

Chapter 35

Impact of Climate Change on Localized Plant–Microbe Signalling and Technology Advancement in Microbial Quorum Sensing



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Abstract In the natural habitat, plants have association with abundant microbial population having important direct or indirect roles in plant health and growth and a most of the information is available on the plant microbiota structure. Most of the studies are available on microbial mechanisms on physiological processes with respective to the host plants. In plants, the secreted components could form microbial communities at rhizosphere, endosphere and phyllosphere regions of plants. In each niche, a group of microbial colonies can be established and respond to specific conditions appeared during interaction with plants. Overall, the plant microbiome communities played a major role in control of diseases, nutrient acquisition enhancement and tolerance to stress or aiding in plant growth promotion. In this present chapter, the habitats and features of microbial communities have been discussed in relation to plant growth followed by factors responsible for the plant–microbe interactions, secreting components and signalling mechanisms between plant and microbe communications, and the role quorum sensing in communication and plant protection. The application of synthetic biology tools in deploying plant microbiome in plant protection, plant breeding and plant health for more sustainable agriculture has been also discussed.

Keywords Climate change · Microbe · Plant · Quorum sensing · Signalling · Technology advancement

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35.1 Introduction

In nature, plants host highly dynamic and diverse microbiota and create a unique microbial ecology. Microbial assemblages from the soil mostly associated with host plants (rhizosphere, phyllosphere and endosphere) and specific plant organs called as plant halobiont and termed as plant microbiota or the plant microbiome show a wide range of functions for supporting the plant health and growth (Philippot et al. 2013). These microbiota contribute nutrition in the host plants, protect from the pathogens and pests and improve the tolerance against stress. The functionality of plant–microbe interactions and factors involved may potentially help researchers to deploy this towards enhanced plant growth and better crop productivity. Most of the earlier surveys focussed on plants and microbes interactions (pathogenic), and after assuming that, some are pathogenic and the others are neutral or beneficial for plant development (Philippot et al. 2013). Beneficial microorganisms involved in the agriculture or plant biomass production by aiding acquisition or availability nutrients and promoting stress tolerance (Kavamura et al. 2013) and these specific microbial groups nitrogen-fixation and fungi belongs to mycorrhiza) involved in promoting the plant growth (Chagnon et al. 2013). The plant–microbe interactions are influenced by a basic principles, such as (1) defence or symbiotic responses which will be activated based on signals from microbes that are perceived by plant immune receptors, (2) modulation of host cell functions which will be mediated by transport effector molecules like microbial DNA and/or protein into the plant cell, and (3) during symbiotic and pathogenic interactions formation of specialized microbial organs (e.g. nodules and galls) which will be developed for nutrient exchanging.

The communication between plant and microflora is known to be initiated by a specific signalling molecule in the environment and they will increase in response to specific microbial population and help to coordinate protective mechanism against adverse conditions called quorum sensing (QS). Under plant and cell communication, microbes can secrete extracellular signal molecules called autoinducers. These plant–microbe interactions can be altered by external conditions, including temperature, moisture and nutrient status. At the plant rhizosphere region, some symbionts (N_2 -fixing bacteria or fungi) are known as microbial biofertilizer. For better understanding and practices in agriculture, these plant microbes are important for microbiome-based solutions. The application of knowledge of synthetic biology can significantly aid in understanding of individual or a package of strains in combination with model plants. Under synthetic biology approaches, application of selective microbes for plant developments can create new avenues for the development and use of microbial functions in enhancing crop productivity.

The present chapter discussed the topics of plant and microbe interaction and secretion of various signalling chemical components along with the responsible factors for effective interactions between plant and microbe. In continuation, role of quorum sensing in this communication is also discussed with mechanisms involved and advancements using synthetic biology at molecular level.

