

Running Title: ACTINOBACTERIA FOR SUSTAINABLE AGRICULTURE

Enhanced plant growth, nutrient acquisition, and crop protection by using Actinobacteria: advancements in soil, plant, and microbial multifactorial interactions

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ABSTRACT

Agricultural areas of land are deteriorating every day with population increase, rapid urbanization, and industrialization. To feed today's huge populations, more crop production is

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required from smaller areas, which triggers the continuous application of higher doses of inorganic fertilizers. These cause damage to soil health and therefore, nutrient imbalance conditions arise in arable soil. Under these conditions, the benefits of Actinobacteria as an alternative tool for replacing harmful chemicals with microbial inoculum and promoting eco-friendly sustainable farming practices have been possible through recent technological advances. They are multifunctional traits involved in the production of different types of bioactive compounds responsible for plant growth promotion and biocontrol of phytopathogens have reduced the use of chemical fertilizers and pesticides. There are some well-known groups of nitrogen-fixing Actinobacteria like *Frankia* which undergo mutualism with plants and offer enhanced symbiotic trade-offs. In addition, to nitrogen fixation, increasing availability of major plant nutrients in the soil by solubilization of immobilized forms of phosphorus and potassium compounds in soil, production of phytohormones like indole-3-acetic acid, indole-3-pyruvic acid, gibberellins, and cytokinins, improving organic matter decomposition by releasing cellulases, xylanase, glucanases, lipases and proteases, suppression of soil-borne pathogens by the production of siderophores, ammonia, hydrogen cyanide, and chitinase are some of those important features of Actinobacteria which have been found useful for combating biotic and abiotic stresses in plants. Thus the influence of Actinobacteria on improving soil fertility and plant health has motivated to compile those important findings associated with sustaining plant productivity in the long run.

Key Words: Actinobacteria, plant growth promoters, biocontrol agents, metabolites, sustainable agriculture.

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INTRODUCTION

With an increase in the world population, the demand for agricultural productivity is also increasing. To cope with rising food demand, there has been large-scale application of chemically synthesized pesticides and fertilizers to boost agricultural productivity (Zhang *et al.*, 2018). With advances in agricultural equipment and innovative methods of application, traditional methods have reached their limits of efficiency (Pivoto *et al.*, 2018). For HYVs (high yielding varieties), chemical fertilizers are often used conventionally in higher doses to increase productivity. These chemicals not only become accumulated in crop plants and seeds but also cause pollution of soil and water, including groundwater (Kumar *et al.*, 2007, Heidarpour *et al.*, 2019). In this context, scientists have found several sustainable ways for switching to eco-friendly farming activities (Mishra, 2013, Khoshru *et al.*, 2020a). A number of studies have pointed out different ways to combat this problematic situation of chemical usage in agriculture. Among the solutions, microorganisms with multifunctional traits have been found to reduce the use of chemical fertilizers and pesticides, by producing or releasing different types of bioactive compounds (Janardhan *et al.*, 2014), enzymes (Verbon and Liberman, 2016; Turan *et al.*, 2016, Khoshru *et al.*, 2020b), antimicrobial substances or biocontrol compounds (Dhanasekaran *et al.*, 2005; Liu *et al.*, 2018), and others are plant growth

promoters (Pérez-Montaña *et al.*, 2014; Sarikhani *et al.*, 2016 and 2020; Tang *et al.*, 2016; Gange and Gadhave 2018; Khoshru *et al.*, 2020c). Considering this point, plant growth-promoting rhizobacteria (PGPR) are a good choice since rhizobacteria can demonstrate mutual relationships with plants and share nutrients; these findings have been critically supported by several studies (Tang *et al.* 2016; Zhang *et al.* 2016; Rosier *et al.* 2018; Raklami *et al.* 2019; Sarikhani *et al.* 2020; Khoshru *et al.* 2020a). PGPR are naturally occurring (Rosier *et al.*, 2018), free-living rhizosphere-colonizing bacteria that enhance plant yield, growth and soil fertility and decrease the percentages of pathogens as well as reducing biotic or abiotic stresses (Vessey, 2003; Kumar *et al.*, 2014; Sarikhani *et al.*, 2019; Khoshmanzar *et al.*, 2020). Actinobacteria are among these bacteria equipped with multifunctional plant growth promoting traits and many plant growth beneficial properties (El-Tarabily and Alkhajeh, 2016; Monteiro *et al.*, 2017) (Fig. 1).

