**The Use of Synthetic Microbial Communities (SynComs) for Plant Health**

**Samuel J. Martins1\*, Josephine Pasche1, Hiago Silva1,2, Gijs Selten3, Noah Savastano4, Lucas Magalh**ã**es Abreu2, Harsh Bais4, Karen Garrett1, Nattapo Kraisitudomsook1, Corné C.M.J. Pieterse3 Tomislav Cernava5,6**

1Department of Plant Pathology, University of Florida, Gainesville, FL, 32611, USA.

2Departamento de Fitopatologia, Universidade Federal de Viçosa, Viçosa, MG 36570‑900, Brazil

3Plant-Microbe Interactions, Department of Biology, Utrecht University, Padualaan 8, 3584 CH Utrecht, The Netherlands

4Department of Plant and Soil Sciences, 311 AP Biopharma, 590 Avenue 1743, University of Delaware, Newark DE 19713, USA.

5Graz University of Technology, Graz, Austria

6Graz University of Technology, School of Biological Sciences, Faculty of Environmental and Life Sciences, University of Southampton, Southampton, SO17 1BJ, U.K.

**\*Correspondence:**

Corresponding Author

[sj.martins@ufl.edu](mailto:sj.martins@ufl.edu)

**Abstract**

Despite the numerous benefits of plant probiotics to the plant, maintaining consistent results between applications is still a challenge. Cultivation-independent methods associated with reduced sequencing costs have considerably improved the overall understanding of microbial ecology in the plant environment. As a result, now is possible to engineer a consortium of microbials aiming for plant health. This consortium is known as synthetic microbial community (SynComs) and each species in these communities have to be carefully chosen to mimic the desired function of the microbiome. Microbial biofilm formation, production of secondary metabolites and ability to induce plant resistance are some of the microbial traits to take in consideration while designing SynComs. Using machine learning, we can target microbial functions aiming at desired plant phenotypes, which are more likely to lead to a stable microbial consortium that thrive under environmental stressors, as compared to the classical selection of single microbial activities or taxonomy. However, ensuring microbial colonization and a long-term plant phenotype stability are still some of the challenges to overcome with SynComs, as the synthetic community may change over time with the microbial horizontal gene transfer and retained mutations. In this review, we explored the advance made with SynCom regarding to plant health focusing on bacteria, as they are the most dominant microbial form compared with other members of the microbiome and most of the SynCom studies used bacteria.

**Keywords**: food security, plant-microbiome interaction, phytobiome, inoculants, metagenomics, plant growth promoting (PGP), dysbiosis, eubiosis, Induced Systemic Resistance (ISR), biofilm, microbial volatiles organic compounds (mVOCs)

# 1. Introduction

As our global population faces a steady increase along with the number of diseases in existence, the importance of beneficial microbes for human health has gained more attention as an alternative treatment. Some of these beneficial microbes, often termed probiotics, have been studied with positive outcomes through fecal microbiome transplantation from healthy donors to disease patients to treat infectious diseases and to overcome resistance to powerful immunotherapies (Erdmann, 2022). These probiotics act by antagonizing specific pathogens and/or by inducing host immunity (Sanders et al. 2019). Similar to the human gut, the plant rhizosphere, which is defined as the narrow area of soil around the root under direct influence of root exudates, is colonized by diverse microbes. These microbes play a crucial role in plant physiological processes, in addition to being the first line of defense against invading pathogens/parasites (Berg et al. 2020; Trivedi et al. 2020). For instance, when isolated and applied to the plant, these microbes can act as probiotics and increase the levels of the plant nutrient uptake, control diseases, alleviate environmental stress, and promote growth (Martins et al. 2015; Martins et al. 2022; Poudel et al. 2022). Despite the numerous benefits of these probiotics to the plant, maintaining consistent results between applications is a challenge, especially under field conditions, where there are other native microbials and plants are under constant abiotic stressors. The use of beneficial microbes for plant health has promised for over 100 years to become a reliable sustainable approach in agriculture, but still presents the same problems as before. To enhance probiotics performance and reliability, a better understanding the microbial interactions as a community and the factors that contribute to the probiotic success and failures in the environments are needed.

In recent years, cultivation-independent methods based on profiling of marker genes or shotgun metagenome sequencing, associated with a reduced sequencing costs have considerably improved the overall understanding of microbial ecology in the plant environment. As a result, we can now engineer a small consortium of microbials that can mimic the observed function and structure of the microbiome in natural conditions (de Souza et al. 2020). This consortium is known as synthetic microbial community (SynComs) and each species in these communities has to be carefully chosen in order to mimic the function of the microbiome and preserve the symbiotic interactions within the plant (Shayanthan et al. 2022). To effectively manipulate and engineer a SynComs among the approximately 10 billion microorganisms present in one gram of soil has been a major challenge in microbial ecology. In this review, we explored the advance made with SynCom regarding to plant health focusing on bacteria, as they are the most dominant microbial form compared with other members of the microbial community and most of the SynCom used bacteria.

# 2. From Single Microbes to Synthetic Microbial Communities (SynComs)

To feed our growing population, it is imperative to increase agricultural productivity 70% by the year 2050 (Singh et al. 2020). In order to meet this goal, a possible sustainable solution that is explored involves alterations of the microbes in the rhizosphere, where the majority of plant microbials are found. The beneficial microbes associated with the suppressive soils were coined “plant growth promoting rhizobacteria” (PGPR) by Kloepper and Schroth (1978), who also showed that there are bacteria in the rhizosphere that specifically influence plant growth. These realizations sparked a world of research opportunity, as the influence of these suppressive soil microbials could have more beneficial effects than previously known. The question of disease suppression was addressed by Broadbent et al. (1971), who determined that some strains of *Bacillus* and *Streptomyces* had suppressive qualities against damping-off, caused by *Rhizoctonia solani*. Later on, Schroth and Hancock (1982) determined that inoculating soil with *Pseudomonas* spp. could allow a soil to become suppressive to deleterious rhizobacteria (including *Pseudomonas*, *Enterobacter*, *Klebsiella*, *Citrobacter*, *Flavobacterium*, *Achromobacter*, and *Anthrobacter*) in sugar beet (*Beta vulgaris* subsp. *vulgaris*). Though single-strain inoculation showed promise, the importance of the community of microbes became increasingly prominent, as microbial communities and their interactions are beneficial to plants and their resistance to diseases (Qu et al. 2020). In the same train of thought as fecal microbiome transfer from stick to healthy patients, the idea of transferring a percentage of soil is being explored to transfer the beneficial microbiome and turn conducive soils into suppressive soils (Jiang et al. 2022).

The transfer of rhizosphere microbials from one community into another has been addressed through different methods, each with its own set of strategies and challenges. The most classical of these approaches is soil transfer, which involves a donor and recipient soil. The donor soil is disease-suppressive, while the recipient is conducive to the disease of interest. (Jiang et al. 2022). A study done by Mendes et al. (2011) sought to understand the possibility of using this soil transfer method to control disease. They specifically focused on a soil that was previously identified as suppressive to *Rhizoctonia solani* infections. The team transferred a portion of the suppressive soil into a conducive soil in a 1:9 (w/w) ratio. The conclusion of this experiment was the transference of soil partially conferred soil disease suppressive to *Rhizoctonia solani* infections in sugar beet (*Beta vulgaris subsp. vulgaris*) as the result of microbials in the soil. Another approach to this microbiome transference is the extraction of the soil microbials. The rhizosphere microbiome transplant (RMT) approach eliminates the abiotic factors of soil, and the microbials from the suppressive rhizosphere are extracted for transplant into the recipient soil (Jiang et al. 2022). The strategy begins very similarly to the soil transfer approach, as a disease-suppressive soil is identified, but the microbiome will be prepared into a slurry that will be added to the conducive soil, as described by (Elhady et al. 2018; Silva et al. 2022; Zhou et al. 2019). There are slight variations between these protocols, but the methods begin with a donor soil extracted from the rhizosphere is taken for extraction. Soil is extracted in a 1:10 ratio of soil to salt buffer, and the solution is then shaken or blended (Zhou et al. 2019). After the vigorous mixing, the supernatant is passed through sieve and centrifuged (Silva et al. 2022). The remaining microbiome slurry is resuspended in water to then transplant into the recipient soil (Elhady et al. 2018). One additional benefit of this method is the delivery of microbes in an exact proportion that was found in the suppressive soil.

Another approach that are being explored recently is isolation of key taxa microbes and delivery them in a synthetic microbial community (SynComs). The number of microbes present in a SynCom for crop health seems to vary from 3 to 23 and more than half of the SynCom studies utilized between 3 and 7 microbes (Figure 1A; Supplementary Table 1).

A comparison of a pie chart

Description automatically generated**Fig. 1**. Fig. 1. Number of microbes used in synthetic microbial communities (SynComs) when the authors used in vivo experiments (n=34), excluding model plants. The blue dashed line represents the mean value (A). Top 5 bacterial genera used in an in vivo SynCom study, excluding model plants (B). The five most frequently used genera in synthetic microbial communities (SynComs) across 34 studies (B).

# Additionally, the top 5 bacteria used in a SynCom are *Bacillus, Pseudomonas, Enterobacter, Streptomyces,* and *Pantoea*, respectively (Figure 1B). Despite beneficial organisms being identified, plant colonization and maintaining the long-term stability of a SynCom are still challenges to be overcome, as the synthetic community may change over time with the horizontal gene transfer among microbes and retained mutations (Jiang et al. 2022; Shayanthan et al. 2022).

In contrast to selecting microbes based on single microbial *in vitro* activities or taxonomy as it has been conducted in the classical method, SynComs development should take into consideration multiple attributes. These attributes include microbials associated with desirable plant phenotype(s) and microbial traits that will give the microbials fitness to persistence in different environments and colonize plants. These microbial traits include exometabolites, such as secondary metabolites and volatiles organic compounds, a robust biofilm formation, and the ability to chemically trigger the plant defense mechanisms.

**3. Modes of Action of SynComs**

**3.1 The potential of microbial volatiles organic compounds (VOCs) in SynComs**

Microorganisms mostly occur in mixed-species communities in which biological diversity is accompanied by chemical diversity. The latter is partially constituted of secondary metabolites that are purposefully produced by microorganisms. One specific type of such metabolites are volatile organic compounds (VOCs) that are often secreted as mediators for molecular communication or as antimicrobial compounds (Cernava et al. 2015; Weisskopf et al. 2019) (Figure 2).

**A diagram of a plant with different types of plants

Description automatically generatedFig. 2**. Roadmap to design a synthetic microbial community (SynCom) involving plant phenotypes and microbial traits.

Microbe-produced VOCs comprise a broad spectrum of small molecules that can dissipate the atmosphere at ambient temperatures (Schmidt et al. 2015). One of their key characteristics is that they can reach long distances not only in the air, but also in soil (Schulz-Bohm et al. 2018; Terra et al. 2018). This makes them highly efficient as mediators of intra- as well as inter-specific communication that can even extend beyond organisms of the same kingdom, e.g., bacterial-fungal or bacterial-plant interactions via volatiles (Martins et al. 2019; Schmidt et al. 2016; Weisskopf et al. 2019). An even more complex interplay was deciphered when tomato plants were inoculated with a specific *Bacillus* *amyloliquefaciens* strain (Kong et al. 2021). Plants that were inoculated with this bacterium released a specific VOC that was received by neighboring plants resulting in a modulation of their rhizosphere microbiome. Other VOCs that exhibit strong antimicrobial effects on certain pathogens have become the focus of research due to their potential for biotechnological applications (Wiltschi et al 2020). Pathogen suppressiveness in certain soils can be partially attributable to VOCs that are likely of microbial origin (Ossowicki et al. 2020). Unambiguous results were obtained in binary systems where specific pathogens were challenged with the VOCs of isolated bacteria (Cernava et al. 2015; Mülner et al. 2019). In fact, many bacteria known for their high potential in plant protection, such as *Bacillus* spp. and *Pseudomonas* spp., were shown to produce bioactive VOCs that inhibit pathogen growth without direct contact (Asari et al. 2016; Mülner et al. 2019). When isolated and grown under laboratory conditions, these bacteria usually produce distinct mixtures of VOCs that are detectable with headspace sampling and subsequent analysis via gas chromatography–mass spectrometry (Cernava et al. 2015). A study by Mülner and colleagues (2019) has demonstrated that specific mixtures of VOCs have a significantly stronger inhibitory effect on phytopathogenic fungi than the individual components present in them. What is even more interesting, is that microorganisms will alter their VOC emission when exposed to volatiles of other bacteria or fungi. Rybakova and colleagues (2022) have shown that VOC production in the beneficial bacterium *Serratia plymuthica* specifically responds to the presence of three different pathogenic fungi. This knowledge opens new possibilities for the design of SynComs where the integrated strains mutually direct each other’s VOC production in a certain direction. Such SynComs might not only be applicable for plant protection against pathogens and pests, but also to improve plant growth (Türksoy et al. 2022). For the design of such SynComs, it is not only important to select compatible strains, but also to ensure that they are present in appropriate concentrations, otherwise they may cause undesirable effects (Cordovez et al. 2018). It was previously observed that certain microbial VOCs positively affect plant growth at low concentrations while being detrimental after a certain threshold is reached (Cordovez et al. 2018; Song et al. 2022). The design of SynComs might also benefit from VOC producers with dual functions, i.e., such that can inhibit the growth of pathogens while simultaneously promoting plant growth (Asari et al. 2016). Overall, microbial VOCs can elicit various desirable effects in plant production and their targeted activation in SynComs will be an important milestone.

