Chapter 6
Soil–Microbes–Plants: Interactions and Ecological Diversity

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Abstract In interactions between plants and soil, microorganisms have significant roles. Ecological stability is contributed by the biogeochemical cycling of elements. An emerging body of research is distinguishing the impacts that root-associated microbial communities can have on plant fitness and growth. Rocks and minerals are weathered by the activities of plants, which exude various types of hormones, with a crucial role in the supply of organic matter and formation of soils. Various types of plant species have distinctive biological characteristics that show constraint to precise soil types. Plant–microbe interactions in soil are contributing to a new, microbially based perspective on plant community and ecology. These microorganisms are soil dwellers, diverse, and their interactions with plants vary with respect to specificity, environmental heterogeneity, and fitness impact. The key influences on plant community structure and dynamics are effected by two microbial procedures: microbial intervention of niche diversity in resource use and response dynamics among the soil community and plants. The hypothesis of niche diversity is based on various interpretations that the nutrients of soil are found in different chemical forms: the plant requires accessing these enzymes and nutrients, and the microorganisms of the soil are a major source of these enzymes. Plant–microbe interactions are a significant establishing force for extensive spatial gradients in species abundance. The positive response (a homogenizing force) and negative response (a diversifying force) of virtual balance may contribute to detected latitudinal (and altitudinal) diversity patterns. The microbially based perception for the ecology of plants promises to contribute to our understanding of long-standing issues in ecology and to disclose new areas of future investigation.

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6.1 Introduction

The soil is the most important factor for plants and their associated microorganisms, which have a crucial role in the modification and formation of soil (Marschner 2012). According to the origin of the parent material, climate, and vegetation, soil has various properties formed by the weathering of rocks and minerals (Jenny 1980). Directly or indirectly, plants derive soil carbon; mostly the plants are involved in the weathering process by microbial activities that depend on root-derived carbon, and physical and chemical processes are also involved secondarily (Six et al. 2004). Microbial diversity and soil functionality are the important regulating factors in the elements of biogeochemical cycling, that is, carbon, nitrogen, and phosphorus, and as such contribute to the stability and quality of the ecosystem (Van Der Heijden et al. 2008). Microbial ecology has developed rapidly in general and in soil–plant interactions in particular, led by molecular and isotope labeling technologies (Dawson et al. 2002). Concern for preserving ecosystem services and food provision are in urgent need of solutions in East Asian countries such as Korea, Japan, and China (Davis et al. 2011). The East Asian Federation of Ecological Societies (EAFES), which promote collaboration of ecological and environmental sciences, was established by these three countries in 2003 (Kim et al. 2018). Maintenance and establishment of microbial populations in rhizospheric soil have been completed successfully by the transfer of molecular and genetic information. The microbial soil communities also have an important major function in the protection of plants from abiotic stresses and phytopathogens (Johansson et al. 2004). In the environment, the microorganisms are rarely encountered as single-species populations, but observations have shown an enormous biodiversity and abundance variability in a small quantity of samples from various habitats (Sogin et al. 2006). It is suggested that the establishment of microbial populations in the rhizospheric environment (physical, chemical, and biological) is inherent in the interactions of microbes (Bais et al. 2006). The coevolution of various species has led to specialization and adaptation; consequently, the relationships in large variety can expedite sharing, whether symbiotic, mutualistic and antagonistic, endosymbiotic, parasitic, or pathogenic relationships (Toby et al. 2010). In microbial interactions, various secondary metabolites, also known as bioactive compounds that execute various important functions in the interactions of rhizospheric ecology, have been detected (Quiñones et al. 2005). A quorum-sensing mechanism resides in a stimuli–response system which is widely related in cellular concentration studies, and the microbes interact with each other. Production of the signaling molecules (auto-inducers) permits messaging of cells and reacting to the environment in a synchronized way (Waters and Bassler 2005). The microbially associated molecular patterns (MAMP) during interactions with the host cells are preserved in various taxa of microbes, permitting continuous proliferation during interactions with the animal and plant cells and adaptability to the interactions of microbes with various hosts (Table 6.1) (Braga et al. 2016).

The belowground microbial communities have a significant function in the productivity, microbial diversity, and composition of various plants (Van Der

Table 6.1 Microbial interaction studies

Organisms involved	Type of interaction	Compounds/mechanisms involved	Findings	References
Moniliophthora roreri and *Trichoderma harzianum*	Phytopathogen–endophyte	T39 butenolide, harzianolide, sorbicillinol	Compounds dependent on the phytopathogen presence and were spatially localized in the interaction zone.	Braga et al. (2016)
Trichoderma atroviride and *Arabidopsis* sp.	Endophyte–plant	Indole acetic acid-related indoles	Plant root colonization promotes growth and enhances systemic disease resistance in the plant by endophytes.	Salas-Marina et al. (2011)
Xylella fastidiosa and *Methylobacterium mesophilicum*	Phytopathogen–endophyte	Hydroxamate type	Genes related to energy production, stress, transport, and motility were upregulated in the phytopathogen, but genes related to growth were downregulated.	Lacava et al. (2004)
Burkholderia gladioli, *B. seminalis*, and orchid	Phytopathogen–endophyte–plant	Extracellular polysaccharides; altering hormone metabolism	By using extracellular polysaccharides and by altering hormone metabolism, the endophyte strain probably interacts with the plant, as was suggested by genomic analysis.	Araújo et al. (2016)
Bradyrhizobium diazoefficiens and *Aeschynomene afraspera*	Symbiont–plant	C35 hopanoids	C35 hopanoids are essential for symbiosis and are related to evasion of plant defense, utilization of host photosynthates, and nitrogen fixation.	Barrière et al. (2017)
Stachybotrys elegans and *Rhizoctonia solani*	Mycoparasite–host	Trichothecenes and atranones	Mycoparasite-induced alterations in *Rhizoctonia solani* metabolism, growth, and development by the production of mycotoxins. The biosynthesis of many antimicrobial compounds by *R. solani* was downregulated.	Chamoun et al. (2015)
Candida albicans and *Pseudomonas aeruginosa*	Microbial community	Quorum sensing	The *Pseudomonas aeruginosa* QS system may block the yeast-to-hypha transition or activate the hypha-to-yeast reversion of *Candida albicans*. Farnesol produced by *C. albicans* downregulates the QS system of *P. aeruginosa*.	Polke et al. (2017)

(continued)

Table 6.1 (continued)

