



# A Deeper Insight into the Symbiotic Mechanism of *Rhizobium* spp. from the Perspective of Secondary Metabolism

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## 14.1 Introduction

Growth of an organism is determined by mineral nutrient availability, and among all the mineral nutrients, nitrogen is the most crucial for plant growth as it is a component of proteins, nucleic acids and other cellular constituents. Atmosphere comprises about  $10^{15}$  tonnes of gaseous nitrogen out of which about  $1.4 \times 10^8$  metric tonnes of nitrogen is fixed biologically all over the globe every year. This accounts for about 90% of the total nitrogen being fixed in terrestrial environment, and the rest 10% is fixed by lightning (Postgate 1982; Zahran 1999). An additional  $1.4 \times 10^8$  metric tonnes of nitrogen being fixed each year by utilization of nitrogenous fertilizers, fossil fuels and planting of legumes (Vitousek et al. 1997; Gage 2004). The prokaryotes are the so far only known source of biological nitrogen fixation being carried out by 87 species in 38 genera of bacteria, 2 genera of archaea and 20 genera of cyanobacteria (Dixon and Wheeler 1986). Nitrogen fixation can be accomplished by both free living (*Clostridium*, *Azotobacter*, *Beijerinckia*, *Rhodospirillum* and *Chromatium*) and symbiotic nitrogen-fixing bacteria (*Rhizobium*, *Bradyrhizobium*, *Mesorhizobium*, *Sinorhizobium*, *Azorhizobium* and *Frankia*). Symbiotic nitrogen fixation in Leguminosae family is associated with class alphaproteobacteria, family *Rhizobiaceae*, whereas filamentous, gram-positive actinomycete, *Frankia*, induces nodules on a variety of woody plants from the family Betulaceae, Casuarinaceae, Rosaceae, Myricaceae, Rhamnaceae, Elaeagnaceae, Coriariaceae and Datisceae (Benson and Clawson 2000).

*Rhizobium* is a genus of gram-negative motile bacteria which has the ability to fix atmospheric nitrogen. *Rhizobium* species forms a symbiotic nitrogen-fixing association with roots of leguminous plants such as soybean, pea and alfalfa. An equivalent term used by other researchers is 'root nodule bacteria' (RNB) (Zakhia

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et al. 2004; Howieson and Brockwell 2005). Soil-inhabiting bacteria, *Rhizobium*, form specific root structure, nodules generally of two types, determinate and indeterminate. Differ mainly in that indeterminate nodules are elongated in shape and have persistent meristem that continuously form new nodule (Handberg and Stougaard 1992).

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## 14.2 Historical Perspective of *Rhizobium*

Beijerinck (1888) was the first to isolate and culture microorganism from root nodules of different legume species and named it as *Bacillus radicola*. Later on, the name *Rhizobium* was proposed by Frank (1889) for nitrogen-fixing bacteria of legumes. The word *Rhizobia* is derived from the Greek word *rhíza*, meaning “root”, and *bios*, meaning “life”. The term *Rhizobium* is usually used as a singular form of rhizobia. Genera other than *Rhizobium* were identified later; this includes *Sinorhizobium* (Chen et al. 1988), *Bradyrhizobium* (Jordan 1982) and *Mesorhizobium* (Jarvis et al. 1997). Nobbe and Hiltner (1896) developed the technology for inoculation of legume with *Rhizobium* spp. and granted US patent for it (Das et al. 2017). Mass production of *Rhizobium* inoculants began in 1895 in the USA, mostly by employing peat-based inoculants (Roughley and Vincent 1967). Besides peat-based formulation used worldwide, vermiculite, mineral soil, bentonite, perlite and coal are used as rhizobial inoculants (Stephans and Rask 2000; Temprano et al. 2002; Das et al. 2017).

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## 14.3 Rhizobial Genome

*Rhizobium* has a large and complex multipartite genome with genome size varying from 5.4 to 9.2 Mb and plasmid number ranges from 0 to 7 (MacLean et al. 2007). The genome organization reflects the adaptive potential and the lifestyle of species (MacLean et al. 2007; González et al. 2006). Comparative genomic studies reveal the evolutionary pattern of rhizobia-legume symbiosis. Outcomes of genome comparisons were quite interesting as it revealed that no gene is common and specific to all rhizobia (Amadou et al. 2008; Laranjo et al. 2014).

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## 14.4 *Rhizobium*: Plant Symbiosis

The bacteria colonize plant cells within root nodules and convert atmospheric nitrogen into ammonia, a process known as nitrogen fixation (O’Gara and Shanmugam 1976). The ammonia is used by the plants as a nitrogen source. In turn the rhizobia are supplied with nutrients (Lodwig and Poole 2003) and are protected inside the nodule structure (van Rhijn and Vanderleyden 1995). However, in ineffective nodules no nitrogen is fixed, yet rhizobia are still supplied with nutrients, and in this case, the rhizobia could be considered parasitic (Denison and Kiers 2004). Other

genera of rhizobium such as *Azorhizobium*, *Mesorhizobium*, *Sinorhizobium* and *Bradyrhizobium* have also got the ability to fix nitrogen. The rhizobium-legume association is unique and specific in that each rhizobial strain has definite host range varying from narrow to exceptionally wide (Perret et al. 2000).