**3.2. Other microbial secondary metabolites**

Microbial plant symbionts produce and secrete a large number of secondary metabolites (SM) of diverse biosynthetic origins that play pivotal roles in interspecies interactions, from communication to direct antagonism. Knowledge about the diversity and functions of SM produced by members of the plant microbiome traditionally came from studies conducted with single strains isolated from specific niches, such as plant growth promoting rhizobacteria (PGPR) selected as antagonists of plant pathogens and used biological control agents (BCAs) (Paulsen et al. 2005, Borris et al. 2007). In this context, the production and excretion of few major groups of SM by BCAs inoculated and maintained at high cell densities result in direct pathogen suppression (antibiosis) or the activation of defense mechanisms in the host plant (induced systemic resistance) (Raaijmakers et al. 2002, Ongena et al. 2007).

Several species of *Bacillus* and members of the *Pseudomonas fluorescens* clade are dominant PGPR taxa that produce complex mixtures of SM with a wide range of bioactivities towards prokaryotes and eukaryotes. Lipopeptides are amphiphilic molecules with surfactant properties that interact with lipid bilayers and cause damage to the cell membranes of susceptible organisms. Plant-associated *Bacillus* produce antifungal and antibacterial cyclic lipopeptides of the iturin, fengycin, surfactin and kurstatin biosynthetic families; these SM are active against many plant pathogens and may also induce systemic disease resistance in some plants (Ongena & Jacques 2008). Fluorescent pseudomonads are also prolific producers of many linear and cyclic lipopeptides with antimicrobial activities (Zhao et al. 2019). Interestingly, lipopeptides produced by plant pathogenic *Pseudomonas* can act as phytotoxins (Götze & Stallforth 2020). Phloroglucinols and phenazines are other well-known bioactive SM produced by fluorescent pseudomonads in the rhizosphere of wheat and other crops cultivated in soils that are suppressive to soilborne pathogens (Raaijmakers et al. 2002). A third group of prominent PGPR is composed of Actinobacteria, especially those of the genus *Streptomyces* that produce thousands of bioactive metabolites in their secondary metabolism, a feature that has traditionally attracted the attention of researchers looking for new pharmaceuticals (Bérdy 2012).

In natural microbial communities, complex interspecies interactions govern the biosynthesis and excretion of SM through quorum sensing control mechanisms (Chodkowski & Shade 2017). In this context, most SM are present at subinhibitory concentrations in the medium, where they may participate in formation of biofilms, mediate cell mobility, or function as signaling molecules affecting quorum sensing-dependent phenotypes, including the production of other SM by different microbial species (Raaijmakers & Mazzola 2012, Chevrette et al. 2022). On the other hand, the accumulation of antifungal molecules such as 2,4 diacetylphloroglucinol and phenazines, produced by fluorescent pseudomonads, and several cyclic lipopeptides of *Bacillus* and *Pseudomonas* spp. in the rhizosphere of crops planted in naturally suppressive or artificially inoculated nonsterile soils provide evidence that major SM produced by dominant PGPR can reach inhibitory concentrations in nature (Raaijmakers et al. 1999, Nielsen et al. 2003, Kinsella et al. 2009, Mavrodi et al. 2012).

Recent microbiome-based studies use culture-independent multi-omic approaches combined with dedicated databases and analysis pipelines to characterize the biosynthetic gene clusters (BGCs) responsible for biosynthesis of microbial SM. These studies have uncovered a large number of microbial BGCs responsible for the biosynthesis of polyketides, nonribosomal peptides, terpenes, aryl polyenes, ribosomally synthesized and post-translationally modified peptides (RiPPs), and metabolites of mixed origin in the metagenomes of plant-associated microbes (Carrión et al. 2019, Dror et al. 2020, Tracanna et al. 2021). In one study involving the protection of sugar beet seedlings against damping-off caused *Rhizoctonia solani* in a suppressive soil, metagenomic analyses of the root endosphere showed an expressive enrichment of bacteria-derived BCGs in the endophytic compartments of plants subjected to pathogen inoculation in the suppressive soil. Interestingly, only 12 out of 117 enriched BGCs could be linked to known bioactive SM produced by PGPR (Carrión et al. 2019). In another study, partial sequencing of the adenylation domain of nonribosomal peptide synthetases and functional metagenomics were used to study the diversity of nonribosomal peptides in the rhizosphere microbiome of wheat planted in soils classified as suppressive or conducive to root rot caused by *Fusarium culmorum*. More than 50,000 unique domains were detected, and functional annotations showed that siderophores and cyclic lipopeptides are enriched in the rhizosphere of plants in suppressive soils (Tracanna et al. 2021).

Collections of culturable bacteria representing the dominant taxa in the plant microbiome can be used to test the insights gained from culture-independent studies. Helfrich et al. (2018) conducted thousands *in vitro* pairwise confrontations with dominant members of the phyllosphere microbiome of *Arabidopsis thaliana* and found that most potent inhibitors belonged to the orders *Bacillales* and *Pseudomonadales*. A single strain of *Brevibacillus* was the top inhibitor in dual confrontations and MALDI imaging mass spectrometry showed the accumulation of several SM in the inhibition zones induced by this strain. The mixture of antibacterial SM produced by this strain contained the cyclopeptides, streptocidins and marthiapeptide A, and the novel metabolites macrobrevin and phosphobrevin (Helfrich et al. 2018). In another study, the microbiome-informed isolation of fluorescent pseudomonads from the rhizosphere of sugarbeet cultivated in a suppressive soil inoculated with *R. solani* led to the discovery of strain capable of protecting the plants against damping-off through the production of a chlorinated cyclic lipopeptide, later identified as a new metabolite, thanamycin (Mendes et al. 2011).

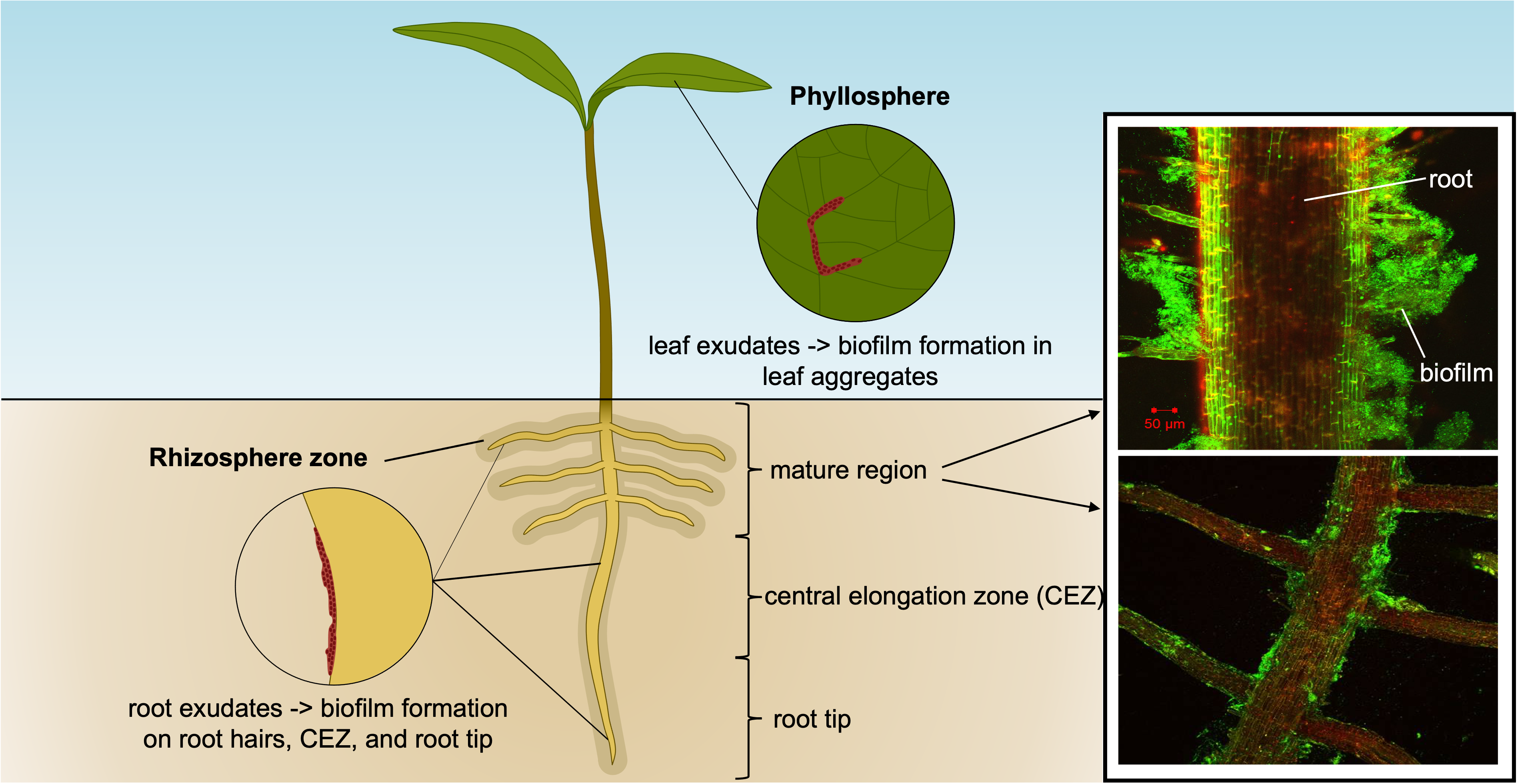
Synthetic communities containing key taxa selected from the plant microbiome can be used for studying more complex roles of SM in interspecies interactions. A three-member syncom was composed of *Bacillus cereus*, *Flavobacterium johnsoniae* and *Pseudomonas koreensis*, three taxa that co-exist in the rhizosphere of soybean and interact in distinct ways *in vitro*. In dual cultures, *P. koreensis* partially inhibits the growth of *F. johnsoniae*, but in tripartite interactions *B. cereus* protects the latter (Lozano et al. 2019). The novel alkaloids koreenceines are produced by *P. koreensis* in co-cultures with the other members of the syncom and induce extensive reprogramming of gene expression in both bacterial partners, while also having direct antimicrobial effects on *F. johnsoniae* (Hurley et al. 2022). Meta-metabolomic analysis showed that several SM are only produced in tripartite interactions, such as a biotransformation derivative of the cyclic lipopeptide lokisin produced by *P. koreensis*, while the relative concentration of several SM of *B. cereus*, including siderophores and the antibiotic kanosamine, varied in response to the presence or absence of koreenceines in the medium (Chevrette et al. 2022).

The utility of SynComs for studying the function of microbial SM in pathogen suppression *in situ* was shown in the work of Carrión et al. (2019). Metagenome data provided evidence for the key role of BGCs from *Flavobacterium* and chitinases from *Chitinophaga* in the suppression of *R. solani* by the endophytic root microbiome of sugarbeet. Accordingly, a minimal two-strain SynCom composed of *Flavobacterium* and *Chitinophaga* isolates representing dominant haplotypes found in the root endosphere protected sugarbeet seedlings against damping-off. Gene expression analyses and site-directed mutagenesis confirmed the production of chitinases by *Chitinophaga* and showed that a specific BGC from *Flavobacterium*, responsible for the biosynthesis of a yet unknown nonribosomal peptide-polyketide hybrid, was crucial for maintaining the level of plant protection provided by SynCom.