Organisms involved	Type of interaction	Compounds/mechanisms involved	Findings	References
Vibrio fischeri and fishes or squids	Symbiont–fish	Quorum sensing	In symbiotic association with fishes and squids, the auto-inducer molecule reaches a threshold and luminescence genes are activated.	Fuqua et al. (1994)
Rhizobium leguminosarum and plants	Symbiont–plant	Quorum sensing	The quorum-sensing system in these bacteria is related to different functions: nodulation efficiency, growth inhibition, nitrogen fixation, and plasmid transfer.	Gonzalez and Marketon (2003)
Xanthomonas or *Xylella* and grapevines or citrus	Pathogen–host	Quorum sensing	Quorum-sensing signaling molecules control the expression of virulence factor as well a s biofilm formation.	Mansfield et al. (2012)
Pantoea stewartii and *Zea mays*	Pathogen–host	Quorum sensing	Quorum-sensing mutants of *Pantoea stewartii* were not able to disperse and migrate in the vasculature, consequently decreasing the disease.	Koutsoudis et al. (2006)
Pseudomonas syringae and tabacco and bean	Phytopathogen–plant	Quorum sensing	Quorum-sensing system allows this bacterium to control motility and exopolysaccharide synthesis essential on biofilm formation and leaves colonization.	Quiñones et al. (2005)
Streptomyces coelicolor and other *Actinomycetes* spp.	Microbial community	Prodiginines, ctinorhodins, coelichelins, acyl-desferrioxamines, and other compounds	The 227 compounds differentially produced in the interactions were unique.	Bentley et al. (2002)
Aspergillus nidulans and *Streptomyces rapamycinicus*	Microbial community	Aromatic polyketides	Activation of fungal secondary metabolite genes that were otherwise silent led physical interaction between the microorganisms. The actinomycete triggered alterations in fungal histone acetylation.	Bertrand et al. (2014)

Pseudomonas sp.	Microbial community	Pyoverdines (siderophore)	Pyoverdines act as signaling molecules, activating a cascade that results in the production of several virulence factors. It is essential to infection and biofilm formation.	Jimenez et al. (2012)
Burkholderia sp., *Rhizopus* sp., and rice	Symbiont phytopathogen plant	Rhizoxin, bongkrekic acid, enacyloxins	In the absence of the endosymbiont the fungus does not form spores. The phytotoxin rhizoxin is the causal agent of rice seedling blight produced by the endosymbiont; fungus induces the growth of the endosymbiont.	Depoorter et al. (2016)
Vibrio sp. and diverse marine bacteria strains	Microbial community	*N*,*N*-bis-(2,3-Dihydroxybenzoyl)-*O*-serylserine: exogenous siderophore	Siderophores and iron-regulated outer membrane proteins produced by marine bacteria and other species only in the presence of exogenous siderophores.	Kanoh and Kamino (2001)

Heijden et al. 2008). As such, experimental observations have confirmed that microbial diversity in the rhizospheric regions influences plant growth plants and the efficiency, nutrient accessibility, and functioning of an ecosystem (Delgado-Baquerizo et al. 2016). Furthermore, the significance of the soil–plant response is demonstrated by various observations, whereby the changes in the composition of community microbial response allow the simultaneity of plant and community arrangements. Although the effects of soil and plant–microbial interactions on ecological dynamics have been widely apparent, a brief observation indicates how the rhizospheric microbial communities stimulate the evolutionary process of plant communities (Lambers et al. 2009). A short generation time and a very high degree of genetic diversity are found in the microbes, with the capability to develop on ecologically significant timescales (Jessup et al. 2004). The microbial community structure is altered very rapidly because of these characteristics, which in turn may shape the way that the populations of plants react to innovative selective pressures in their environment (Whitham et al. 2006). Genetic differentiation in fully associated microbes derived from local adaptation in plants has been verified by various new observations (Richardson et al. 2009). For example, fungal endophytes have been recognized to colonize in stress conditions such as high temperatures, salinity, and drought, and heavy metal-resistant strains of mycorrhizae have been shown to expedite plant colonization of adulterated mine tailings (Calvo et al. 2014). The complex interactions with plant-associated microbes affect plant ecology. The functions of both plant-associated microbes and the hosts in the ecosystem have been identified, but the mechanism is not clarified (Hardoim et al. 2015). The immobile plants have developed a number of mechanisms that restrain the product of their interactions. The wide range of chemical compounds synthesized, secreted, and accumulated by the plant roots pass into the soil as root exudates (Chapin et al. 2002). These root exudates include various carbon-containing primary and secondary compounds, enzymes, water content, H^+ ions, and mucilaginous substances (Berg and Smalla 2009). These exudates of the plant roots structure and shape the bacterial community. In bulky soil, the density of microbes is 100 times less than in the rhizospheric soil (Baudoin et al. 2003). The composition of microbes alters and produces a response in the related plant routines.

Long-term effects of the soil microbes on their synchronicity with that plant species are described (Jentsch et al. 2007). There are two types: response-positive soil–plant microbial content emphasizes the spatial splitting of the microbial populations, whereas a negative response results in plant replacement, which requires recolonization of locally explicit roots (Lambers et al. 2008). The genome-wide association observed by experimental methods has facilitated our discoveries of the interactions of plant loci and associated communities. The diversity of the microbiome and its functions potentially affects the performance of host plants (Bodenhausen et al. 2014). The plant microbiome system performs important roles among plants and the community of microbes. An intricate assortment of volatile compounds is produced by the plant growth-promoting rhizobacteria (PGPR), which are distinctive among microbial species (Swamy et al. 2016). Plant growth is stimulated by the volatile compounds released by PGPR that suppress the disease-motivating induced systemic resistance (ISR) or alienate phytopathogens such as nematodes or insects. Biotic and abiotic stress factors affect the worldwide crop production and cause millions of dollars in losses (Wang et al. 2013). PGPR or plant-associated microbes were found to assist plants by producing various enzymes and hormones, improving the nutrient uptake, stimulating the root and shoot growth such as indole acetic acid, 1-aminocyclopropane-1-carboxylate (ACC) deaminases, and solubilizing phosphate, and enhancing the uptake of nutrients from environmental strains such as heavy metals, salts, nutrient deficiency, and drought (Gravel et al. 2007). The stress of biotic factors includes interactions with other organisms and infection by pathogens or damage by insect pests, and some plant growth-promoting bacteria have been used as bio-control agents against phytopathogens. This chapter explores symbiotic microbial communities and plant–host relationships, and these interactions require communication between various microorganisms that are involved in the rhizospheric system.

6.2 Fundamentals of Plant–Microbe Interactions

6.2.1 *Functions and Diversity*

The microorganisms that reside in the soil include a variety of phylogenetic groups and other major functional groups such as producer, consumer, and decomposer. Exceptionally, thousands of genomes are found in each gram of soil and form the genetic diversity (Bardgett et al. 2008). Interactions among soil microbes and plants span the range from mutualistic to pathogenic (Reynolds et al. 2003). The soil microbes are ultimately accountable for the bulk of terrestrial vegetation and annual nutrient demand as decomposers. In this order, the plant photo-synthetically fixed carbon is the major source for decomposition by microbes (Gougoulias et al. 2014). The microbes and plants form their relationship simultaneously, mutualistic and competitive, and also compete for soil nutrients (Van Der Heijden et al. 2008). The mycorrhizal fungi and PGPR increase the fitness of the host plant by providing mineral resources and safeguarding against other pests (Parnell et al. 2016; Prasad et al. 2015). Various other nonmycorrhizal fungi, rhizospheric bacteria, protozoa, and nematodes have also been revealed to protect plants from soil pathogens such as fungi, bacteria, actinobacteria, protozoa, nematodes, and viruses (Igiehon and Babalola 2018; Singh et al. 2019). These types of pathogens are responsible for various diseases such as damping-off, vascular wilt, and root rot diseases (Weller 1988).