35.2 Plant and Microbes

35.2.1 *Favourable Zones in Plant for Microbial Growth*

The matrix of soil is the diverse microbial reservoir and in interaction with plants and plant parts (Vogel et al. 2009). The microbial population present in the soil is important for processes happening in relation to health of the plant (suppresses plant diseases and infecting plant tissues) (Mendes et al. 2011). These soil microbiomes impart a degree of resistance against “invaders” and show intrinsic and extrinsic activities (van Elsas et al. 2012). Microbial populations at plant region are considered as an active component of the host, being also responsive to changes in environmental (biotic and abiotic) conditions. Segregating the plant–microbe population involves three major compartments: so-called rhizosphere, phyllosphere and endosphere (Hirsch and Mauchline, 2012).

35.2.1.1 **Microbiome at Rhizosphere and Secreting Components**

In 1904 Hiltner coined the rhizosphere term (Curl and Truelove 1986) and referring to the environment at the root region of plant where the soil at the root of plants and microorganisms (Sugiyama et al. 2014). The microbial population residing at rhizosphere region is organized differentially than the bulk soil and is driven by root exudates and the effect of increased microbial biomass in the rhizosphere.

Rhizodeposits (organic or inorganic compounds) are the components which influence the rhizosphere microbial community at rhizosphere, and this is known as “rhizosphere effect” (Berendsen et al. 2012), which is influenced by the genotype of plant (Bulgarelli et al. 2012), and each plant sp. is specific to microbial populations and coevolution of plants and microbes (Bais et al. 2006). In rhizodeposits, some of them are involved in activation of microbial populations (e.g. glucose) or can activate specific groups of organisms (e.g. flavonoids) (Jones et al. 2004).

These rhizodeposits are directly released to surroundings for microorganisms at roots throughout the plant life (Haichar et al. 2008) and plant growth (Chaparro et al. 2014). Microbial aggregation starts at the germination stage, and microorganisms will be distributed according to root type and zones during root growth (Philippot et al. 2013). Alcohols and sugars will be released in the early stages of plant growth (seedlings), followed by amino acids and phenolic compounds at further plant growth (Chaparro et al. 2014). This selectively will follow the phenomenon like attraction by offering a carbon at the early stage of development, and later selects certain microorganisms by releasing specific compounds (Chaparro et al. 2014). At the root region, microorganisms more number belongs to gram-negative bacteria, gram-positive bacteria, proteobacteria (α , β , γ) etc., usually represent at high level (Philippot et al. 2013).

The rhizosphere microorganisms can have beneficial effects as plant growth-promoting rhizobacteria (PGPR), for plant growth and health (Philipot et al. 2013). PGPR can suppress the diseases from the various sources by a mechanism like creating food (nutrients) competition or antibiosis or parasitism (Philipot et al. 2013).

35.2.1.2 Microbiome at Phyllosphere and Secreting Components

The second component at plant and microbe's interacting location is aerial tissues called phyllosphere (Vorholt 2012a, b). The phyllosphere region is characterized as nutrient poor by comparing with the rhizosphere (Andreote et al. 2014). At phyllosphere, microbial communities play a major role in plant protection from pathogens, nitrogen fixation and phytohormones biosynthesis (Kishore et al. 2005).

The phyllosphere is habituated with bacteria, yeasts, filamentous fungi, viruses, algae and bacteria which are more abundant (10^6 and 10^7 cells cm^2) than fungi and archaea (Vorholt 2012a, b). At the level of community composition, the genus level of bacteria mainly belongs to *Sphingomonas*, *Pseudomonas*, *Bacillus*, *Methylobacterium*, *Arthrobacter*, *Pantoea* and *Massilia* present at phyllosphere (Bulgarelli et al. 2013). On phyllosphere region, these bacteria, fungi and other microorganisms occur through the immigration from air, soil, water, seeds or through animal sources and get stabilized (Vorholt 2012a, b). After the stabilization, the microbial communities will depend on nutritive sources (carbon) from leaf surface and leaf veins (Vorholt 2012a, b). The phyllosphere microbiome structure may vary due to a large flux in atmospheric conditions on the day and night (Vorholt 2012a, b; Lindow 1996). These phyllosphere organisms can live under harsh and variable conditions (Andrews and Harris, 2000).