**3.3. Biofilms**

Biofilms are microbial communities within an extracellular matrix, adhering to a fixed surface (Lakshmanan et al. 2012; Vlamakis et al. 2013). Bacterial biofilms can be found on plant surfaces, specifically on colonizing seeds through the release of seed exudates (Martins et al. 2018), on leaves (Beattie and Lindow 1999), and roots (Lakshmanan et al. 2012). During biofilm formation, bacteria grow to form microbial colonies, composed of one (homogenous) or multiple (heterogeneous) bacterial species. In heterogeneous microbial colony formation, different bacterial species can migrate or be enveloped into the microbial colony. This heterogeneity can enhance survival and growth of the biofilm (Beattie and Lindow 1999). In the root, biofilm formation process initiates in the rhizosphere, where the bacteria feed on these root exudates, increasing their growth (Lakshmanan et al. 2012). Signaling from the plant triggers bacterial cells to express matrix genes and form a biofilm, adhering to the root surface via an extracellular matrix (Vlamakis et al. 2013). Compounds such as surfactin, activates kinase C and kinase D, which in return both influence the activity of the *Spo0A-P* pathway that controls multiple genes involved in biofilm formation (Vlamakis et al. 2013). Other kinases and external signals influencing biofilm formation can be produced by plants and other soil microorganisms (Vlamakis et al. 2013). Signaling between microbes of different species in a singular biofilm may have enhanced benefits. For example, microbe-microbe enhancements include increased biofilm formation, colonization, and synergism (Niu et al. 2020). *Bacillus* species present in soil positively influenced biofilm formation and growth of *Bacillus subtilis* by activating kinase D (Shank et al. 2011). The exact mechanisms of microbe-microbe enhancement within biofilms are still unknown (Niu et al. 2020).

During the formation of biofilms, small autoinducer (AI) molecules regulate quorum sensing (QS), most commonly AHLs N-acyl homoserine lactones. A certain level of AHLs is produced by bacteria until the bacterial population grows to a specific threshold. Then, AHLs bind to global transcription regulators, LuxR or LuxR-like proteins, to trigger QS-controlled gene activity, including virulence factors involved in bacterial colonization (Lakshmanan et al. 2012). However, our knowledge of root regions that triggers or deters biofilm formation in plant growth promoting rhizobacteria (PGPR) is not well understood. Conventionally, it is speculated that root tip, a highly metabolically active site, may secrete majority of exudates, leading to increased microbial association. The temporal secretion patterns within the specific region of roots are not fully understood (Figure 3).

**Fig. 3**. Root and leaf exudates trigger microcolonies and biofilm formation by plant growth promoting rhizobacteria (PGPR). The biofilm formation in roots is more prominent compared to the phyllosphere regions. The root regions such as tip, CEZ and maturation zones may facilitate biofilm formation based on secretion patterns and profiles. The confocal micrographs in the inset shows root colonization by PGPRs (in green) in different crop species localized at the maturation root region.

The method of microbial inoculation has been found to influence the site of root bacterial colonization. Bacteria concentration increases closer to the point of inoculation, for plants inoculated as seeds. Generally, bacterial colonization increases in root locations where root exudates are released, including at the root elongation zone and on root hairs (Hassan et al. 2019). The factor of root surface roughness influences colonization in that more bacteria colonize roots where the root surface is rougher. Time also is a factor that influences bacterial distribution, as the location of root bacterial colonization changes with time (Benizri et al. 2010). Factors contributing to the location of bacterial colonization on roots should be further investigated.

Biofilm quantification: Biofilms can be harvested from soil and observed using the buried slide technique. The technique involves placing a sterile slide in soil for 1 to 3 weeks, then removing the slide and staining to observe soil microbial community. Although, the method is not ideally representative of the microbial distributions within the soil because the microscope slide is a new substrate which alters the composition of microbial species in comparison to the soil populations (Cunningham et al. 2011). Quantification of biofilms in the rhizosphere involves marking bacteria with fluorescent proteins, and quantifying the number of bacteria via flow cytometry (Knights et al. 2021). Eight fluorescent proteins ranging from blue to far-red can tag a range of bacterial species, for studies of biofilms composed of multiple bacterial species (Schlechter et al. 2018).

Beneficial biofilm and its role in plant protection: When exposed to pathogen infection. Plants promote signaling in the rhizosphere to attract beneficial microbes. These microbes protect the plants against biotic and improve tolerance to abiotic stressors, such as salinity, drought, and temperature stress (Martins et al. 2014; Trivedi et al. 2020). To mitigate salinity stress in the rhizosphere, EPS produced by microbes for biofilm formation and adherence can bind cations such as Na+. EPS binds to Na+ and makes Na+ unavailable to plants, thus reducing Na+ plant uptake, which helps to maintain the K+/Na+ balance in plant roots under salinity stress (Gupta et al. 2017; Morcillo and Manzanera 2021). Additionally, biofilms improve salinity tolerance by forming a layer of water around bacterial cells, which improves bacterial adhesion to the plant root and mitigates salinity stress. EPS also encourage plant growth under salinity stress by improving soil aggregation. However, the influence of EPS compositional change and physical and chemical properties on plant salinity stress is still largely unknown (Morcillo and Manzanera 2021). Bacterial biofilm formation has also been found to improve drought tolerance (Martins et al. 2018). Under drought stress, bacterial EPS in the rhizosphere decrease plant water loss and increase bacterial survival due to their increased water content (Roberson and Firestone 1992). This increased water content also provides plants with water in the rhizosphere, allowing more time for plants to adjust their metabolic activity to drought conditions (Morcillo and Manzanera 2021). EPS also mitigate drought stress by improving the soil structure to retain more water in the soil (Zheng et al. 2018), although the exact influence of EPS on plant physiology is not well understood (Morcillo and Manzanera 2021).

EPS-producing bacteria in the rhizosphere may also mitigate heat and cold stress. EPS improve heat tolerance, likely due to matrix formation that also improves soil water content. EPS also produce heat shock-related proteins that protect microbes from heat, to mitigate heat shock. Although, few studies have investigated the mitigation of heat stress and heat shock by EPS-producing bacteria. More research is needed regarding EPS improvement of plant heat stress tolerance. Additionally, in colder temperatures, EPS binding of Na+ cations can improve osmotic balance in cold-stressed plants (Morcillo and Manzanera 2021).

**Plant resistance mechanisms triggered by SynComs**

To cope with pathogenic microbes, plants developed sophisticated defense mechanisms. In a first line of defense, these resistance mechanisms depend on the perception of microbe derived compounds called MAMPs (microbe-associated molecular patterns). Examples of MAMPs include bacterial flagellin, bacterial peptidoglycan, fungal chitin and oomycetal β-glucans ((Gómez-Gómez and Boller 2000; Miya et al. 2007; Tyler 2002). These MAMPs are recognized by the plant’s pattern recognition receptors (PRRs), which trigger a cascade of reactions that lead to transcriptional reprogramming and activation of the plant’s first line of defense called MAMP-triggered immunity (MTI) (Boller and Felix 2009; Galletti et al. 2011; Jones and Dangl 2006; Newman et al. 2013). As the plant is putting a substantial amount of energy in its defense systems, a prolonged state of MTI can lead to growth inhibition due to growth-defense trade-offs (Gómez-Gómez et al. 1999; Zipfel et al. 2006). For that reason, it is vitally important for the plant to be selective about activating its defense systems against microbes that can activate MTI.

SynComs and the plant immune system

MAMPs are evolutionary conserved across the bacterial, fungal and oomycetal kingdoms. Commensal and beneficial microbes in the plant microbiome possess similar MAMPs as their pathogenic counterparts. It is therefore highly unlikely that SynComs consisting of commensal and/or beneficial microbes will not activate the plant’s defense systems. As a matter of fact, in many SynCom studies the bacterial strains used didn’t cause disease themselves. When the SynCom-treated plants were subsequently challenged with a pathogen, they actually developed less disease symptoms than non-treated control plants (Berendsen et al. 2018; Berg and Koskella 2018; Carrion et al. 2019; Dúran et al. 2018, 2021; Gómez-Pérez et al. 2022; Hu et al. 2016; Li et al. 2021; Liu et al. 2022; Ma et al. 2021; Niu et al. 2017; Prigigallo et al. 2022; Vogel et al. 2021), either through direct competition with the pathogen, or via the onset of a plant-mediated induced systemic resistance (ISR) or systemic acquired resistance (SAR) (de Kesel et al. 2021; Pieterse et al. 2014). Phenotypic data of these studies revealed that in absence of the pathogen, the SynComs had either no effect (Ma et al. 2021; Niu et al. 2017) or significantly increased plant growth (Berendsen et al. 2018; Dúran et al. 2018; Liu et al. 2022), suggesting that the SynComs are able to circumvent growth-defense trade-offs that result from the activation of plant defenses. So how do plants accommodate plant growth-promoting microbes, such as provided in a SynCom, while at the same time being able to ward off pathogens? To answer this question it is interesting to investigate the role of different plant defense systems, such as MTI, ISR and SAR during interactions of the plant with plant-beneficial SynComs.

*SynComs and evasion of local host immunity*

Flagellin is one of the major MAMPs in bacterial communities. Treating wildtype Arabidopsis plants with the immunogenic flagellin epitope flg22 of pathogenic Pseudomonas aeruginosa PO1 or from beneficial Pseudomonas simiae WCS417 leads to highly similar root defense transcriptome changes and suppression of plant growth (Stringlis et al. 2018a). This suggests that the initial response of plant roots to MAMPs of beneficial and pathogenic microbes is highly similar. However, live beneficial rhizobacteria have been shown to actively suppress this flg22-induced root MTI response (Yu et al. 2019a). Yu et al. (2019b) showed that of the tested root microbiota, 42% were able to quench local Arabidopsis root immune responses that are triggered by flg22. This shows that suppression of local MTI is an important function of the root microbiome, possibly to accommodate colonization by beneficial microbiota. A flg22-induced root MTI response can lead to a growth-defense trade-off phenomenon called root growth inhibition (RGI) (Garrido-Oter et al. 2018; Gómez-Gómez et al. 1999; Huot et al. 2014). Interestingly, Teixeira et al. (2021) demonstrated in Arabidopsis that a 35-member SynCom was able to revert flg22-induced RGI. Additionally, a mono-association study in which 151 rhizobacterial strains were individually inoculated on Arabidopsis roots indicated that roughly 40% of this selection of bacterial strains have the ability to suppress RGI (Ma et al. 2021). The mechanisms by which RGI can be suppressed can be multiple. Yu et al. (2019b) demonstrated that lowering environmental pH through the production of gluconic acid by the Pseudomonas rhizobacteria plays a role in the suppression of flg22-triggered MTI. Additionally, two studies found Variovorax and Bradyrhizobium species to be able to revert RGI by degrading auxin in the root compartment (Conway et al. 2022; Finkel et al. 2020). Another study found two Janibacter species to avoid RGI by degrading flg22 (Ma et al. 2021). Especially bacteria from the Variovorax genus seem to be good RGI suppressors as they were able to revert RGI in multiple studies (Finkel et al. 2020; Qi et al. 2022; Teixeira et al. 2021).

*SynComs and dysbiosis*

The beneficial effects that a SynCom can have on the plant are much more evident when growth inhibition responses like RGI are reverted by the SynCom. So what is the role of MTI in plant interactions with complex microbial communities when it seems to stand in the way for beneficial functions of the microbiome? A SynCom study with the peptidoglycan receptor mutant bak1bkk1, the flagellin-chitin receptor mutant efrfls2cerk1, and the chitin receptor mutant lyk5, indicated that a non-functional MTI response leads to a higher amount of bacterial and fungal cells in the rhizosphere (Wolinska et al. 2021). Similar MAMP receptor mutants, as well as the MTI response mutant rbohD, which is impaired in the production of reactive oxygen species (ROS), displayed a phenomenon called “dysbiosis” in the phyllosphere (Chen et al. 2020; Pfeilmeier et al. 2021; Wolinska et al. 2021). Dysbiosis is a state of imbalance in the microbial community that can have adverse side-effects on the plant, such as the loss of disease resistance mediated by the bacterial community or the increase in opportunistic pathogens that can subsequently harm the plant (Pfeilmeier et al. 2021). Adiitionally, Arabidopsis mutants impaired in the response to the defense hormones salicylic acid, jasmonic acid or ethylene displayed a significant shift in microbial community composition, both in a natural microbiome setting as well as in a SynCom setting (Bodenhausen et al. 2014; Lebeis et al. 2015). Hence, besides its function in the first line of defense against pathogens, MTI and its associated defense responses also seem to be important to prevent dysbiosis in plant-associated microbial communities, as dysbiosis can possibly lead to resilient beneficial communities turning into consortia that can easily be invaded by pathogenic microbes or that can cause disease in the plant themselves.