6.2.2 *The Interconnection Between Plants and Soil Microbes*

The soil is the source of nutrients for plants: it is an intricate ecosystem accommodating various bacteria, fungi, protists, and animals. Plants demonstrate a diverse arrangement of interactions with these soil-dwelling microorganisms, which span the full range of environmental potentials such as competitive, exploitative, neutral, commensal, and mutualistic (Ratnadass et al. 2013). Various interactions were observed, which focused on improving the effects of pathogens such as herbivory and infection or tempering abiotic stress conditions through modern plant science (Shoresh et al. 2010), although the ecological interactions positively stimulate the growth of plants by long-standing interest in characterization. For example, in the second half of the nineteenth century the root symbiotic relationship was documented as mycorrhizal fungi and bacteria (Smith and Read 2010), and the bacterial cultures such as *Azotobacter chroococcum* or *Bacillus megaterium*, which improve the growth and crop yield when the seeds were coated by this culture (Burr et al. 1978). *Pseudomonas* sp. and *Azospirillum* sp. had been described as having plant growth-promoting effects, isolated in the 1980s. The diversity and abundance of the root microbiome is documented through metagenomics, which has shifted from individual microbial strains since the twentieth century (Hartmann et al. 2009). The rhizospheric niche is a hotspot of ecological richness observed from such types of sequencing, with plant roots hosting a massive array of microbial taxa (Van Der Heijden et al. 2008). In the current scenario, research has altered toward accumulating reasonably premeditated uninspired groupings that comprise the strains representing the overriding rhizospheric taxa, with the aim of reiterating the advantageous functions of microbes under controlled experimental conditions. To gain a systematic understanding in this research field, how soil microbes boost the plant growth and defense is a major goal, and to use these facts to inform the best strategy of microbial societies design to carry out specific functions (Fig. 6.1) (Johnson 2010).

6.2.3 Soil and Plant

For host health and improvement, the microbiota colonized in soil by microorganisms such as Archaea, Bacteria, Fungi, and viruses offer key functions (Xu 2006). The association of the microbiome with plants is measured as its second genome. It is also a contributing factor for the health of plants, growth, suitability, and productivity consequently (Björkman et al. 2011). The rhizosphere, endosphere, and phyllosphere have a specific microbial community with specific functions associated with the environment. The densities of the plant microbiome are greater than the number of plant cells and also contain better expressed genes than the host cells, as illustrated by these culture-independent methods (Hardoim et al. 2015). The next-generation sequencing technologies used for metagenomics analysis demonstrate that the current methods have cultured only 5% of bacteria, revealing that many microorganisms and their functions remain unknown (Walker et al. 2014). The microbial gratitude of plant exudates in the region of rhizosphere occurs by the collaboration of plant microbes (Sugiyama et al. 2014). The plants have the capability to recruit the microorganisms by their exudates (Compant et al. 2010).

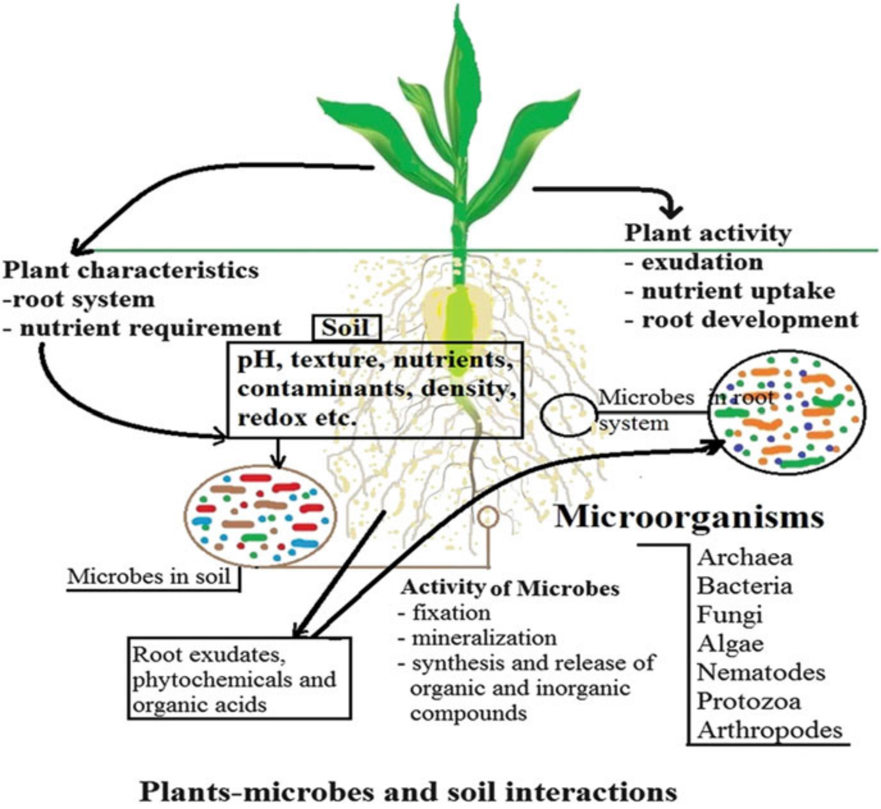

Fig. 6.1 Interactions among plants, microbes, and soil with microbial activity

The exudates are composed of amino acids, carbohydrates, and organic acids and vary according to the plant and its biotic or abiotic condition (Badri and Vivanco 2009). The specific microbial communities are selected from different plants when matching with rhizospheric settlement of two medicinal plants, *Matricaria chamomilla* (chamomile) and (*Solanum distichum*) nightshade, even with being harvested under the same conditions, and they access various analyzing 16*S* rRNA genes (structural) and analyzing the nitrogen fixing-*nifH* genes (functional) microbial community. Furthermore, the plant exudate of the same plant contrasts according to the developmental stages of plants, which selects the exact communities of microbes (Pérez-Montaño et al. 2014). The plant legume–Rhizobia secreted flavonoids and strigolactone as a signal molecule for arbuscular mycorrhizal fungi (AMF) showing specific interactions (Badri et al. 2009). A great diversity of the microbial community exists in the bulk soil, produced only by environmental factors and soil textures (Zornoza et al. 2015). The more specialized community of some species is found in the rhizospheric regions and the plant root exudates, and some species have the capability to enter the roots of plants and establish therein

