Structural and Functional Dynamics of Bacterial World for Sustainability

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1 Introduction

The vast diversity in plant-associated microbes has been an area of interest and research for over a century. The fact that bacteria residing in the root nodules of leguminous plants fix the atmospheric nitrogen made scientists believe that plants are associated with an abundance of diverse microbes. Plants have evolved with a multitude of microorganisms that profoundly benefit plant growth and development in particular as well as the ecosystem in general. The study of plant-associated microorganisms is quite interesting and needful due to functional potential and remarkable structural dynamics of these microorganisms associated with plants. There is an urgent need to meet the increasing global demand of food as well as combat the severe climatic conditions for the growth of plant crops. In addition to this, the soil would not be conducive for plant growth as it will be nutritionally depleted and contaminated with inadequacy of water resources as well (Singh & Trivedi, 2017). The sustainable ecosystem functioning globally needs an innovative production system that would maintain soil fertility and adequate water resource. The use of available natural resources, such as plant-associated microbiomes, is the most suitable approach to contribute to an improved and sustainable plant crop production system (Altieri, 2018; Bender et al., 2016; Eyhorn et al., 2019). A vast diversity of microbiomes improves ecosystem functioning (Isbell et al., 2015). Due to their broad range of genetic and metabolic diversity, the bacteria are highly adapted to varied ecological niches (Toft & Andersson, 2010). Microorganisms,

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particularly bacteria, have lived in association with plants since ancient times and are beneficial to their host plant. These microbes associated with plants acquire soil nutrients by regulating all biogeochemical processes in the soil resilience to abiotic stresses, and pathogen control, destruction of pollutants, hence enhancing crop productivity, overall environmental quality and hence an increase of ecological adaptations (Schlaeppi & Bulgarelli, 2015). This chapter reviews and highlights the significance, composition, structural and functional dynamics of the plant-associated bacteria.

2 Diversity and Composition of Plant-Associated Bacteria

The plant microbiome encompasses the entire microbial community of plants including bacteria as well as fungi. Microbiome can be defined as the definite number of genes that are found in association with the host plant in a particular environment (Boon et al., 2014). It is believed that the microbiome interacts with the host plant dynamically to build up a symbiotic association that has a remarkable impact on the overall functioning of the host plant (Foo et al., 2017). The most significant type of plant-associated bacteria in the microbiome, that promote ecosystem functioning and sustainability and the potential of host plants, reviewed so far include the rhizobacteria and *Actinobacteria* (Ana et al., 2020).

2.1 Plant-Associated Rhizobacteria

The rhizobacteria include the variety of bacteria that inhabit the rhizosphere of the host plant thus benefitting the surrounding environment. The common plant-associated bacterial species belong to the genera *Lactobacillus*, *Acetobacter*, *Azospirillum*, *Serratia*, *Bacillus* and *Psuedomonas* (Backer et al., 2018). The host plant develops a symbiotic association with these rhizobacteria. The host plant enables the association of these bacteria by producing various secretions like carbohydrates, organic acids, minerals and root exudates that are utilized by rhizobacteria for their nutrition and development of symbiotic association with the host plant (Hassan et al., 2019; Braga et al., 2018). The rhizobacteria may invade either the inner structures, leading to endophytic establishment or the intercellular spaces of the host plant (Abbas et al., 2019; Akram et al., 2016).

The rhizobacteria, once in an established association, favours the host plant growth and development directly or indirectly (Backer et al., 2018; Akram et al., 2016). Directly, the host plant synthesizes some important nutrients like potassium (K), zinc (Zn) and silicon (Si) that lead to the growth of host plants (Backer et al., 2018; Rijavec & Lapanje, 2016; Angulo et al., 2014). Besides, the rhizobacteria generally synthesize various phytohormones like gibberellins (gibberellic acid, GA_3), auxins (indoleacetic acid, AIA), cytokinins, ethylene and abscisic acid

(ABA), to further enhance growth, cell division and overall development of the host plant. These phytohormones can further stimulate the secretion of the enzyme 1-aminocyclopropane 1-carboxylate deaminase (ACC), which mitigates the amount of ethylene hormone in the roots of the crops, thus improving the root length and density (Backer et al., 2018; Angulo et al., 2014; Penrose & Glick, 2001). The rhizobacteria indirectly promote plant growth through the modification of the rhizosphere environment, bringing about an inner resistance and adaptation in the host plant to cope with the external environment, such as protection against herbivores, insects and pathogenic microorganisms, and stimulate the synthesis of both physical and chemical obstructions and against abiotic stress. In turn, these substances allow the rhizobacteria to be more competitive in niche invasion and inhibit the interference by other pathogenic bacteria and fungi. These changes are brought about by the bacteria through the production of peculiar organic compounds and secondary metabolites (Takishita et al., 2018; Cappellari et al., 2017; Bhattacharyya & Jha, 2012). The common example includes the secretion of terpenoids (volatile secondary metabolite) by the bacterial species associated with mint and grape plants that prevents these plants against some harmful soil-borne pathogens (Cappellari et al., 2017; Salomon et al., 2016). Certain bacteria have been proven to facilitate the availability of important nutrients like iron to plants (Liu et al., 2017). The plant-associated bacteria especially some species of *Bacillus* and *Pseudomonas* have been reported to serve as biofertilizers, pesticides and stress-resistant for many important agricultural crops (Naeem et al., 2018; Hussain et al., 2016; Turatto et al., 2017; Chatterjee et al., 2017).

