Microbial Based Land Restoration Handbook

Plant-microbe interaction is a powerful and promising link to mitigate the various kinds of stresses like drought, salinity, heavy metals, and pathogenic effects. It is more beneficial for crop improvement and sustainable approaches for reclamation of problematic soils. Taking a multidisciplinary approach, this book explores the recent uses of plant-microbe interactions in ecological and agricultural revitalization beyond normal agriculture practices and offers practical and applied solutions for the restoration of degraded land to fulfill human needs with food, fodder, fuel, and fiber. It provides a single comprehensive platform for soil scientists, agriculture specialists, ecologists, and those in related disciplines.

Features

- Presents cutting-edge microbial biotechnology as a tool for restoring degraded lands
- Explores the aspects of sustainable development of degraded lands using microbe inspired land remediation
- Highlights sustainable food production intensification in nutrient poor lands through the innovative use of microbial inoculants
- Explains the remediation of polluted land for regaining biodiversity and achieving United Nations Sustainable Development Goals
- Includes many real-life applications from South Asia offering solutions to today's agricultural problems

This book will be of interest to professionals, researchers, and students in environmental, soil, and agricultural sciences, as well as stakeholders, policy makers, and practitioners with an interest in this field.

Microbial Based Land Restoration Handbook VOLUME 1

Plant-Microbial Interaction and Soil Remediation

Edited by
Umesh Pankaj and Vimal Chandra Pandey



CRC Press is an imprint of the Taylor & Francis Group, an **informa** business

First edition published 2023 by CRC Press 6000 Broken Sound Parkway NW, Suite 300, Boca Raton, FL 33487-2742

and by CRC Press 4 Park Square, Milton Park, Abingdon, Oxon, OX14 4RN

CRC Press is an imprint of Taylor & Francis Group, LLC

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ISBN: 9780367702267 (hbk) ISBN: 9780367705862 (pbk) ISBN: 9781003147091 (ebk)

DOI: 10.1201/9781003147091

Typeset in Times

by KnowledgeWorks Global Ltd.

Dedication

This book is dedicated to our beloved mothers.

—Umesh Pankaj and Vimal Chandra Pandey

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13.1 INTRODUCTION

Organic crop production concerns the use of natural materials for plant nutrition in association with limited eco-friendly pesticides, along with ecological engineering concepts. Use of inorganic nutrient sources and/or pesticides, even though they have contributed to food production, established significant adverse effects on soil fertility, as well as macro- and microfauna biodiversity. The issue has assumed center stage since it has been established that the use of inorganic chemical nutrients has decelerated the soil microbial growth vigor (Wang et al. 2018), led to a reduction in composition (Fierer et al. 2012), impacted the diversity of soil microbial population, particularly the bacterial communities (Li et al. 2014; Huang et al. 2019), and could weaken the plant-microbe linkages since carbon from plant biomass is sparsely available to microbes (Huang et al. 2019). Relative abundance of Protecbacteria and Actinobacteria was positively correlated with the chemical N application rate, while a reverse in Chloroflexi in sesame (Wang et al. 2018) and Acidobacteria (Ramirez et al. 2012) has been noticed. Hence, the typical role of microbes is considered to be an acceptable solution to plant nutrition, and microbial biocontrol approaches have been

DOI: 10.1201/9781003147091-13 **273**

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recognized for pest and disease management globally. Soil microbiota, which primarily involves beneficial bacteria and fungi, has diverse modes of action. Culturable microbes isolated and cultured from this source are reported to contain little or no toxic compounds to non-target species as well as human beings; albeit the successful use depends on sound awareness of the physiological reaction of plants to the bioagents. The plant-microbe generally establish an intimate, dynamic relationship that allows them to coexist (Nihorimbere et al. 2011) through synergistic effect (Mendes et al. 2011) to boost plant health. To further understand the processes, an understanding of the Tritrophic relationship between the soil, plant and the microbes is required.

In essence, soil microbes have a central role to play in controlling soil health and preserving plant quality. The techniques that manipulate soil microbiota are required to make the conducive soil into a suppressive one. This can also be accomplished by supplementing exogenous microbiota provided by selective biocontrol agents, organic amendments, for example, compost. Restoration of soil fertility and promotion of soil suppressiveness have been reported as a result of organic manure applications. Furthermore, integration of organic amendments and biocontrol agents effectively manage several soilborne pathogens. Research conducted elsewhere in the world has indicated that rhizosphere inhabiting microorganisms are a potential and effective management tactic to manage pests and diseases (Kerry 2000), besides serving as a supply of plant nutrients. This chapter explores the microbial biodiversity of oilseed crops, their mechanism of nutrient availability and abiotic and biotic stress mitigation in oilseed crops, and the tritrophic interactions between soil, plant and microbes.