*SynComs and plant-derived metabolites*

One way to keep order in the root and leaf microbiome is by the production of antimicrobial compounds such as ROS, phytoalexins, or indole glucosinolates (Favaron et al. 2009; Ferrari et al. 2007; Pascale et al. 2020; Tsuji et al. 1992; Voges et al. 2019; Wolinska et al. 2021). These compounds are known to be released to repress pathogens, though it is likely that they can also affect beneficial and commensal members of the plant microbiome and its representatives in SynComs. Expectedly, plant-associated microbial communities have developed mechanisms to cope with these antimicrobial compounds. For instance, Stringlis et al. (2018b) demonstrated that antimicrobial coumarin production in plant roots can inhibit fungal pathogens, such as Fusarium oxysporum f. sp. raphani and Verticillium dahliae JR2, while ISR-inducing rhizobacterial strains P. simiae WCS417 and Pseudomonas capeferrum WCS358 were insensitive to the antimicrobial effect of coumarins. In an in vitro screen that included P. simiae WCS417, Voges et al. (2019) showed that the majority of SynCom members across bacterial families were unaffected by the catecholic coumarins sideretin, fraxetin and esculetin, which generate ROS compounds in iron-deficient conditions. Interestingly, the bacterial strains that were sensitive to these coumarins were also found in high abundance on plant roots that were grown under iron-deficient conditions during which coumarins secretion is typically enhanced (Voges et al. 2019). A similar study focusing on the release of antimicrobial benzoxazinoids (BXs) by wheat and maize showed that Beta- and Gammaproteobacteria are largely resistant to these compounds (Schandry et al. 2021). Interestingly, when tested in a SynCom, these BX-resistant Beta- and Gammaproteobacteria were able to make the whole community, which also included BX-susceptible members, resistant against BXs. These findings suggest that microbes with resistance against certain antimicrobial compounds might be able to confer the whole microbial community resistant against these compounds.

*SynComs and plant protection against pathogens*

SynComs of well-characterized bacterial or fungal communities are used to empirically test functions of much more complex microbial communities in the root or phyllosphere microbiome (Vorholt et al. 2017). Mono-association and small SynCom studies show that for a SynCom to have a disease resistance enhancing effect, the level of complexity can be modest, as only one or a few strains can be enough to enhance disease resistance in a plant host against certain pathogens (Berendsen et al. 2018; Berg and Koskella 2018; Carrion et al. 2019; Li et al. 2021; Liu et al. 2022; Niu et al. 2017; Prigigallo et al. 2022). How does that hold up when increasing the complexity of SynComs? Only few studies investigated the ability of SynCom members to provide pathogen protection in the context of increasing SynCom complexity. For instance, in a potato study, increasing SynCom complexity had stronger effects on the level of resistance against Phytophthora infestans (de Vrieze et al. 2018). In another study, SynComs consisting of bacterial members versus multi-kingdom members were compared in terms of circumventing growth-defense tradeoffs when the plant was grown under different light intensities (Hou et al. 2021). In this study, a multi-kingdom SynCom consisting of bacteria, fungi and oomycetes was able to prevent the growth-defense tradeoffs that were apparent when plants under low light were grown in absence of microbes or exposed to bacterial SynComs (Hou et al. 2021). When bacteria are left out of the multi-kingdom SynCom it can, however, lead to severe dysbiosis (Dúran et al. 2018), indicating that bacterial community members are important for maintaining a healthy microbiome.

In conclusion, SynCom research has made evident that microbial communities have developed evasion strategies to avoid immune responses that the plant has evolved to cope with pathogens. The interplay between the plant’s defense mechanisms and the microbial communities in its various compartments is necessary, however, as it avoids dysbiosis and allows the plant to maximally benefit from plant-growth promoting rhizobacteria in its associated microbiome.

**4. Edaphic factors and *in situ* microbiome manipulations** (Mara Cloutier) up to 1 page

**5. Network Analysis**

Conventionally, the selection of microbes for plant health has essentially followed the *in vitro* screening approach targeting the selection of well-known microbial taxa for the control of specific pathogen/pest/parasite or aiming at improving some plant phenotypes, such as plant growth, nitrogen fixation, and phytohormone production (Glick, 2012; de Souza et al. 2020). As a result, the application of these inoculants often fails and/or are unable to establish in the environment (Besset-Manzoni et al. 2019; Zimmer et al., 2016). Therefore, it is crucial that we identify relevant microbes with key traits in each system. The use of machine learning for SynComs selection is a powerful tool for understanding microbes and plant as a system and how phytobiome structure will influence crop health. Phytobiome is defined as a network of interactions between plants, their environment, and their associate micro- and macroorganisms (APS 2016). The positions of microbes in the network can indicate their importance within the microbial community. For instance, highly interactive members of the core microbiome, known as “hub” microbes, strongly shape the phytobiome communitys (Muller et al., 2018; Trivedi et al., 2020) by suppressing the growth and diversity of other microbes within and across kingdoms (Agler et al. 2016). Hub microbes may play significant roles in plant health by suppressing pathogenic microbes and/or promoting the expression of disease resistance genes (Poudel et al. 2016). Identifying these hub microbes in each plant species could be key to create a successful and effective SynComs (Toju et al. 2020).

**Conclusion**

In conclusion, cultivation-independent methods associated with reduced sequencing costs have considerably improved the overall understanding of microbial ecology in the plant environment making the possible to engineer synthetic microbial communities (SynComs) for plant health. Using machine learning with plant and microbial trait phenotypes as input, we are able to get compositions of SynComs. The composition number of microbes in the SynComs is still a practical challenge to overcome due to a lack of industrial technologies and difficulties in handling the microbes (Shayanthan et al. 2022). Moreover, though a single SynCom can provide plant resilience to multiple pathogens (Santhanam et al. 2015), it is unrealistic to think that one SynComs will act as ‘*one size fits all*’. For a more likely successful scenario, SynCom should contain microbes with multiple beneficial traits as discussed in this review (robust biofilm formation, production of desired secondary metabolites and mVOCs, capable of inducing plant resistance) and possess synergistic interactions among themselves.

**6. Conflict of Interest**

# 7. Author contributions

# 8. Acknowledgement

This work was supported by the USDA National Institute of Food and Agriculture, Hatch project 1024881. The authors also thank UF/IFAS Communications and the Graphic Designer Heather Griffith for designing the figure 2.

# 9. Literature Cited

Agler, M. T., Ruhe, J., Kroll, S., Morhenn, C., Kim, S.-T., Weigel, D., et al. 2016. Microbial hub taxa link host and abiotic factors to plant microbiome variation. PLoS Biol. 14:e1002352.

American Phytopathological Society 2016. Phytobiomes: A roadmap for research and translation. Available at [www.phytobiomes.org/Roadmap/Documents/PhytobiomesRoadmap.pdf](http://www.phytobiomes.org/Roadmap/Documents/PhytobiomesRoadmap.pdf).

Asari, S., Matzén, S., Petersen, M. A., Bejai, S., & Meijer, J. (2016). Multiple effects of Bacillus amyloliquefaciens volatile compounds: plant growth promotion and growth inhibition of phytopathogens. FEMS Microbiology Ecology, 92(6), fiw070.

Beattie, G.A. and Lindow, S.E. 1999. Bacterial colonization of leaves: a spectrum of strategies. *Phytopathology*, 89:353-359.

Benizri, E., Baudoin, E. and Guckert, A. 2001. Root colonization by inoculated plant growth-promoting rhizobacteria. *Biocontrol Sci. Technol.*, 11:557-574.

Bérdy, J. (2012). Thoughts and facts about antibiotics: where we are now and where we are heading. The Journal of antibiotics, 65(8), 385-395. <https://doi.org/10.1038/ja.2012.27>

Berendsen, R. L., Vismans, G., Yu, K., Song, Y., de Jonge, R., Burgman, W. P., et al. 2018. Disease-induced assemblage of a plant-beneficial bacterial consortium. Isme Journal. 12:1496–1507.

Berg G, Rybakova D, Fischer D, Cernava T, Vergès M-CC, Charles T, et al. Microbiome definition re-visited: old concepts and new challenges. Microbiome. 2020;8:103.

Berg, M., and Koskella, B. 2018. Nutrient- and dose-dependent microbiome-mediated protection against a plant pathogen. Current Biology. 28:2487.

Besset-Manzoni, Y., Joly, P., Brutel, A., Gerin, F., Soudiere, O., Langin, T., & Prigent-Combaret, C. (2019). Does *in vitro* selection of biocontrol agents guarantee success in planta? A study case of wheat protection against Fusarium seedling blight by soil bacteria. *PLoS One*, *14*(12), e0225655.

Bhattacharyya, P. N., & Jha, D. K. (2012). Plant growth-promoting rhizobacteria (PGPR): Emergence in agriculture. In *World Journal of Microbiology and Biotechnology* (Vol. 28, Issue 4, pp. 1327–1350). https://doi.org/10.1007/s11274-011-0979-9

Bodenhausen, N., Bortfeld-Miller, M., Ackermann, M., and Vorholt, J. A. 2014. A synthetic community approach reveals plant genotypes affecting the phyllosphere microbiota. PLoS Genet. 10.

Boller, T., and Felix, G. 2009. A renaissance of elicitors: perception of microbe-associated molecular patterns and danger signals by pattern-recognition receptors. Annu Rev Plant Biol. 60:379–406.

Carrion, V. J., Perez-Jaramillo, J., Cordovez, V., Tracanna, V., de Hollander, M., Ruiz-Buck, D., et al. 2019. Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. Science. 366:606.

Cernava, T., Aschenbrenner, I. A., Grube, M., Liebminger, S., & Berg, G. (2015). A novel assay for the detection of bioactive volatiles evaluated by screening of lichen-associated bacteria. Frontiers in microbiology, 6, 398.

Chen, T., Nomura, K., Wang, X. L., Sohrabi, R., Xu, J., Yao, L. Y., et al. 2020. A plant genetic network for preventing dysbiosis in the phyllosphere. Nature. 580:653.

Chen, X. H., Koumoutsi, A., Scholz, R., Eisenreich, A., Schneider, K., Heinemeyer, I., Morgenstern, B., Voss, B., Hess, W. H., Reva, O., Junge, H., Voigt, B., Jungblut, P. R., Vater, J., Süssmuth, R., Liesegang, H., Strittmatter A., Gottschalk, G., Borriss, R. (2007). Comparative analysis of the complete genome sequence of the plant growth–promoting bacterium Bacillus amyloliquefaciens FZB42. Nature Biotechnology, 25(9), 1007-1014. <https://doi.org/10.1038/nbt1325>

Chevrette, M. G., Thomas, C. S., Hurley, A., Rosario-Meléndez, N., Sankaran, K., Tu, Y., Hall, A., Magesh, S., Handelsman, J. (2022). Microbiome composition modulates secondary metabolism in a multispecies bacterial community. Proceedings of the National Academy of Sciences, 119(42), e2212930119.<https://doi.org/10.1073/pnas.2212930119>

Chodkowski, J. L., & Shade, A. (2017). A synthetic community system for probing microbial interactions driven by exometabolites. Msystems, 2(6), e00129-17. <https://doi.org/10.1128/mSystems.00129-17>

Conway, J. M., Walton, W. G., Salas-Gonzalez, I., Law, T. F., Lindberg, C. A., Crook, L. E., et al. 2022. Diverse MarR bacterial regulators of auxin catabolism in the plant microbiome. Nat Microbiol. 7:1817.

Cordovez, V., Schop, S., Hordijk, K., Dupré de Boulois, H., Coppens, F., Hanssen, I., ... & Carrión, V. J. (2018). Priming of plant growth promotion by volatiles of root-associated Microbacterium spp. *Applied and environmental microbiology*, *84*(22), e01865-18.

Cunningham, A.B., Lennox, J.E., and Ross, R.J. 2011. Collecting soil biofilms by the buried slide technique - instructions for students. *Biofilms: The Hypertextbook*, http://www.hypertextbookshop.com/biofilmbook/v004/r003/

De Kesel, J., Conrath, U., Flors, V., Luna, E., Mageroy, M. H., Mauch-Mani, B., et al. 2021. The induced resistance lexicon: do’s and don’ts. Trends Plant Sci. 26:685–691.