#### 14.4.1 Mechanism of Root Nodule Formation

The process of nodule formation involves a complex series of steps (Vincent 1974; Newcomb 1981a, b). Plants of Leguminosae family usually secrete a variety of organic compounds such as amino acids and flavonoids which are recognized by bacterial NodD protein. Rhizobium is generally chemotactic towards the plant roots due to the secretion of such compounds (Bergman et al. 1988; Caetano-Anolles et al. 1988; Kurrey et al. 2016). Nodulation takes place due to specific and complex interaction between the plant and the *Rhizobium*. The initial attachment usually involves a protein called “rhicadhesin” which is found on the surface of all leguminous plants. Upon binding of these compounds with NodD protein, nodulation genes get activated. *Rhizobium* secretes Nod factors, lipochito-oligosaccharides which get recognized by the leguminous plant, and triggers early step of nodulation (Pawlowski and Bisseling 1997; Spaink 1992). Host specificity of rhizobia is determined by terminal sugar residues of lipochito-oligosaccharides secreted by rhizobia (Denarie and Cullimore 1993; Fisher and Long 1992; Stokkermans and Peters 1994). When the root hair of the plant comes in contact with bacterium, the growing root hairs get curled and form a pocket for the particular rhizobia (Mylona et al. 1995). The bacteria invade the plant by forming a new infection thread. The infection threads progress towards the primordium, and the bacteria are released into the cytoplasm of the host cells, surrounded by a plant-derived peribacteroid membrane (PBM) (Verma and Hong 1996). This separation usually occurs to suppress plant defence responses which are likely to harm the bacteria. The bacteria produce cytokinin which facilitates division of plant cells to form nodules and the nodule formation initiates on the root hairs. Afterwards, the nodule primordium develops into a mature nodule. The bacteria differentiate into their endosymbiotic form, which is usually known as bacteroid. Bacteroids, altogether with the surrounding PBMs, are called symbiosomes (Roth and Stacey 1989; Guan et al. 1995).

Rapid cell division starts in the infected tissue. The area of N<sub>2</sub> fixation is usually pink or red in colour due to the presence of “leghaemoglobin” required for active oxygen transport (Appleby 1984; Kannenberg and Brewin 1989). The formed nodule establishes a direct vascular connection with the host for nutrient uptake. In the process of nodule formation, certain genes called *nod* genes are involved and are known as nodulin genes (van Kammen 1984). The “early nodulin genes” encode products which get expressed before the commence of N<sub>2</sub> fixation and are involved in infection and nodule development. However, the “late nodulin genes” interact with the bacterium and aid in metabolic specialization of the nodule (Nap and Bisseling 1990).

### 14.4.2 The Infection Thread

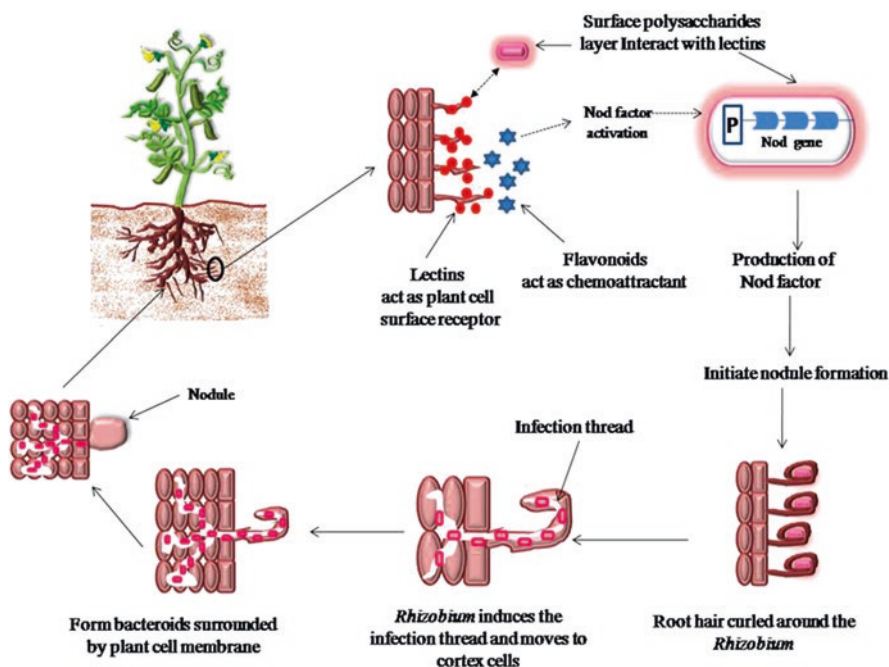
The invasion of root tissues is initiated by intracellular ‘tunnels’ known as infection threads, which initially arise in root hair cells (Callaham and Torrey 1981). In uninfected root hairs, the nucleus is paired to the tip by microtubules which facilitate new wall material to the growing apex (Lloyd et al. 1987; Ridge 1988). The bacterial infection usually removes the nucleus from the tip and facilitates the pathway for incorporation of wall precursors. Initially, the infection thread develops as an invagination of root hair wall, and the nucleus migrates towards the base of the root hair. The new wall material synthesized is thereafter directed to the tip of the invagination to produce an interior growing cylinder of wall material bounded by a membrane, and the bacteria embedded in a matrix (Gage 2004). Infection thread structures develop subsequently in the underlying cortical cell layers and facilitate the bacteria in the infection thread to spread from one cell to adjacent cell (Libbenga and Harkes 1973). During this process of tissue invasion, the wall of the infection thread limits the rhizobia to the extracellular space, thus preventing its contact with the plant plasma membrane (VandenBosch et al. 1989). Cell invasion can only arise by endocytosis from unwalled infection droplets that evolve from infection threads at a particular stage of development.