13.2 MICROBIAL DIVERSITY IN OILSEED CROP SOIL ECOLOGY

The soil ecosystem around the plant root system is regarded as one of the most active interfaces on earth (Berendsen et al. 2012), where nutrient related interactions takes place between plants, soil and microbes, particularly the bacterial community in the rhizosphere (Jiménez et al. 2020). Depending on the terrestrial microhabitat of the organisms, their behavior and interaction with other organisms varies. Among the different microbes, rhizobacteria and mycorrhizal fungi are the most influential class in the rhizosphere, reported to take part in soil aggregation at various levels (Rillig and Mummey 2006). Diversity of microbiomes has been well documented in oilseed based production systems. Groundnut and soybean, two important leguminous oilseed crops inherently associated with bacterial strains through nodule-bacteria symbiosis to fix atmospheric nitrogen. Chloroflexi, Acidobacteria, Actinobacteria, and Proteobacteria (Levy et al. 2018) are the common phylae associated with oilseed crops. Among them, Acidobacteria is the most abundant phylae found in the terrestrial ecosystem (Barns et al. 1999). A wide variety of bacterial species associated with soybean rhizosphere is enriched with bacterial species through the nodule-bacteria association (Ziegler et al. 2013), which produces siderphores for aiding phosphate solubilization and nitrogen fixation. Other than Bradyrhhizobium, rhizosphere fungal communities with highest abundance of Ascomycota and Basidiomycota were noticed (Sugiyama, 2019). A few specific microbes found in groundnut rhizosphere are Alcaligenes faecalis, Agrobacterium tumefeciens, Azotobacter chrocooccum, Aerobacter aerogenes, Bacillus subtilis, B. cereus, Citrobacter freundii, Clostridium

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perfringens, Enterobacter aerogenes, Flavobacterium lutescens, Klebsiella pneumoniae, Micrococcus varians, M. luteus, Proteus vulgaris, Pseudomonas fluorescens, P. aeruginosa, Streptococcus faecalis, S. pyogenes, Rhizobium japonicum and Serratia marcescens in a sandy loam soil (Babadoko and Pacy 2011).

Irrespective of the nutrient source, the population of Proteobacteria was multiplied linearly with plant-derived carbon substrates (Philippot et al. 2013), needing further exploration (Wang et al. 2018) in sesame soils. A little over 189 plant growth promoting endophytic bacteria have been reported in Sunflower (leaves, stems, flowers and roots) in its short span of a life cycle (Bashir et al. 2020) of one-fourth of a year. Bacterial strains belonging to Klebsiella, Enterobacter, Novosphingobium, Asticcacaulis, Grimontella, Microbacterium, Pantoea, Chryseobacterium, Herbaspirillum, Variovorax, Moraxella, Mitsuaria, Shinella, Sphingobium, Serratia and Xanthomonas (Ambrosini et al. 2012) as well as Enterobacter and Burkholderia were noticed in sunflower. Recently, phosphorus mobilizer Alcaligenes faecalis has also been isolated by Shahid et al. (2012) from the roots of sunflower. It is of particular interest to note that microbiomes associated with soybean (Xu et al. 2009) and canola (Farina et al. 2012) remained dynamic at various growth stages of the plant, possibly due to nutritional balances (Chaparro et al. 2013). A high abundance of Proteobacteria, Actinobacteria and Bacteroidetes were noticed in Canola (Cordero et al. 2020). Bacillusbrevis, B. amyloliquefaciens, B. megaterium, Erwinia amylovora, P. fluorescens, P. chlororaphis, P. putida, P. marginalis, P. syringae, Micrococcus luteus, Comamonas acidovorans (Graner et al. 2003), Agrobacterium, Burkholderia, Enterobacter (Dunfield and Germida, 2003), Serratia plymuthica and S. proteamaculans (Abuamsha et al. 2011) have been reported in oilseed rape. For example, canola harbored 20% more microbes at the rosette stage over the normal population and decreased as the plant approach senescence stage. Analysis of canola microbiome revealed the abundance of *Enterobacter*, Burkholderia, Agrobacterium and Pseudomonas genera (Farina et al. 2012), with the majority belonging to the *Proteobacteria* phylum.