(Chandra and Enespa 2019). Moreover, the microbial community varies among different organs after entering the plant, such as roots, top leaves, fruits, bottom leaves, flowers, and stems. Plants can be protected from pathogens by mutualistic microorganisms, either by inducing plant resistance or by antibiosis (De Coninck et al. 2015). High tolerance to pathogens is produced in plants by the induced systemic resistance (ISR) mechanisms. Whether the mechanisms of ISR suppressed the growth of the pathogen or the disease does not occur in the soil is still being investigated (Pineda et al. 2010). The disease of damping-off in several agricultural crops caused by the *Rhizoctonia solani* fungal pathogen is suppressed in soil by the microbiome observed (Berendsen et al. 2012). The oligonucleotide microarray (PhyloChip) using 16*S* rDNA has the capability to recognize more than 33,000 taxa of bacteria and Archaea in the seedlings of sugar beet grown in the rhizospheric region in suppressive and conductive soils (Hoitink and Fahy 1986). These observations predicted that in the suppressive soil the bacterial groups would be present. The Proteobacteria, particularly the Pseudomonadaceae, were all more abundant in suppressive soil than in conducive soil as noted by various authors, focusing thereby in this bacterial group (Choudhary et al. 2009). Using the random transposon mutagenesis techniques they were able to recognize the genes accountable for the biosynthesis of nine amino acid-chlorinated lipopeptides in *Pseudomonas* sp., an antifungal manufactured by *Pseudomonas* sp. that controls the pathogen (Ramaswamy et al. 2007). Other antifungals produced by rhizosphere-associated *Streptomycetes* were identified by the same PhyloChip diversity analysis (Chandra and Enespa 2017). These isolates were capable of producing chemically diverse volatile organic compounds (VOCs) with an antifungal effect as well as the plant growth-promoting properties. The various bacterial groups can perform similar roles in the same environment (Mendes et al. 2013). Strains of *Methylobacterium* that protect the plants against pathogen attack and affected communities of endophytes after inoculation were reported by various investigators (Ardanov et al. 2012). Consequently, investigators started inoculating plants with a pool of microorganisms with complementary traits using these concepts, such as various control mechanisms, with the aim of defining the various methods that were used for the inoculation of microorganisms (Lynch et al. 2004). The core microbiome of a healthy host is defined by the first methods, or the function of microbiomes can be understood by sequencing methods. In this manner, the modulation of microbial communities is beginning to be studied as "microbiome engineering." Plant breeding programs select a beneficial interaction between the plant lines and the rhizospheric microbiome or by redirecting the rhizospheric microbiome or stimulating beneficial microorganisms (Pieterse et al. 2012). The ecological processes can be altered by microbiome engineering such as the variation in diverse communities and the changing structure of microbe interaction networks and the extinction of microbial species in the microbiome, transfer of genes horizontally, and transmutations which can restructure the genomes of microorganisms by modifying the processes of evolution (Mueller and Sachs 2015). Briefly described, the sum of plant solutions for the environment and to the present microbiome such as endophytes and pathogens are the phenotype of the plant; this microbiome also replies to the environment, and these interact with each other (Gaiero et al. 2013). The gut and plant rhizospheric microbiomes demonstrate similarity with each other, as has been observed. Both are open systems, with oxygen gradient, H_2O, and pH resulting in huge numbers and microorganism diversity because of the altered conditions of survival (Herbst et al. 2016). The compositions of plant rhizosphere and gut microbiome differ between each other, but the acquisitions of nutrients, modulation of the immune system, and protection against infections have several similarities (Hacquard et al. 2015). The similarities between host-associated microbiome ecology include various conditions of abiotic shape and the microbial community structure; the microbiome of host coevolution (Braga et al. 2016); the microbiome of the core region can be vertically transmitted; the microbiome structure varies during the life cycle; the microbiomes associated with the host are self-possessed prokaryotic and eukaryotic microorganisms; functional diversity is the key in a microbiome; and the diversity of microbes is destroyed by human interventions (Lloyd-Price et al. 2016).

6.2.4 Secondary Metabolism

Microorganisms produce a large variety of compounds, secondary metabolites that are not necessary for the growth, improvement, and reproduction of the manufacturing organisms (Bourgaud et al. 2001). However, these metabolites are known as bioactive compounds and work in defence mechanisms, competition, and signaling, as well as in ecological interactions (Kliebenstein 2004). Microorganisms react by exchange of metabolic activity to establish a microbial interaction network, which leads to difficult regulatory replies and connecting to the biosynthesis of secondary metabolites (Zhao et al. 2005). The metabolites involved for interactions can be parasitic, antagonistic, or competitive, and their functions are being studied especially just now as a result of the beginning of new methods, for example, the technology of imaging mass spectrometry (IMS) and metabolomics (Gemperline et al. 2017). The competitive and cooperative microbial interactions are related to siderophores and can also have other functions such as signaling and antibiotic activity (West et al. 2007). In the interaction of bacteria, tolerance and discussing and improving the adaptation of bacteria in various environments, hopanoids are important (Sikkema et al. 1995). The compounds synchronized in fungi differentially in collaboration are often bioactive secondary metabolites, for example, diketopiperazines, trichothecenes, atranones, and polyketides. We present examples of such studies in these sections on secondary metabolites that elaborate various types of interactions in microbes.

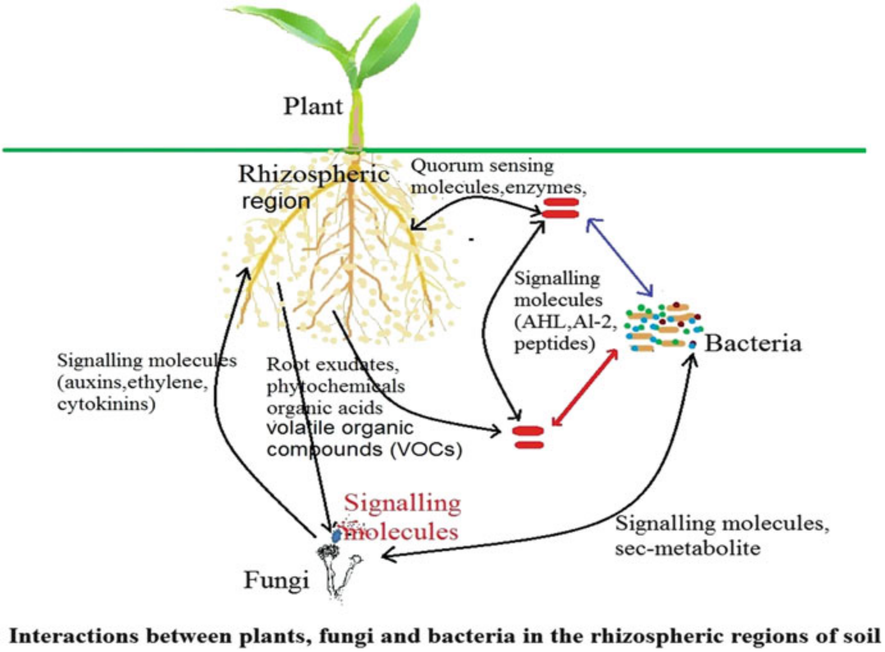

Fig. 6.2 Microbes and plant interactions using signaling molecules between rhizosphere and soil

6.2.5 *Plant Community Ecology and Soil Symbiotic Interactions*

Global climate changes can affect the ecology of plants in a terrestrial ecosystem in terms of both above- and belowground diversity (Bobbink et al. 1998). The dynamic changes in soil microbial ecology drive the plant communities of terrestrial regions that may result in adaptations in the functions of the ecosystem and stabilize the mechanisms essential for the maintenance of species diversity and synchronicity (Shade et al. 2012). These mechanisms of plant–plant interactions are contributed in the entire plant ecosystem by the microbes (Bever et al. 2010). Habitually, challenging the plant species have been supposed to have resilient intraspecific interactions negative for the high overlap in resource tradition, although the cohabitation of opposing plant species in local diversity explains the mechanism of success in finding the community (Hausch et al. 2018). Feedback might be one reason for neglecting a soil microbial community. In the rhizospheric region, the microbial communities communicate with each other and with the variety of mechanisms of the plant root, with bacterial AHLs (*N*-acylhomoserine lactones) and AI-2 (autoinducer-2) (Bogino et al. 2013). The composition of microbial communities is influenced directly by this and in some circumstances leads to the growth of improved plant health when the roots of plants establish beneficial interactions with root microbes (Fig. 6.2) (Berendsen et al. 2012).