35.2.1.3 Microbiome at Endosphere and Secreting Components

Inner plant tissues can be considered as endosphere region, and the associated microorganisms with the host plant are termed as endosphere microbiome, and these microorganisms reside internally in plant tissues without showing any visible symptom (Hardoim et al. 2008; Mostert et al. 2000; Berg et al. 2014). The endosphere region is composed of the endorhizosphere and endophyllosphere (Truyens et al. 2015).

These endophytic organisms are beneficial or commensal (Malcolm et al. 2013) and, under beneficial role, promote plant development and health (Khan et al. 2012a, b; Waqas et al. 2014), characterized by produced antibiotics and toxicants (Schardl et al. 2013; Gond et al. 2015; Yaish et al. 2015). Endophytes can also involve in altering the expression of plants gene defence and metabolic pathways (Rosenblueth and Martínez-Romero 2006; Mathys et al. 2012; Ownley et al. 2009).

The structure of endosphere is driven by type of soil, soil pH, phylogeny of host and microbes (Baker et al. 2009) and local edaphic conditions (Yandigeri et al. 2012;

Marques et al. 2015). After crossing all these barriers finally, the microbes establish themselves at endosphere. Common microbial population are bacterial phyla, firmicutes (Robinson et al. 2015; Manter et al. 2010) and fungi, including Ascomycota and Basidiomycota (Glynou et al. 2016; Higgins et al. 2014; Toju et al. 2013).

35.2.2 Contribution from Plants to Microbe Interactions by Chemicals and Signals

Plants are multicellular and sessile organisms, which have three well-defined parts: (1) root, (2) stem and (3) shoot (López-Bucio et al. 2005; Ross et al. 2005), and root system is different in its morphology and physiology in the environment. During embryogenesis primary root contrast to be formed, adventitious and lateral roots are formed post-embryonically. Widespread communication occurs between microorganisms (fungal and bacterial species) and plants, and the signalling molecules of both partners have a significant role. Plants can recognize and adjust their defines and growth responses against the microbe-derived compounds (Van Loon et al. 1998). Region of rhizosphere is a complex and associated with increased number of bacterial abundance and other microbial community activities associated with different plant species (Zeng et al. 2017).

At the rhizosphere region, in a sophisticated manner organism will interact with each other and with the plant by chemical communication, and in a response, plants release different metabolites by ‘signalomics’ at the rhizosphere. Diverse group of compounds from the root system are collectively termed as root exudates. These compounds belong to three main classes: (1) low molecular, (2) high molecular and (3) volatile organic compounds (VOC) (Schulz and Dickschat 2007; Badri and Vivanco 2009; Aulakh et al. 2001).

Microorganisms and their products may respond in various ways (positive or negative or neutral) at the roots (Morgan et al. 2005; Broeckling et al. 2008). Interactions and communication are important in rhizosphere to enhance plant growth. For biotechnology improvement, rhizosphere region is important to biomass production and can be achieved by inoculating or by engineering plants to modify the nature and level of exudate compounds. Plants can produce molecules like elicitors which are involved in defence responses (Mackey and McFall 2006). Exogenous methyl jasmonate, nitric oxide and salicylic acid induce the accumulation of secondary metabolites which play a major role in communication (Noritake et al. 1996).

Usually, the organic carbon forms are present in rhizodeposits to make plant–microbe trophic interactions, and these microbes will respond to various carbon sources (Neumann et al. 2014; Eichorst and Kuske 2012). Under labile chemically recalcitrant substrate conditions, few bacterial communities (*Burkholderiales* and *Pseudomonales*) will show growth (Goldfarb et al. 2011). The types of release

sugars by plant influence the microbial diversity; for example, *pseudomonads* (accepts wide range of sugars) can use trehalose (Raaijmakers and Weller 2001) in the tomato rhizosphere (Ghirardi et al. 2012). After sugars, amino acids are abundant class of compounds in the rhizosphere, and they impact rhizosphere microorganisms as signal molecules and nutrient sources which are important in biofilm formation (Moe 2013). Other compounds like phenolics impact the rhizosphere microbiota taxa. For example, the pathogen *Agrobacterium* spp. that shows trophic-mediated communication causes crown gall tumours by the insertion or transfer of T-DNA (bacterial genome) into plant genome and induces tumour cells to produce opines, and these opines are low molecular weight molecules (Chen et al. 2016).

