Phyllosphere:**
- **Endophytes:**
- **bulk soil:**

# Composizione del microbiota

## Glossario

- **Rhizosphere:** The region of soil in the vicinity of plant roots that is influenced by plant-derived nutrients and oxygen availability; it is not a region of definable size or shape, but instead consists of a gradient in chemical, biological and physical properties that change both radially and longitudinally along the root.
- **Phyllosphere:** All the aboveground organs of plants, including the leaf, flower, stem and fruit.
- **Endophytes:**
- **bulk soil:**

# Composizione del microbiota

## Glossario

- **Rhizosphere:** The region of soil in the vicinity of plant roots that is influenced by plant-derived nutrients and oxygen availability; it is not a region of definable size or shape, but instead consists of a gradient in chemical, biological and physical properties that change both radially and longitudinally along the root.
- **Phyllosphere:** All the aboveground organs of plants, including the leaf, flower, stem and fruit.
- **Endophytes:** The microorganisms residing within plant tissues (the endosphere), such as leaves, roots or stems.
- **bulk soil:**

# Composizione del microbiota

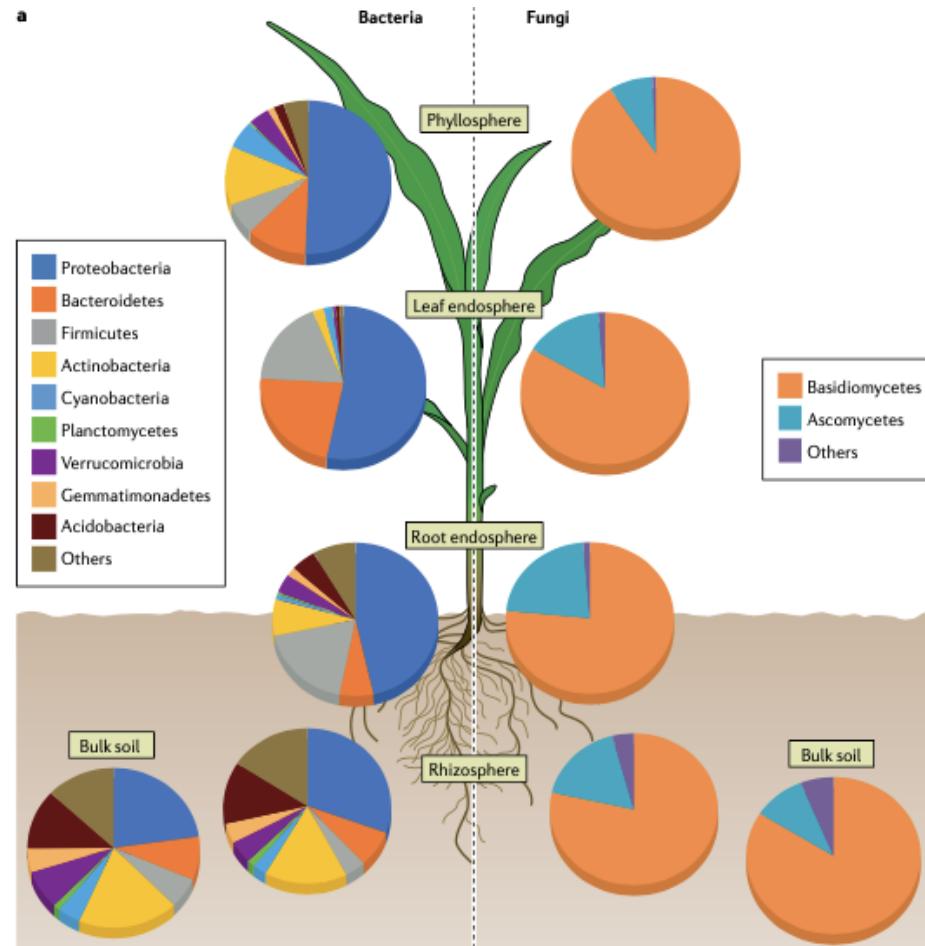
## Glossario

- **Rhizosphere:** The region of soil in the vicinity of plant roots that is influenced by plant-derived nutrients and oxygen availability; it is not a region of definable size or shape, but instead consists of a gradient in chemical, biological and physical properties that change both radially and longitudinally along the root.
- **Phyllosphere:** All the aboveground organs of plants, including the leaf, flower, stem and fruit.
- **Endophytes:** The microorganisms residing within plant tissues (the endosphere), such as leaves, roots or stems.
- **bulk soil:** is soil outside the rhizosphere. bulk soil is not penetrated by plant roots