Soybean, accommodated more bacterial communities during the seedling stage than maturity stage with abundance of the phyla *Actinobacteria*, *Acidobacteria*, *Proteobacteria* (Wang et al. 2020) *Bacteroidetes*, *Nitrospirae*, *Firmicutes* and *Verrucomicrobia* (Xu et al. 2009). *Acidobacteria* plays a pivotal role in carbon cycling through degradation of plant parts, including cellulose and lignin. Notwithstanding this fact, their relationship in the rhizosphere is yet to be explored (Ward et al. 2009). *Proteobacteria* and *Actinobacteria* genera have been demonstrated to exhibit traits associated with the plant disease suppression (Mendes et al. 2011), while *Bacteroidetes* have a significant role in nitrogen cycling by denitrification (Chaparro et al. 2012).

13.3 PLANT-SOIL-MICROBE: TRITROPHIC INTERACTION

13.3.1 Soil-Microbe Interactions

Soil is a warehouse of microbes to the tune of 1×10^4 to 5×10^5 , can be detected per gram of soil, the diversity of which varies with soil texture and nutrient composition (Schloss and Handelsman 2006). The majority of the complex rhizosphere microbiome

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food webs are reliant on the plant released nutrients (Mendes et al. 2013). Soil pH, nutrient content and temperature do play a key role in the soil microbial composition and population. It has also been reported that soil deficit in micronutrients render the plants more susceptible to the pathogens infection. For example, lowering the concentration of secondary (Ca and Mg) and micro nutrients (Na and Fe) and increasing the concentration of K, Cu and Zn in the soil was found to minimize the root rot incidence (*Macrophomina phaseolina*) in sesame (Narayanaswamy and Gokulakumar 2010). Manganese is one of the key elements that make the plants immune to the pathogens through inhibition of the induction of aminopeptidase, an enzyme essential for fungal growth (Dordas 2008). Soil deficit in manganese (Mn) decrease the metabolism of nitrogen and affects photosynthetic rate of the plants. This can be corrected by the addition of *B. subtilis* to the soil that reduce Mn⁴⁺ to Mn²⁺, which can easily be taken up by the plants. When entered into the plant system, the reduced form of Mn strengthens the plant defense mechanism (Hoagland and Arnon 1938).

The beneficial effects of arbuscular mycorrhizal fungi (Gianinazzi et al. 2010) may influence CO₂ fixation by plants, through an increase in the "sink effect" and supply of photo-assimilates to the roots (Begum et al. 2019). Soilborne fungi deposits metabolites into the soil and affects the beneficial microbes' density. Addition of micronutrients to the soil eliminates this issue by suppressing the effect of pathogenic species in the soil. The investigation of Duffy and Defago (1997) confirmed that whenever the external supplementation limited the soil micronutrient zinc, it resulted in a drastic reduction in the composition of fusaric acid produced by *Fusarium oxysporum* f.sp. *radices-lycopersici* and enhanced the antibiotic production of *P. fluorescens* CHAo.

Soil salinity is another factor limiting the oilseed productivity that can be managed through the application of salt tolerant PGPR (Rodriguez and Redman 2008). Under salinity, due to the elevated level of Na⁺, growth of the plant and uptake of K will be affected (Islam et al. 2015). Application of salt tolerant PGPR protects the plants from harmful effects of excessive concentration of Na⁺ by binding Na⁺ in the root zone through the production of exopolysaccharides and biofilms (Ourashi and Sabri 2012). Application of PGPR under salt stress conditions is reported to improve the availability of N, P, K, Zn, Fe, Cu and Mn, macro- and micronutrients. The key appliance of disease suppression by the microbes, antibiosis and competition could not be easily transferred from one soil unit to another, whereas the unique clampdown effect triggered by parasitism and predation is easily transferable between soils, as it involves only a few microbial taxonomic classes. Thus, soil properties play a significant role in the suppression of soilborne disease causing microbes, either directly or indirectly, due to the close association of several factors. Knowledge of soil factors is very important for the adaption of biocontrol treatments in various soil environments. It will also provide a basis for the inclusion of biocontrol agents with the best agronomic practices to exploit and manipulate the soil microbiota for improvised disease control.

13.3.2 Mechanisms

While contact between microbes and plants occur at every phase of plant growth and development by signaling molecules, when soil is also taken into account,

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biochemical, physiological and molecular processes also come into the picture. In principle, plants, typically transfer about 20 to 40% of phytosynthetically fixed carbon to their roots in order to sustain root growth. Biochemically, plants produce an array of compounds with different molecular weights, as released as root exudates, which are used as cues for attraction of soil microbes (Haichar et al. 2014). Thus, the root system plays a crucial role in interacting with the microbe-soil complex, functions as a chemical factory and mediates this interaction. In return, these microbes interact with the plant in various ways, as the plant released volatile compounds are made up of CO₂, alcohol and aldehydes (Dudareva et al. 2004). To access nitrogen from the soil, plants are reliant on soil microbes, which possess the metabolic routes to depolymerize and convert the organic forms of N (Bonkowski 2004; Richardson et al. 2009) under organically managed conditions.

