

## Roads to Construct and Re-build Plant Microbiota Community

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**Plant microbiota has influenced plant growth and physiology significantly. Plant and plant-associated microbes have flexible interactions that respond to changes in environmental conditions. These interactions can be adjusted to suit the requirements of the microbial community or the host physiology. In addition, it can be modified to suit microbiota structure or fixed by the host condition. However, no technology is realized yet to control mechanically manipulated plant microbiota structure. Here, we review step-by-step plant-associated microbial partnership from plant growth-promoting rhizobacteria to the microbiota structural modulation. Glutamic acid enriched the population of *Streptomyces*, a specific taxon in anthosphere microbiota community. Additionally, the population density of the microbes in the rhizosphere was also a positive response to glutamic acid treatment. Although many types of research are conducted on the structural revealing of plant microbiota, these concepts need to be further understood as to how the plant microbiota clusters are controlled or modulated at the community level. This review suggests that the intrinsic level of glutamic acid *in planta* is associated with the microbiota composition that the external supply of the biostimulant can modulate.**

**Keywords :** beneficial microbe, microbial engineering, microbiome, *Streptomyces*

Agriculture aims to provide stable food for humankind. Due to the population growth, the world population is expected to be 10 billion by 2050 (Béné et al., 2015). Humans need to produce more than twice as many crops as we do now, but climate change is threatening crop productivity (Foley, 2011). Plant microbiomes play a critical role in plant development and health (Badri and Vivanco, 2009; Berendsen et al., 2018; Chaparro et al., 2012). Therefore, maintaining a healthy microbiome is an essential factor in the growth and yield of crops in the agricultural system (Etesami and Beattie, 2017; Turner et al., 2013). For the next green revolution, more research and investigation are needed to understand the various roles and mechanisms of the plant microbiome (Langridge, 2014; Schmalzer, 2016).

The plant-associated microorganism can survive either inside or outside of the plant tissues. The microbes within the plant roots, stem, leaves, and seeds (endosphere) and as well as the leaf (phyllosphere) or flower surface (anthosphere), have a significant impact on the growth and nutrient acquisition of the host (del Carmen Orozco-Mosqueda et al., 2018; Liu and Brettell, 2019; Liu et al., 2017). It is judged that certain microorganisms can influence the many factors that promote the soundness of plants, and the microbes can also affect and receive each other within the community, so the complexity is very high (Hassani et al., 2018). Rhizosphere microbes contribute to the health and development of plants by being present around of root tissue of plants. The microbes are affected by the variety of crops, which are improved species of crops, and are controlled by the pH and moisture content of the soil (Adejumo and Orole, 2010). This change in microbial clusters is ultimately acting in a direction that affects the productivity of crops, so their importance is perceived as higher (San-

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toyo et al., 2017). In plants, microbes were recognized and found to exist where surviving was possible, and this area was found to exist everywhere in plants. This co-existing concept is known as the ‘plant holobiont’ (Jacoby and Kopriva, 2019; Rosenberg and Zilber-Rosenberg, 2016; Zilber-Rosenberg and Rosenberg, 2008). This review briefly introduces plant growth-promoting bacteria (PGPB) to plant microbiota, especially the possibility of modifying or engineering the plant microbiota community structure with plant probiotics or biostimulators.

### Plant-Microbiota Interactions and Communications

At the ecology level, community members of the plant-associated microbiota are driven by evolutionary relationships. Also, phytobiome has emerged as an ideal concept for understanding the interactions of various factors considered in plant growth (Beans, 2017; Parakhia and Golakiya, 2018). It is assumed to be a general structure according to the relationship with the host and the nutrient security strategy (Hamonts et al., 2018). These interactions are known as multiple pathways of plant-microbiota, and these interactions have both positive and negative directions (van der Heijden and Hartmann, 2016). Since the integrity of plant growth soil does not reflect the various effects of individual factors on the environment, the utility of the factors involved has reached its limit. Therefore, scientists have noted the microbiota link between specific factors and interactions in crop production. The interaction between plants and microbes has developed a continuous relationship within the ecosystem, and in this ecosystem, various factors are involved in the interaction.

Among them, PGPB is presented as a particular microbial community that positively interacts with the host plant (Adair and Douglas, 2017; Huang et al., 2014). The PGPB doing are various beneficial activities to the host plant and biocontrol effect against phytopathogens and promote the plant growth. PGPB can colonize the rhizosphere or endosphere of the plant and play beneficial roles in protecting from various pathogens attacks, improving growth, health, and productivity (Kloepper et al., 1980; Santoyo et al., 2016). As a result, the PGPB has excellent adaptability to plants (Berg et al., 2016; Haney et al., 2015).

