

Chapter 10

The Rhizosphere Microbiome: Microbial Communities and Plant Health



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Abstract Exploration of rhizosphere and rhizosphere microbiome has been the research focus for last many decades. The rhizosphere is a junction for intercommunication among plants, insects, and microorganisms. It serves as diverse habitat with a nutrient-rich niche by providing a platform interaction among plants-soil-microorganism trio along with energy and matter trade-off. The rhizosphere microbiome also influences plant vigour, health, and defence against stresses by interfering with nutrient uptake, chemical signalling, and enzyme activity. Interaction among the microbiome, the environment, and the genetic makeup of host is well-known to contribute towards host health. The present chapter summarises the major effects of microbial communities present in rhizosphere on plant health and diseases.

10.1 Introduction

10.1.1 *Rhizosphere: Hotspot of Root–Microbe Interaction*

Rhizosphere acts as hotspot of root–microbe interaction. The etymology of rhizosphere can be expressed as rhiza (Greek), meaning root, and “sphere,” meaning region influenced by roots. Lorenz Hiltner in the year 1904 was the first to use this term to describe the effects of root exudates on the proliferation of advantageous and deleterious microbes around roots (Hartmann et al. 2008). Rhizosphere is regarded as one of the most diverse ecosystems in the universe with huge energy flow (Barriuso et al. 2008). It is the region where intense biogeochemical activities take place depending on root architecture, exudates, and mucilage which influence the

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microorganisms feeding on these compounds within the soil matrix. Besides this, the pH and redox gradients of the rhizosphere are also assumed to influence rhizospheric microbial communities (Schmidt et al. 2011; Shrivastava et al. 2014; Prasad et al. 2015, 2020). The roots exudation effectively widens the functional boundary of the belowground plant–microbe interface as it may control the soil microbial community in their locale, prevent or defend against herbivores, invigorate beneficial symbioses, alter the physiochemical properties of the soil, or slow down the growth of competing plant species resulting in entirely different environment at the root interface compared to bulk soil (Bais et al. 2004, 2006; Hinsinger et al. 2005). This narrow region bordering and affected by plant roots is a junction for microbial colonisation and activity, termed as rhizodeposition. During rhizodeposition, various major processes take place like depletion of border cells and root cap, soluble root exudates, insoluble mucilage, organic carbon, carbon flow to rhizosphere symbionts, and lysis of root cells (Jones et al. 2009).

Rhizosphere is categorised into three zones based on microorganisms existing in close proximity to roots, and the influence of root exudates on them as endorhizosphere, rhizoplane, and ectorhizosphere. Endorhizosphere is made up root endodermis and cortex. Rhizoplane refers to the root facet where soil particles and microorganisms cohere and involves epidermis, cortical layers, and mucilaginous polysaccharides. The third zone is ectorhizosphere consisting of soil immediately adjoining the root (Prashar et al. 2013).

10.2 Rhizosphere Microbiome: Diversity of Microbial Communities

The complex soil communities of microorganisms associated with plant roots are regarded as the plant microbiome which is also considered as the plants' other genome. The root microbiome is dynamic and plays a key role in various nutrient cycling like nitrogen and phosphorus in addition to provide protection against various biotic and abiotic stresses, thus contributing towards plant health and increased productivity (Bender et al. 2016; Lladó et al. 2017; Berendsen et al. 2012; Kumar et al. 2020; Nath et al. 2018). Root–microbe interactions may be beneficial to the plant or to the microbes or to neither of them. Both plants and microbes can be benefitted directly through mutualistic relationship or indirectly via decomposition, nutrient cycling and solubilisation (Glick 1995), emanation of growth hormones (Narula et al. 2006), induction of the resistance (Pieterse et al. 2001), and antagonism of pathogens (Kloepper et al. 2004). According to two contrary schools of thoughts, the root exudation is an “active” or “passive” process. Cook et al. (1995) hypothesised that plants may actively moderate the root microbiome for their welfare by specifically influencing microbe in a targeted manner. Other school of thought is that root exudation is a passive process releasing waste products (Jones et al. 2009; Dennis et al. 2010).