The chemical composition of root secretions and its type can alter the microbial diversity of the soil and may prevent the population spurt of harmful microbes; hence, the importance of root and microbe secretion is increasingly recognized (De-la-Peña and Loyola-Vargas 2014). The plant roots may also secrete strigolactones, a terpenoid and flavonoids (Bais et al. 2006; Venturi and Fuqua 2013; Massalha et al. 2017), besides carbohydrates, organic acids, vitamins and are reported to attract and support the beneficial bacteria development such as Enterobacter cloacae in the spermosphere and rhizosphere for their carbon requirement (Madhaiyan et al. 2010). As a complementary interaction, the microbes release volatile phytohormones promoting plant growth and bestow immunity to the plants. Rhizodeposits produced account from 5 to 30% of the total plant fixed C (Bekku et al. 1997; Hutsch et al. 2002; Dennis et al. 2010) into their direct surroundings; spermosphere, phyllosphere, rhizosphere and mycorrhizosphere (Frey-Klett et al. 2007; Raaijmakers et al. 2009; Vorholt 2012) are found to be the main sources of organic carbon that attract microbes toward them (Whipps 1990). Plants identify those compounds released by the microbes and change their growth and defense responses accordingly (Bais et al. 2006).

The compounds released by the plants may either be low molecular weight compounds (sugars and simple polysaccharides such as fructose, glucose, maltose, mannose, etc., amino acids such as arginine, aspartic, cysteine and glutamine; organic acids viz., acetic acid, ascorbic, benzoic and malic acids and phenolic compounds) or high molecular weight compounds (mucilage and proteins), which serve as signaling molecules to attract microbes since microbes use these compounds as carbon source for their nutrition (Schulz and Dickschat 2007). ATP-binding cassette (ABC) transporters have a significant role to play in the development of exudate compounds (Badri et al. 2008), which are primarily released through diffusion, vesicle transportation and ion exchange (Neuman and Romheld 2007) from the plant roots. It is an interesting phenomenon that when a pathogen infests a plant, it damages root cells and allows the mucilage to escape, which raises the amount of carbon in the rhizosphere, and attracts the beneficial microbes (Campbell and Greaves 1990) toward the roots. Any change in the composition of root exudates can, therefore, alter the diversity of soil microbial consortia. Chemotaxis is yet another process through which the roots release carbohydrates and amino acids to attract the beneficial microbes (Somers et al. 2004).

Plants physiologically change their rhizosphere under unfavorable conditions to allow the microbes to colonize the root zone. Under waterlogged conditions, soil could not hold oxygen within its particles. Physiological alteration of the plants during such adverse conditions contributes oxygen to the rhizosphere, which are otherwise utilized by the rhizosphere microbes. Under these oxygen rich environments, iron loving bacteria uses the excess free oxygen to oxidize the soluble mineral FeS, and Fe plaque gets precipitated on the root surfaces as oxidized coatings (Uren 2007). Due to the accumulation of iron on the surface of rhizosphere, plants can easily get Fe out of the soil. The other physiological adaption includes acidification of the rhizosphere, which is possible through the reduction of pH a variety of ways, for example, reduction of insoluble manganese oxide by the roots and the production of organic acids (Figure 13.1). These metabolites serve as signaling molecules that help the colonization of microbes by the rhizosphere (Berg and Smalla 2009). Microbes also use quorum-sensing mechanisms to change their metabolism. Plants secrete a number of chemicals that mimic the quorum signals provided by the bacteria that lead to the alteration of bacterial activity in the rhizosphere (Bauer and Mathesius 2004). Since rhizosphere microbes viz., Pseudomonas, Bacillus, Paenibacillus, actinomycetes and arbuscular mycorrhizal fungi and (AMF) enhance nutrient absorption (Cummings, 2009), as well as resistance to biotic (De Vleesschauwer and Hofte 2009) and abiotic stresses (Zhang et al. 2008; Berendsen et al. 2012; Selvakumar et al. 2012) termed rhizosphere soil microbiomes and the associated microbial community as the second genome of the plant.

Production of the iron chelating compound for e.g. siderophores, commonly produced by fungi as well as bacteria, is pronounced in fluorescent pseudomonads known for the suppression of soilborne pathogenic microbes. Uptake of ferric ion

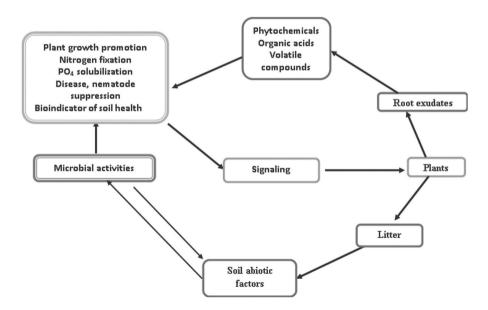


FIGURE 13.1 Role of soil microorganism in plant growth and molecular signaling.