### Direct or Indirect Mechanisms of PGPB

The PGPB has direct or indirect mechanisms to promote plant growth and protection (Santoyo et al., 2012). Many PGPB strains produce 1-aminocyclopropane-1-carboxylate

(ACC) deaminase, a pivotal enzyme to control the production of a phytohormone, ethylene, which involves plant growth well as defense activity (Saleem et al., 2007). The PGPB generally has pathogens suppression mechanisms through activation of the host defense systems (Compant et al., 2005; Ryan et al., 2008; Santoyo et al., 2012, 2016). The direct mechanism for suppressing pathogens by the syntheses and secretes of various antibiotics such as iturin A, bacillomycin D and enzymes like proteases, chitinases, and other antibiotic metabolic groups are siderophore and mycosubtilin lipopeptides (Glick, 2012; Hernández-León et al., 2015; Leclère et al., 2005; Martínez-Absalón et al., 2014; Santoyo et al., 2012). Certain PGPB strains, *Pseudomonas fluorescences*, *Streptomyces globisporus*, *Burkholderia vietnamiensis*, *Bacillus subtilis* have been isolated from diverse disease suppressive soil systems (Cha et al., 2016; Colombo et al., 2019; Kim et al., 2019b; Singh et al., 2019; Thomashow and Weller, 1988; Weller et al., 2012; Yang et al., 2009). Those beneficial bacteria strains have antifungal compounds; however, researchers needed additional evidence to be involved in those function.

Phylum Actinobacteria has been known as the most diverse bacterial group in nature and includes the genus of *Streptomyces* can be isolated from many different environments (Worsley et al., 2020). These Gram-positive bacteria have a high GC content and show a remarkable range of morphologies (Behie et al., 2017). The genus has also represented numerous functional secondary metabolites, and nearly 17% of the metabolites have biological activities (Harir et al., 2018). Notably, Actinobacteria produce two-thirds of all known antibiotics used in the clinic today, but also a vast array of anticancer, immunosuppressants, anthelmintics, herbicides, and antiviral compounds in addition to extracellular enzymes (Behie et al., 2017). Streptomyces is a core group in agro-ecosystems and can improve plant health and migrate from the rhizosphere to the endosphere (Kim et al., 2019a). Streptomyces have been screened and characterized by plant rhizosphere or endosphere for their potential for biocontrol activity against *Rhizoctonia solani*, *Fusarium graminearum*, and PGPB effect (Araujo et al., 2019; Colombo et al., 2019; Vurukonda et al., 2018).

### Plant-Associated Microbial Community in Ecosystem

The relationship between the plants and microbes, including these multiple elements, was defined as the concept of eco-holobiome (Liu et al., 2019; Singh et al., 2020). In the ecosystem, essential interactions with multiple hosts could

affect the overall microbiota community structure and plant health via a linked microbial interaction network (Singh et al., 2020). Plant volatile organic compounds (VOC) influence the microbiota community structure of phyllosphere, and the secretion of root exudates are known to affect soil microbiota structural configuration (Brilli et al., 2019; Liu et al., 2019). Plant VOC compounds activate disease defense mechanisms and are utilized to evade herbivore attacks, attract pollinators, or communicate with other plants (Dudareva et al., 2013). Recent research demonstrated that the anthosphere microbiota interacts with pollinators and plants (Kim et al., 2019a).

In the eco-holobiome, we must understand the structure of the microbiota communities and the function of core or keystone microbes. It is necessary to reveal what changes occur in the plant-microbial interactions through microbiota that reacts according to the external environment and the process of change within the communities. The control mechanisms of microbiota community structure may be accessed in various ways. If we reveal the community structure control factors and secure the technology, a more beneficial microbiota community can be artificially built to increase plant growth and adaptability to the environment. Microbiota consists of numerous microbes. Therefore, it is necessary to understand the community's constituent microorganisms, and the construction of an artificial community with several selected strains is being attempted (Berendsen et al., 2018).