De Souza, R. S. C., Armanhi, J. S. L., & Arruda, P. (2020). From Microbiome to Traits: Designing Synthetic Microbial Communities for Improved Crop Resiliency. *Frontiers in Plant Science*, *11*. <https://doi.org/10.3389/fpls.2020.01179>

De Vrieze, M., Germanier, F., Vuille, N., and Weisskopf, L. 2018. Combining different potato-associated Pseudomonas strains for improved biocontrol of Phytophthora infestans. Front Microbiol. 9.

Dror, B., Wang, Z., Brady, S. F., Jurkevitch, E., & Cytryn, E. (2020). Elucidating the diversity and potential function of nonribosomal peptide and polyketide biosynthetic gene clusters in the root microbiome. Msystems, 5(6), e00866-20. <https://doi.org/10.1128/mSystems.00866-20>

Dúran, P., Reinstadler, A., Rajakrut, A. L., Hashimoto, M., Garrido-Oter, R., Schulze-Lefert, P., et al. 2021. A fungal powdery mildew pathogen induces extensive local and marginal systemic changes in the Arabidopsis thaliana microbiota. Environ Microbiol. 23:6292–6308.

Dúran, P., Thiergart, T., Garrido-Oter, R., Agler, M., Kemen, E., Schulze-Lefert, P., et al. 2018. Microbial interkingdom interactions in roots promote Arabidopsis survival. Cell. 175:973.

Elhady, A., Adss, S., Hallmann, J., & Heuer, H. (2018a). Rhizosphere microbiomes modulated by pre-crops assisted plants in defense against plant-parasitic nematodes. *Frontiers in Microbiology*, *9*(JUN). https://doi.org/10.3389/fmicb.2018.01133

Erdmann, J. (2022). How gut bacteria could boost cancer treatments. *Nature*, *607*(7919), 436-439.

Favaron, F., Lucchetta, M., Odorizzi, S., da Cunha, A. T. P., and Sella, L. 2009. The role of grape polyphenols on trans-resveratrol activity against Botrytis cinerea and of fungal laccase on the solubility of putative grape PR proteins. Journal of Plant Pathology. 91:579–588.

Ferrari, S., Galletti, R., Denoux, C., de Lorenzo, G., Ausubel, F. M., and Dewdney, J. 2007. Resistance to Botrytis cinerea induced in Arabidopsis by elicitors is independent of salicylic acid, ethylene, or jasmonate signaling but requires PHYTOALEXIN DEFICIENT3. Plant Physiol. 144:367–379.

Finkel, O. M., Salas-Gonzalez, I., Castrillo, G., Conway, J. M., Law, T. F., Teixeira, P., et al. 2020. A single bacterial genus maintains root growth in a complex microbiome. Nature. 587:103.

Galletti, R., Ferrari, S., and de Lorenzo, G. 2011. Arabidopsis MPK3 and MPK6 play different roles in basal and oligogalacturonide- or flagellin-induced resistance against Botrytis cinerea. Plant Physiol. 157:804–814.

Garrido-Oter, R., Nakano, R. T., Dombrowski, N., Ma, K. W., McHardy, A. C., Schulze-Lefert, P., et al. 2018. Modular traits of the Rhizobiales root microbiota and their evolutionary relationship with symbiotic rhizobia. Cell Host Microbe. 24:155.

Gharde, Y., Singh, P. K., Dubey, R. P., & Gupta, P. K. (2018). Assessment of yield and economic losses in agriculture due to weeds in India. *Crop Protection*, *107*, 12–18. <https://doi.org/10.1016/j.cropro.2018.01.007>

Glick, B. R. (2012). Plant growth-promoting bacteria: mechanisms and applications. Scientifica 2012, 963401. doi: 10.6064/2012/963401

Gómez-Gómez, L., and Boller, T. 2000. FLS2: an LRR receptor-like kinase involved in the perception of the bacterial elicitor flagellin in Arabidopsis. Mol Cell. 5:1003–1011.

Gómez-Gómez, L., Felix, G., and Boller, T. 1999. A single locus determines sensitivity to bacterial flagellin in Arabidopsis thaliana. Plant Journal. 18:277–284.

Gómez-Pérez, D., Schmid, M., Chaudhry, V., Velic, A., Maček, B., Kemen, A., et al. 2022. Proteins released into the plant apoplast by the obligate parasitic protist Albugo selectively repress phyllosphere-associated bacteria. bioRxiv.

Gopal, M., Gupta, A., & Thomas, G. v. (2013). Bespoke microbiome therapy to manage plant diseases. *Frontiers in Microbiology*, *4*(DEC). https://doi.org/10.3389/fmicb.2013.00355

Götze, S., & Stallforth, P. (2020). Structure, properties, and biological functions of nonribosomal lipopeptides from pseudomonads. Natural Product Reports, 37(1), 29-54. <https://doi.org/10.1039/C9NP00022D>

Guglielmi, G. (2018). Gut microbes join the fight against cancer. Nature, 557(7706), 482-484.

Gupta, G., Snehi, S.K. and Singh, V. 2017. Role of PGPR in biofilm formations and its importance in plant health. *Biofilms Plant Soil Health*, 27:27-40.

Hassan, M.K., McInroy, J.A. and Kloepper, J.W. 2019. The interactions of rhizodeposits with plant growth-promoting rhizobacteria in the rhizosphere: A review. *Agriculture*, 9:142.

Helfrich, E. J., Vogel, C. M., Ueoka, R., Schäfer, M., Ryffel, F., Müller, D. B., Probst, S., Kreuzer, M., Piel, J., & Vorholt, J. A. (2018). Bipartite interactions, antibiotic production and biosynthetic potential of the Arabidopsis leaf microbiome. Nature Microbiology, 3(8), 909-919. <https://doi.org/10.1038/s41564-018-0200-0>

Hou, S. J., Thiergart, T., Vannier, N., Mesny, F., Ziegler, J., Pickel, B., et al. 2021. A microbiota-root-shoot circuit favours Arabidopsis growth over defence under suboptimal light. Nat Plants. 7:1078.

Howard, M. M., Bell, T. H., & Kao-Kniffin, J. (2017). Soil microbiome transfer method affects microbiome composition, including dominant microorganisms, in a novel environment. In *FEMS Microbiology Letters* (Vol. 364, Issue 11). Oxford University Press. https://doi.org/10.1093/femsle/fnx092

Hu, J., Wei, Z., Friman, V. P., Gu, S. H., Wang, X. F., Eisenhauer, N., et al. 2016. Probiotic diversity enhances rhizosphere microbiome function and plant disease suppression. mBio. 7.

Huot, B., Yao, J., Montgomery, B. L., and He, S. Y. 2014. Growth-defense tradeoffs in plants: a balancing act to optimize fitness. Mol Plant. 7:1267–1287.

Hurley, A., Chevrette, M. G., Rosario-Meléndez, N., & Handelsman, J. (2022). THOR’s Hammer: the Antibiotic Koreenceine Drives Gene Expression in a Model Microbial Community. Mbio, e02486-21. <https://doi.org/10.1128/mbio.02486-21>

Jiang, G., Zhang, Y., Gan, G., Li, W., Wan, W., Jiang, Y., Yang, T., Zhang, Y., Xu, Y., Wang, Y., Shen, Q., Wei, Z., & Dini-Andreote, F. (2022). Exploring rhizo-microbiome transplants as a tool for protective plant-microbiome manipulation. *ISME Communications*, *2*(1). https://doi.org/10.1038/s43705-022-00094-8

Jones, J. D. G., and Dangl, J. L. 2006. The plant immune system. Nature. 444:323–329.

Kinsella, K., Schulthess, C. P., Morris, T. F., & Stuart, J. D. (2009). Rapid quantification of Bacillus subtilis antibiotics in the rhizosphere. Soil Biology and Biochemistry, 41(2), 374-379. <https://doi.org/10.1016/j.soilbio.2008.11.019>

Kloepper, J. W., & Schroth, M. N. (1978). *Plant growth-promoting rhizobacteria on radishes.* https://www.researchgate.net/publication/284682983

Knights, H.E., Jorrin, B., Haskett, T.L. and Poole, P.S. 2021. Deciphering bacterial mechanisms of root colonization. *Environ. Microbiol. Rpt.*, 13:428-444.

Lakshmanan, V., Kumar, A.S. and Bais, H.P. 2012. The ecological significance of plant-associated biofilms. *Microbial biofilms: Current research and applications. Caister Academic Press, Norfolk*, 43-60.

Lebeis, S. L., Paredes, S. H., Lundberg, D. S., Breakfield, N., Gehring, J., McDonald, M., et al. 2015. Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. Science. 349:860–864.

Lee, S. M., Kong, H. G., Song, G. C., & Ryu, C. M. (2021). Disruption of Firmicutes and Actinobacteria abundance in tomato rhizosphere causes the incidence of bacterial wilt disease. *ISME Journal*, *15*(1), 330–347. https://doi.org/10.1038/s41396-020-00785-x

Li, Y., He, F., Guo, Q., Feng, Z., Zhang, M., Ji, C., Xue, Q., & Lai, H. (2022). Compositional and functional comparison on the rhizosphere microbial community between healthy and Sclerotium rolfsii-infected monkshood (Aconitum carmichaelii) revealed the biocontrol potential of healthy monkshood rhizosphere microorganisms. *Biological Control*, *165*. https://doi.org/10.1016/j.biocontrol.2021.104790

Li, Z. F., Bai, X. L., Jiao, S., Li, Y. M., Li, P. R., Yang, Y., et al. 2021. A simplified synthetic community rescues Astragalus mongholicus from root rot disease by activating plant-induced systemic resistance. Microbiome. 9.

Liu, H., Qiu, Z., Ye, J., Verma, J. P., Li, J., and Singh, B. K. 2022. Effective colonisation by a bacterial synthetic community promotes plant growth and alters soil microbial community. Journal of Sustainable Agriculture and Environment. 1:30–42.

Lozano, G. L., Bravo, J. I., Garavito Diago, M. F., Park, H. B., Hurley, A., Peterson, S. B., Stabb, E. V., Crawford, J. M., Handelsman, J. (2019). Introducing THOR, a model microbiome for genetic dissection of community behavior. MBio, 10(2), e02846-18. <https://doi.org/10.1128/mBio.02846-18>

Ma, K. W., Niu, Y. L., Jia, Y., Ordon, J., Copeland, C., Emonet, A., et al. 2021. Coordination of microbe-host homeostasis by crosstalk with plant innate immunity. Nat Plants. 7:814.

Martins SJ, Medeiros FHV, Lakshmanan V, Bais HP. Impact of seed exudates on growth and biofilm formation of *Bacillus amyloliquefaciens* ALB629 in common bean. *Frontiers in Mic­­­robiology*, v.8, p.1-9, 2018. doi:10.3389/fmicb.2017.02631

Martins SJ, Medeiros FHV, Souza RM, Vilela LAF. Is curtobacterium wilt biocontrol temperature dependent? *Acta Scientiarum. Agronomy*, v.36, p­­­­.409, 2014. doi:10.4025/actasciagron.v36i4.18018

Martins SJ, Taerum SJ, TriplettL,Emerson JB, Zasada I, de Toledo BF (g), Kovac J, Martin K, Bull CT. Soil bacterivores and other bacterial predators for plant and human health. *Phytobiomes Journal,* v. 6, 184-200, 2022. doi:10.1094/PBIOMES-11-21-0073-RVW

Martins, S. J., Faria, A. F., Pedroso, M. P., Cunha, M. G., Rocha, M. R., & Medeiros, F. H. V. (2019). Microbial volatiles organic compounds control anthracnose (Colletotrichum lindemuthianum) in common bean (Phaseolus vulgaris L.). *Biological Control*, *131*, 36-42.

Martins, Samuel Julio, Flavio Henrique Vasconcelos de Medeiros, Ricardo Magela de Souza, Amanda Flausino de Faria, Eduardo Lopes Cancellier, Helbert Rezende de Oliveira Silveira, Mário Lúcio Vilela de Rezende, and Luiz Roberto Guimarães Guilherme. 2015. “Common Bean Growth and Health Promoted by Rhizobacteria and the Contribution of Magnesium to the Observed Responses.” *Applied Soil Ecology* 87:49–55.