Plant hormones and hormone-like compounds present in small amounts but impact the microbes at rhizosphere. Some of the phytochemicals release signals described for symbiotic or parasitic interactions, for example, flavonoids for symbiotic nitrogen fixation between rhizobia and legumes. These phenolics (acetosyringone) and phytoalexins are involved in parasitic interactions between phytopathogenic bacteria and plants (Subramoni et al. 2014; Kalia 2013).

Hormones involved in plant immunity and defence reactions; for example, the salicylic acid (SA) enriches *A. thaliana* (Lebeis et al. 2015), and the citric acid or malic acid (organic) acts as a signals bacterial chemotaxis towards plants called plant growth-promoting rhizobacteria (Zhang et al. 2014a, b), and they will involve in biofilm formation for the colonization of root bacteria (niche) to protect the bacteria from abiotic and biotic factors.

35.2.3 Contribution from Microbes to Plant Interactions

Rhizosphere-associated microorganisms can influence their host plant by releasing different signalling molecules and are good for plant defences against diseases, etc. Plant beneficial microorganisms are rhizobial bacteria, mycorrhiza, plant growth-promoting fungi (PGPF) and plant growth-promoting rhizobacteria (PGPR) (Cameron et al. 2013).

Plant at initially recognize this as non-self by pattern recognition receptors (PRRs), called microbe-associated molecular patterns (MAMPs) (Zamioudis and Pieterse 2012). These MAMPs trigger the immune defence in the roots (Millet et al. 2010; Vos et al. 2013). PGPR and PGPF are the components involved in plant defence response, which is known as induced systemic resistance (ISR) and acts against pathogens and insects (Pieterse et al. 2014). ISR depends on the jasmonic acid and ethylene signalling pathways (Conrath, 2006).

Rhizosphere microorganisms elicit plant responses not only via MAMPs, Nod and Myc factors released by rhizobia and mycorrhiza (Zamioudis and Pieterse 2012). Small secreted proteins (SSPs) and promoting mycorrhization are produced by mycorrhiza by altering hormonal signalling in the host plant (Plett and Martin 2015), and actually, these molecules function as signal compounds (Hartmann and Schikora 2012).

Other QS molecules from bacteria are less studied and include the *Xanthomonas* diffusible signal factor (DSF) and cyclodipeptides released by *Pseudomonas aeruginosa*, which affect gene expression for the abscisic acid and salicylic acid in plants (Ortiz-Castro et al. 2011; Xu et al. 2015).

Antimicrobials produced by rhizosphere *pseudomonads* and 2,4-Diacetylphloroglucinol (DAPG) present on roots (Weller et al. 2012) affect the development of root, and these occur via an auxin-dependent signalling pathway (Brazelton et al. 2008). Pyocyanin, a phenazine from *P. aeruginosa*, induces ISR and controls the development of root (Ortiz-Castro et al. 2014; Powers et al. 2015).

VOCs are the signalling molecule from microbes and involved as growth promoters or inhibitors (Bailly and Weiskopf 2012; Zamioudis et al. 2015). 2,3-Butanediol (2,3-BD) from *Bacillus* strains was demonstrated on plants to promote the growth of *Arabidopsis* (Ryu et al. 2004) and to induce ISR towards phytopathogenic *Erwinia* (Ryu et al. 2004). 2,3-BD produced by a *Pseudomonas chlororaphis* induces ISR against the *Erwinia* in tobacco (*Nicotiana tabacum*) (Han et al. 2006).