Fig. 1 Beneficial impacts and interaction of Actinobacteria with plant and rhizosphere to imply the acquisition of nutrients, growth promotion and plant protection

Today's world requires high output yield and enhanced crop production as well as better soil fertility achieved in an ecofriendly way (Yasari *et al.*, 2009). Actinobacteria as bio-inoculants and bio-pesticides are an alternative to chemical fertilizers, and they can be used for improving crop production under multiple stress conditions such as temperature, pH, salinity and drought (Cheng *et al.*, 2018a). *Streptomyces* represent the most abundantly occurring Actinobacteria genus in the soil (Panneerselvam *et al.*, 2020). First of all, due to their higher growth rate, they achieve efficient colonization with plant root and can withstand adverse growth circumstances through the formation of spores. *Streptomyces* produce many enzymes and organic compounds that are beneficial to plant growth (Vonothini *et al.*, 2008; Syed *et al.*, 2009; Polak *et al.*, 1992). Soil Actinobacteria are known to produce active compounds in the rhizospheric area of plants, many of which are very important in agriculture (Suzuki *et al.*, 2000). Khan *et al.* (2010) reported that phosphorus could be implicated in an assortment of metabolic process of plant hosts, as energy transfer, photosynthesis, macromolecular biosynthesis, signal transduction and respiration. Phosphorus availability to hosts plants is facilitate through soil phosphorus cycle. Richardson and Simpson (2011) noted that Actinobacteria solubilize and mineralize directly inorganic phosphorus or mediate organic phosphorus availability through microorganism turnover and increase the root system. These Actinobacteria lower soil pH through section of different types of organic acids and thus facilitate the phosphorus availability to hosts plants (Kaur *et al.*, 2016). Among all microorganisms, Actinobacteria have also been reported as showing potential for solubilizing the insoluble organic and inorganic phosphorus compounds into simpler forms for the plants to absorb easily. Phosphorus improves plant yield by the establishment and development of the entire root system and consequently improving shoots (Khan *et al.*, 2010). Moreover, solubilization of phosphorus is a common process among microbes involving archaea, bacteria, and fungi. Sahu *et al.* (2007) demonstrated the phosphate-solubilizing potential of Actinobacteria in the estuarine environment. The positive influence of pure Actinobacterial strains on plants through multifunctional attributes such as rock phosphate solubilization has been briefly described by Hamdali *et al.*, (2008a, b). Several reports on plant growth-promoting Actinobacteria with a vast number of phosphate solubilizing microbes have been represented in a number of studies (Dastager *et al.*, 2010; Verma *et al.*, 2013; Singh *et al.*, 2014; Anwar *et al.*, 2016). According to Karlidag *et al.* (2007), plant growth promotion is also improved by K-solubilizing Actinobacteria. Similarly, Iron is a necessary co-factor for numerous enzymatic reactions for virtually all organisms and an essential nutrient. The Fe-chelating compounds producing microbes show both direct and