As cell divisions in the plant root facilitate the formation of body of the nodule, the infection threads start penetrating individual target cells within the nodule. The bacterioids are released into the plant cytoplasm itself, enveloped in plasma membrane of the plant (Robertson et al. 1978). Thereafter, the bacteria and plant cells differentiate and initiate symbiotic nitrogen fixation and metabolite exchange (Sutton et al. 1981; Verma and Long 1983) (Fig. 14.1).

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## 14.5 Rhizobia as Biocontrol Agent and Biofertilizer

*Rhizobium* spp. has boosted legume production worldwide by enhanced nitrogen fixation, plant growth promotion and suppression of soilborne pathogens such as *Rhizoctonia solani*, *Pythium* spp., *Fusarium* spp., and *Macrophomina phaseolina* in both legumes and nonlegumes (Table) (Antoun et al. 1978; Malajczuk et al. 1984; Chakraborty and Purkayastha 1984; Ehteshamul-Haque and Ghaffar 1993; Nadia et al. 2007; Das et al. 2017). Ehteshamul-Haque and Ghaffar (1993) deployed biocontrol potential of *Rhizobium leguminosarum*, *Sinorhizobium meliloti* and *Bradyrhizobium japonicum* by soil drenching and seed coating of sunflower, okra, mung bean and soybean. Antimicrobial activity of *Rhizobium* spp. strains ORN 24 and ORN 83 has been exploited against *Pseudomonas savastanoi*, olive knot disease (Maurad et al. 2009). Buonassisi et al. (1986), inoculated seeds of snap bean with *Rhizobium leguminosarum* bv. *phaseoli* (isolated from nodules of commercial snap bean) to control fusarium foot rot of beans caused by *Fusarium solani* f. sp. *phaseoli*. Inoculation of pea and sugar beet seeds with *R. leguminosarum* bv. *viciae* strain R12 significantly reduced the occurrence of pythium damping-off (Bardin



**Fig. 14.1** Mechanism of nodule formation in rhizobium-legume symbiosis

et al. 2004). Different strains of *Rhizobium* were reported to reduce incidence of root rot of chickpea, *Rhizoctonia solani*, and increased the nitrogen fixation, phosphorus uptake and plant growth (Hemissi et al. 2011). Seed treatment of chickpea with PGPR + *Mesorhizobium ciceri* provided enhanced plant growth (seedling emergence and shoot length) and reduced fusarium wilt of chickpea significantly over their single treatment (Kumari and Khanna 2014). Co-inoculation of common bean with *Rhizobium* and *Pseudomonas* strains was reported to have increased number of nodules and produce higher yield (Sanchez et al. 2014) (Table 14.1).

## 14.6 Mechanism of Biological Control by Rhizobia

The mechanism associated with biological control of phytopathogens by rhizobia consists of antibiotic production, siderophore production, HCN production, production of lytic enzymes, phosphate solubilization, competition and induction of plant defence (Arora et al. 2001; Huang and Erickson 2007). Antagonistic activity against a wide range of pathogens is due to its ability to produce wide range of secondary metabolites such as HCN, siderophore, rhizobitoxin, lytic enzymes, IAA production and phosphate solubilization (Antoun et al. 1978; Presmark et al. 1993; Nautiyal, 1997; Biswas et al. 2000; Deshwal et al. 2003; Pandey and Maheshwari 2007).

**Table 14.1** Biological control potential of *Rhizobium* spp.

S. N.	Producer	Host	Target plant pathogen	Disease manage	References
1	<i>Rhizobium japonicum</i>	<i>Glycine max</i>	<i>Fusarium solani</i>	Root rot	Al-Ani et al. (2012)
			<i>Macrophomina phaseolina</i>	Charcoal rot	
2	<i>Rhizobium</i> sp.	<i>Cicer arietinum</i>	<i>Fusarium oxysporum</i> f. sp. <i>ciceris</i>	Wilt	Arfaoui et al. (2005)
3	<i>Rhizobium meliloti</i>	<i>Arachis hypogaea</i>	<i>Macrophomina phaseolina</i>	Root rot	Arora et al. (2001)
			<i>Pythium</i> sp.	Brown rot of groundnut	Bardin et al. (2004)
			<i>Fusarium solani</i> f. sp. <i>phaseoli</i>	Wilt	Buonassisi et al. (1986)
4	<i>Mesorhizobium loti</i> MP6	<i>Brassica juncea</i>	<i>Sclerotinia sclerotiorum</i>	Sclerotinia rot	Chandra et al. (2007)
			<i>Rhizoctonia solani</i>	Root rot	Dubey and Maheshwari (2011)
			<i>Fusarium oxysporum</i> F. <i>solani</i>	Wilt	
			<i>Fusarium oxysporum</i> f. sp. <i>lentis</i>	Wilt	Essalmani and Lahlou (2002)
5	<i>Rhizobium</i> sp.	<i>Phaseolus vulgaris</i>	<i>Fusarium solani</i> f. sp. <i>phaseoli</i>	Wilt	Estevez de Jensen et al. (2002)
6	<i>Rhizobium</i> sp.	<i>Arachis hypogaea</i>	<i>Sclerotium rolfsii</i>	Stem rot	Ganesan et al. (2007)
7	<i>Rhizobium</i> sp.	<i>Glycine max</i>	<i>Cylindrocladium parasiticum</i>	Red crown rot	Gao et al. (2012)
8	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i>	<i>Pisum sativum</i> <i>Lens culinaris</i>	<i>Pythium</i> spp.	Root rot	Huang and Erickson (2007)
9	<i>Rhizobium</i> sp.	<i>Olea europaea</i>	<i>Pseudomonas savastanoi</i>	Olive knot	Kacem et al. (2009)
10	<i>Sinorhizobium fredii</i> KCC5	<i>Cajanus cajan</i>	<i>Fusarium udum</i>	Wilt	Kumar et al. (2010)
11	<i>Ensifer meliloti</i> , <i>Rhizobium leguminosarum</i>	<i>Trigonella foenum-graecum</i>	<i>Fusarium oxysporum</i>	Wilt	Kumar et al. (2011)
			<i>Phytophthora cinnamomi</i>	Root rot	Malajczuk et al. (1984)
12	<i>Rhizobium</i> sp. NBRI9513	<i>Cicer arietinum</i>	<i>Fusarium</i> spp.	Wilt	Nautiyal (1997)
			<i>Rhizoctonia bataticola</i>	Dry root rot	
			<i>Pythium</i> sp.	Damping-off	