Indole is another bacterial VOC produced by PGPRs (Blom et al. 2011) and affects *Arabidopsis* root development via the auxin signalling pathway (Bailly et al. 2014) and also functions as a protectant for plants against attacks from herbivorous insects (Erb et al. 2015).

A further phytohormone like compounds, including gibberellins, auxins, and cytokinins, affect growth, hormonal signalling, organ development and immune responses, in plants (Spaepen et al. 2007).

35.2.4 Climatic Responses on Plant–Microbe Interactions

Seasonal variation on microbial community will change drastically due to the continuously the concentrations levels of atmospheric CO₂, and surface temperatures will increase as predicted (IPCC Climate Change 2007). The changes directly show impact on soil water levels and are expected to (Le Houérou 1996) increase drought in the world and affect terrestrial microorganisms such as plants. All land plants have excellent symbiotic relation with microorganisms (Brundrett 2009), and these plant growth-promoting microorganisms (PGPM) colonize at root, and some can also enter into root (endophytic) (Stone et al. 2000). Climate change with altered environmental conditions induces changes in plants and root secretions. These changes fluctuate the availability of chemoattractants or signal compounds (Haase et al. 2007). Similarly, the elevated temperature induces similar changes, and together they influence the plant and microbe associations. Change in climate will influence the diversity and activities and shows direct influence on plant and microbial communities (Drigo et al. 2008).

35.2.4.1 Direct Impact of Climate Change

On planet, most of plants are in association with mycorrhizal (Brundrett 2009), and most of these plants have symbiotic association with AMF (Fitter and Moyersoen 1996). These AMF are enhancing plant nutrient uptake or in exchange for carbohydrates from rhizosphere (Newsham et al. 1995; Sanders et al. 1998; Augé 2001). Climatic change alters the soil communities as the soil community differ plant growth rates have been reviewed extensively. Mostly, the microbial communities respond to warming and other agitations (Allison and Martiny 2008) and shifts in microbial community which leads to changes in ecosystem function (Bodelier et al. 2000).

Warming conditions alter the microbial soil respiration rates, and given no changes in community composition the microbial activity is defined as the factor with Q10. While decomposition of soil organic matter, soil respiration, and growth of microbial biomass generally increase with temperature (Bradford et al. 2008). Initially, warming can alter microbial communities (Zogg et al. 1997), or it may take many years (Rinnan et al. 2007, 2013). This is clear that temperature is coupled with soil and its moisture (Zak et al. 1999), and the bacterial communities mostly will respond to moisture pulses (Cregger et al. 2014). Drought amplifies fungal and bacterial groups (Briones et al. 2014) and leads to shift from one member to another in soil fungal and bacterial communities (Kaisermann et al. 2015).

35.2.4.1.1 Microbial–Plant Interactions

Under warming of soil, plants (Parmesan and Yohe 2003) start flowering earlier and leafing out will occur (Wolkovich et al. 2012). As a result of warming up at arctic region, the woody shrubs have replaced grasses (Pearson et al. 2013). Plant community transitions may be facilitating by the soil communities which are tightly coupled with plants, and these communities show a strong effect on survival of plant, expression and phenology (Wagner et al. 2014).

35.2.4.2 Indirect Effects

35.2.4.2.1 Climate Change on Plant and Microbial Population

Under climate change, the plant species migrations between the soil community and the plant (positive or negative relationship) (van der Putten 2012). Microbial population in soil will respond fast to climate change (van der Putten 2012). At local community level, the climate change can alter plant establishment and plant productivity (Bever et al. 2010). If plants that successfully establish, they induce higher levels of defines compounds (polyphenols) (Engelkes et al. 2008). Geographic

disconnects might influence the composition and functioning of the microbial community (van der Putten 2012).

Above ground level, plant structures change due to climate change (Durán et al. 2014), and compared to aboveground level, communities belowground are structured by different environmental conditions (Fierer and Jackson 2006) with different life history characteristics. Due to these, plants are experiencing changes in global climate than soil community (Kardol et al. 2010). By changing distribution levels, the soil communities will respond to climate stress.