indirect improvement of plant growth by beneficial Actinobacteria, including *Streptomyces*, *Micrococcus*, *Microbacterium*, *Kocuria*, *Corynebacterium* and *Arthrobacter* (Tiwari *et al.*, 2011). There are numerous reports of Actinobacteria involved in nitrogen fixation, such as members of the genus *Frankia*, which are widespread endophytic Actinobacteria symbiotically associated with plant roots and that fix atmospheric nitrogen for host plants. Symbiotic association with Actinobacteria lead legume crops undergo biological nitrogen fixation and meet their own needs without depending external sources. Actinobacteria strains have been proved to be effective in a multidimensional way. They are involved in numerous plant growth promoting activities such as siderophore production, IAA, complementing mycorrhizal fungi and maintaining the ecological balance in the soil system. The ability to produce phytohormones is extensively distributed among IAA-producing Actinobacteria and may potentially be employed to improve plant growth (Tomilova *et al.*, 2016; Sharma *et al.*, 2016). Merckx *et al.* (1987) and Khamna *et al.* (2010) reported that the involvement of Actinobacteria is crucial in plant growth promotion through siderophore as well as IAA production, which resulted in enhanced nutrient uptake. Moreover, metabolites produced by Actinobacteria restricted fungal phytopathogens like *C. gloeosporioides* (potato dry rot), *A. brassicicola* (rose apple anthracnose), *F. oxysporum* (chinese cabbage leaf spot), *S. rolfii* (damping-off of balsam) and *P. digitatum* (orange green mold), exhibiting reduced disease symptoms. There is much evidence that proves Actinobacteria are potential bio-inoculants and biocontrol agents for plant growth improvement. All these special qualities of this group make them an inevitable tool in this current agricultural practices (Poovarasan *et al.*, 2016; Panneerselvam *et al.*, 2017; Panneerselvam *et al.*, 2020). Given all these special aspects, we concentrate on Actinobacteria as an alternative tool for sustainable farming practices and for reducing harmful chemical usage to promote eco-friendly sustainable agriculture, so that we can reduce some environmental damage and transform chemical farming into organic farming. This review has been focused on the interaction and current situation of Actinobacteria related to plant growth development, secondary metabolite production, biocontrol activity and soil nutrient management for sustaining agricultural productivity.

TAXONOMY, PHYSIOLOGY AND MULTIFUNCTIONAL ACTINOBACTERIA IN SUSTAINABLE AGRICULTURE

The term “Actinobacteria, formerly known as Actinomycetes” was derived from the Greek term *aktis* or *aktin*, representing ‘Ray Fungi’ (Williams, 1990). These bacteria are Gram positive, aerobic, spore-forming with a high percentage of guanine (G) and cytosine (C) in their DNA (>55mol %) (Krogus-Kurikka *et al.*, 2009). Members of Actinomycetales are commonly referred to as Actinobacteria (Goodfellow, 2012). Actinobacteria possess both bacterial (cell wall shows peptidoglycan structure) and fungal properties (filamentous appendages). The Actinobacteria phylum is the largest in bacteria classified into 6 classes; namely, *Coriobacteriia*, *Actinobacteria*, *Thermoleophilia*, *Rubrobacteria*, *Acidimicrobiia* and *Nitriliruptoria* (Goodfellow, 2012). Actinobacteria are categorized with bacteria in the same class as *Schizomycetes* in the strict taxonomic context, but limited to the *Actinomycetales* order (Goodfellow, 2012). The class Actinobacteria is further divided into sixteen orders, which are *Actinopolysporales*, *Glycomycetales*, *Actinomycetales*, *Jiangellales*, *Streptosporangiales*, *Micrococcales*, *Bifidobacteriales*, *Catenulisporales*, *Frankiales*, *Kineosporiales*, *Micromonosporales*, *Pseudonocardiales*, *Propionibacteriales*, *Streptomycetales*, *Corynebacteriales* and *Incertae sedis* (Zhi *et al.*, 2009; Goodfellow, 2012). With the recent development of new sequencing technology has allowed a better grading of higher taxa unknown to the vast majority of researchers and has introduced new methods to rebuild phylogeny reconstruction.