# Composizione del microbiota

## Spatial plant microbiota

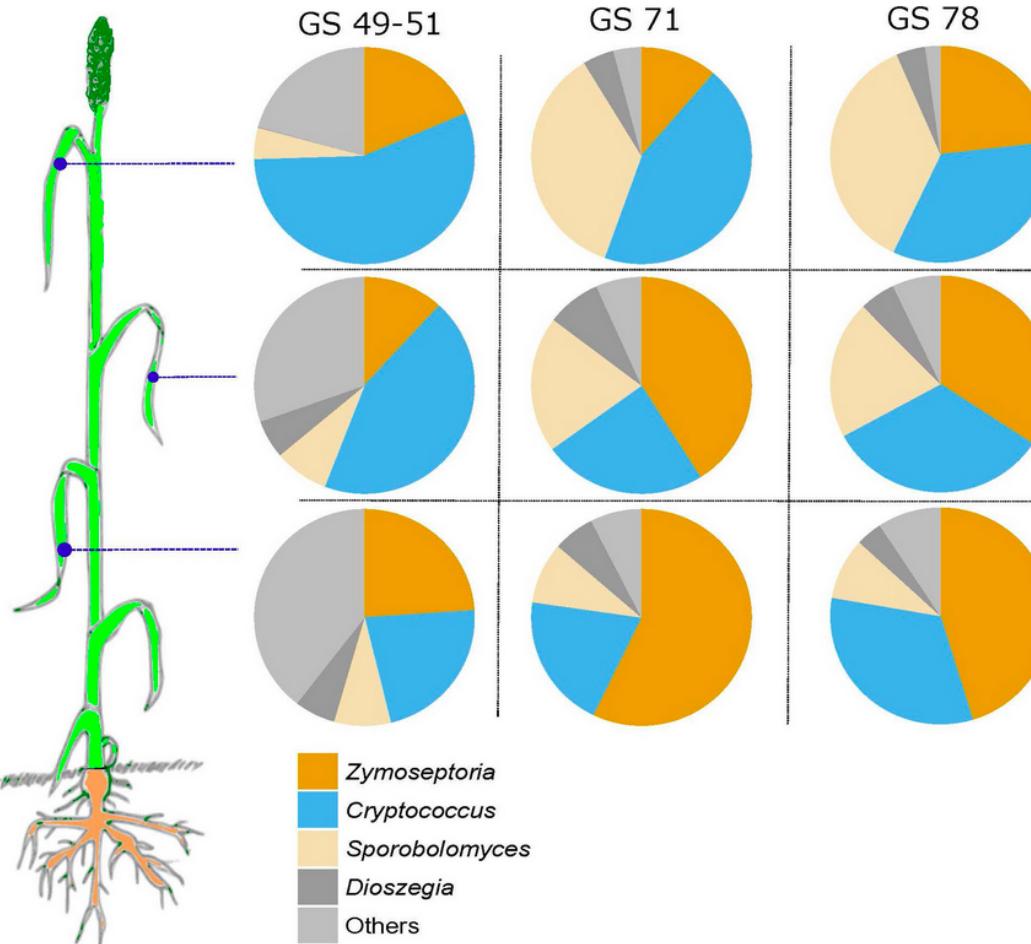
(Singh, Raina, Kumar, Singh, and Prasad, 2019)