By releasing nearly one half of their total photosynthetic fixed carbon, rhizosphere microbiome provides unique locale for a diverse conglomeration of microorganisms which are an important part of food chain that consumes the bulk of nutrients exuded by plant roots (Lynch and Whipps 1990; Bonkowski et al. 2009). It has been estimated that rhizosphere microbiome can harbour approximately hundred billion microbial cells per gram of root (Egamberdieva et al. 2008) which is many times more than (10^8) in bulk soil (Foster 1988). The rhizospheric microbial communities are different from those present within the root and are reduced in diversity compared with the microbial communities of bulk soil. Organisms like nitrogen-fixing bacteria, arbuscular mycorrhizae, plant growth-promoting rhizobacteria (PGPR), biological control agents, and mycoparasitic saprobes have been well documented for their beneficial impact on plant vigour (Singh et al. 2019). Rhizospheric microorganisms which are detrimental to plant health are various plant pathogens particularly oomycetes fungi, bacteria, and nematodes. Apart from these, rhizosphere also serves as a stockpile for certain human pathogens such as *Pseudomonas*, *Staphylococcus*, and *Stenotrophomonas* (Berg et al. 2005).

10.3 Rhizosphere Microbiome: Vigour and Well-Being

The diverse rhizospheric microbial population plays a key role towards plant vigour and yield as it protects against pathogens and produce phytohormones (Lu et al. 2018; Singh et al. 2019). Approximately nearly 5–20% of total carbon fixed through photosynthesis is exuded as root exudates and functions either as substrate, chemoattractant, or signalling molecules (Mendes et al. 2013). These chemicals allure advantageous microbes that elicit pest resistance, water holding, and the synthesis phytohormones like auxins and may influence plant phenotype. Interactions among microbes-root exudates-plant physiology aggressively influence rhizospheric microbial population and alters the plants phenotypic traits. At molecular level, cross-talk differs depending upon propinquity to other microbes and management practices, etc.

Naturally occurring plant communities are influenced by rhizosphere microorganisms either directly or indirectly (van der Heijden et al. 1998, 2006, 2008; Schnitzer et al. 2011). Microbial species diversity below ground has been found to be an indicator of aboveground plant diversity and productivity (Hooper et al. 2005; Lau and Lennon 2011). The underground microbial richness ensures plant productivity under diverse climatic conditions (Wagg et al. 2011). Thus, microorganisms present both in rhizosphere and bulk soil may be utilised as a bench mark of soil quality. The plant beneficial and plant pathogenic microorganisms are discussed below:

10.3.1 *The Beneficial Rhizo-Microorganisms*

The plant growth-promoting microbes present in rhizosphere including bacteria, fungi, actinomycetes, protozoa, and algae act through a variety of important mechanisms like biofertilisation, root growth stimulation, rhizoremediation, abiotic stress control, and direct disease control. The beneficial effects of different rhizosphere microorganisms like *Proteobacteria* (*Pseudomonas* and *Burkholderia*) and *Firmicutes* (*Bacillus* sp.) and for fungi imperfecti (deuteromycetes) genera like *Trichoderma*, *Gliocladium*, and *Piriformospora indica* along with non-pathogenic *Fusarium oxysporum* are well documented (Kogel et al. 2006; Prasad 2008; Qiang et al. 2012; Deshmukh and Shinde 2016; Prasad et al. 2020). Among these rhizosphere microbial communities, bacteria are the most abundant (Kaymak 2010). Recently, much more information has been generated pertaining to diverse rhizospheric communities like in case of *Planctomycetes* (Hol et al. 2010; Jogler et al. 2012). The increased plant vigour by the incorporation of these microorganisms as biological control agents is well documented (Saharan and Nehra 2011; Bhattacharyya and Jha 2012). Microorganisms associated with plant microbiome can benefit the plants either by increasing the nutrient use efficiency, acting as biocontrol agents against various pathogens, or promoting plant growth by production of auxins (Singh et al. 2019).