Further Nouioui *et al.* (2018) reported twenty orders of Actinobacteria viz. *Actinomycetales*, *Acidothermales*, *Micrococcales*, *Corynebacteriales*, *Bifidobacteriales*, *Micromonosporales*, *Pseudonocardiales*, *Cryptosporangiales*, *Sporichthyales*, *Nitriliruptorales*, *Streptosporangiales*, *Catenulisporales*, *Frankiales*, *Geodermatophilales*, *Glycomycetales*, *Propionibacteriales*, *Jiangellales*, *Kineosporiales*, *Nakamurellales*, and *Streptomyetales* based on the whole-genome sequences in the latest re-classification. Different types of soil Actinobacteria e.g. *Streptomyces*, *Actinoplanes*, *Nocardia*, *micromonospora*, and *Streptosporangium* have been extensively used to enhance the properties of soil and found to increase crop yield (Wahyudi *et al.*, 2019), among which the members of *Streptomyces* sp. have been found to play major role due to higher production of different plant beneficial enzymes and metabolites (Kekuda *et al.*, 2014). Actinobacteria can promote and protect the plant growth by using various enzymes such as cellulose, protease, pectin, α -amylase, xylanase, lipase, chitinase and lignin (Nascimento *et al.*, 2002; Vonothini *et al.*, 2008; Syed *et al.*, 2009; Sreevidya *et al.*, 2016; Zang *et al.*, 2018; Siddharth and Rai, 2019; Sharma and Thakur, 2020), siderophore production (Lee *et al.*, 2012), nitrogen (N) fixation (Prakash and Cummings, 1988), phosphate solubilization (Farhat *et al.*, 2015; Anwar *et al.*, 2016), indole-3-acetic acid (IAA-C₁₀H₉NO₂) production (Myo *et al.*, 2019), and plant growth regulators like hormones (Passari *et al.*, 2016). Actinobacteria play an important role in management of phytopathogens by suppressing the growth of several types of plant pathogens e.g. *Fusarium* sp., *Pythium* sp., *Alternaria* sp., *Botrytis* sp., *Rhizoctonia* sp., *Helminthosporium* sp., *Phytophthora* sp., *Phanerochaete* sp., *Aspergillus* sp., *Oidium* sp., *Curvularia* sp., *Sclerotium* sp., *Colletotrichum* sp., and *Pyricularia* sp. by secreting antimicrobial products (Lu *et al.*, 2008; Prapagdee *et al.*, 2008; Hamadali *et al.*, 2008; Gopalakrishnan *et al.*, 2013; Goudjal *et al.*, 2014; Sreevidya *et al.*, 2016). Actinobacteria has a major role in the decomposition of organic materials through which the nutrient recycling process in soil get fastened by virtue of lignocellulotic enzymes released by this group of bacteria (Das *et al.*, 2007). Actinobacteria can adapt more easily to harsh environments than other microorganisms. They can grow in alkaline as well as acidic soil and keep the soil properties in balanced conditions (Phoebe *et al.*, 2001; Trenozhnikova and Azizan, 2018). Hence, to establish sustainable agriculture Actinobacteria are an excellent choice because they can show dual nature, both promoting plant growth and presenting effective biocontrol activity (Coombs *et al.*, 2004; Meguro *et al.*, 2006).

Further insights into the studies conducted on structural community of Actinobacteria in soil using next generation sequencing of 16S amplicons from soil DNA have found a total abundance of $16.68 \pm 5.93\%$ Actinobacteria in rice rhizosphere soil (Imchen *et al.*, 2019). Related studies have also found the population of Actinobacteria was 45% higher in rhizosphere as compared to non-rhizospheric soil (Jang *et al.*, 2019). DNA-SIP techniques have found application of biochar to have beneficiary impact on increasing the population of Actinobacteria in the oxisol (Yu *et al.*, 2020). Compared to rice plants, millets rhizosphere has 42.22% total abundance making it the dominating phylum among other bacterial phylum in this crop type (Prabha *et al.*, 2019). Several uncommon actinobacteria related have been found to be associated with the rhizosphere of alpine plants among which *Kitasatospora* genus and certain clades of *Streptomyces* genera including, *Streptomyces subrutillus*, *S. avidinii*, *S. chinensis*, *S. mirabilis*, *S. olivochromogenes*, *S. brevispora*, *S. spororaveus*, *S. anulatus*, *S. camponoticapitis*, *S. erringtonii* and *S. scabrisporus* have been some of the peculiar strains to be identified from rhizosphere soil (Oberhofer *et al.*, 2019). Furthermore in banana endophytes, actinobacteria constituted 9.30% of the total bacteria identified with the population remaining unaffected by infestation of phytopathogenic fungal pathogens (Kaushal *et al.*, 2020). These findings clearly demonstrates the structural diversity of actinobacteria to shift in accordance to