35.2.4.2.2 Climate Change Alters Plant Phenology and Microbial Communities

In the growing season, warming may affect the plant species in earlier leafing out and flowering (Wolkovich et al. 2012) and impacts root phenology, interactions of plant-rhizosphere (Iversen et al. 2015). If root growth peaks early, phenologies of belowground and aboveground synchronous, because they are asynchronous (Abramoff and Finzi 2015). Phenology of root varies by species because it has complex interactions (Abramoff and Finzi 2015). As per IPCC 2013 due to climate change, variation in root–shoot phenology will impact rhizosphere interactions and may influence the soil microbial groups (Zhang et al. 2014a, b).

35.2.5 *Microbes in Plant Growth Promotion*

To enhancing productivity conventional agricultural practices, have a threat due to the global climate changes and anthropogenic activities in the agroecosystems. To overcome such negative roles of climatic challenges research on plant growth-promoting microbes (PGPM) playing a major role in agro-ecosystems to their original shape. PGPM are the soil and plant growth influencing rhizosphere microorganisms, colonize plant roots with beneficial activities (Antoun and Prevost 2005). PGPM are of two main groups: plant growth-promoting fungi (PGPF) and plant growth-promoting rhizobacteria (PGPR). PGPR are soil bacteria that colonize the plant roots and enhance the growth in a mutualistic manner (Kapulnik and Okon 2002).

35.2.5.1 Plant Growth-Promoting Rhizobacteria (PGPR)

PGPR stimulate plant growth, form association with roots, leaves and/or in tissues (Glick 2012) and belong to *Rhizobium*, *Pseudomonas*, *Azotobacter*, *Klebsiella*, *Alcaligenes*, *Arthrobacter*, *Bacillus*, *Serratia*, etc. (Ahemad and Kibret 2014). They provide direct assistance in plant growth by nitrogen (N) fixation, phosphate solubilization (Sharma et al. 2013), iron (Fe) sequestration (Sayyed et al. 2013),

phytohormones synthesis (Maheshwari et al. 2015) and phytopathogens control (Mishra and Arora 2012).

Biological Nitrogen Fixation (BNF) BNF is the conversion of atmospheric N to ammonia under the symbiotic process (Dixon and Kahn 2004) and well-developed process, and a vast array of microbes belongs to archaea and bacteria. Bacteria under N-fixing process will form obligate symbiotic association with legumes to form root nodules by colonizing plant's root system (known as rhizobia). Several studies show that at field conditions PGPR increase N content in legume plants (Bruijn 2015).

Phosphate-Solubilizing Bacteria (PSB) PSB involved in uptake of phosphate by plants and species are *Pseudomonas*, *Bacillus* and *Rhizobium* (Bossis et al. 2000). PGPR play a significant role in secretion of siderophores and are Fe-binding extracellular compounds (Krewulak and Vogel 2008; Boukhalfa et al. 2003),

Other than above-mentioned mechanisms, PGPB can produce broad spectrum of antimicrobial compound called as hydrogen cyanide (HCN) to control root diseases by plant-associated *pseudomonads* (Ramette et al. 2003). PGPR trigger ISR response against plant pathogens (Ramos et al. 2008) and involved in the synthesis of hydrolytic enzymes, which lyse the hyphae of fungi (Maksimov et al. 2011).

In the agriculture sector, members of the genus *Bacillus* sp. produced products which are important and being considered as microbial pesticides, fungicides or fertilizers (Fravel 2005). Another important PGPR organism such as *Pseudomonas* is considered as biocontrol and PGP activities (Tewari and Arora 2015) involved in biocontrol activity against plant pathogenic fungi (Tewari and Arora 2014). *Pseudomonas* produces a variety of components at the rhizospheric region (Fernando et al. 2005).