10.3.1.1 **Enhancement of Nutrient Recovery**

Different nutrients like N, P, and S are present in most of the soils but are not readily available for plant uptake. Microorganisms convert these organic nutrients into available forms via different processes like production of extracellular enzymes which solubilises and fixes nutrients into available forms.

They also enhance the solubility of certain nutrients such as Fe due to various oxidation and reduction reactions. They are also reported to release organic acids which are responsible for releasing nutrients from minerals and increased rate of weathering (Coyne and Mikkelsen 2015).

The most classical example is the symbiotic relationship between arbuscular mycorrhizal and roots of higher plants thereby increasing the supply of various nutrients such as copper, iron, nitrogen, phosphorus, and zinc (Prasad et al. 2017). Arbuscular mycorrhizal fungi are also reported to produce many enzymes responsible for solubilising organic P and, thus, can absorb soluble P from the soil at very low concentrations compared to plant roots alone.

Microorganisms play a vital role in nitrogen cycle as they can convert atmospheric nitrogen into fixed nitrogen. Above 90% nitrogen is fixed by nitrogen-fixing bacteria which fulfils up to 1/5th of the N required by cultivated crops. Nitrogen-fixing bacteria are either free-living/nonsymbiotic (*Azotobacter*, *Cyanobacteria*, *Beijerinckia*, *Clostridium*, and *Anabaena* species) or mutualistic/symbiotic (*Azospirillum*, *Frankia*, and *Rhizobium* species).

Azospirillum is an example of free-living nitrogen-fixing bacteria and is known to enhance rice yields (Tejera et al. 2005). Mutually beneficial relationship between bacteria and plant roots is popularly called as symbiotic. Such mutual relationship starts with the entry of bacteria into root hair followed by multiplication and formation of nodules on the host roots and enlargement of both plant and bacterial cells in association with each other. *Rhizobium*, *Bradyrhizobium*, *Sinorhizobium*, and *Mesorhizobium* comprise of large group of rhizobacteria known to establish symbiotic relationship by formation of nodules on roots of leguminous plants, thus fixing nitrogen to ammonia and solubilising it into available form. *Frankia* has been reported to be associated with non-leguminous host plants (Bhattacharyya and Jha 2012).

Besides N fixation, the ability of rhizosphere microorganisms for P solubilisation is another important trait associated with plant phosphate nutrition. Phosphorus (P) is one of the major macronutrients required by plants. It is applied to soil as chemical phosphatic fertilisers. However, a major part of this phosphatic fertiliser applied to soil gets immobilised, precipitates as orthophosphate and gets adsorbed by Fe and Al oxides via ligand exchange and becomes unavailable to plants.

Growth-promoting phosphate solubilising bacterial strains employ following strategies to convert phosphorus into soluble form:

- (a) Lowering of soil pH by producing low molecular weight mineral-dissolving compounds such as organic acids (mainly gluconic and keto-gluconic acids), O₂/CO₂ exchange, protons, and hydroxyl ions through which their hydroxyl and carboxyl groups chelate the Fe, Al, and Ca ions bound to phosphate, thereby competing for adsorption sites with phosphate. Inorganic acids are less effective compared to organic acids for phosphate solubilisation at same pH level (Kim et al. 1997). Many times, phosphate starvation may enhance phosphate solubilisation (Gyaneshwar et al. 1999).
- (b) Release of extracellular enzymes (biochemical phosphate mineralisation). Key mode of action for mineralisation of organic P in soil is the release of nonspecific acid phosphatases (NSAPs) or alkaline phosphomonoesterases (Jorquera et al. 2008) which is responsible for dephosphorylation of phosphoester or phosphoanhydride bonds of organic matter; phytases causing phytate degradation; phosphonatasases; and C–P lyases to split the C–P bond of organophosphonates. These enzymes hydrolyse the organic P into the soil.
- (c) Substrate degradation leading to liberation of phosphate and mineralisation (McGill and Cole 1981).