the plant type, soil amendments and environment. This demonstrates that actinobacteria have preferences for certain soil and plant types and is a commensal microorganism for plant ecosystem.

BENEFICIAL IMPLICATIONS FOR THE RHIZOSPHERE BY THE INTERACTION OF ACTINOBACTERIA AND ITS MAJOR ATTRIBUTES IN PLANT GROWTH PROMOTION

Plant growth promoting microorganisms (PGPMs) are mainly colonizers of the rhizoplane and rhizosphere region (Gopalakrishnan *et al.*, 2015a and 2013; Sarikhani *et al.*, 2020). Within the phylum Actinobacteria, the genus *Streptomyces* is predominant and present ubiquitously in soil or water, existing both as rhizosphere-colonizing bacteria and plant endophytes. As some of the *Streptomyces* are endophytic, they can easily grow in the host cell without harming the host's internal appearance (Kumar *et al.*, 2014; Marella, 2014). They assist the growth of plant by providing different types of nutrients (e.g. soluble phosphorus), and increases the water uptake as well as the retention capacity of the plant (Schütze *et al.*, 2014). In return, Actinobacteria receives nutrients such as sugars from the plant, which help them proliferate their growth in soil. *Streptomyces* spp. also produce some catalytic enzymes and provides them to the host systems, wherein these enzymes easily breaks down several complex biomolucular compounds into simpler chemical units (Nascimento *et al.*, 2002; Syed *et al.*, 2009). Actinobacteria, mainly *Streptomyces* and some other beneficial strains, possess various plant growth promoting (PGP) attributes (Gopalakrishnan *et al.*, 2013; Anwar *et al.*, 2016). Thus, *Streptomyces* are considered as plant growth-promoting *Streptomyces* (PGPS) which have the ability to increase plant growth by direct or in-direct biosynthetic pathways (Vurukonda *et al.*, 2018). These common PGP attributes are shown in Fig. 2 (Saito *et al.*, 2003; El-Tarabily *et al.*, 2008; Khamna *et al.*, 2010). There are two different ways by which Actinobacteria can influence plant growth. The direct way of influence on plant has been through facilitation of plant growth by releasing microbial metabolites and providing biological nutrients such as phosphorus and nitrogen are ideal than agrochemicals which caused serious environmental damage and also expensive (Tanvir *et al.*, 2018). Whereas indirectly the Actinobacteria influences the plant by minimizing the deleterious effects of pathogenic microbe by production of antagonistic compounds. Table I shows the lists of Actinobacteria that help regarding plant growth promoting attributes in plant growth.

Fig. 2 Major PGP attributes of Actinobacteria

TABLE I

Beneficial effects of Actinobacteria on growth promotion attributes and growth enhancement in different host systems