Actinomycetes in PGP Activities *Micromonospora* spp., *Streptomyces* spp., *Thermobifida* spp. and *Streptosporangium* spp. are involved in control process against root pathogenic fungi by phytohormones production (Solans et al. 2011), enzymes for degrading fungal cell wall (Anitha and Rabeeth 2010) and antibiotics production.

35.2.5.2 Plant Growth-Promoting Fungi (PGPF)

PGPF attributes of rhizospheric fungi, species include *Aspergillus*, *Penicillium*, and *arbuscular mycorrhizal fungus* (AMF) etc., gained attention due to the involvement in growth of plant and disease control. PGPF produces the plant hormones and involves in decomposition of organic matter and soil solubilization (Khan et al. 2012a, b). In plants, AMF involved in the growth promotion by nutrient uptake, particularly phosphorus (P) and disease suppression (Brundrett 2002; Maherali and Klironomos 2007).

35.3 Quorum Sensing: Microbial Role

Quorum sensing (QS) is coordinational behaviour that occurs between two different organisms by a communication, and this helps the bacteria to respond to scavenging of extracellular nutrients, extracellular hydrolytic enzymes, siderophores, biosynthesis of exopolysaccharides, pigments, antibiotics, aiding motility and for biofilms growth.

35.3.1 Biocommunication and Mechanisms

Rhizosphere around the roots is comprised of the microorganisms and various chemicals secreted from roots are involved in the regulation of beneficial and pathogenic microorganisms at the rhizosphere (Sharma et al. 2013). Release of chemicals involved through a communication and may export signals to the extracellular environment. The plants as root exudates and generated due to the organic carbon utilization (Bais et al. 2006). Due to its microbial activity it is very high at roots than the non-rhizosphere soil is a hotspot for a variety of microorganisms.

During QS, organisms differentiate species-specific signals and interspecies behaviour modulations which enable them to specifically coordinate with species and with other diverse groups. Mycorrhizal fungi come under this category by supporting the growth of bacteria and degrading of complex organic materials to simple for fungi. By extending its hyphae, helps the plant growth by supplying enough nutrients or minerals.

QS in bacteria releases exoenzymes to convert complex food/carbon to simpler molecules and facilitates easy uptake by plants or any other associated cells.

Generally, bacterial QS falls into three classes: (1) AHL-dependent, (2) peptide-mediated QS, and (3) both gram-positive and gram-negative bacteria is luxS-encoded autoinducer 2 (AI-2) QS. In the gram-negative bacteria, QS is mediated by AHL.

In gram-positive bacteria, two types of QS systems are reported—one is autoinducing peptide (AIP), and the other is a two-component signal transduction. Gram-positive bacteria produce a signal peptide precursor which is later cleaved at the double-glycine sequence and obtained active AIP, and the two-component signal transduction will regulate AIP which leads to QS.

Autoinducer 2 (AI-2) is observed both in gram-positive and gram-negative bacteria. For interspecies communication, AI-2 helps more (universal language) and characterized *Vibrio harveyi* for the regulation of bioluminescence.

35.3.1.1 Mechanism in Rhizosphere

At the rhizosphere region, proteobacteria as a major colonizer produce QS signals and are capable to produce acyl-HSL signals with different specificities by the LuxI family.

In the rhizosphere, actinobacteria is a major organism and QS is dependent on the production of different chemicals class switch includes A-factor of *Streptomyces griseus* and similar compounds found in other *Actinobacteria*.

35.3.1.2 Quorum Sensing in Soil Microorganisms

Soil is a natural media for growth of microorganisms and plant. Several types of microorganisms inhabit the soil and create microenvironment by supporting the biogeochemical cycle, and they show additional benefit for plant growth by developing interactions (Sindhu et al. 2016).

35.3.2 Synthetic Biology in Quorum Sensing

In the present scenario, most of the studies discussed the importance of QC in microbiomes and how it will influence the composition and function of these communities. Synthetic biology is a field where scientists design systems (biological) with predictable design or output to manipulate QS in natural consortia, and it can be used as a tool to construct synthetic co-cultures with desired behaviour. Early studies made the QS circuits for programming cell behaviour. Synthetic biology provides new tools for investigating QS.