(continued)

**Table 14.1** (continued)

S. N.	Producer	Host	Target plant pathogen	Disease manage	References
13	<i>Rhizobium</i> sp.	<i>Glycine max</i>	<i>Macrophomina phaseolina</i>	Charcoal rot	Omar and Abd-Alla (1998)
14	<i>Bradyrhizobium</i> sp.	<i>Helianthus annuus</i>	<i>Rhizoctonia solani</i>	Collar rot	Siddiqui et al. (2000)
15	<i>Rhizobium</i> sp.		<i>Macrophomina phaseolina</i>	Charcoal rot	Romesh Sagolshemcha et al. (2017)
16	<i>Rhizobium</i> sp.	<i>Vicia faba</i> , <i>Cicer arietinum</i> , <i>Lupinus albus</i>	<i>Fusarium oxysporum</i>	Wilt	Shaban and El-Bramawy (2011)
			<i>Fusarium solani</i> ,		
			<i>Macrophomina phaseolina</i>	Charcoal rot	
			<i>Rhizoctonia solani</i>	Rot	
			<i>Sclerotium rolfsii</i>	Collar rot	
17	<i>Bradyrhizobium japonicum</i>	<i>Solanum lycopersicum</i>	<i>Macrophomina phaseolina</i>	Charcoal rot	Siddiqui and Shaukat (2002)
			<i>Fusarium solani</i>	Wilt	
			<i>Rhizoctonia solani</i>	Damping-off, root rot, stem rot and stem canker	
18	<i>Rhizobium leguminosorum</i>	<i>Cicer arietinum</i>	<i>Fusarium oxysporum</i> f. sp. <i>ciceris</i>	Wilt	Singh et al. (2010)
19	<i>Rhizobium</i> sp. RS12	<i>Cicer arietinum</i>	<i>Macrophomina phaseolina</i>	Dry root rot	Smitha and Singh (2014)

### 14.6.1 Antibiotic Production

Antibiotic production is one of the major mechanisms of biological control of phytopathogens. Several workers have reported different rhizobial strains to produce variety of antibiotics (Ligon et al. 2000; Raaijmakers et al. 2002; Deshwal et al. 2003; Bardin et al. 2004; Chandra et al. 2007; Das et al. 2017). Hirsch (1979) reported that 97 strains of *R. leguminosarum* produces bacteriocins, characterized as small and medium based on their size. *R. leguminosarum* plasmid pRL1J1 carries genes for nodulation and bacteriocin production, encodes for medium bacteriocin (Hirsch et al. 1980). *R. leguminosarum* bv. *trifolii* T24 produces a potent antibiotic, trifolitoxin that promote clover nodulation have been reported by Triplett and Barta (1987). Different strains of *R. leguminosarum* bv. *viciae*, *R. leguminosarum* bv. *trifolii*, *R. meliloti*, *B. japonicum* and *S. meliloti* have been reported to secrete diverse group of antibiotics having potential for inhibition of phytopathogens (Chakraborty



and Purkayastha 1984; Bardin et al. 2004; Deshwal et al. 2003; Hafeez et al. 2005; Chandra et al. 2007; Gopalakrishnan et al. 2015) (Table 14.2).

## 14.6.2 Production of Antimicrobial Secondary Metabolites

### 14.6.2.1 HCN Production

HCN are volatile, secondary metabolite produced during the early stationary phase of rhizobacteria (Rezzonico et al. 2007; Knowles and Bunch 1986). HCN is inhibitor of various metalloenzymes such as cytochrome C oxidases of respiratory electron transport. It disrupts the energy supply to the cell and is highly toxic; even at low concentration, it has deleterious effect on growth and development of aerobic plant pathogens (Corbett 1974; Gehring et al. 1993; Deshwal et al. 2003; Siddiqui et al. 2006; Martínez-Viveros et al. 2010). Beauchamp et al. (1991) and Antoun et al. (1998) have reported that 12.5 and 3% of the total strains of rhizobia screened were HCN producers, respectively. HCN production has also been reported in *Mesorhizobium loti* MP6, retarding the growth and development of *S. sclerotiorum* causing white rot in *Brassica campestris* (Chandra et al. 2007). Six *Rhizobium* spp. strains (an isolate from root nodules of chickpea) has been reported to produce HCN, reducing the incidence of chickpea wilt by *Fusarium oxysporum* f. sp. *ciceris* (Arfaoui et al. 2006).