# Composizione del microbiota

## Temporal plant microbiota

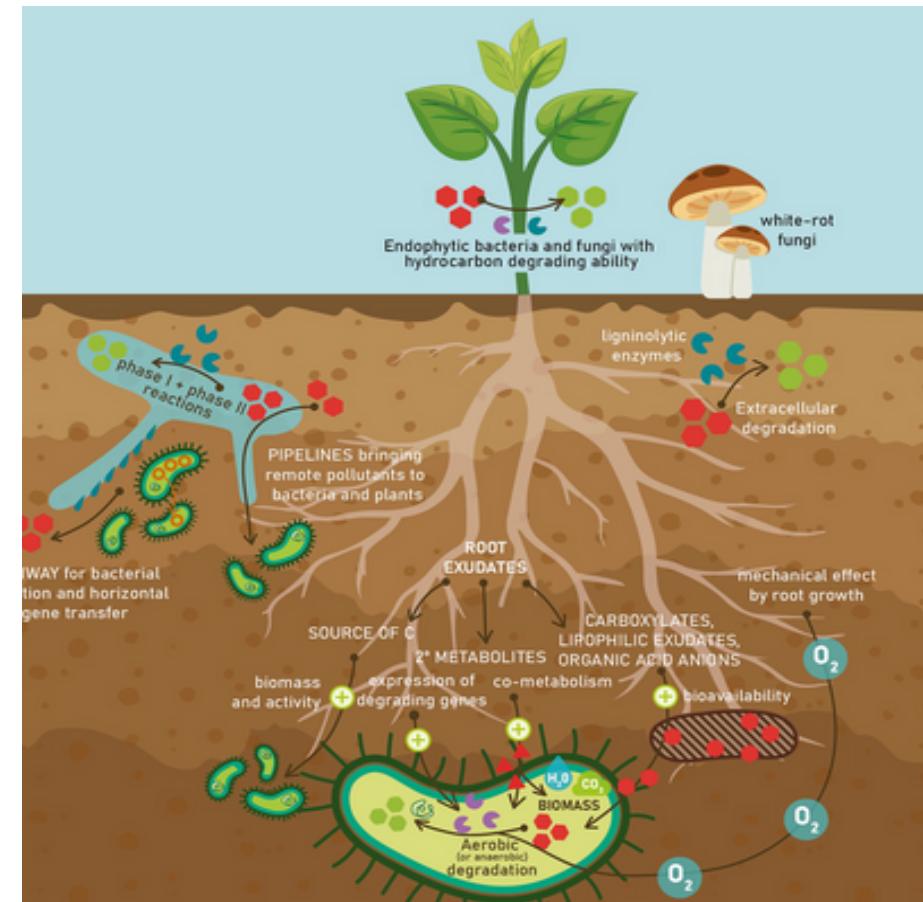
(Sapkota, Jørgensen, and Nicolaisen, 2017)



# Composizione del microbiota

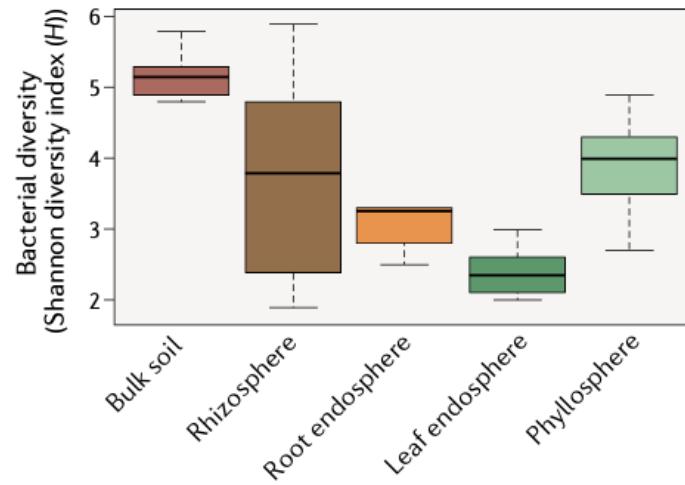
## Microbiota reservoir

- Although the assemblies of root-associated bacteria and fungi differ substantially from the above-ground communities, both represent a **subset of the microbiota derived from soil communities** and enriched in different plant-associated niches
- This suggests that **soil functions as a common reservoir** for both belowground and aboveground plant microbiota

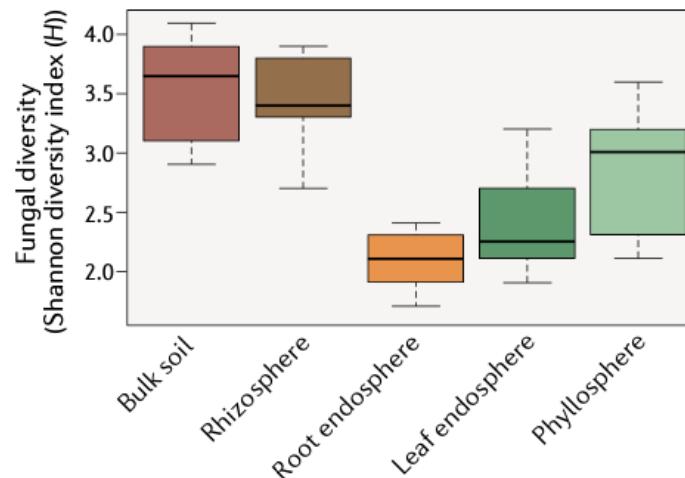


(Agnello, Morelli, and Del Panno, 2020)