Microorganisms engaged in phosphorus solubilisation are primarily arbuscular mycorrhizae and phosphorus-solubilising bacteria (Fankem et al. 2006). Out of the total microbiota prevalent in the soil, phosphorus-solubilising bacteria (PSB) account for 1–50%, while phosphorus-solubilising fungi (PSF) are meagre (0.1–0.5%) for P solubilisation capability. Among bacteria, ectorrhizospheric types (*Pseudomonas striata*, *Bacillus megaterium*, *B. circulans*, *B. subtilis*, *B. polymyxa*, *Bacillus sircalmous*, and *Enterobacter*) and endosymbiotic *Rhizobia* have been

reported as most efficient phosphate solubilisers (Igual et al. 2001; Subbarao 1988; Kucey et al. 1989). Besides bacteria, fungi (*Penicillium* and *Aspergillus*), actinomycetes, algae (*Cyanobacteria*), mycorrhiza, and a nematophagous fungus *Arthrobotrys oligospora* are well documented for their P solubilisation activity (Whitelaw 2000; Duponnois et al. 2006). Phosphate-solubilising bacteria belong to genera *Arthrobacter*, *Bacillus*, *Beijerinckia*, *Burkholderia*, *Enterobacter*, *Erwinia*, *Flavobacterium*, *Microbacterium*, *Pseudomonas*, *Rhizobium*, *Rhodococcus*, and *Serratia* (Ahmad et al. 2008). *Kocuria turfanensis* strain 2M4 acts as phosphate solubiliser which is also reported to produce IAA and siderophores (Goswami et al. 2014).

Iron (Fe) holds fourth rank among the most abundant nutrient on the earth; still Fe deficiency is a widespread problem particularly in arid and semi-arid regions. This is because Fe is not readily assimilated due to presence of rarely soluble ferric ion (Fe^{+3}). Hence, the amount of iron available for assimilation is very low (Aloni et al. 2006). Rhizospheric microorganisms play a key role to overcome Fe deficiencies and greatly influence the Fe uptake by production siderophores, which form Fe^{3+} chelates and are transported through plasma membrane (Awad et al. 1994; Sabry et al. 1997; De Felipe and Fijación 2006). They are mostly produced by microorganisms growing under low stress of iron. Most of the siderophores produced by bacterial genera such as *Streptomyces* and *Pseudomonas* are catecholates, whereas siderophores produced by fungi are hydroxamates (Das et al. 2007).

Siderophores have been associated with improved plant vigour, e.g. PGPR (*Aeromonas*, *Azadirachta*, *Azotobacter*, *Bacillus*, *Burkholderia*, *Pseudomonas*, *Rhizobium*, *Serratia*, and *Streptomyces* sp.) increased chlorophyll level as in comparison with uninoculated plants (Berg et al. 1980).

10.3.1.2 Plant Growth Regulators

A huge and diverse variety of rhizosphere microbiome is capable of producing growth hormones such as auxins, cytokinins, gibberellins, and ethylene. Plant growth-promoting rhizobacteria (PGPR) produce organic substances also known as exogenous hormones (phytohormones) in extremely low amounts which can control different morphological and physiochemical processes of the plants. PGPR are well documented for production of phytohormones influencing root system architecture (RSA) with an increasing rate of nutrient and water uptake. The most common effect is a reduction of growth rate of primary root and increased number of lateral roots and root hairs. Further, PGPR can also modify chemical makeup and structure of cell wall of root (Zhang et al. 2007). PGPR are also known to produce growth hormones along with secondary metabolites which interfere with the plant auxin pathway (Prasad et al. 2005). Exogenous production of IAA influences a vast range of plant processes. For example, low concentrations of IAA can encourage elongation of primary root, whereas high concentration of IAA encourages lateral roots formation, decreased root length, and increased number of root hairs (Remans et al. 2008). The PGPR (*Pseudomonas*, *Rhizobium*, *Bradyrhizobium*,