To produce the responses in eukaryotes such as plants and fungi, bacteria employ signaling molecules. The plant growth-promoting rhizobacteria (PGPR) produce volatile organic compounds and initiate the induced systemic resistance (ISR) in plants, promoting growth in *Arabidopsis thaliana* (Choudhary and Johri 2009); thus, the expression of defence genes is stimulated that can be effective against microbes such as fungi, bacteria, oomycetes, and viruses (Pieterse et al. 2009). Although regulating the activities of bacteria in a density-dependent fashion, the molecules of quorum sensing (QS) also stimulate a plant-beneficial response range in the host plants (Lareen et al. 2016). The plant "priming" is included by them in which disclosure to signaling molecules of quorum primes the plant to return more strongly and quickly to biotic challenges (Mauch-Mani et al. 2017).

The exposure to AHL produced by *Serratia liquefaciens* MG1 and *Pseudomonas putida* IsoF increased the systemic resistance of tomato plants in contrast to the fungal foliar pathogen *Alternaria alternata* by inducing the ethylene and salicylic acid-dependent defence genes (Lareen et al. 2016). In *Arabidopsis* the AHL *N*-3-oxo-tetradecanoyl-L-homoserine lactone also supports pathogen defense of the accumulation of phenolic compounds by enhanced deposition of callose, cell wall lignification, and stomata closure in response to *Pseudomonas syringae* infection. Significantly, the increases in salicylic acid and oxylipin levels are associated with AHL activities. Plant hormone activity stimulation is used further by several microbes to accept the processes elaborated in the early stages of legume–rhizobia interactions and root mycorrhization that indicate the inter-domain communication for their successful establishment. A potential of microbial species or derivatives of metabolites modified the improvement of plants and fungi as observed in this study (Bloemberg and Lugtenberg 2001).

6.2.6 Soil Communities Affected by Bacteria and Fungi Interaction

The site enriched as plant nutrients in rhizospheric regions is a highly reasonable environment for the microorganisms (Hodge 2004). Secondary metabolites such as antibiotics, toxins, lytic enzymes, and siderophores are produced by the microbes to outcompete competitors to establish inside roots at the rhizosphere and occupy the similar niches (Lareen et al. 2016). The large gene clusters that are involved in detoxification, secretion of antibiotics, and siderophores are possessed by some rhizospheric microbes (Compant et al. 2010). Some rhizosphere microbes possess these large gene clusters involved in detoxification, production/release of antibiotics, and siderophores, such as *Bacillus amyloliquefaciens* and *Pseudomonas fluorescens* (Tewari and Arora 2013; Chandra and Singh 2016). Various common antibiotic compounds are secreted by the microbes such as 2,4-diacetylphloroglucinol (DAPG), hydrogen cyanide, oomycin A, and phenazine. In the soil these antibiotics (phenazines) inhibit the growth of pathogens such as *Fusarium oxysporum* produced by *Pseudomonas chlororaphis* (Lee et al. 2013; Raaijmakers et al. 2002; Enespa and Chandra 2017). Furthermore, various microbes released the lower concentrations of antibiotic compounds and have led to the recommendation that the primary functions of these molecules is in statement rather than inhibition or exclusion of opponents (Taylor et al. 2007). This range of functions in the soil suggests antimicrobial compounds as key in establishing microbial communities (Torsvik and Øvreås 2002). In the rhizospheric regions these antimicrobial compounds are the key to establishing microbial communities subjected to a wide range of functions in the soil (Badri and Vivanco 2009). The microorganisms produce the secondary metabolites in addition to antibiotic compounds to modify the signaling of the plant and its metabolism (Berendsen et al. 2012) to obtain nutrients. The plant can modify the arrangement of root exudates and encourage the release of more positive exudates by this reprogramming, in the rhizospheric region, which leads to a selective improvement of respective microbes in the rhizosphere (Shtark et al. 2010). This action recommends that in the regions of the rhizosphere the secondary metabolites and the antimicrobial compounds establish the microbial communities, which assist in the competitive niche exclusion (Hibbing et al. 2010). As a prerequisite the competitiveness for the formation and the dominancy of these communities required a harmonized message among the microbes as well as the sensitivity and the transformation of ecological signals (Cray et al. 2013).

6.2.7 Soil Resources and Microbial Interactions

Plant species synchronicities govern the soil resources by resource partitioning and sharing (Schoener 1974). The efficiency of nutrient uptake is increased by the root symbionts and allows the host to maintain in a low-nutrient environment, thus directly subsidizing to the competitive exclusion of other plants (Langley and Hungate 2003). Different forms of nitrogen or phosphorus in the soil can modify availability by the rhizosphere microbes and affect the plant–plant interactions through the intervention of source separating (Palacios et al. 2014). Common mycorrhizal networks (CMNs) formed by symbiotic fungi can also transfer micronutrients. In nature, different plant species commonly share the broadly specific mycorrhizal fungi (Brooker et al. 2015). CMNs with labeled carbon, nitrogen, and phosphorus transfer the resources directly from one plant to another. Soil microbial mediation resource distributing and involvement are driven by the community dynamics of the plant (Selosse et al. 2006).

6.2.8 Host Response to Microbes and Soil Community Feedback

In plant populations, the coexistence of plant species is affected indirectly via the feedback of dynamic density and composition of the rhizospheric microbes, such as the competition or inhibition of symbionts (Bever 2003). Three hypotheses have been proposed by ecologists to explain the mechanism that produces the low diversity of plant communities (Wright 2002). The novel symbionts reside in those regions that were invaded by invasive plants, as suggested by the empty niche hypothesis (Hierro et al. 2005). These symbionts are well organized for obtaining the resources and favor accompanying hostile plants rather than other plants (Johnson 2010). The invasive plants and their symbionts obstruct the capability of the native community of symbionts to obtain the positions and reduce the acts of native plants indirectly, suggested by the hypothesis of degraded mutualistism (Downer 2014). Growth improvement and survival of exotic seedlings near the natural recognized symbionts is demonstrated by the positive feedback (Bever et al. 2010). The interactions of symbiotic microbes have a high relationship with the monodominancy of plant coexistence and the ecology of invasion (Kulmatiski et al. 2008).

6.3 Role of Root Exudates Shaping the Rhizospheric Microbial Community

The microbes of soil are attracted to the plant root exudates, the volatile organic carbon, and rhizodeposition chemotactically, and then thrive in the carbon-rich environment (Somers et al. 2004; Shrivastava et al. 2014). The exudates of plant root differ among the species of plants, so in various plant species the differences in the rhizospheric microbiome are expected. Strong confirmation for species-specific microbiomes of plant have been provided by more recent observations (Fiehn et al. 2008). The root exudates of plants can be shaped via the microbial community. Various types of sugars, amino acids, organic acids, nucleotides, flavonoids, antimicrobial compounds, and enzymes are characterized in root exudates (Haas and Défago 2005).