### 14.6.2.2 Siderophore Production

Iron is one of the key components of metabolic molecules such as ribonucleotide reductase, cytochromes, etc. (Guerinot 1994). Some microbes are equipped with the ability to produce siderophores, an iron-binding compound of low molecular weight (Matzanke 1991; Andrews et al. 2003). Siderophores scavenges iron ( $\text{Fe}^{3+}$ ) from environment under iron stress condition which in turn determines the colonization of bacteria on plant roots leaving pathogens (Crowley and Gries 1994; Siddiqui 2006; Martínez-Viveros et al. 2010). Rhizobia has been endowed with the ability to produce a range of siderophores varying from catechol and hydroxamate type (Modi et al. 1985; Roy et al. 1994; Persmark et al. 1993), rhizobactin type (Smith et al. 1985), citrate type (Guerinot et al. 1990), phenolate type (Patel et al. 1988), vicibactin type (Carson et al. 1992), anthranilic acid (Rioux et al. 1986) to dihydroxamate type (Carson et al. 2000). Arora et al. (2001) reported that *M. phaseolina* causing charcoal rot of groundnut was inhibited by siderophore-producing strains of *Rhizobium meliloti* under in vitro condition. Seed treatment with hydroxamate siderophore producer, *Mesorhizobium loti* MP6, reduced the occurrence of white rot of *Brassica campestris* (Chandra et al. 2007).

### 14.6.3 Lytic Enzyme Production

Chitinases, cellulases,  $\beta$ -1,3-glucanase  $\beta$ -1,4-glucanase,  $\beta$ -1,6-glucanase, proteases, pectinase and amylases are some of the lytic enzymes produced by microorganisms



**Table 14.2** Representative list of secondary metabolites of important *Rhizobium* species (KEGG database accessed on April 25, 2018)

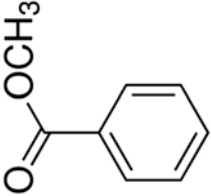
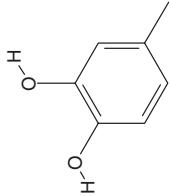
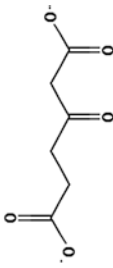
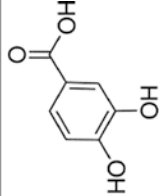
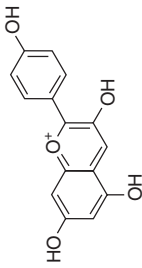
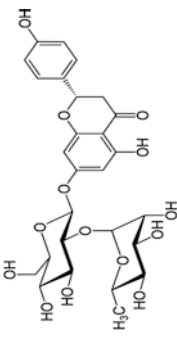
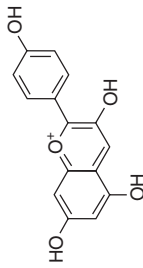
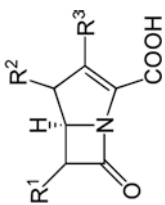
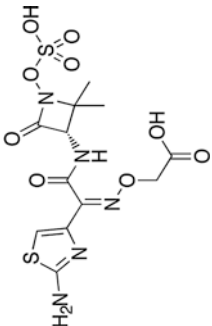
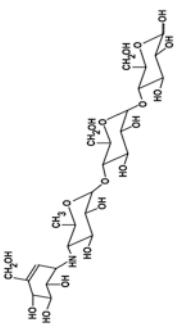
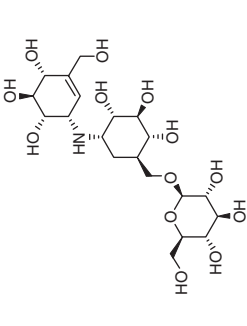
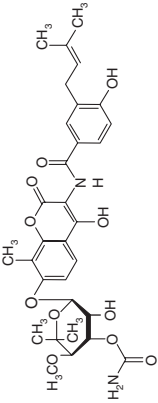
<i>Rhizobium</i> species	Type of secondary metabolite	Biosynthesis pathway	Structural formula
1. <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> 3841	a) Methylbenzoate	Xylene degradation	
	b) Methylcatechol	Benzoate degradation	
	c) 3-Oxoadipate	Catechol ortho cleavage	
	e) 3,4-Dihydroxybenzoate	Terephthalate degradation	

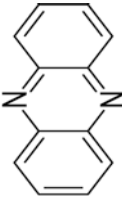
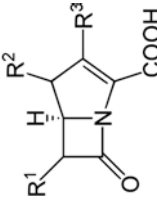
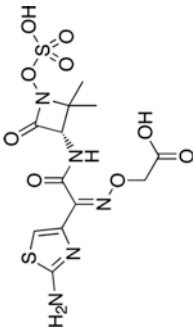
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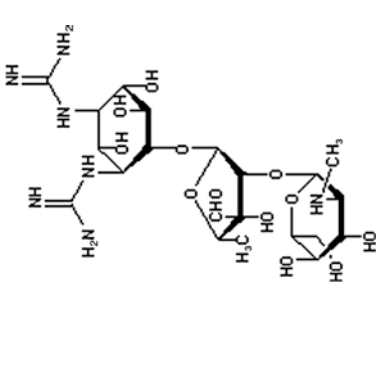
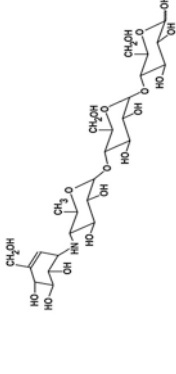
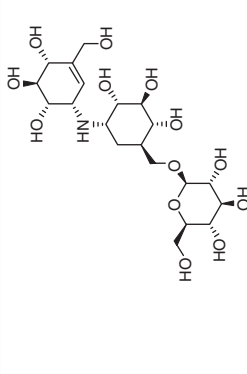
<i>Rhizobium</i> species	Type of secondary metabolite	Biosynthesis pathway	Structural formula
	f) Pelargonidin	Flavonoid biosynthesis	
	g) Naringenin	Flavanone biosynthesis	
	h) Paspaline	Paspaline biosynthesis	
2. <i>Mesorhizobium opportunistum</i>	a) Carbapenem	Carbapenem biosynthesis	