Agrobacterium, *Enterobacter*, and *Klebsiella*) produce IAA in plants majorly through indole-3-pyruvic acid and indole-2-acetic aldehyde pathways (Joo et al. 2005). Root growth promotion by the free-living rhizobacteria like *Enterobacter cloacae*, *Alcaligenes faecalis*, *Acetobacter diazotrophicus*, *Azospirillum* sp., *Pseudomonas* sp., and *Xanthomonas* sp. is reported to be associated with IAA secretion. Auxins like 2,4-diacetylphloroglucinol (DAPG) produced by biocontrol fluorescent pseudomonads induce systemic resistance in plants (Bakker et al. 2007), enhance exudation by roots (Phillips et al. 2004), and stimulate branching of roots (Walker et al. 2011).

PGPR such as *Arthrobacter giacomelloi*, *Azospirillum brasilense*, *Bradyrhizobium japonicum*, *Bacillus licheniformis*, *Pseudomonas fluorescens*, and *Paenibacillus polymyxa* are well documented to produce cytokinins. Cytokinins play a vital role in enhancing cell division, differentiation of root meristem, and root hair proliferation. Besides they also prevent formation of lateral roots and elongation of primary root (Riefler et al. 2006). Several PGPR are known to produce both cytokinins and gibberellins, e.g. *Pseudomonas* and *Bacillus* sp. (Han and Lee 2005). Thus, plant organogenesis and root architecture are regulated by ratio of auxins and cytokinins (Aloni et al. 2006).

Another key phytohormone is ethylene which is produced in small quantities but is responsible for inhibiting elongation of roots, promoting senescence and abscission of different plant organs, and ripening of fruits (Perrig et al. 2007). Higher concentration of ethylene leads to inhibited plant growth by inducing premature senescence, thus leading to poor plant growth and yield (Li et al. 2005). Various biotic and abiotic stresses induce plants to synthesise 1-aminocyclopropane-1-carboxylate (ACC). The increased level of ethylene in response to stress conditions causes termination of important cellular mechanisms such as elongation of roots and bacterial nitrogen fixation in leguminous crop plants thereby causing premature senescence (Jackson 1991; Glick 2012; Ahmad et al. 2013).

PGPR are also capable to produce phytohormones like abscisic acid or gibberellic acid (Dodd et al. 2010). ABA is responsible for causing stomatal closure thereby reducing rate of transpiration and plays a key role under drought stress conditions (Bauer et al. 2013). Besides this it is known for its key role in root development particularly the lateral roots (De Smet et al. 2006). Whereas gibberellins encourage both elongation of primary root and extension of lateral roots (Yaxley et al. 2001). A number of PGPR, viz. *Achromobacter xylosoxidans*, *Acinetobacter calcoaceticus*, *Azospirillum* spp., *Azotobacter* spp., *Bacillus* spp., *Herbaspirillum seropedicae*, *Gluconacetobacter diazotrophicus*, and *Rhizobium*, have been well documented for gibberellins production (Bottini et al. 2004; Dodd et al. 2010). Additionally, both of these phytohormones also induce resistance in plants. Thus, PGPR produced phytohormones and can regulate jasmonate and salicylic acid pathways involved in plant resistance.

In spite the fact that production of phytohormones by PGPR has been well studied, the genetic factors responsible for biosynthesis are still not, and the knowledge about role of bacterial mutants in phytohormones production is scanty. Thus, the role of bacterial synthesised towards plant hormonal balance is not well studied.