# Composizione del microbiota



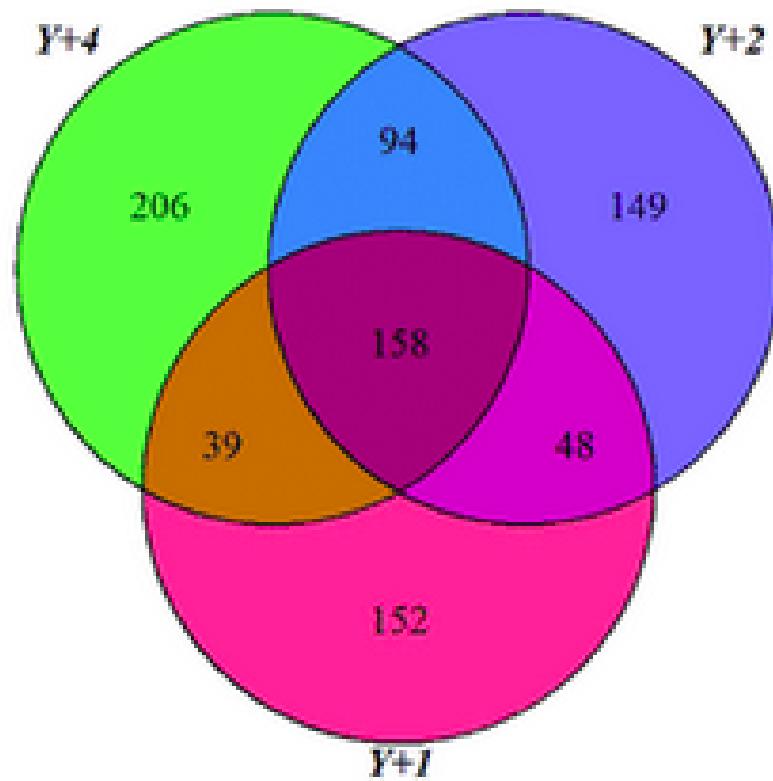
- There are clear differences among the microbial communities in different plant compartments, which indicates that the **plant compartment is a major selective force** that shapes the composition of plant-associated microbiota