6.4 Types of Root Exudates

6.4.1 Amino and Organic Acids

The growth of soil-borne pathogens affected the compositions of root exudates from different cultivars (Berendsen et al. 2012). Analysis of root exudate and its evaluation for the responses of soil-borne pathogens such as *Fusarium oxysporum* and *Fusarium solani* to the susceptible peanut cultivar Ganhua-5 (GH) and the mid-resistant cultivar Quanhua-7 (QH) were selected (Li et al. 2013). Ingredients such as total amino acids, sugars, and alanine in the root exudates of the mid-resistant cultivar were significantly less than in the susceptible cultivars, but substances such as total phenolic acids, *p*-hydroxybenzoic acid, benzoic acid, and *p*-coumaric acid were significantly higher than in the susceptible cultivars. In the composition of root exudates, these differences of susceptible and resistant cultivars might be presumed to adjust the mechanism of resistance in the rhizospheric regions of peanut (Lattanzio et al. 2006). Soil-borne pathogens such as *Fusarium oxysporum* and *F. solani* considerably enhanced the germination of spores and the growth of mycelia from both the susceptible and mid-resistant cultivars by treatment with root exudates compared with a control (Balendres et al. 2016). The effects of other factors must be measured if the root exudates do not inhibit the growth of pathogens directly (Jones et al. 2004). The colonization of organic acids controlled and improved the formation of the biofilm of the root microbiome observed previously (Lugtenberg and Kamilova 2009). The bacterium *Bacillus amyloliquefaciens* facilitated the colonization of banana root exudates, which released organic acids as demonstrated by Yuan et al. (2015). The organic acids from the root exudates of banana were significant in attracting and beginning the colonization of PGPR in plant roots (Haas and Défago 2005). Biofilm formation was induced significantly by fumaric acid, although the greatest chemotactic response was evoked by malic acid (Enespa and Dwivedi 2014). The residues of various amino acids, such as histidine, proline, valine, alanine, and glycine, and the carbohydrates such as glucose, arabinose, mannose, galactose, and glucuronic acid, are secreted primarily by the rice plant, and a higher chemotactic response is induced by the endophytic bacteria *Corynebacterium flavescens* and *Bacillus pumilus* (Kong et al. 2004).

6.4.2 Sugars

The plant pathogens effected the infection by the secretion of a quantity of sugar. The Glc-derived carbon efflux restricted the *Arabidopsis* vacuolar sugar transporter SWEET2 from roots and inhibited infection by *Pythium*. The secretion of SWEET 2 modulated sugar in restraining the loss of carbon to rhizosphere was proposed by some scientists. The decreased substrate availability in the rhizosphere subsidized the resistance to *Pythium* (Nega 2014).

6.4.3 Other Antimicrobial Compounds

Root exudates also participated in belowground plant defense. The “phytoanticipins” and “phytoalexins” are formed by antimicrobial action of low molecular weight (Baetz and Martinoia 2014). A biotic stress such as pathogen infection of the plant root that was previously produced released a defensive compound, phytoanticipins. The manufacture of diterpene rhizathalene-A deficiency in the roots of *Arabidopsis* was found to be more vulnerable to insect herbivory, as observed in a new study. Thus, the root is considered as a part of a constitutive direct defense system by rhizathalene-A (Enespa and Dwivedi 2014). Phytoalexins are not detected in healthy plants: these are known as inducible defensive compounds. The soil-borne pathogen *Fusarium graminearum* is inhibited by five phenylpropanoid root-derived aromatic root exudates, demonstrated as antifungal activity (Lanoue et al. 2010). Generally, the phenolic defensive compounds and terpenoid secreted by the root have very strong antibacterial and antifungal activity. Terpenoids form the largest class of plant defensive compounds both above and below ground (Bais et al. 2004). Volatile organic compounds (VOCs) are secreted from the roots as plant protective compounds, and the rhizospheric regions secrete terpenoids, which are nonvolatile. Also, the root exudates secrete a group of plant defensive phenolics known as phenylpropanoids (Massalha et al. 2017). Phenylpropanoids are cinnamic acid rapidly accumulated and secreted by barley plant resist fungal attack infection such as *Fusarium graminearum*. The exudates of roots are phenolic compounds that have antimicrobial activity and also attract soil-borne microorganisms, which also affects the soil microbial community natively (Barsainya et al. 2016). The amino acid canavanine is also a chemical compound that stimulates a specific group of microbes which inhibit the growth of other soil microbes. The specific rhizosphere microbial community shapes the plants via root exudates (Venturi and Keel 2016).

6.5 Effects of Environmental Factors on Root Exudates

The root exudates of various compositions are produced with various genotypes by plants. The exudates of roots are also affected by abiotic and biotic factors (Wardle et al. 2011). Nutrient availability, organic matter content, structure, pH, and texture are the physicochemical properties of soil affecting the microbial requirement and availability of root exudates by root plants (Schmidt et al. 2011). The secondary metabolism of soil microbes can also affect the exudates by some biotic factors (Badri and Vivanco 2009).

6.5.1 Temperature

Since the beginning of global warming and climate change, cold waves and extreme heat consequentially have affected the harvesting of various crops (Wassmann et al. 2009). To explicate the effects of temperature on root exudates, it was also studied that the strawberry plant grew at 5–10 °C and were linked at 20–30 °C growing-stage plants (Vigo et al. 2000). In the plants growing at low soil temperature, more amino acids were found in exudates, significantly affecting the pathogenicity of *Rhizoctonia fragariae* (Harrier and Watson 2004). The content of organic acid increased with the elevation of temperature in Japanese cucumber grown hydroponically in a growth chamber at high and low temperatures, and a few other compounds identified significantly inhibited the growth of root and germination as demonstrated in this plant (Enespa and Dwivedi 2014).

6.5.2 Soil Moisture Content

Cereal harvesting globally is reduced by flooding and drought conditions: the moisture content of soil affects the release of root exudates, confirmed in various reports (Römheld and Kirkby 2010). Wilting of plants increased temporarily with the discharge of amino acids from the plant roots, which might be related to the incidence of pathogens in the rhizosphere. Plants that grow normally in moist and dried sand include peas, soybeans, wheat, barley, and tomatoes; the sand is remoistened for the liberation of amino acids (Curl and Truelove 2012). In temporarily dried sand, the total quantity of amino nitrogen was many times higher than in the normal moist sand (Certini 2005).

6.5.3 Nutrition and Soil pH

The status of soil pH and the availability of nutrients such as C, N, and P have been found to affect the initiation of plant root exudates and the formation of specified chemical niches in the soil region, along with the abundance of phytopathogens and beneficiary microbes (Kõljalg et al. 2013). The composition of arbuscular mycorrhizal (AM) fungi and bacteria was significantly affected and correlated with changes in pH, phosphate, and soil carbon content in maize plants in a long-term fertilization trial (Toljander et al. 2008). The fungal community of arbuscular mycorrhiza (AM) in 425 individuals and 28 other plant species modified the structure of the AM fungal community by soil pH. In Fe-deficient soil, the phenolic of root secretion was induced and rehabilitated the microbial community in the rhizosphere (Lindsay and Norvell 1978).