35.3.2.1 Synthetic Biology to Manipulate QS Signal and QS-Mediated Cell Phenotypes

Till today, there are a several QS systems available and, for example, AI-1 or acyl-homoserine lactone (AHL) and AI-2 QS systems. In QS systems, well-known systems are AHL (discussed earlier). Synthetic biologists frequently use the AHL QS systems due to the few components, and without specific transporters, they can enter into cell through cell membrane.

For the characterizing responses in AHL and to engineer cells, there are many efforts made by scientists and they did manipulation in the regulator protein LuxR. Wang et al. expressed LuxR to detect different ranges of AHL by a series of varied expression levels using constitutive promoters (Wang et al. 2015; Shong and Collins 2013; Zeng et al. 2017).

35.3.2.2 Synthetic Biology for Plant Microbiome

Plant microbiomes are the main components in plant health and crop yield. Engineered microbiomes can promote plant health by reducing the environmental impacts in agriculture (Busby et al. 2017; Compant et al. 2019). For the growth of

plant and productivity, QS plays a major role in plant–microbiome interactions. Some pathogens depend on QS for the virulence production in some of the crops, and the community interactions can inhibit virulence. Virulence of *Pectobacterium carotovorum* can be attenuated by the degradation of AHL signals (Garge and Nerurkar 2016). Similarly, Valente et al. showed a crosstalk mechanism between species (Valente et al. 2017). In synthetic biology concern, engineers have used the QS to engineer commensal bacteria with desired behaviour. Zuniga et al. engineered a Rhizobacterium *Cupriavidus pinatubonensis* to produce indoleacetic acid by an autoinducer-regulated method (Zúñiga et al. 2018) so that the bacteria autonomously produced indoleacetic acid (IAA) to promote plant growth. QS is also an important process to facilitate interactions between species in other ecologically important microbiomes (coral microbiome).

35.3.2.3 Synthetic Biology in Plant Breeding

In agriculture, effective application of microorganisms is important for improved plant response to the environment and plant yield with the pathogen resistance. Under mutualism, plant and microbe will interact with each other and the plant secretion will influence microbiome composition (genotype-dependent) and population and is an evolutionary process. Using modern tools of synthetic biology, pathogen-resistant potato varieties were developed. Mendes et al. (2011) in common bean shown that the microbial taxa selected in breeding for resistance involved in complementing plant protection and finding out of such traits will help breeders to select plant traits with enriched microbial groups.

35.4 Conclusion

For the growth of plant, tolerance to adverse environmental conditions and plant health, a good plant and soil microbiota interactions are essential. Microorganisms adapted at different parts of the plant showed great impacts particularly in secreting of various chemicals, plant–microbe communication, plant growth promotion, etc. Understanding of plant–microbe and microbe–microbe interactions will provide a great help in future to modulating microbes in controlling disease and enhancing plant productivity. Plant-associated microbiota can act against harmful pathogens, thereby resulting in avoiding outbreaks in pathogen attack and increasing plant productivity. Plant-associated microbiomes also aid in stabilization of ecosystem and biodiversity enhancement. In the plant and microbial communication, QS plays a vital role against abiotic factors, environmental challenges and biosurfactant production in rhizosphere, for plant growth promotion, and is proven to be effective in improving the soil quality by soil remediation. In the coming future, these studies will further help in understanding the QS mechanisms and their role in soil fertility and crop productivity. Agriculture plays a major role for economic growth.

Therefore, a major focus on the exploitation of eco-friendly beneficial microorganisms in sustainable crop production in the coming decades would be of paramount importance. It is also critical to explore all potential applications of synthetic biology tools such as genetic engineering for the microbial flora at rhizosphere and generate engineered plants which can alter QS and show multiple functions in agriculture. Screening and identification of quorum quenching compounds for autoinducers or their receptors are another interesting areas for the plant microbial interaction and growth.

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