### Artificial Community and Functional Synthetic Community (SynCom)

The microbiome is considered a "second genome" of various hosts such as humans, animals, and plants. In plants, the microbiome has been reported to have many functions that can improve plant health and growth (Berg et al., 2016). The microbial partners provide beneficial functions to the plant, based on modulating hormonal signaling and anti-pathogens activity. Also, they have nutrient absorption activities from the soil to the host to enhance plant growth in general. Thought, a single microbe may not affect the more complex ecological system in nature. With the development of next-generation sequencing technology, it is possible to reveal the microbial community structure including uncultured microorganisms (Berg et al., 2016; van der Heijden and Hartmann, 2016). A new approach to plant-microbiome research is to structure a community with artificially selected microorganisms, named synthetic community (SynCom) (Vannier et al., 2019). Members of SynCom can be selected based on in-depth analyses

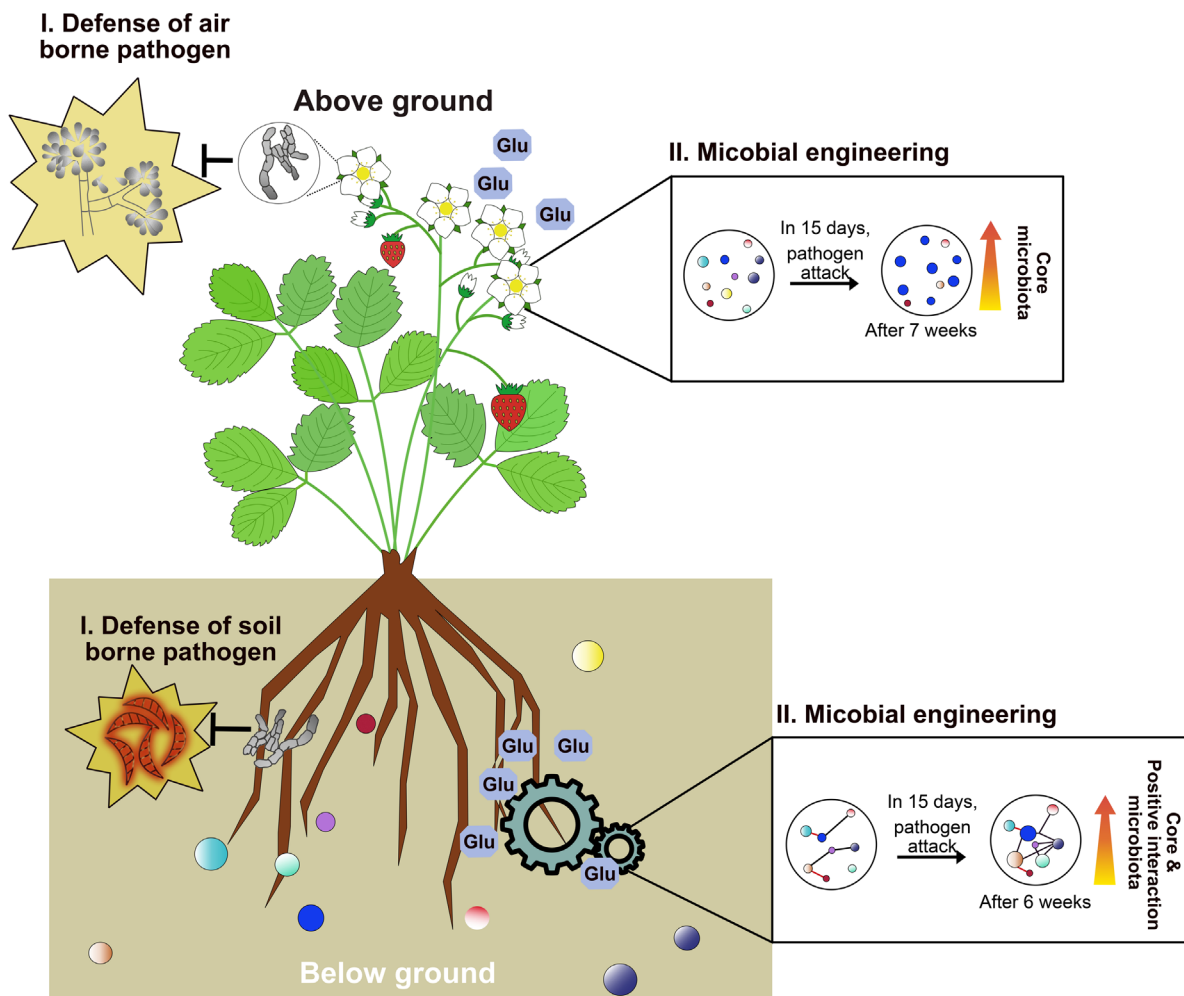
of functional keystone taxa and hub microbes. Outstanding questions remain regarding the microbial role in plant defense, many of which may now be answered utilizing a novel synthetic community approach. But they also have a bottleneck in that some groups are not represented in the total microbiome community, and members of the SynCom are not sustainable to have multiple functions. Also, those studies have relied upon culture-dependent methods. In situ, manipulation of microbiome structures remains limited, as plant-associated compounds (Rodriguez and Durán, 2020).