b) Monobactam	Monobactam biosynthesis	 <p>The image shows the chemical structure of Monobactam biosynthesis. It features a central 5-membered beta-lactam ring fused to a 6-membered thiazolidine ring. The thiazolidine ring has a methyl group and a sulfonamide group (-SO<sub>2</sub>NH<sub>2</sub>) attached. The beta-lactam ring is linked to a side chain containing a thiazolidine ring, which is further substituted with a methyl group and a sulfonamide group.</p>
c) Acarbose	Acarbose biosynthesis	 <p>The image shows the chemical structure of Acarbose biosynthesis. It is a complex oligosaccharide consisting of a central pyranose ring linked to a pyridose ring, which is further linked to a thiazolidine ring. The structure is highly branched and contains multiple hydroxyl groups and a methyl group.</p>
d) Validamycin	Validamycin biosynthesis	 <p>The image shows the chemical structure of Validamycin biosynthesis. It is a complex oligosaccharide consisting of a central pyranose ring linked to a pyridose ring, which is further linked to a thiazolidine ring. The structure is highly branched and contains multiple hydroxyl groups and a methyl group.</p>
e) Novobiocin	Novobiocin biosynthesis	 <p>The image shows the chemical structure of Novobiocin biosynthesis. It is a complex oligosaccharide consisting of a central pyranose ring linked to a pyridose ring, which is further linked to a thiazolidine ring. The structure is highly branched and contains multiple hydroxyl groups and a methyl group.</p>

(continued)

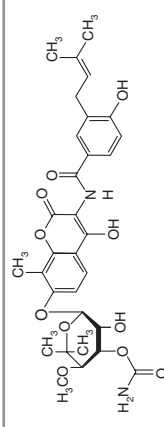
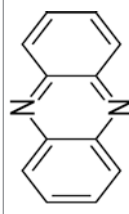
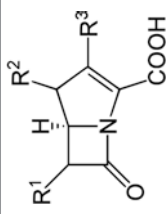
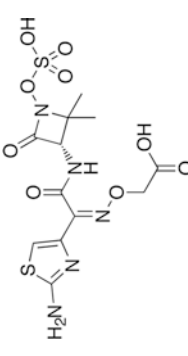
**Table 14.2** (continued)

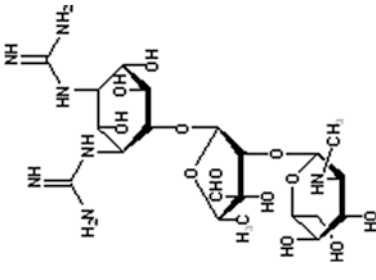
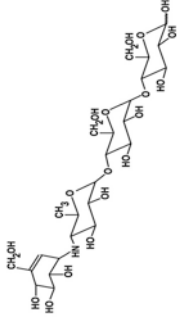
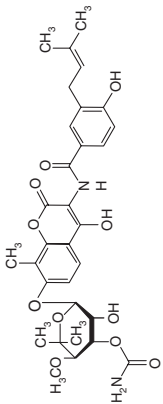
<i>Rhizobium</i> species	Type of secondary metabolite	Biosynthesis pathway	Structural formula
	f) Phenazine	Phenazine biosynthesis	
3. <i>Azorhizobium caulinodans</i>	a) Carbapenem	Carbapenem biosynthesis	
	b) Monobactam	Monobactam biosynthesis	

c) Streptomycin	Streptomycin biosynthesis	 <p>The image shows the chemical structure of Streptomycin, a complex aminoglycoside antibiotic. It consists of a streptidine ring system linked to a 2-deoxystreptose sugar, which is further linked to a 2-deoxy-L-xylofuranose sugar. The structure is highly detailed, showing various hydroxyl groups, amino groups, and methyl groups.</p>
d) Acarbose	Acarbose biosynthesis	 <p>The image shows the chemical structure of Acarbose, a tricyclic alpha-glucosidase inhibitor. It features a central pyridine ring substituted with a methyl group and a hydroxyl group, and is linked to a complex sugar chain consisting of a 2-deoxy-L-xylofuranose unit and a 2-deoxy-D-ribofuranose unit.</p>
d) Validamycin	Validamycin biosynthesis	 <p>The image shows the chemical structure of Validamycin, a cyclic aminoglycoside antibiotic. It consists of a 2-deoxy-L-xylofuranose sugar linked to a 2-deoxy-D-ribofuranose sugar, which is further linked to a 2-deoxy-D-ribofuranose sugar. The structure is highly detailed, showing various hydroxyl groups and amino groups.</p>