Mavrodi, D. V., Mavrodi, O. V., Parejko, J. A., Bonsall, R. F., Kwak, Y. S., Paulitz, T. C., Thomashow, L., Weller, D. M. (2012). Accumulation of the antibiotic phenazine-1-carboxylic acid in the rhizosphere of dryland cereals. Applied and Environmental Microbiology, 78(3), 804-812. <https://doi.org/10.1128/AEM.06784-11>

Mendes, R., Kruijt, M., De Bruijn, I., Dekkers, E., Van Der Voort, M., Schneider, J. H., Piceno, Y. M., DeSantis, T. Z., Andersen, G. L., Bakker, P. A. H. M., Raaijmakers, J. M. (2011). Deciphering the rhizosphere microbiome for disease-suppressive bacteria. Science, 332(6033), 1097-1100. <https://doi.org/10.1126/science.1203980>

Miya, A., Albert, P., Shinya, T., Desaki, Y., Ichimura, K., Shirasu, K., et al. 2007. CERK1, a LysM receptor kinase, is essential for chitin elicitor signaling in Arabidopsis. Proc Natl Acad Sci USA. 104:19613–19618.

Morcillo, R.J. and Manzanera, M. 2021. The effects of plant-associated bacterial exopolysaccharides on plant abiotic stress tolerance. *Metabolites*, 11:337.

Muller, E. E. L., Faust, K., Widder, S., Herold, M., Martı́nez Arbas, S., and Wilmes, P. (2018). Using Metabolic Networks to Resolve Ecological Properties of Microbiomes. Curr. Opin. Syst. Biol. 8, 73–80. doi: 10.1016/j.coisb.2017.12.004

Mülner, P., Bergna, A., Wagner, P., Sarajlić, D., Gstöttenmayr, B., Dietel, K., ... & Berg, G. (2019). Microbiota associated with sclerotia of soilborne fungal pathogens–a novel source of biocontrol agents producing bioactive volatiles. *Phytobiomes Journal*, *3*(2), 125-136.

Newman, M. A., Sundelin, T., Nielsen, J. T., and Erbs, G. 2013. MAMP (microbe-associated molecular pattern) triggered immunity in plants. Front Plant Sci. 4.

Nielsen, T. H., & Sørensen, J. (2003). Production of cyclic lipopeptides by Pseudomonas fluorescens strains in bulk soil and in the sugar beet rhizosphere. Applied and environmental microbiology, 69(2), 861-868. <https://doi.org/10.1128/AEM.69.2.861-868.2003>

Niu, B., Paulson, J. N., Zheng, X. Q., and Kolter, R. 2017. Simplified and representative bacterial community of maize roots. Proc Natl Acad Sci USA. 114:E2450–E2459.

Niu, B., Wang, W., Yuan, Z., Sederoff, R.R., Sederoff, H., Chiang, V.L. and Borriss, R. 2020. Microbial interactions within multiple-strain biological control agents impact soil-borne plant disease. *Frontiers Microbiol.*, 11:585-404.

Ongena, M., & Jacques, P. (2008). Bacillus lipopeptides: versatile weapons for plant disease biocontrol. Trends in Microbiology, 16(3), 115-125. <https://doi.org/10.1016/j.tim.2007.12.009>

Ongena, M., Jourdan, E., Adam, A., Paquot, M., Brans, A., Joris, B., Arpigny, J. Thonart, P. (2007). Surfactin and fengycin lipopeptides of Bacillus subtilis as elicitors of induced systemic resistance in plants. Environmental Microbiology, 9(4), 1084-1090. <https://doi.org/10.1111/j.1462-2920.2006.01202.x>

Ossowicki, A., Tracanna, V., Petrus, M. L., van Wezel, G., Raaijmakers, J. M., Medema, M. H., & Garbeva, P. (2020). Microbial and volatile profiling of soils suppressive to Fusarium culmorum of wheat. Proceedings of the Royal Society B, 287(1921), 20192527.

Pascale, A., Proietti, S., Pantelides, I. S., and Stringlis, I. A. 2020. Modulation of the root microbiome by plant molecules: the basis for targeted disease suppression and plant growth promotion. Front Plant Sci. 10.

Paulsen, I. T., Press, C. M., Ravel, J., Kobayashi, D. Y., Myers, G. S., Mavrodi, D. V., DeBoy, R. T., Seshadri, R., Madupu, R., Dodson, R.j., Durkin, A., S., Brinkac, L. M., Daugherty, S. C., Sullivan, S. A., Rosovitz, M. J., Gwinn, M. L., Zhou, L., Schneider, D. J., Cartinhour, S. W., Nelson, W. C., Weidman, J., Watkins, K., Tran, K., Khouri, H., Pierson, E. A., Pierson, L. S., Thomashow, L. S., Loper, J. E. (2005). Complete genome sequence of the plant commensal Pseudomonas fluorescens Pf-5. Nature Biotechnology, 23(7), 873-878. <https://doi.org/10.1038/nbt1110>

Pfeilmeier, S., Petti, G. C., Bortfeld-Miller, M., Daniel, B., Field, C. M., Sunagawa, S., et al. 2021. The plant NADPH oxidase RBOHD is required for microbiota homeostasis in leaves. Nat Microbiol. 6:852.

Pieterse, C. M. J., Zamioudis, C., Berendsen, R. L., Weller, D. M., van Wees, S. C. M., and Bakker, P. 2014. Induced systemic resistance by beneficial microbes. Annual Review of Phytopathology. 52:347–375.

Poudel M, Mendes R, Soares LA, Bueno CG, Meng Y, Folimonova SY, Garrett KA, Martins SJ. The role of plant-associated bacteria, fungi and viruses in drought stress mitigation. *Frontiers in Microbiology*, v.12, 2021 doi:10.3389/fmicb.2021.743512

Poudel, R., Jumpponen, A., Schlatter, D. C., Paulitz, T. C., Gardener, B. B. M., Kinkel, L. L., et al. 2016. Microbiome networks: A systems framework for identifying candidate microbial assemblages for disease management. Phytopathology. 106:1083–1096.

Prigigallo, M. I., Cabanas, C. G. L., Mercado-Blanco, J., and Bubici, G. 2022. Designing a synthetic microbial community devoted to biological control: the case study of Fusarium wilt of banana. Front Microbiol. 13.

Qi, M. S., Berry, J. C., Veley, K. W., O’Connor, L., Finkel, O. M., Salas-Gonzalez, I., et al. 2022. Identification of beneficial and detrimental bacteria impacting Sorghum responses to drought using multi-scale and multi-system microbiome comparisons. Isme Journal. 16:1957–1969.

Qu, Q., Zhang, Z., Peijnenburg, W. J. G. M., Liu, W., Lu, T., Hu, B., Chen, J., Chen, J., Lin, Z., & Qian, H. (2020). Rhizosphere Microbiome Assembly and Its Impact on Plant Growth. In *Journal of Agricultural and Food Chemistry* (Vol. 68, Issue 18, pp. 5024–5038). American Chemical Society. https://doi.org/10.1021/acs.jafc.0c00073

Raaijmakers, J. M., & Mazzola, M. (2012). Diversity and natural functions of antibiotics produced by beneficial and plant pathogenic bacteria. Annual review of phytopathology, 50, 403-424. <https://doi.org/10.1146/annurev-phyto-081211-172908>

Raaijmakers, J. M., Bonsall, R. F., & Weller, D. M. (1999). Effect of population density of Pseudomonas fluorescens on production of 2, 4-diacetylphloroglucinol in the rhizosphere of wheat. Phytopathology, 89(6), 470-475.

Raaijmakers, J. M., Vlami, M., & De Souza, J. T. (2002). Antibiotic production by bacterial biocontrol agents. Antonie van Leeuwenhoek, 81(1), 537-547. <https://doi.org/10.1023/A:1020501420831>

Roberson, E.B. and Firestone, M.K. 1992. Relationship between desiccation and exopolysaccharide production in a soil Pseudomonas sp. *Appl. Environ. Microbiol.*, 58:1284-1291.

Rudrappa, T., Czymmek, K.J., Paré, P.W. and Bais, H.P. 2008. Root-secreted malic acid recruits beneficial soil bacteria. *Plant Physiol.*, 148:1547-1556.

Rybakova, D., Müller, H., Olimi, E., Schaefer, A., Cernava, T., & Berg, G. (2022). To defend or to attack? Antagonistic interactions between Serratia plymuthica and fungal plant pathogens, a species-specific volatile dialogue. Frontiers in Sustainable Food Systems, 6:1020634

Sanders ME, Merenstein DJ, Reid G, Gibson GR, Rastall RA. Probiotics and prebiotics in intestinal health and disease: from biology to the clinic. Nat Rev Gastroenterol Hepatol. 2019;16:605–16.

Santhanam, R., Luu, V. T., Weinhold, A., Goldberg, J., Oh, Y., & Baldwin, I. T. (2015). Native root-associated bacteria rescue a plant from a sudden-wilt disease that emerged during continuous cropping. Proceedings of the National Academy of Sciences, 112(36), E5013-E5020.

Schandry, N., Jandrasits, K., Garrido-Oter, R., and Becker, C. 2021. Plant-derived benzoxazinoids act as antibiotics and shape bacterial communities. bioRxiv.

Schlechter, R.O., Jun, H., Bernach, M., Oso, S., Boyd, E., Muñoz-Lintz, D.A., Dobson, R.C., Remus, D.M. and Remus-Emsermann, M.N. 2018. Chromatic bacteria–A broad host-range plasmid and chromosomal insertion toolbox for fluorescent protein expression in bacteria. *Frontiers Microbiol.*, *9*:3052.

Schmidt, R., Cordovez, V., De Boer, W., Raaijmakers, J., & Garbeva, P. (2015). Volatile affairs in microbial interactions. The ISME journal, 9(11), 2329-2335.

Schmidt, R., Etalo, D. W., De Jager, V., Gerards, S., Zweers, H., De Boer, W., & Garbeva, P. (2016). Microbial small talk: volatiles in fungal–bacterial interactions. *Frontiers in microbiology*, *6*, 1495.

Schroth, M. N., & Hancock, J. G. (1982). Disease-Suppressive Soil and Root-Colonizing Bacteria. In *New Series* (Vol. 216, Issue 4553).

Schulz-Bohm, K., Gerards, S., Hundscheid, M., Melenhorst, J., de Boer, W., & Garbeva, P. (2018). Calling from distance: attraction of soil bacteria by plant root volatiles. The ISME Journal, 12(5), 1252-1262.

Shank, E.A., Klepac-Ceraj, V., Collado-Torres, L., Powers, G.E., Losick, R. and Kolter, R. 2011. Interspecies interactions that result in Bacillus subtilis forming biofilms are mediated mainly by members of its own genus. *Proc. Natl. Acad. Sci.*, 108:E1236-E1243.

Shayanthan, A., Ordoñez, P. A. C., & Oresnik, I. J. (2022). The Role of Synthetic Microbial Communities (SynCom) in Sustainable Agriculture. In *Frontiers in Agronomy* (Vol. 4). Frontiers Media S.A. https://doi.org/10.3389/fagro.2022.896307

Silva, J. C. P., Nunes, T. C. S., Guimarães, R. A., Pylro, V. S., Costa, L. S. A. S., Zaia, R., Campos, V. P., & Medeiros, F. H. V. (2022). Organic practices intensify the microbiome assembly and suppress root-knot nematodes. *Journal of Pest Science*, *95*(2), 709–721. <https://doi.org/10.1007/s10340-021-01417-9>

Singh, B. K., Trivedi, P., Egidi, E., Macdonald, C. A., & Delgado-Baquerizo, M. (2020). Crop microbiome and sustainable agriculture. In *Nature Reviews Microbiology* (Vol. 18, Issue 11, pp. 601–602). Nature Research. https://doi.org/10.1038/s41579-020-00446-y

Song, G. C., Jeon, J. S., Sim, H. J., Lee, S., Jung, J., Kim, S. G., ... & Ryu, C. M. (2022). Dual functionality of natural mixtures of bacterial volatile compounds on plant growth. Journal of experimental botany, 73(2), 571-583.

Stringlis, I. A., Proietti, S., Hickman, R., van Verk, M. C., Zamioudis, C., and Pieterse, C. M. J. 2018a. Root transcriptional dynamics induced by beneficial rhizobacteria and microbial immune elicitors reveal signatures of adaptation to mutualists. Plant Journal. 93:166–180.

Stringlis, I. A., Yu, K., Feussner, K., de Jonge, R., van Bentum, S., van Verk, M. C., et al. 2018b. MYB72-dependent coumarin exudation shapes root microbiome assembly to promote plant health. Proc Natl Acad Sci USA. 115:E5213–E5222.