### Engineering Plant Microbiota Community

Several plant-microbiota manipulation strategies are considered, with each factor being bottom-up or top-down. The strategies will be based on understanding how microbes have evolved and changed together in the various organisms on Earth. Plant microbiomes make a lasting and long-term contribution to plant health. During the past years, biostimulators in agriculture have been used as tools for functional and eco-friendly materials to improve plant productivity (Backer et al., 2018; Vargas-Hernandez et al., 2017). In the next movement, new biostimulators are enabling the translation of the fundamental microbiota community. And the modulated microbiota should contribute to improving plant health and growth. The engineering strategies of the plant microbiota community enhance microbial diversity and enrichment of functional members. Plant exudates have been suggested as potential modulators of the plant microbiota community (O'Banion et al., 2020).

Root exudates are made up of carbon, nitrogen, flavonoids, peptides, and fatty acids (Badri et al., 2009). These substances serve as signals for host-associated microbial partners and anti-, fungi, and bacterial effects (Bais et al., 2006). Also, the root exudate compounds have important tasks as chemical signaling molecules in plant microbiome interactions in rhizosphere (Bakker et al., 2012). For example, host-associated and multi-generation microbiota have been selected from bulk soil, rhizosphere, and seed, which are directly or indirectly entered into tissues as stems, leaves, and flowers. Some recent relevant studies involving the techniques mentioned above are reviewed below. 'Cry for help' theory is proposed as the host-mediated microbe selection mechanism in nature (Huang et al., 2019). The theory explains a particular compound as coumarin, which enriches a specific microbe to improve host health (Bakker et al., 2018; Berendsen et al., 2018).

We have a novel 'defensbiome' concept to enhance plant health with pre-, pro-, and post-biotics, which can engineer



**Fig. 1.** Summary diagram for glutamic acid re-build microbial community. In the phyllosphere, *Streptomyces globisporus* SP6C4 and microbes can protect the host from gray mold and blossom blight disease (I: defense of airborne pathogens). And application of glutamic acid (5  $\mu\text{g/ml}$ ) re-build the population of the functional core strain, *S. globisporus* SP6C4 (II: microbial engineering). In rhizosphere, the beneficial microbe community is critically contributing to disease suppressiveness against *Fusarium* wilt (I: defense of soil borne pathogen). Bacillaea, Burkholderea, and Streptomycetacea in the rhizosphere microbiota community responded to glutamic acid treatment (II: microbial engineering).

the plant microbiota community structure. The pre-, pro-, and post-biotics are considered biostimulators. The definition of biostimulator is a substance or microorganism applied to the host to enhance micronutrient uptake or abiotic stress tolerance to more efficiency of plant quality. The first of scientific literature was defined by Kauffman et al. (2007): “biostimulator are materials, other than fertilizers, that promote plant growth when applied in low quantities.” Over the years, the word biostimulator has been used frequently in scientific literature, defining the range of substances and modes of action (Calvo et al., 2014; Du Jardin; 2015; Sparks, 2012). The biostimulator has more advantages over biotic and abiotic factors (Vargas-Hernandez et

al., 2017). Glutamic acid re-build the population of *Streptomyces*, a core strain in the strawberry anthosphere. In addition to this, glutamic acid modulated several beneficial microbes in the tomato rhizosphere (Kim et al., 2021) (Fig. 1). *Streptomyces*, which increased the population again, have a positive interaction with Bacillaceae and Burkholderiaceae. All of these bacteria positively affect plant health against various pathogens. Additionally, glutamic acid affects the microbiota community but does not trigger the activation of plant resistance genes, suggesting that glutamic acid modulates plant microbiota structure directly (Kim et al., 2021).

## Concluding Remarks and Perspectives

Thus, we have new strategies considering both plant and microbial communities. In this paper, we would like to present the current level of plant microbiota community engineering. Also, we propose a new biostimulator concept that changes community structure and enriches the core microbe for plant health. In plant-microbiota co-adaptation, the plants affect their microbiota through stimulating exudates, and the microbial partners undergo adaptation in the ecosystem. A lack of shared history between the host plant and microbiota may rarely know the development of niche saturation. Common root exudate compounds quickly exploit the soil microbiota in specific conditions such as disease infection or abiotic factors. The microbiota community's fundamental changes are already having in toolboxes: the host, soil, and microbe interactions. However, we need to have better tools for designing the plant microbiota community to take advantage of plant health. If we figure out the modulator that globally coordinated approaches, that will fill critical knowledge gaps on co-development in the plant microbiota ecosystem. Finally, the engineering of microbiota is engaged in agriculture-associated problems with feasible strategies in eco-friendly ways.

## Conflicts of Interest

No potential conflict of interest relevant to this article was reported.

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