# Composizione del microbiota

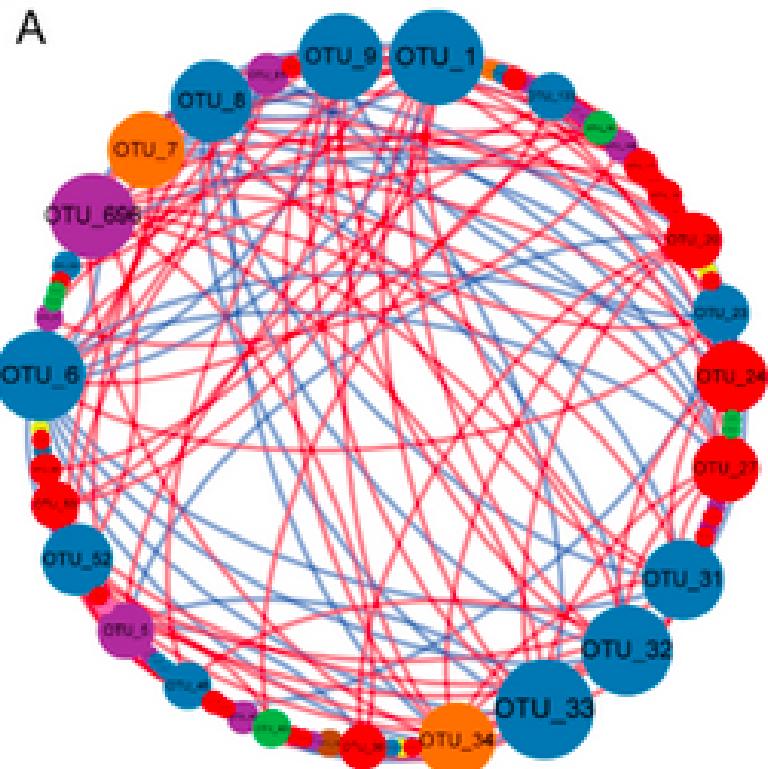
## CORE MICROBIOTA

- The plant core microbiota consists of members of the microbial community that are **persistent and are ubiquitous in almost all the communities** associated with a particular host
- The core microbiota contains key microbial taxa that carry **genes with functions that are essential** for host fitness
- Many members of the core microbiota of different plant species are **common at the genus level**
- The identification of a co-occurring core of plant-associated microorganisms also provides a useful starting point for studies of how to build **SynComs** to manipulate plant–microbiome interactions for increased **growth and productivity**