Within the rhizosphere, both living (like root exudates) and non-living (like pH, oxygen, type of soil, metals, etc.) factors may influence the effect of PGPR's favourable traits that can lead to distinct expression patterns with different effects on host plant (Drogue et al. 2013). Root exudation by plants may influence the expression of PGPR genes particularly those encoding for plant favouring traits. The expression of *phlA* gene of *Pseudomonas protegens* was enhanced four times near the roots of maize and wheat compared to those of legumes and cucumber. Sugar content in the root exudates largely influenced synthesis of antimicrobial compounds by fluorescent pseudomonas like DAPG, pyoluteorin, and pyrrolnitrin (Duffy and Défago 1999). Root exudates play a key role in tryptophan biosynthesis pathways (Spaepen et al. 2007). In the absence of exogenous tryptophan supply, bacterial IAA biosynthesis is insignificant. In addition, root exudates also contain vitamins and organic acids which can significantly increase IAA biosynthesis in PGPR (Shukla et al. 2011; Zakharova et al. 2000; Somers et al. 2004). Thus, the composition of root exudates can precisely modify genes encoding for plant favouring traits.

In conclusion, rhizosphere microbiota may lessen impact of various living and non-living stresses on plants. But performance of microorganisms is affected by numerous factors such as not consistent efficiency under geographically different climatic conditions and narrow shelf life. More basic knowledge needs to be generated pertaining to beneficial interactions among microorganisms and plant roots both at cellular and molecular level, as well as the effect of beneficial microbes on virulence spectrum of phytopathogens.

10.3.2 The Deleterious Rhizo-Microorganisms

The rhizosphere in addition to beneficial microorganisms also attracts soil-borne pathogens which are deleterious for plant vigour and well-being. It provides a battlefield where the complex rhizosphere microbiome interacts with soil-borne pathogens and influences the phytopathogens and impacts their pathogenicity causing major yield reductions of food, feed, and fibre crops. Predominant soil-borne plant pathogens include nematodes (*Meloidogyne*, *Heterodera*, *Longidorus*, *Paratrichodorus*, etc.), true fungi, bacteria, and viruses. Among these, viruses need vectors (nematodes, insects, and fungi) to invade plant roots (Campbell 1996).

Plants show a variety of symptoms in response to infection with fungal soil-borne pathogens such as pre- and post-emergence damping off of seedlings (*Pythium* sp.), root rots (*Rhizoctonia* sp.), wilts (*Fusarium* sp.) etc. In response to infection by root rot causing phytopathogens, there is increased mortality of root tips causing reduced root growth leading to poor absorption of water and nutrients. This could be due to destruction of root hairs. As a result, plant shows retarded growth and may exhibit nutritional deficiency.

Two important phenomena, viz. fungistasis and rhizodeposition, that occur in the rhizosphere determine the fate of the pathogen and its ability to initiate infection. Fungistasis refers to reduced rate of germination due to exogenously induced

dormancy (Dobbs and Hinson 1953; Lockwood 1977). The fungistatic mechanisms facilitated by soil microorganisms include the presence of volatile or soluble inhibitory substances or lack of essential nutrients for spore germination (Ko and Lockwood 1967; Liebman and Epstein 1992).

Soil-borne fungal plant pathogens, viz. *Rhizoctonia*, *Fusarium*, *Sclerotium*, *Pythium*, and *Phytophthora*, perpetuate in the soil as chlamydospores, oospores, sclerotia, or hyphae or survive on plant debris (Bruehl 1987). The root exudates stimulate these resting propagules to germinate and invade roots of susceptible plants. This stimulus is particularly important for less virulent phytopathogens which remain in dormant phase in the absence of either nutrients or fungistasis. The microorganisms prevalent in rhizosphere are governed by the resistance or susceptibility level of the crop varieties grown.