6.5.4 Other Soil Microorganisms

The growth of plants and their exudates was improved and developed by the microbial activity of soil. The permeability of root cells and root metabolism was affected by the plant exudations, which were also affected by microbes (Bais et al. 2006). The root exudates and other released compounds are absorbed by microorganisms. Secondary metabolites produced by the soil microbes affected the metabolism and the signaling of plants and are considered as a "plant secondary genome," which is delivered to the plant hosts with derived microbial compounds. Antibiotics such as penicillin and polymyxin and the microbes increased the exudation of organic materials, rehabilitated cell permeability, and amplified the outflow (Sparbier et al. 2012). The microbes of soil induced the exudation of phenolic compounds for improving the Fe absorption of plant in low-Fe availability soil (Marschner 2012).

6.6 Ecological Diversity and Its Interactions

Four major groups of organisms have the greater impact on the performance of plants and the ecological processes that form very close associations with the plant roots. In specific groups of organisms, a plant is exposed to more than one of these groups at any time, and the interactions between them can change the outcome for the plant.

6.6.1 Nitrogen Fixation Symbiotically

In terrestrial ecosystems, N_2 is the most limiting nutrient for plant growth. Although molecular nitrogen is found abundantly in the atmosphere, eukaryotes do not have the capability to fix the atmospheric nitrogen into ammonia (Chandra et al. 2019; Codispoti et al. 2001). In actual fact, this capability is limited to various species of bacteria and Archaea with various life strategies (Bäckhed et al. 2005). Several of these reside in free form in soil and water, such as *Azotobacter* and *Clostridium*, in the intercellular spaces of plants, the phyllosphere, and rhizosphere regions occupied by other microbes such as *Azospirillum*, *Azoarcus*, and *Gluconacetobacter*; and still others are highly specific symbionts such as *Frankia*, connected to *Alnus*, *Myrica*, *Ceanothus*, *Elaeagnus*, and *Casuarina*; and legume symbionts mutually known as rhizobia (Beattie 2007). In the terrestrial ecosystem, the diazotrophs are the main providers for biological nitrogen fixation symbiotically. In the field of agriculture, legume plants form symbiotic relationships, so it is mainly focused on exploration (Lambers et al. 2009). The wide distribution of legume plants in temperate, tropical, and arid regions is significant in natural ecosystems. The order Rhizobiales is mostly known for legume symbionts, but some species known as nodulate legumes are in the order Burkholderiales (Peix et al. 2015). The genera of *Rhizobium*, *Sinorhizobium*, *Mesorhizobium*, *Bradyrhizobium*, *Azorhizobium*, and *Allorhizobium* have the capability to nodulate the legumes and fix nitrogen. *Ensifer*, *Blastobacter*, *Burkholderia*, and *Ralstonia*, similar to other genera, contain both legume symbionts and nonsymbiotic species (Sawada et al. 2003; Rasolomampianina et al. 2005). The relationship among the bacterial symbionts and legumes depends on fine molecular communication. The legume roots produce flavonoids and respond to nodulating bacteria by producing *N*-acetyl-D-glucosamine, which promotes the physiological changes in the roots of the host to nodulation, known as Nod factors (Chandra and Enespa 2017). The structure of Nod factors has dissimilarities, dependent on the various strains and species to determine the host specificity, although in nature symbiotic promiscuity is common and could be beneficial for inhabiting new soils (Shamseldin 2013). The highly immoral legumes are successful invasive species as observed by some scientists. For the institution and growth of many pioneer species of legumes, this is a crucial association. From these relationships the growth of other plant species in nitrogenous enrichment soil is consequently expedited (Sharpley et al. 1994). So, it promotes the succession of plants. In consequence, when the level of nitrogen increased, it displaced the other species and promoted spatial heterogeneity. Thus, it is shown that the functioning of terrestrial ecosystems depends on the key symbiosis relationship (Laliberté et al. 2013).

6.6.2 Fungal Mycorrhiza

A plant root and a specialized fungus show a symbiotic, nonpathogenic, and permanent association known as mycorrhiza in both natural and cultivated environments. This is an ancient symbiotic association found in plants and evolved by primitive plants during the colonization of land (Rodrıguez-Echeverrıa et al. 2007). The carbohydrates exchanged by plants for mineral nutrients such as phosphorus, nitrogen, potassium, calcium, and zinc are repossessed by the mycelia of fungi from enormous soil volumes in the symbiotic relationship (Korhonen et al. 2015). The mycorrhizal fungi are involved in other various processes such as plant protection against abiotic stress (Rapparini and Peñuelas 2014). The essential nutrients are available to the plants by the breakdoown of complex organic molecules, which synthesized the plant growth hormones such as auxins, citokinins, and gibberellins (Pieterse et al. 2009). On the basis of morphology and physiology, the mycorrhizal association is classified into three main groups. (1) The fungal mycelia surround the root and penetrate the intercellular spaces, known as ectomycorrhizae. (2) The mycelium does not coat the root; however, there is contact among the fungi and the root through constructions inside the root cells that are specialized for nutrient exchange and storage, known as endomycorrhizae (Taylor and Peterson 2005). (3) Both ecto- and endomycorrhizae are intermediate and include the ectendo-, arbutoid, monotropoid, and orchid mycorrhizae. The mycorrhizal associations most widespread by far are the ectomycorrhizae and the arbuscular mycorrhizae (Rodrıguez-Echeverrıa et al. 2007). Seed plants belonging to the families Betulaceae, Fagaceae, Pinaceae, Rosaceae, Myrtaceae, Mimosaceae, and Salicaceae show ectomycorrhizal association. Although there are more ectomycorrhizal plant species than endomycorrhizal plants, the dominant species of boreal, temperate, and many subtropical forests involve ecologically significant associations (Brundrett 2002). In this symbiosis the fungi involved are almost exclusively basidiomycetes and ascomycetes. Both hypogeous and epigeous genera, such as *Amanita*, *Boletus*, *Leccinum*, *Suillus*, *Hebeloma*, *Gomphidius*, *Paxillus*, *Clitopilus*, *Lactarius*, *Russula*, *Laccaria*, *Thelephora*, *Rhizopogon*, *Pisolithus*, and *Scleroderma*, are common genera of basidiomycetous fungi (Read et al. 2000).