# Composizione del microbiota

## HUB MICROBIOTA

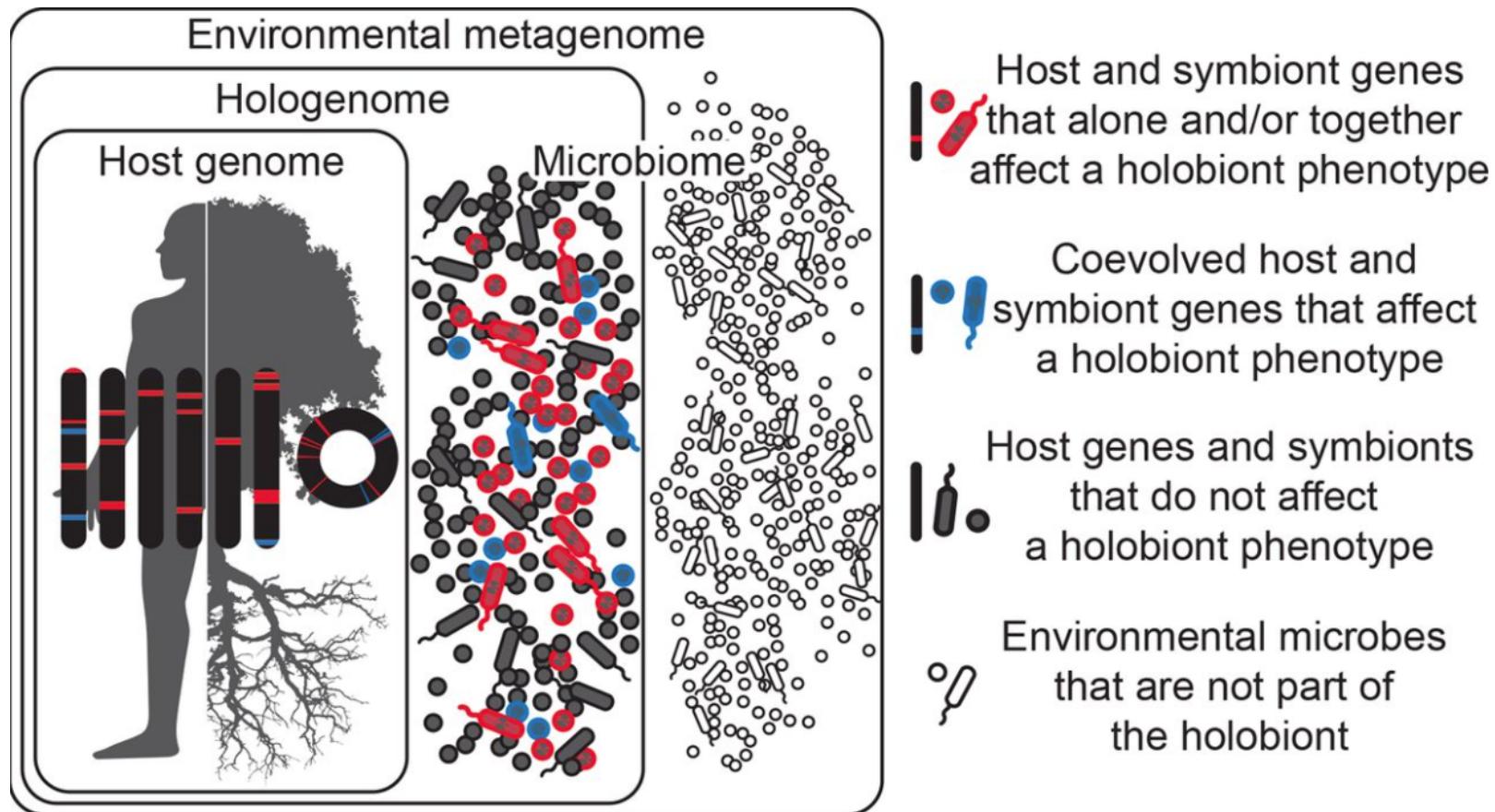


- Within the core microbiota, a few members, such as 'hub microorganisms', can **influence the community structure** through strong biotic interactions with the host or with other microbial species, rather than simply by their own high abundance
- These hub species may represent **keystone species** that can exert strong direct and indirect effects on microbiome assembly and that **function as mediators** between the plant and its associated microbiome.
- For example, *Albugo laibachii* and *Dioszegia* spp. have been identified as highly interactive hubs in the phyllosphere of *A. thaliana* [Agler, et al. 2016]

# Plant Holobiont

---

# Plant Holobiont

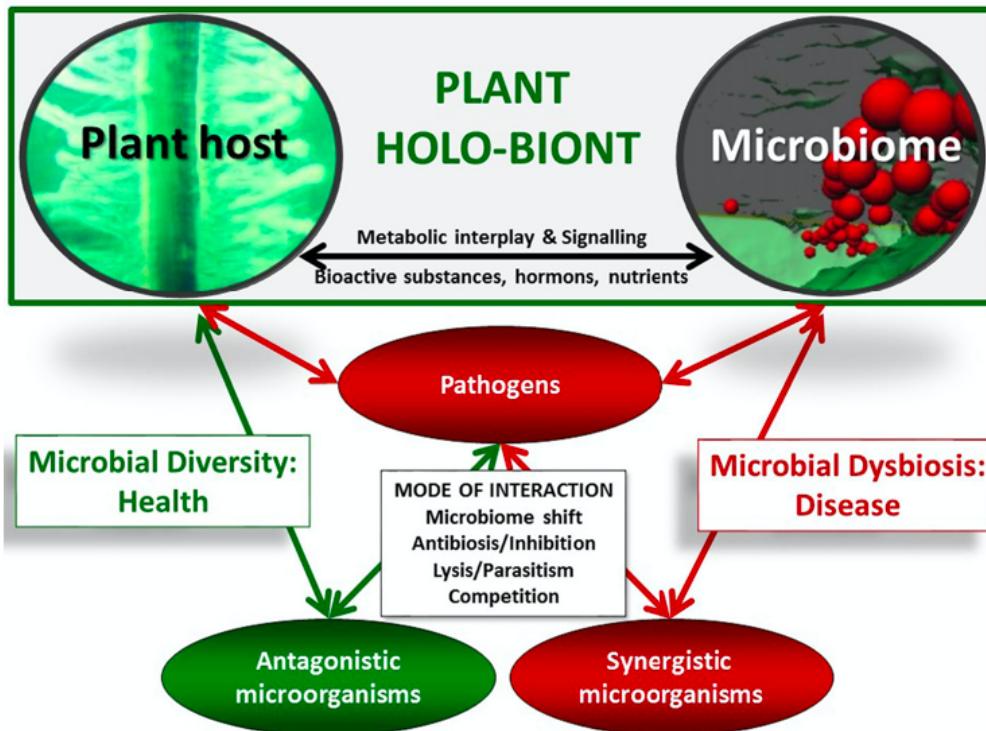


(Berg, Köberl, Rybakova, Müller, Grosch, and Smalla, 2017)

Plants and their associated microorganisms form a holobiont and have to be considered as co-evolved species assemblages consisting of bacterial, archaeal and diverse eukaryotic species

# Plant Holobiont

## Holobiont functions



- Microbial diversity and balance is a key for healthy plants
- Microbial species have the ability to contribute multiple aspects to the system
  - seed germination and growth
  - nutrient supply
  - resistance against biotic stress factors
  - resistance against abiotic factors
  - physiology and production of bioactive metabolites
- The presence of microbes in plants became initially noticeable when diseases appeared. However, the vast majority of microbes in

# Questions about the lesson



Slack (<https://bit.ly/3upNjCt>) -  marco.chiapello@unito.it

# Feedbacks



<https://bit.ly/3B8iTr2>