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(Fe³⁺) from the soil into their cells renders the iron inaccessible to the pathogens, which creates a competition (Kloepper et al. 1999) between *Pseudomonas* and pathogens for nutrients. The 3-hydroxy-2-butanone, an elicitor compound production by the *Bacillus* spp. provided a persuasive effect on the infestation of the pathogens (Rudrappa et al. 2008). Another significant plant-soil-microbe interaction is through fixation of atmospheric nitrogen (von der Weid et al. 2002) and solubilization of phosphorus (Deepa et al. 2010).

The essential components of soil nitrogen cycle are mineralization and immobilization of nitrogen by soil microbes. Microbial enzymes breakdown organic nitrogenous molecules to produce ammonia (NH₂), which increases the quantity of plant-available nitrogen in soils. A proportion of the nitrogen in the transformed organic material is utilized by microbial tissue, while the rest is liberated (mineralized) as inorganic nitrogen. Some of the genus of nitrogen fixing bacteria includes Alcaligenes, Beijerinckia, Campylobacter, Derxia, (Rennie 1980), Azospirillium, (Li and Castellano 1987), Klebsiella, Pantoae, Bacillus, Azotobacter (Kennedy et al. 1997), Pseudomonas, and Burkholderia. In general, summer recorded the largest population of ammonifying bacteria in soil under diverse crops, while winter reported the lowest. Insoluble IP, such as Ca₃(PO₄)₂, AlPO₄, and FePO₄, as well as insoluble/soluble organic phosphorus (OP), such as phytate, which accounts for 80% of soil OP, require phosphorus-solubilizing microorganisms (PSM) to convert into orthophosphate, which may be taken by plants and bacteria. The majority of P in soils exists in inorganic insoluble form (Ca₃(PO₄)₂) and organic insoluble/soluble form (phytate and nucleic acid) and, hence, only a small amount can be directly digested by plants (Neal et al., 2017). To solubilize the insoluble inorganic phosphates as well as insoluble/soluble organic phosphates, phosphorus-solubilizing microorganisms (PSM) are essential, which convert insoluble form into orthophosphate, which may be taken by the plants. Fertilizer use degrades soil quality and decreases phosphorus availability (Liu et al. 2018). Application of phosphorus solubilizing microorganisms with multiple P source using abilities gives a new strategy to improving soil quality in order to reach the goal of sustainable agriculture.

PGPR plays a crucial mechanism of reducing the quantum of ethylene in the plants during stress condition since its production (Glick et al. 2007) accelerates due to the accumulation of 1-aminocyclopropane-1-carboxylic acid (ACC), a precursor in the biosynthetic pathway of ethylene (Zapata et al. 2017). This interrupts normal functioning of the plant through impairment in the root growth (Figure 13.1). When PGPR are integrated, they release ACC deaminase and disintegrate and α -ketobutyrate (Singh et al. 2015), thus reducing ethylene concentration in the root zone and root growth is not compromised (Glick et al. 2007). Furthermore, in the plant roots, synthesis of indole acetic acid, activates the enzyme ACC synthase to transform S-adenosylmethionine to ACC (Gravel et al. 2007), which is subsequently absorbed by PGPR through root exudation and ultimately disintegrates through bacterial ACC deaminase, thus preventing the plant from suffering the negative effects of ethylene (Yaish et al. 2015). Yang et al. (2008) were of the optimistic view that PGPR usage might reduce the external application of fertilizers.

A wide range of microorganisms use the mechanism of competition toward the ecological niches and food through which they contribute to the reduction of Microbial Based Land Restoration Handbook, Volume 1

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pathogen infestation. Compounds released by root exudates in response to the chemical signals from soil microbes are a function of soil type (Rovira 1969), biotic, abiotic components (Tang et al. 1995) and plant age (De-la-Pena et al. 2010). As they are associated by identifying the compounds secreted by the roots against particular beneficial microbes, it may be possible to culture the beneficial microbes on their own in the roots that provide protection from deleterious species.