Teixeira, P., Colaianni, N. R., Law, T. F., Conway, J. M., Gilbert, S., Li, H. F., et al. 2021. Specific modulation of the root immune system by a community of commensal bacteria. Proc Natl Acad Sci USA. 118.

Terra, W. C., Campos, V. P., Martins, S. J., Costa, L. S. A. S., da Silva, J. C. P., Barros, A. F., ... & Oliveira, D. F. (2018). Volatile organic molecules from Fusarium oxysporum strain 21 with nematicidal activity against Meloidogyne incognita. *Crop Protection*, *106*, 125-131.

Toju, H., Abe, M. S., Ishii, C., Hori, Y., Fujita, H., and Fukuda, S. 2020. Scoring species for synthetic community design: network analyses of functional core microbiomes. Front. Microbiol. 11:1361.

Tracanna, V., Ossowicki, A., Petrus, M. L., Overduin, S., Terlouw, B. R., Lund, G., Robinson, S. L., Warris, S., Schijlen, E. G. W. M., van Wezel, G. P., Raaijmakers, J. M., Garbeva, P., Medema, M. H. (2021). Dissecting disease-suppressive rhizosphere microbiomes by functional amplicon sequencing and 10× metagenomics. MSystems, 6(3), e01116-20. <https://doi.org/10.1128/mSystems.01116-20>

Trivedi P, Leach JE, Tringe SG, Sa T, Singh BK. Plant-microbiome interactions: from community assembly to plant health. Nat Rev Microbiol. 2020;18:607–21.

Trivedi, P., Leach, J.E., Tringe, S.G., Sa, T. and Singh, B.K. 2020. Plant–microbiome interactions: from community assembly to plant health. *Nature Rev. Microbiol.*, 18:607-621.

Tsolakidou, M. D., Stringlis, I. A., Fanega-Sleziak, N., Papageorgiou, S., Tsalakou, A., & Pantelides, I. S. (2019). Rhizosphere-enriched microbes as a pool to design synthetic communities for reproducible beneficial outputs. *FEMS Microbiology Ecology*, *95*(10). https://doi.org/10.1093/femsec/fiz138

Tsuji, J., Jackson, E. P., Gage, D. A., Hammerschmidt, R., and Somerville, S. C. 1992. Phytoalexin accumulation in Arabidopsis thaliana during the hypersensitive reaction to Pseudomonas syringae pv. syringae. Plant Physiol. 98:1304–1309.

Türksoy, G. M., Carron, R., Koprivova, A., Kopriva, S., Wippel, K., & Andersen, T. G. (2022). Modulation of Arabidopsis growth by volatile organic compounds from a root-derived bacterial community. *BioRxiv*, doi: 10.1101/2022.04.12.488003

Tyler, B. M. 2002. Molecular basis of recognition between Phytophthora pathogens and their hosts. Annual Review of Phytopatholy. 40:137–167.

Vlamakis, H., Chai, Y., Beauregard, P., Losick, R. and Kolter, R. 2013. Sticking together: building a biofilm the Bacillus subtilis way. *Nature Rev. Microbiol.*, 11:157-168.

Vogel, C. M., Potthoff, D. B., Schafer, M., Barandun, N., and Vorholt, J. A. 2021. Protective role of the Arabidopsis leaf microbiota against a bacterial pathogen. Nat Microbiol. 6:1537.

Voges, M., Bai, Y., Schulze-Lefert, P., and Sattely, E. S. 2019. Plant-derived coumarins shape the composition of an Arabidopsis synthetic root microbiome. Proc Natl Acad Sci USA. 116:12558–12565.

Vorholt, J. A., Vogel, C., Carlstrom, C. I., and Muller, D. B. 2017. Establishing causality: opportunities of synthetic communities for plant microbiome research. Cell Host Microbe. 22:142–155.

Weisskopf, L., Schulz, S., & Garbeva, P. (2021). Microbial volatile organic compounds in intra-kingdom and inter-kingdom interactions. *Nature Reviews Microbiology*, *19*(6), 391-404.

Weller, D. M., Raaijmakers, J. M., McSpadden Gardener, B. B., & Thomashow, L. S. (2002). Microbial populations responsible for specific soil suppressiveness to plant pathogens. In *Annual Review of Phytopathology* (Vol. 40, pp. 309–348). https://doi.org/10.1146/annurev.phyto.40.030402.110010

Wiltschi, B., Cernava, T., Dennig, A., Casas, M. G., Geier, M., Gruber, S., ... & Wriessnegger, T. (2020). Enzymes revolutionize the bioproduction of value-added compounds: From enzyme discovery to special applications. Biotechnology advances, 40, 107520.

Wolinska, K. W., Vannier, N., Thiergart, T., Pickel, B., Gremmen, S., Piasecka, A., et al. 2021. Tryptophan metabolism and bacterial commensals prevent fungal dysbiosis in Arabidopsis roots. Proc Natl Acad Sci USA. 118.

Yin, C., Hagerty, C. H., & Paulitz, T. C. (2022). Synthetic microbial consortia derived from rhizosphere soil protect wheat against a soilborne fungal pathogen. *Frontiers in Microbiology*, *13*. https://doi.org/10.3389/fmicb.2022.908981

Yu, K., Liu, Y., Tichelaar, R., Savant, N., Lagendijk, E., van Kuijk, S. J. L., et al. 2019b. Rhizosphere-associated Pseudomonas suppress local root immune responses by gluconic acid-mediated lowering of environmental pH. Current Biology. 29:3913.

Yu, K., Pieterse, C. M. J., Bakker, P., and Berendsen, R. L. 2019a. Beneficial microbes going underground of root immunity. Plant Cell Environ. 42:2860–2870.

Zhao, H., Liu, Y. P., & Zhang, L. Q. (2019). In silico and genetic analyses of cyclic lipopeptide synthetic gene clusters in Pseudomonas sp. 11K1. Frontiers in Microbiology, 10, 544. <https://doi.org/10.3389/fmicb.2019.00544>

Zheng, W., Zeng, S., Bais, H., LaManna, J.M., Hussey, D.S., Jacobson, D.L. and Jin, Y. 2018. Plant growth‐promoting rhizobacteria (PGPR) reduce evaporation and increase soil water retention. *Water Resources Res.*, 54:3673-3687.

Zhou, D., Feng, H., Schuelke, T., de Santiago, A., Zhang, Q., Zhang, J., Luo, C., & Wei, L. (2019). Rhizosphere Microbiomes from Root Knot Nematode Non-infested Plants Suppress Nematode Infection. *Microbial Ecology*, *78*(2), 470–481. https://doi.org/10.1007/s00248-019-01319-5

Zimmer, S., Messmer, M., Haase, T., Piepho, H.-P., Mindermann, A., Schulz, H., et al. (2016). Effects of soybean variety and *Bradyrhizobium* strains on yield, protein content and biological nitrogen fixation under cool growing conditions in Germany. Eur. J. Agron. 72, 38–46. doi: 10.1016/j.eja.2015.09.008

Zipfel, C., Kunze, G., Chinchilla, D., Caniard, A., Jones, J. D. G., Boller, T., et al. 2006. Perception of the bacterial PAMP EF-Tu by the receptor EFR restricts Agrobacterium-mediated transformation. Cell. 125:749–760.