(continued)

Table 14.2 (continued)

<i>Rhizobium</i> species	Type of secondary metabolite	Biosynthesis pathway	Structural formula
	e) Novobiocin	Novobiocin biosynthesis	
	f) Phenazine	Phenazine biosynthesis	
4. <i>Sinorhizobium meliloti</i> 1021	a) Carbapenem	Carbapenem biosynthesis	
	b) Monobactam	Monobactam biosynthesis	

c) Streptomycin	Streptomycin biosynthesis	
d) Acarbose	Acarbose biosynthesis	
e) Novobiocin	Novobiocin biosynthesis	



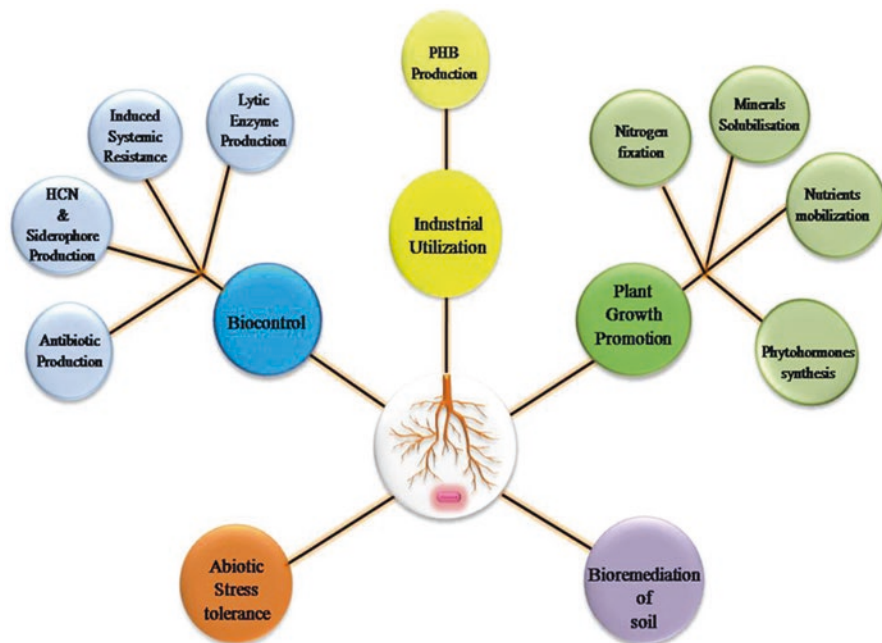
for disease reduction (Chatterjee et al. 1995; Diby et al. 2005; Gupta et al. 2006; Ruiz Duenas and Martinez 1996; Szekeres et al. 2004). There are reports of rhizobial isolates producing chitinase to inhibit pathogenic microbes (Chernin et al. 1955; Mazen et al. 2008). Mazen et al. (2008) reported that seed treatment with chitinase-producing *Rhizobium* spp. alone or co-inoculated with mycorrhizal fungi leads to reduction of damping-off of fababean. *Rhizobium* strains isolated from *Sesbania sesban* has been reported to be produce chitinase (Sridevi and Mallaiah 2008). *R. leguminosarum* isolate TR2 and *Ensifer meliloti* isolate TR1 and TR4 showed  $\beta$ -1,3-glucanase and chitinase activity, respectively, and inhibited fusarium wilt of fenugreek (Kumar et al. 2011). *Rhizobium* sp. Strain RS12, with chitinase-producing ability, suppresses diseases of chickpea caused by *F. oxysporum*, *S. sclerotiorum* and *M. phaseolina* by preventing mycelia growth and development (Smitha and Singh 2014).

#### 14.6.4 Phosphate Solubilization

Phosphorus is present in soil in immobile form and thus become unavailable to microbe and plant (Gyaneshwar et al. 2002). Group of rhizobia have been reported to be potent phosphate solubilizers, some of them as *R. leguminosarum* mobilizes phosphorus making it available to plant (Rodriguez and Fraga 1999; Mehta and Nautiyal 2001). *Rhizobium* inoculated *P. vulgaris* showed significant difference in acid phosphatase activity in its rhizospheric zone (Makoi et al. 2010). Bradyrhizobium strains that have been reported by Deshwal et al. (2003) for their ability to produce siderophores, phosphate solubilization and IAA, conferring it strong root colonizing, growth promotion and vigorous antagonistic activity against *M. phaseolina* (charcoal rot of peanut). Co-inoculation of *Rhizobium* and phosphate solubilizing bacteria have been reported to have synergistic effect increasing nodulation, shoot and root nitrogen and phosphorus content (Rugheim and Abdelgani 2009).

### 14.7 Induction of Plant Defence Mechanisms

Systemic resistance in host is induced by up regulating the expression of defence-related genes encoding for antioxidant enzymes, hydrolytic enzymes and pathogenesis-related proteins. Defence-related enzymes such as polyphenol oxidase, L-phenylalanine ammonia lyase, peroxidase, chalcone synthase and isoflavone reductase play crucial role in induction of plant defence to pathogenic attack (Arfaoui et al. 2005; Dutta et al. 2008). Rhizobia have ability to induce defence arsenal by triggering production of plant defensive enzymes, phytoalexins, phenolics and flavonoids (Mavrodi et al. 2001; Yu et al. 2002). Phenolics plays a crucial role in plant defence by activating plant defence genes, acting directly as structural barriers and modulating the pathogenicity, preventing growth and spread of pathogens (Ramos et al. 1997 and Dihazi et al. 2003). Mishra et al. 2006 reported that inoculation of rice with strains of *Rhizobium leguminosarum* bv. *phaseoli* and *R.*