2.2 Plant-Associated Actinobacteria

The *Actinobacteria* were previously known as Actinomycetes and form the largest group of prokaryotes. *Actinobacteria* can inhabit plant roots endophytically or remain attached to epidermal or subcortical root cells. The endophytic bacteria have been described to enter the host plant through root hairs, stomas, wounds and sprouting hydathodes, while in free-living bacteria, structures like flagella, fimbria, exopolysaccharides and lipopolysaccharides may enable the bacterial attachment to the plant roots (Kandel et al., 2017). *Actinobacteria* are generally Gram-positive bacteria and either may be aerobic or anaerobic displaying distinct morpho-chemical characteristics of these particular moneran taxa (Bhatti et al., 2017; Sousa & Olivares, 2016; Barka et al., 2016; Trujillo et al., 2014).

The study *Actinobacteria* has a vast scientific and commercial importance, owing to their ability to synthesize a wide variety of secondary metabolites with potential biological activities including antimicrobial, anti-inflammatory, and anti-tumour, besides the production of plant growth regulators under abiotic and biotic stress conditions (Manivasagan et al., 2014). These bacteria thus promote the growth and development of important crop plants like tomato and corn, and are also responsible for inhibiting the growth of phytopathogens, and can even facilitate the availability of nitrogen to many plants. Nitrogen-fixing bacteria include members of the *Frankia* family, etc. Some of them are used as alternative for nitrogen fertilizers (Bhatti et al., 2017). The important actinobacterial genera include *Microbacterium*, *Micrococcus*, *Streptomyces* and *Frankia*, which have been reported to provide protection to their host plants against diseases and pathogens as well as enhance the growth of these plants (Bhatti et al., 2017; Barka et al., 2016; Vurukonda et al., 2018).

3 Plant-Bacteria Association: A Boon to Plant Growth

The scientists have unveiled the vast significance of the relationship between plants and bacteria; nature has endowed the plants with the ability to promote this association with the bacteria so that these get the ultimate benefit from these minute creations of nature. Apart from these useful bacteria, there are a number of harmful microbes that act as pathogens (e.g., *Agrobacterium, Pseudomonas*, etc.), thus causing a hurdle in plant growth. The most significant benefit of plant-associated bacteria includes their antimicrobial activity against these plant pathogens, through the production of siderophores (chelating agents that chelate ferric ions), certain volatile compounds, antibiotics and enzymes besides regulating the phytohormone levels. These associated microbes restrict the plant pathogen growth also through competition for nutrition as well as microenvironments and hence overall niche (Ellis, 2017; Kumar et al., 2018). A remarkable feature of these plant-associated bacteria is that they render resistance to their host plants thus boosting their immune system (Hunter, 2016). The Actinobacteria are able to control the wilt caused by *Fusarium* sp.; some actinobacteria were able to control the pathogen that caused a lot of damage to some cereal plants; besides, these microbes also promote plant growth through biofertilization by facilitating the availability and uptake of nutrients by plants (Trivedi et al., 2017; Durán et al., 2018). Another important benefit of the microbiome is the stimulation of plant growth and development through the production of phytohormones like auxins, gibberellins and cytokinins and decreasing ethylene concentration in the host plants (Backer et al., 2018; Angulo et al., 2014; Penrose & Glick, 2001). The plant-associated bacterial species enhance the resistance of their host plants to many unfavourable and stressful conditions that are non-conducive to plant growth. The bacteria growing in the rhizosphere of the *Hibiscus* plants enhance their germination and growth under non-conducive conditions (Kumar et al., 2019; Shahzad et al., 2017; Yuan et al., 2019).

The extensive use of pesticides in agriculture has a detrimental impact on the soil, and the microorganisms associated with plants are an anecdote to it; these microbes are able to degrade the harmful contaminants in the soil. The contamination of the soil leads to changes in the composition of the microorganisms inhabiting these soils. Many scientists have proposed some models that advocate human intervention and supervision for the efficient establishment of beneficial bacteria and other microorganisms in the contaminated soils and optimized phytoremediation through the plant-microbe interaction (Thijs et al., 2016; Yergeau et al., 2015).

4 Conclusion

The plant-associated bacteria and other microorganisms are believed to be important natural resources that would serve as an ultimate alternative to face the global demand for food. In order to evolve and perpetuate the concept of sustainable agriculture besides the proper functioning of our ecosystem, there is a need to research and explore the functional potential of the microbes associated with plants and select more efficient microbial groups that would enable the mitigation of pesticide and chemical fertilizer use, enhance plant growth and accomplish this sustainability (Johns et al., 2016). There is a need to augment the research on the molecular aspects of plant microbial functioning that would include sampling, extraction, amplification of DNA, development of bioinformatics in addition to the conventional techniques for proper understanding and application of plant microbiomes in sustainable agriculture. Despite the fact that ample data and knowledge have been generated from time to time regarding the functional and structural aspects of plant-associated microorganisms, there is still more scope to unravel the structural complexities and functional intricacies involved with these minute but worthwhile creatures of the universe.

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