The arbuscular mycorrhizae are ubiquitous, occurring over a broad ecological range. Almost all the natural and cultivated plant species have arbuscular mycorrhizae and are ubiquitous (Öpik et al. 2010). Also, all the angiospermic families form the associations of endomycorrhizae, with some exceptions. Some gymnospermic plant species of *Taxus* and *Sequoia* show the infection. The bryophytes and pteridophytes are also infected by these fungi, phylogenetically. The phylum Glomeromycota shows obligate symbionts that talso form these associations (arbuscular mycorrhizal fungi, AMF) (Redecker et al. 2013). In this association little specificity has traditionally been recognized, but recent observations have revealed more genetic and functional diversity than was estimated formerly (Romero et al. 2012). Ecosystem productivity and plant diversity are increased by the presence of AMF. The high functional diversity of AMF and the specificity are explained by this and the consequence of the interaction with various plant species (Bever et al. 2001). A wider range of plant species benefited by a rich AMF community is more competent at exploiting soil resources (Pérez-Jaramillo et al. 2016). For the positive correlation between AMF and plant diversity, an alternative explanation comes from the observation that plant growth has a detrimental effect by AMF. At the site, the plant diversity increased by a richer fungal community because no plant has a greater advantage with all AMF (McCann 2000). Plant diversity is increased in the absence of mycorrhizal fungi in some circumstances. The highly mycotrophic species dominate plant communities in this case or by ectomycorrhizal species. Removal of the mycorrhizal fungi leads to a decrease of the dominant species and the subsequent modest issue of the subsidiary species (Van Der Heijden and Horton 2009). An underground net links several plants established by the external mycelium of mycorrhizal fungi. Nutrients loss reduces this fungal network also by the sequestering of nitrogen, phosphorus, and carbon within their biomass (Smith and Smith 2012). The external mycelium moves nutrients according to fungal needs, but there is also a transfer of nutrients between plants through the hyphal network (Smith et al. 2010). In ectomycorrhizae the carbon transfers between plants, but these also occur through arbuscular mycorrhizae (Jeffries et al. 2003). The nutrient flow between plants contrasts with the colonization of mycorrhizal content of soil nutrients and the physiological status of plants (Marschner 2011). So, in the greenhouse studies the obtained results have been very adjustable. The external hyphae of mycorrhizal fungi transfer of nutrient rates were high, having important ecological consequences such as establishment of the growth of new seedlings of mycorrhizal plants that augments the transfer of nutrients (Smith et al. 2010).

6.6.3 Pathogenic Fungi

Fungus inhabitants in the soil can have lethal outcomes on the growth of plants, and historically focus has been on agricultural systems for obvious economic reasons. Ecologists have been on track to explore the diversity of microorganisms and the role of fungal pathogens in the natural ecosystem in the past two decades (Pringle et al. 2009). The ascomycetes group found in soil are fungal pathogens that attack plants. In agricultural systems, various genera of pathogenic ascomycetes have been identified and isolated from natural systems (Boer et al. 2005). Sand dunes studies in coastal areas have focused on the deterioration of innovator plant species. In the Netherlands, *Verticillium* and *Fusarium* species were isolated from declining stands of the dune grass *Ammophila arenaria*, and species of *Fusarium*, *Cladosporium*, *Phoma*, and *Sporothrix* were involved in the degeneration of *Leymus arenarius* in Iceland. Dieback of the endemic Hawaiian tree koa (*Acacia koa*), a keystone species in the upper-elevation forests, caused by the systemic wilt pathogen *Fusarium oxysporum* f. sp. *koae*, is another example (Gilbert 2002). Killing of big trees and opening gaps in the forest by other root rot fungi is part of the dynamic of temperate forests. The basidiomycete *Phellinus weirii* that specifically damages *Pseudotsuga menziesii* in North American temperate forests is a well-studied example (Hansen and Goheen 2000). *Pythium* and *Phytophthora*, two genera of Oomycota, are also fungal-related species. *Pythium* is accountable for seedlings mortality in tropical and temperate forests of natural and agricultural systems. A high mortality of new seedlings was caused in the vicinity of parent trees by the pathogenic *Pythium* spp., which is correlated to parent trees in the rhizospheric regions. The life stage of the plants not only depends on the impact of pathogenic fungi and oomycetes, but also depends on the overall history of pathogens, virulence, and also on specificity (Packer and Clay 2003). The seed decay, seedling diseases, foliage diseases, systemic infections, cankers, wilts, and diebacks, root and butt rots, and floral diseases are classified by the fungal pathogens of non-crop plants. The plant populations affected by the fungal pathogens are assumed to be subsidized by the genetic and species diversity of plants and succession in natural systems (Simard et al. 2015).

6.6.4 Nematodes

The most abundant metazoans are known as nematodes. On the basis of ecological observations, they are usually classified by their feeding habits: they can be bacterial feeders, fungal feeders, omnivores, or plant feeders (Bongers and Ferris 1999). We focus on the plant feeders in this section: to feed on plant roots, one group of nematodes have specialized mouth structures (stylets). Nematodes feeding on the roots of plants are a highly specialized obligate parasite that evolved through close interactions with plants, which explains their high impact on the plant populations that they attack (Rodrıguez-Echeverrıa et al. 2007). The plant-parasitic nematodes belowground are subdivided into four groups: sedentary endoparasites, sedentary semi-endoparasites, migratory endoparasites, and ectoparasites (De Deyn et al. 2004). Sedentary endoparasites, such as *Meloidogyne* spp. and *Heterodera* spp., are completely surrounded and protected by their host's root tissue for most of their life cycle, (Nicol et al. 2011). To cultivate permanent and highly specialized feeding sites, they interact with the plant root within the root tissues that act as nutrient sinks (Vovlas et al. 2005). *Rotylenchulus* spp. are known as sedentary semi-endoparasites exposed partially in the root tissue for part of their life cycles while the juveniles and young females feed ectoparasitically in the rhizosphere (Khan 2015). In *Pratylenchus* spp., the migratory endoparasites hatch and develop to maturity inside the root tissues of the plant host: causing extensive damage, they migrate within the roots and do not establish a permanent feeding site (Jones et al. 2013). Additive and synergistic interactions are developed by plant-feeding nematodes with pathogenic fungi and bacteria, and some, such as *Xiphinema* and *Longidorus*, are vectors of plant viruses. The changes caused by nematodes promote the nutrient influx of soil, and the microbial biomass of soil increases and constructs the damaged root growth of neighboring plants (Jones et al. 2016).

6.7 Conclusions

The various studies discussed in this chapter indicate that the structure of microbial communities of the soil certainly does have an effect on the suppression of phytopathogens. Niches can be created by microbes for selected plant species and niche space limited for others, depending on the properties of pathogens, symbionts (mycorrhizal fungi), and accumulated nutrients such as N-fixation and weathering of rock phosphate microbially, with the successful establishments of C- and N-fixing microbes such as Cyanobacteria and the concurrent weathering of parent material by organic acids. In the same way, we expect that high variability in the distribution of microbes that are known symbionts with species of plants, such as mycorrhizal fungi, will strongly influence which plants can invade particular sites. Conclusively, plant communities move into sparsely vegetated regions and alter the functioning of these ecosystems. The microbial community is limited by carbon in plant-free areas with numerous groups such as zoosporic fungi particularly linked with increased amine-containing compounds and nitrification. The barren soil is colonized by the plants, and by competitive exclusion of algae we anticipate the plants to decrease the plentitude of zoosporic fungi. The available nitrate is mostly taken up by plants; therefore, the plants should decrease the export of nitrate from the watershed. Thus, the rhizospheric regions of plants provide better interactions for crop productivity.

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