**Fig. 14.2** Multifaceted role of *Rhizobium* sp.

*leguminosarum* bv. *trifolii* induces production of phenolics such as ferulic acid, gallic acid and tannic and cinnamic acids, reducing infection by *Rhizoctonia solani*. Induction and accumulation of phytoalexins such as medicarpin and maackiain in response to *Rhizobium* species in planta, protect it from phytopathogens (Weigand et al. 1986; Weidemann et al. 1991). A phytoalexin, glyceollin have been reported to be produced by *Rhizobium* and *Bradyrhizobium* sp. in soybean, which has antimicrobial activity against plant pathogens (Phillips and Kapulnik 1995) (Fig. 14.2).

## 14.8 Microbial Secondary Metabolites and Its Importance

Microbial secondary metabolites are low molecular weight compounds, indispensable for growth of producing microbes but play an important role in nutrition, health and economy of the society (Berdy 2005; Ruiz et al. 2010). Microbial secondary metabolites varied widely in its chemical nature from peptides, polyketides, lipids, steroids, terpenoids and carbohydrate to alkaloids (O'Brien and Wright 2011). They include pigments, toxins, antibiotics, pheromones, antitumor agents, enzyme inhibitors, effectors of ecological competition and symbiosis, receptor antagonist and agonists, immunomodulating agents, pesticides, cholesterol-reducing drugs and growth promoters of plants and animals (Demain 1998). These metabolites are not synthesized during logarithmic growth phase but are synthesized during subsequent

production stages; stationary phase (idiophase) and metabolites known as idiolites (Demain and Fang 2000; Gonzalez et al. 2003; O'Brien and Wright 2011). Production of secondary metabolites are brought about by addition and biosynthesis of an inducer or exhaustion of nutrients, generate signal which regulate metabolic pathways leading to chemical differentiation (Bibbs 2005; Ruiz et al. 2010). Microbial secondary metabolites are major source of essential agricultural products and contributes to about half of the pharmaceutical market (Demain and Sanchez 2009). In addition to its use as anti-infective drugs, they are used as immunosuppressants to facilitate organ transplantation (Verdine 1996; Barber et al. 2004; Demain and Schez 2009). Autoinducers of secondary metabolites includes oligopeptides of gram-positive bacteria, N-acylhomoserine lactone of gram-negative bacteria and butanolides of the actinomycetes (Kawaguchi et al. 1988; Demain 1998).

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## 14.9 Rhizobial Formulations

Field applicability of rhizobium for its better exploitation at large scale is determined by a formulation with appropriate inoculum load. Survivability in higher number and for longer period in commercial formulation is major objective of developing an inoculants formulation. Mainly two types of commercial formulation of *Rhizobium* are available in market, they are solid and liquid. Solid inoculants are prepared by blending broth culture with an appropriate carrier material. Selection of carrier material is determined by a number of factors such as survivability of rhizobial cells on carrier material, cost-effectiveness and accessibility, pH buffering moisture absorbing capacity, etc. (Date and Roughley 1977; Brockwell and Bottomley 1995). Peat-based application of rhizobial inoculants is the most widely used method for application of rhizobia worldwide since 1895. A diverse range of carriers such as soil material (peat, clay, charcoal) (Chao and Alexander 1984; Beck 1991; Temprano et al. 2002), perlite (Ronchi et al. 1997; Khavazi et al. 2007), vermiculite (Graham-weis et al. 1987), plant by-products (sawdust, peanut shell, corn cobs) (Sparrow and Ham 1983) and composts (Kostov and Lynch 1998) are used all over the world (Singh et al. 2016; Singh et al. 2017).

Other formulations such as liquid, granular and biofilm-based formulation have been studied, but of all formulations only solid- and liquid-based formulations have been exploited commercially. Liquid formulations are based on broth culture with oil in water suspensions or mineral and organic oil as carriers (Albareda et al. 2008; Bashan 1998). Granular formulations such as peat prills (Fouilleux et al. 1996), peat inoculants coated on sand (Chamber 1983), perlite/alginate beads (Bashan 1986; Hedge and Brahmaaprakash 1992) and polymer-coated beads (Brockwell et al. 1980) have been studied. Biofilm-based formulation is latest and efficient one having greater stability under abiotic and biotic stresses. Bacteria may be grown on carrier material to form biofilm or trapped by a fungal matrix (Seneviratne 2003; Seneviratne et al. 2008; Triveni et al. 2013; Prasanna et al. 2013; Jayasinghearachchi and Seneviratne 2004).

## 14.10 Conclusion and Future Prospects

Currently, there is an increasing threat to agricultural sustainability, soil and ground-water contamination. Biofertilizer and biocontrol agents are used as a highly efficient alternative to chemical fertilizers and chemical pesticides, respectively. *Rhizobium* with promising biofertilization and biocontrol ability can be exploited for increasing legume and nonlegume production. Studies regarding secondary metabolites of *Rhizobium* need to be explored for its greater benefit for agriculture. Genetic engineering approaches can also be used to incorporate genes for secondary metabolites in rhizobial strains lacking it but have potential for biocontrol. Although a number of rhizobial biofertilizer such as solid and liquid formulations are available, better commercial formulations such as polymer and biofilm based need to be urgently introduced in the market.

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