For the successful establishment of the pathogen in the rhizosphere, host signals play a vital role. The life cycle of fungi like formation of surviving structures (oospores, sclerotia, etc.) is influenced by various parameters such as pH level of soil, soil type, and root exudates. At low concentrations, phenolic compounds present in root exudates like p-hydroxybenzoic, Gallic, coumaric, cinnamic, ferulic, salicylic, cinnamic acids, etc. stimulate germination of spores of pathogenic fungi; however, presence of these compounds at higher concentrations causes inhibition of spore germination (Wu et al. 2008). This has been demonstrated in *Veratrum taliense* (Liliaceae), *Phytophthora capsici*, and *Rhizoctonia cerealis* combination (Zhou et al. 2003). Both soil physical characteristics and microbes diversity influence the alkaloid makeup (retrorsine and retrorsine N-oxide) in roots and shoots of *Jacobaea vulgaris* (Joosten et al. 2009). These compounds prevent hyphal growth of various phytopathogenic fungi, for example, *Fusarium* and *Trichoderma* sp. (Hol and Veen 2002). Saponins among diverse group of glycosides also adversely affect plant pathogenic fungi by interfering with membrane integrity (González-Lamothe et al. 2009; Osbourn et al. 2011). Evidence of role of saponins (avenacin) in plants defence against root rot fungi *Gaeumannomyces graminis* var. *avenae* has been well presented (Bednarek and Osbourn 2009; González-Lamothe et al. 2009; Osbourn et al. 2011). Avenacin is also responsible for eliciting other processes in the plant such as callose deposition (Bednarek and Osbourn 2009) thereby inducing resistance.

Oomycete pathogens reproduce asexually by production of motile biflagellate zoospores which invade plant roots and cause infection. The composition of root exudates influence chemotactic attraction of zoospores of *Phytophthora* sp. van West et al. (2002) demonstrated that the zoospores that get attracted towards roots is also due to electrotaxis, whereby roots produce electric currents in response to ion exchange at growing ends. Thus, electrotaxis play a critical role in colonisation of roots by zoosporic pathogens.

10.3.2.1 Nematodes

Plant pathogenic nematodes are either free living, ectoparasitic, or endoparasitic. Nematodes move towards roots of plants in response to root exudates (Bird 1959; Young et al. 1996). Perry (2005) and Curtis et al. (2009) have designated these attractants as long distance (attract nematodes to the general root area), short distance (attract nematodes to the roots themselves), and local attractants (orient the nematodes to the preferred penetration site). In the complex rhizosphere, both volatile (long-distance chemotaxis) and water-soluble compounds (short-distance chemotaxis) act as important signals for nematode scavenging (Rasmann et al. 2012).

Carbon dioxide act as major signal released by plant roots to attract nematodes (Jogler et al. 2012). Besides carbon dioxide, many other compounds like naturally occurring hydroxamic acid (DIMBOA), glutamic, and ascorbic acid can induce chemotaxis in nematodes. On the basis of chemotactic property of root attractants, trap crops have been exploited to attract the nematodes to non-host plants (Franco et al. 1999). For example, *Asparagus officinalis* and *Tagetes* species attract a vast variety of nematodes by releasing glycosides (Bilgrami 1997).

10.4 Role of Root–Microbe Communication in Shaping Rhizo-Microbiome

Being a dynamically active habitat for microorganisms, microbiome not only influences plant growth but also affects human or animal health. Efforts are being made to redesign rhizosphere microbiome favouring plant growth-promoting microorganisms and inhibiting phytopathogens. Several studies conducted in the last 20 years evidently showed that the plant genetic makeup and soil properties are two major factors that outline microbial communities in rhizosphere (Berg and Smalla 2009; Bakker et al. 2012).

The information on rhizodeposition and its role in activating and attracting soil-borne plant pathogens are limited and patchy. The inadequate understanding of the cross-talk between plants and soil-borne phytopathogens is mainly due to a scanty knowledge of the complex physiochemical conditions in vicinity of rhizosphere (Weston et al. 2012). The chemical composition and spatiotemporal production of root exudates also called as “ecometabolomics” needs to be elucidated to understand these complex interactions. The comparatively young researchable area of ecometabolomics is the utilisation of metabolomics techniques to biology with the target to characterise biochemical communications among organisms across various spatiotemporal patterns.

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