13.4 SOIL-PLANT-MICROBE: POSSIBLE INTERVENTIONS

13.4.1 Management Interventions

In developing a successful organic farming protocol, development of a complex microbiome network in a phylogenetic context is the key for a high degree of negative correlation between the biocontrol microbes and disease causing organisms. Utilization of PGPR, which could be a major component of integrated nutrient management program (Yang et al. 2008), has been articulated in the recent past. Endophytic asymbiotic diazotrophic bacteria reported to fix atmospheric nitrogen in canola (Puri et al. 2016) could well be integrated in the organic package for nitrogen supplementation. Disease suppression is a significant phenomenon of healthy soil induced by soil microbes through the combined antagonistic mechanisms of the microbes. In healthy soil, soil microbiota interact with soil organic matter to achieve synergistic results in disease suppression and strengthening the soil structure (Bronick and Lal 2005) through increased microbial activity (Bulluck et al. 2002). The presence of various microbial biomes in the soil provide basal protection against a wide range of biotic stresses and hence become an essential component in the determination of soil health (Kibblewhite et al. 2008). Supplementation of selected beneficial microbiota, along with organic substrates for their proliferation increase suppression against soilborne pathogens (Puglisi et al. 2009) with a rider that efficacy vary, depending on the soil pathogen density (Ruano-Rosa and Mercado-Blanco 2015). In contrast, organic amendments could improve disease severity (Bonanomi et al. 2007) under rare circumstances. Synergistic interaction of microbes is a natural phenomenon seen in organic soil through which many soilborne pathogen are suppressed (Wan et al. 2017).

Compost is typically rich in nutrients with bountiful microbes possibly triggering the process of resistance against various soilborne pathogens. Few notable references include resistance to *F. oxysporum* f.sp. *melonis* in vegetable by sewage sludge compost (Cotxarrera et al. 2002) and *V. dahliae* of cotton by olive mill compost (Aviles and Borrero 2017) through enhanced microbial activity (Berendsen et al. 2012). These soils are typically colonized by a wide group of microorganisms from which several strains have been documented to induce resistance against abiotic stresses (Melero-Vara et al. 2011). Efficiency of beneficial microbes in the soil is a function of physicochemical properties of organic matter such as pH, electrical conductivity, presence of macro and micronutrients content and the pathogen load in the soil (Hadar and Papadopoulou 2012). Use efficiency of cheap sources of P, namely rock phosphates, was improved along with organic amendments and P solubilizers viz., *Aspergillus awamorii*, *P. striata and B. polymyxa*in meeting P nutrition of

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soybean and mustard crops (Qureshi and Narayanasamay 1999 and Qureshi and Narayanasamy 2005). Despite conflicting information, integrated management strategies with the combined use of organic amendments, biocontrol agents and biofertilizers will certainly provide control of various soilborne pathogens (Cretoiu et al. 2013; Zhang et al. 2014). Pre-fumigation of soil combined with the incorporation of organic amendments and/or bio fertilizers induce shifts in the soil microbiota population, which play a crucial role in the control of soilborne pathogens (Deng et al. 2019).

Hence, pre fumigation with composts, biochar and undecomposed plant residues followed by the addition of plant residues, either alone or with organic amendments or biocontrol agents (Himmelstein et al. 2014; Torres et al. 2015), increases disease suppressiveness, thereby suggesting possible recovery in the fertility of the soil. Evidence shows that soil pre-fumigation with ammonium bicarbonate, along with compost, impaired Ralstonia solanacearum, through alteration of the beneficial bacterial and fungal population in the soil and spurt in new beneficial taxa (Antoniou et al. 2017). Addition of compost added macro- and micronutrients to the soil (Evanylo et al. 2008) also improved organic carbon content in the soil (Hemmat et al. 2010), its structure (Celik et al. 2004) and water-holding capacity (Caravaca et al. 2002), thereby raising the crop productivity (Zaccardelli et al. 2013) through containment of the soilborne pathogens (De Corato 2020). Compost may enhance soil microbiota (Zhen et al. 2014), decrease it (Martinez Blanco et al. 2013) or leave it unaffected (Nair and Ngouajio 2012). Addition of green compost, either agro or agro industries wastes, accounted for a greater diversity of microorganism functioning against Verticillium, Rhizoctonia, Pythium and Phytophthora. Composted animal manure has been reported to suppress Fusarium wilt, as it contains Trichoderma, Aspergillus, Penicillium, Streptomyces, Pseudomonas and Bacillus (Xiong et al. 2017). However, to be a successful biocontrol agent, its stability under field conditions is essential for evaluating its efficacy (Sommermann et al. 2018). However, it is postulated that long term supplementation of plant residues combined with biocontrol agents could manipulate soil microbiota (Yang et al. 2019)