**Supplementary Table 1**. *In vivo* experiments using synthetic microbial communities (SynComs) for plant health.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| |  |  |  |  |  | | --- | --- | --- | --- | --- | | Organism | Plant | Subject of Study | Pathogen | Reference | | *Pseudomonas* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Achromobacter* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Delftia* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Enterobacter* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Advenella* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Flavobacterium* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Duganella* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Stenotrophomonas* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Ochrobactrum* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Phyllobacterium* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Comamonas* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Oerskovia* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Rhizobium* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Ancylobacter* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Bacillus* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Rhodococcus* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Sphingopxis* | *Astragalus mongholicus* | root rot disease | *Fusarium oxysporum* | Li et al., 2021 | | *Acinetobacter* | *Zea mays* | desiccation | N/A | Molina Romero et al., 2017 | | *Azospirillum brasilense* | *Zea mays* | desiccation | N/A | Molina Romero et al., 2017 | | *Pseudomonas putida* | *Zea mays* | desiccation | N/A | Molina Romero et al., 2017 | | *Sphingomonas* | *Zea mays* | desiccation | N/A | Molina Romero et al., 2017 | | *Pseudomonas* | *Musa* | Fusarium wilt | *Fusarium oxysporum f. Cubense (TR4)* | Prigigallo et al., 2022 | | *Bacillus* | *Musa* | Fusarium wilt | *Fusarium oxysporum f. Cubense (TR4)* | Prigigallo et al., 2022 | | *Trichoderma* | *Musa* | Fusarium wilt | *Fusarium oxysporum f. Cubense (TR4)* | Prigigallo et al., 2022 | | *Bacillus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Paenibacillus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Pantoea* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Bradyrhizobium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Pantoea* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Rhizobium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Bacillus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Kluyyera* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Acinetobacter* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Staphylococcus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Chryseobacterium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Sphingobium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Sinohizobium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Pseudomonas* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Microbacterium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Agrobacterium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Paenibacillus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Paenibacillus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Sphingomonas* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Microbacterium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Pantoea* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Bacillus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Bacterium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Bacillus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Paenibacillus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Bacillus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Pseudorhodoferax* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Microbacterium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Sphingobium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Chryseobacterium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Erwinia* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Pantoea* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Staphylococcus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Paenibacillus* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Pantoea* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Chryseobacterium* | *Glycine max* | Nutrient Acquisition | N/A | Wang et al., 2021 | | *Bacillus mojavensis* | *Nicotiana attenuata* | Sudden Wilt Disease | *Fusarium-Alternaria* disease complex | Santhanam et al., 2015 | | *Anthrobacter nitroguajacolicus* | *Nicotiana attenuata* | Sudden Wilt Disease | *Fusarium-Alternaria* disease complex | Santhanam et al., 2015 | | *Bacillus megaterium* | *Nicotiana attenuata* | Sudden Wilt Disease | *Fusarium-Alternaria* disease complex | Santhanam et al., 2015 | | *Pseudomonas azotoformans* | *Nicotiana attenuata* | Sudden Wilt Disease | *Fusarium-Alternaria* disease complex | Santhanam et al., 2015 | | *Pseudomonas frederiksbergensis* | *Nicotiana attenuata* | Sudden Wilt Disease | *Fusarium-Alternaria* disease complex | Santhanam et al., 2015 | | *Brevibacterium frigoritolerans* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Lee et al., 2021 | | *Bacillus niacini* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Lee et al., 2021 | | *Solibacillus silvestris* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Lee et al., 2021 | | *Bacillus luciferensis* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Lee et al., 2021 | | *Priestia megaterium* | *Triticum* | Crown rot | *Fusarium pseudograminearum* | Liu et al., 2022 | | *Bacillus* | *Triticum* | Crown rot | *Fusarium pseudograminearum* | Liu et al., 2022 | | *Acinetobacter pittii* | *Triticum* | Crown rot | *Fusarium pseudograminearum* | Liu et al., 2022 | | *Enterobacter asburiae* | *Triticum* | Crown rot | *Fusarium pseudograminearum* | Liu et al., 2022 | | *Bacillus pumilus* | *Triticum* | Crown rot | *Fusarium pseudograminearum* | Liu et al., 2022 | | *Acinetobacter pittii* | *Triticum* | Crown rot | *Fusarium pseudograminearum* | Liu et al., 2022 | | *Xanthamonas* | *Triticum* | Crown rot | *Fusarium pseudograminearum* | Liu et al., 2022 | | *Burkholderia* | *Triticum* | Crown rot | *Fusarium pseudograminearum* | Liu et al., 2022 | | *Pseudomonas* | *Zea mays* | Root rot | *Rhizoctonia solani* | Yin et al., 2022 | | *Rhodococcus erythropolis* | *Zea mays* | Root rot | *Rhizoctonia solani* | Yin et al., 2022 | | *Chryseobacterium soldanellicola* | *Zea mays* | Root rot | *Rhizoctonia solani* | Yin et al., 2022 | | *Pedobacter* | *Zea mays* | Root rot | *Rhizoctonia solani* | Yin et al., 2022 | | *Bacillus subtilis* | *Zea mays* | Fungal root disease | *Rhizoctonia solani* | Ali et al., 2021 | | *Bacillus atrophaeus* | *Zea mays* | Fungal root disease | *Rhizoctonia solani* | Ali et al., 2021 | | *Bacillus licheniformis* | *Zea mays* | Fungal root disease | *Rhizoctonia solani* | Ali et al., 2021 | | *Bacillus altitudinis* | *Zea mays* | Fungal root disease | *Rhizoctonia solani* | Ali et al., 2021 | | *Bacillus pumilus* | *Zea mays* | Fungal root disease | *Rhizoctonia solani* | Ali et al., 2021 | | *Bacillus velezenis* | *Zea mays* | Fungal root disease | *Rhizoctonia solani* | Ali et al., 2021 | | *Bacillus atrophaeus* | *Zea mays* | Fungal root disease | *Rhizoctonia solani* | Ali et al., 2021 | | *Bacillus licheniformis* | *Zea mays* | Fungal root disease | *Rhizoctonia solani* | Ali et al., 2021 | | *Bacillus altitudinis* | *Zea mays* | Fungal root disease | *Rhizoctonia solani* | Ali et al., 2021 | | *Bacillus pumilus* | *Zea mays* | Fungal root disease | *Rhizoctonia solani* | Ali et al., 2021 | | *Bacillus velenzenis* | *Zea mays* | Fungal root disease | *Rhizoctonia solani* | Ali et al., 2021 | | *Pseudomonas putida* | *Solanum tuberosum* | Late blight | *Phytophthora infestans* | De Vrieze et al., 2018 | | *Pseudomonas chloraphis* | *Solanum tuberosum* | Late blight | *Phytophthora infestans* | De Vrieze et al., 2018 | | *Pseudomonas frederiksbergensis* | *Solanum tuberosum* | Late blight | *Phytophthora infestans* | De Vrieze et al., 2018 | | *Pseudomonas fluoroscensz* | *Solanum tuberosum* | Late blight | *Phytophthora infestans* | De Vrieze et al., 2018 | | *Pseudomonas fluoroscensz* | *Solanum tuberosum* | Late blight | *Phytophthora infestans* | De Vrieze et al., 2018 | | *Bacillus* | *Triticum aestivum* | Increasing crop productivity | N/A | Ijaz et al, 2019 | | *Pseudomonas* | *Triticum aestivum* | Increasing crop productivity | N/A | Ijaz et al, 2019 | | *Pseudomonas* | *Triticum aestivum* | Increasing crop productivity | N/A | Ijaz et al, 2019 | | *Bacillus cereus* | *Brassica oleracea* | Modifying root endophytic bacterial composition | N/A | Gadhave et al., 2018 | | *Bacillus subtilis* | *Brassica oleracea* | Modifying root endophytic bacterial composition | N/A | Gadhave et al., 2018 | | *Bacillus amyloliquefaciens* | *Brassica oleracea* | Modifying root endophytic bacterial composition | N/A | Gadhave et al., 2018 | | *Microbacterium oxydans* | *Trifolium pratense* | Prevention of growth reduction factors | N/A | Hartman et al., 2017 | | *Flavobacterium succinicans* | *Trifolium pratense* | Prevention of growth reduction factors | N/A | Hartman et al., 2017 | | *Janthinobacterium lividum* | *Trifolium pratense* | Prevention of growth reduction factors | N/A | Hartman et al., 2017 | | *Pseudomonas* | *Trifolium pratense* | Prevention of growth reduction factors | N/A | Hartman et al., 2017 | | *Bacillus simplex* | *Allium sativum* | Plant Growth | N/A | Zhuang et al., 2021 | | *Pseudomonas cedrina* | *Allium sativum* | Plant Growth | N/A | Zhuang et al., 2021 | | *Pseudomonas baetica* | *Allium sativum* | Plant Growth | N/A | Zhuang et al., 2021 | | *Pseudomonas migulae* | *Allium sativum* | Plant Growth | N/A | Zhuang et al., 2021 | | *Pseudomonas fluorescens* | *Allium sativum* | Plant Growth | N/A | Zhuang et al., 2021 | | *Pseudomonas reinkei* | *Allium sativum* | Plant Growth | N/A | Zhuang et al., 2021 | | *Pseudomonas frederiksbergensis* | *Allium sativum* | Plant Growth | N/A | Zhuang et al., 2021 | | *Flavobacterium* | *Beta vulgaris* | Fungal root disease | *Rhizoctonia solani* | Carrión et al., 2019 | | *Flavobacterium* | *Beta vulgaris* | Fungal root disease | *Rhizoctonia solani* | Carrión et al., 2019 | | *Flavobacterium* | *Beta vulgaris* | Fungal root disease | *Rhizoctonia solani* | Carrión et al., 2019 | | *Flavobacterium* | *Beta vulgaris* | Fungal root disease | *Rhizoctonia solani* | Carrión et al., 2019 | | *Chitinophaga* | *Beta vulgaris* | Fungal root disease | *Rhizoctonia solani* | Carrión et al., 2019 | | *Chitinophaga* | *Beta vulgaris* | Fungal root disease | *Rhizoctonia solani* | Carrión et al., 2019 | | *Chitinophaga* | *Beta vulgaris* | Fungal root disease | *Rhizoctonia solani* | Carrión et al., 2019 | | *Stenotrophomonas maltophilia* | *Zea mays* | Seedling blight disease | *Fusarium verticillioides* | Niu et al., 2017 | | *Ochrobactrum pituitosum* | *Zea mays* | Seedling blight disease | *Fusarium verticillioides* | Niu et al., 2017 | | *Curtobacterium pusillum* | *Zea mays* | Seedling blight disease | *Fusarium verticillioides* | Niu et al., 2017 | | *Enterobacter cloacae* | *Zea mays* | Seedling blight disease | *Fusarium verticillioides* | Niu et al., 2017 | | *Chryseobacterium indologenes* | *Zea mays* | Seedling blight disease | *Fusarium verticillioides* | Niu et al., 2017 | | *Herbaspirillum frisingense* | *Zea mays* | Seedling blight disease | *Fusarium verticillioides* | Niu et al., 2017 | | *Pseudomonas putida* | *Zea mays* | Seedling blight disease | *Fusarium verticillioides* | Niu et al., 2017 | | *Anthrobacter defluvii* | *Brassica napus* | Plant growth and phosphate uptake | N/A | Zheng et al., 2019 | | *Streptomyces prasinopilos* | *Brassica napus* | Plant growth and phosphate uptake | N/A | Zheng et al., 2019 | | *Bacillus megaterium* | *Brassica napus* | Plant growth and phosphate uptake | N/A | Zheng et al., 2019 | | *Burkholderia cepacia* | *Brassica napus* | Plant growth and phosphate uptake | N/A | Zheng et al., 2019 | | *Variovorax paradoxus* | *Brassica napus* | Plant growth and phosphate uptake | N/A | Zheng et al., 2019 | | *Pseudomonas frederiksbergensis* | *Brassica napus* | Plant growth and phosphate uptake | N/A | Zheng et al., 2019 | | *Rhodanobacter* | *Brassica napus* | Plant growth and phosphate uptake | N/A | Zheng et al., 2019 | | *Pseudomonas brassicacearum* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Hu et al., 2016 | | *Pseudomonas fluorescens* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Hu et al., 2016 | | *Pseudomonas fluorescens* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Hu et al., 2016 | | *Pseudomonas fluorescens* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Hu et al., 2016 | | *Pseudomonas fluorescens* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Hu et al., 2016 | | *Pseudomonas fluorescens* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Hu et al., 2016 | | *Pseudomonas protegens* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Hu et al., 2016 | | *Pseudomonas protegens* | *Solanum lycopersicum* | Bacterial Wilt Disease | *Ralstonia solanacearum* | Hu et al., 2016 | | *Agrobacterium* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Agrobacterium* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Asticcacaulis* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Burkholderia* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Dyella* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Ensifer* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Ensifer* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Enterobacter* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Enterobacter* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Enterobacter* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Enterobacter* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Enterobacter* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Lysobacter* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Microbacterium* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Pantoea* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Pantoea* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Pedobacter* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Pedobacter* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Sphingomonas* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Stenotrophomonas* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Stenotrophomonas* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Streptomyces* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Bradyrhizobiaceae* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Xanthomonadaceae* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Variovorax* | *Zea mays* | Nutrient Uptake | N/A | de Souza et al., 2019 | | *Ottowia* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Asticcacaulis* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Enterobacter* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Pantoea* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Microbacterium* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Bosea* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Rhizobium* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Ensifer* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Pedobacter* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Pedobacter* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Chitinophaga* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Sphingomonas* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Streptomyces* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Dyella* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Dyella* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Lysobacter* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Stenotrophomonas* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Stenotrophomonas* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Pseudoxanthomonas* | *Zea mays* | Plant Growth | N/A | Armanhi et al., 2018 | | *Nocardioides* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Micromonospora* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Cellulomonas* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Streptomyces* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Tetrasphaera* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Conexibacter* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Bacillus* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Bacillus* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Bacillus* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Bacillus* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Phenylobacterium* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Asticcacaulis* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Devosia* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Devosia* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Rhizobium* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Pseudolabrys* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Acidovorax* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Herbaspirillum* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Piscinibacter* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Vogesella* | *Oryza sativa* | Nitrogen-use efficiency | N/A | Zhang et al., 2019 | | *Trichoderma harzianum* | *Capsicum* | Root Rot | *Phytophthora capsici* | Ezziyyani et al., 2007 | | *streptomyces rochei* | *Capsicum* | Root Rot | *Phytophthora capsici* | Ezziyyani et al., 2007 | | *Bacillus cereus* | *Capsicum annuum L. var. grossum* | *Phytophthora* blight | *Phytophthora capsici* | Zhang et al., 2019 | | *Bacillus subtilis* | *Capsicum annuum L. var. grossum* | *Phytophthora* blight | *Phytophthora capsici* | Zhang et al., 2019 | | *Serratia* | *Capsicum annuum L. var. grossum* | *Phytophthora* blight | *Phytophthora capsici* | Zhang et al., 2019 | | *Pseudomonas* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Kannan and Sureendar, 2009 | | *Trichoderma harzianum* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Kannan and Sureendar, 2009 | | *Bacillus subtilis* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Kannan and Sureendar, 2009 | | *Pseudomonas* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Kannan and Sureendar, 2009 | | *Bacillus* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Kannan and Sureendar, 2009 | | *Azobacter* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Kannan and Sureendar, 2009 | | *Azospirilum* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Kannan and Sureendar, 2009 | | *Pseudomonas fluorescens* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Kannan and Sureendar, 2009 | | *Bacillus subtilis* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Shanmugam and Kanouja 2011 | | *Bacilus subtilis* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Shanmugam and Kanouja 2011 | | *Bacillus atrophaeus* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Shanmugam and Kanouja 2011 | | *Burkholderia cepacia* | *Solanum lycopersicum* | Vascular Wilt | *Fusarium oxysporum* | Shanmugam and Kanouja 2011 | | *Glomus mosseae* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Mohandas et al., 2009 | | *Trichoderma harzianum* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Mohandas et al., 2009 | | *Pseudomonas Fluorescens* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Mohandas et al., 2009 | | *Pseudomonas aeruginosa* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Wong et al., 2019 | | *Trichoderma harzianum* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Wong et al., 2019 | | *Pseudomonas putida* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Thangavelu and Gopi, 2015 | | *Pseudomonas putida* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Thangavelu and Gopi, 2015 | | *Bacillus cereus* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Thangavelu and Gopi, 2015 | | *Bacillus cereus* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Thangavelu and Gopi, 2015 | | *Bacillus flexus* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Thangavelu and Gopi, 2015 | | *Achromobacter* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Thangavelu and Gopi, 2015 | | *Rhizobium* | *Musa* | *Fusarium* wilt | *Fusarium oxysporum* | Thangavelu and Gopi, 2015 | | *Streptomyces atrovirens* | *Solanum lycopersicum* | Root rot | *Rhizoctonia solani* | Solanki et al., 2019 | | *Trichoderma lixii* | *Solanum lycopersicum* | Root rot | *Rhizoctonia solani* | Solanki et al., 2019 | | *Bacillus aryabhattai* | *Aconitum* | Southern blight | *Sclerotium rolfsii* | Li et al., 2022 | | *Streptomyces fungicidicus* | *Aconitum* | Southern blight | *Sclerotium rolfsii* | Li et al., 2022 | | *Streptomyces rochei* | *Aconitum* | Southern blight | *Sclerotium rolfsii* | Li et al., 2022 | | *Streptomyces enissocaesilis* | *Aconitum* | Southern blight | *Sclerotium rolfsii* | Li et al., 2022 | |
|  |