Incorporation of organic amendments certainly modifies the soil microbiota community (De Corato 2020). Adding compost helps the growth of abundant soil microbiota populations. Amplicon sequence of compost derived microorganisms showed a wide abundance and diversity of bacterial and fungal species (De Corato et al. 2019) in the composted soil. Sustainable production of oilseed to satisfy rising demand is a herculean task. Biotic and abiotic stress exerted on the crop contributes to a greater rise in the crop yield reductions (Selvakumar et al. 2012). Inoculation of oilseed crops with beneficial microbes improves crop production. Among the numerous microorganisms, plant growth promoting rhizobacteria is a versatile community of complex bacterial taxa capable of promoting the supply of plant nutrients, growth and disease suppression (Morrison et al. 2017). Manipulation of soil microbiome in the oilseed ecosystem would support the plant by increasing plant production and decreasing the biotic and abiotic stresses imposed on them. Inoculation of P. fluorescens strain, LBUM677 in Canola (Brassica napus), Soybean (Glycine max) and Corn gromwell (Buglossoides arvensis) was reported to improve oil yield (Cumberford and Hebard 2015), in addition to plant growth promotion effects.

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Generally, oilseed crops grown under stressful conditions suffer iron deficiency. Inoculation of PGPR allows the plants to extract more micronutrient element iron from the soil environment in order to reduce the harmful effects of stress, Recently, inoculation of microbes in the rhizosphere has been suggested to minimize heavy metals and salt stress by enhancing the antioxidant enzyme (Islam et al. 2015). Paenibacillus polymyxa P2b-2R, an endophytic diazotroph isolated from lodge pole pine tree tested on canola increased biomass by 27% 2 months after bacterial inoculation which could fix around 20% of atmospheric nitrogen (Puri et al. 2016). Inclusion of plant growth promoting microbes in the crop packages helps the plant through the systemic activation of defense mechanisms against pests and pathogens. Application of PGPRs are reported to activate the defense genes such as chitinase, proteinase inhibitors and lipoxygenase to protect the plant from infection (Saravanakumar et al. 2007) in peanut and dual inoculation of sulfur oxidizing bacteria, along with Ochrobactrum intermedium (Paulucci et al. 2015) was also beneficial. Further complementary interaction between S-oxidizing bacteria and rhizobia promoted the oil content of groundnut grown in sulfur deficit soils (Anandham et al. 2007). Antagonistic rhizobacteria must be predominant in rhizosphere soils of sunflower (Rangeshwaran and Prasad 2000) in order to contain Sclerotium rot of sunflower.

The sunflower crop is mainly prone to water and salinity stress besides the accumulation of heavy metals which limit crop productivity (Ali et al. 2013). Sunflower growth is also impaired by the deficiency of nitrogen (Dordas and Sioulas, 2008). Jalilian et al. (2012) observed improved productivity of sunflowers when microbes were inoculated in combination with N fertilizers, in addition to upgrading plant water status (Singh et al. 2015). Inoculation of PGP bacteria strains, *Pseudomonas fluorescens* biotype F and *P. fluorescens* CECT 378T were reported to alleviate salinity-induced stress in sunflowers (Kiani et al. 2016). Similarly, the PGPR strains, *Ralstonia eutropha* (B1) and *Chrysiobacterium humi* (B2) protected the crop from metal toxicity by preventing the crop from the uptake of heavy metals viz., Zn and Cd (Ana et al. 2013).

Inoculation of *B. licheniformis* MML2501, *Bacillus* sp. MML2551 and *P. aeruginosa* MML2212 reduced sunflower necrosis disease (SND), which otherwise reduced sunflower productivity by 90% (Bhat et al. 2002; Lavanya et al. 2005). Wherever salinity is a threat to soybean production impairing crop yield (Rahman et al. 2008), either inoculation of PGPR improved crop growth (Kang et al. 2014) through the regulation of stress hormones or through PGPR interaction with *Rhizobium* spp. (Drogue et al. 2013). The beneficial association of PGPR strains *viz.*, *Streptomyces* (Tokala et al. 2002), *Azotobacter* (Wu et al. 2012), *Bacillus* (Atieno et al. 2012), *Serratia* (Zahir et al. 2016), *Azospirillum* (Aung et al. 2013) has been reported, in addition to *Bradyrhizobium diazoefficiens* USDA110 and *B. japonicum* THA6 (Prakamhang et al. 2015). An improvement in the number of root hairs and nodules and secretions of flavonoids was found when Rhizobia was co-inoculated with PGPR over rhizobia inoculation alone (Ramans et al. 2008). Hence, it has been proposed that inoculation of mixture of suitable strains would be more successful for soybean than the inoculation of single bacterial strains.

When performing artificial inoculation experiments, emphasis should be given to the impact of artificially inoculated microbes on the modification of native microbial

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populations. This knowledge is important firstly, to study the adverse effects of inoculated microbiota on natural soil microbial communities and secondly, to consider the indirect effect of inoculated PGPR strains on the plants. Experimental and technical methodology used to describe the effect of PGPR on soil microbiome is an important consideration to be taken into account when analyzing the findings of such studies. Supplementation of bioagents could mobilize soil nutrients and reduce the need of fertilizer application. Soil microbiota, through the production of secondary metabolite compounds, such as 2,4-DAPG (Raaijmakers et al. 1997), iturin and surfactin (Kinsella et al. 2009), tubercidin, phosphalactomycin, candicidin (Shekhar et al. 2006) and lytic enzymes such as β -1,3-glucanase, chitobiase, hydrolases and chitinase (De La Cruz et al. 1993) could allow a strong binding with the plants toward the suppression of pathogens. As an added benefit, growth hormones, auxin (Da Mota et al. 2008) and cytokinin (Timmusk et al. 1993) are also produced, which impart indirect resistance to the plants against abiotic and biotic stresses.

13.4.2 DETERMINANTS

Shaping of the rhizospheric microbiome is dictated by the plant species and the healthy soil (Berg and Smalla 2009; Bakker et al. 2012) underpins the significance of plant-soil-microbe interactions. Furthermore, edaphic features such as soil nutrients, pH and moisture content may have a major effect in the alteration of rhizosphere microbial population (Bakker et al. 2020). Management strategies that are being adopted to enhance nutrient release and to fight pests and diseases could also improve the composition of the soil microbiome population (Lumini et al. 2011). Agricultural practices that ratify and promote beneficial microbes can contribute to improved yield of the crops over the long term. Crop rotation and intercropping have played a major role in altering soil microbial populations. Long term monoculture of a single crop promotes the abundance of soilborne pathogens and decreases crop yield due to a decline in soil chemical properties and soil microbiota composition. Diverse distribution frequencies and transmission mechanisms of biocontrol agents had a direct effect on the rhizosphere. Conventional agricultural practices, which depend primarily on the use of chemical insecticides and fungicides (Krauss et al. 2011), minimize soil microbiome levels. On the other hand, the practice of organic farming would promote microbial diversity (Sugiyama et al. 2010).

13.5 CONCLUSION AND FUTURE PROSPECTS

Increased demand for the production of organic foods has called for more environmentally sustainable agricultural activities. The existence of a healthy microbiota can be the key to acquiring healthier plants. Recently, several studies have started to illustrate the significance of plant-microbiome interaction and its effect on plant health and productivity. Involvement of microbiota will increase natural soil suppression against soilborne pathogens whenever soil properties deteriorate, rendering a decline in crop yields. A significant group of microorganisms play a vital role in enhancing plant health in oilseed environment. A wide range of microbes found in the soil rhizosphere provides an opportunity for genetic variation and exploitation

of microbes. Both bacterial and fungal microbiomes facilitate the growth and development of various oilseed crops, both directly and indirectly under normal and stressful conditions. Root exudates serve as signaling molecules and play a crucial role in the manipulation of microbes. Further research should be carried out to determine the composition of root exudate that will enable the culture of particular beneficial microbes to produce more productive plants. In addition, the ecological function of soil microbiomes should be further explained in order to obtain a deeper understanding of the microbial population network inhabiting the soil. Agronomic practices appeared to be the best methods for increasing soil suppression by microbiomes. As a result, best agronomic methods to increase soil suppression can be put in place that can transfer wild soil microbiota to beneficial microbial consortia. It can be inferred that by following effective agronomic methods such as the addition of compost, crop rotation, intercropping and soil pre fumigation with eco-friendly molecules, problems in the suppression of soilborne diseases can be resolved through the manipulation of soil microbiomes in healthy agroecosystems. Manipulation of microbes by organic farming has been shown to improve the productivity of oilseed crops and reduce their biotic stress. While plant-microbe interactions are very reliable, the underlying mechanisms still need to be studied to optimize and popularize the use of soil microbial cultures in an effective way. In general, a significant change in microbial community composition is imminent after the addition of an amendment, be it organic or inorganic; hence, suitable mechanisms need to be developed for complementary use of organic and/or microbial fertilization, in addition to chemical fertilization. Probing into the interaction of plants and microbes at a molecular level with the aid of stable isotopes and biochemical markers can enhance the understanding for the identification of chemicals involved in the interaction process. Detection and application of a variety of beneficial microbial strains could also play a central role as biofertilizers and biopesticides, which will reduce the use of fertilizers and agrochemicals in oilseed crops.

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