Actinobacteria name	Host	Major PGP traits	Production of growth promoters substance														References			
			IAA	PS	SP	A D	A P	H C N	CP	LP	PP	β -G	Ch P	Ph P	GBs	CKs			N F	O A
<i>Nocardiopsis dassonvillei</i> subsp. <i>dassonvillei</i> D14, <i>Nocardiopsis aegyptica</i> H14	<i>Solanum lycopersicum</i>	IAA, and PS	21.4 μ g/mL	24.84 μ g PO ₄ ³⁻ mL ⁻¹ (D14)	-	-	√	√	-	-	-	-	√	-	-	-	-	√	Djebaili <i>et al.</i> (2020)	
<i>Streptomyces</i> spp. (A20, 5.1, 7.1)	<i>Oriza sativa</i>	IAA, SP and PS	7.98 ± 0.87 μ g/mL	388.53 ± 43.66 μ g/mL	√	√	-	-	-	-	-	-	-	-	-	-	-	√	√	Suarez Moreno <i>et al.</i> (2019)
<i>Streptomyces</i> spp.	<i>Glycine max</i>	IAA, PS and NF	2.08 μ g/mL to 16.70 μ g/mL	2.05±0.06 to 2.72±0.08 μ g/mL	-	-	-	-	-	-	-	-	-	-	-	-	-	√	√	Wahyudi <i>et al.</i> (2019)
<i>S. rochei</i> (WZS1-1) and <i>S. sundarbansensis</i> (WZS2-1)	<i>Mikania micrantha</i>	IAA	absence tryptop- 11.40 ± 0.49 μ g/mL (WZS1-1), 19.72 ± 1.56 μ g/mL (WZS2-1) presence of tryptophan 7.08 ± 0.32 μ g/mL (WZS1-1), 35.76 ± 2.92 μ g/mL (WZS2-1)	√	√	-	-	-	-	-	-	-	-	-	-	-	-	√	√	Han <i>et al.</i> (2018)

<i>Streptomyces</i> spp. (SAI-29)	Chickpea	IAA, SP, CP, ChP, LP, PP, β-G and HCN	14.6 µg/mL	-	11–20 mm	-	-	-	31	11	55 mm	0.3	11	-	-	-	-	-	Sreevidya <i>et al.</i> (2016)	
<i>S. nobilis</i> WA-3, <i>S. Kunmingensis</i> WC-3, <i>S. enissocaesilis</i> TA-3, <i>Streptomyces</i> spp. WA-1, <i>S. djakartensis</i> TB-4 and <i>S. mutabilis</i> WD-3	<i>Triticum aestivum</i>	IAA, SP, PS, AP and HCN	500µg/ml L-tryptophan)-79.5 µg/mL (WA-3), 79.23µg/mL (WC-3), 69.26µg/mL (TA-3)	√	72.13 mg/100 ml (WA-1), 70.36 mg/100 ml (TB-4), 66.0 ± 0.40 (WA-3), 61.46 ± 0.279 (WC-3), 57.83 ± 0.32 (WD-3), 62.9 ± 0.40 (TA-3)	√	√	√	-	-	-	-	-	-	-	-	-	-	√	Anwar <i>et al.</i> (2016)
<i>Streptomyces</i> spp. HM1	<i>Zea mays</i>	IAA	-	-	-	-	-	√	-	-	-	-	√	√	-	-	-	√	√	El-Sayed <i>et al.</i> (2015)
<i>Streptomyces</i> spp.	<i>O. sativa</i>	IAA and SP	43.6 g/mL	-	√	-	-	√	-	-	-	√	√	√	-	-	-	√	√	Gopalakrishnan <i>et al.</i> (2014)
<i>Streptomyces</i> spp., <i>Microbispora</i> spp., <i>Actinomadura</i> spp., <i>Micromonospora</i> spp., <i>Nocardia</i> spp., and <i>Actinoplanes</i> spp.	<i>G. max</i>	IAA, GBs, CKs, SP and HCN	√	√	-	-	-	√	-	-	-	√	-	-	√	-	-	-	√	Dalal and Kulkarni (2014)
<i>Streptomyces</i> spp.	<i>T. aestivum</i>	IAA, PS,	136.5 mg/L	1916 mg/L	47.4 mg/L	-	-	-	-	-	-	-	6.2 U/	0.6	8	-	-	-	√	Jog <i>et al.</i> (2014)

		PhP, ChP and SP										m L	U/ mL					
<i>Streptomyces</i> <i>sp</i> VSMGT1014	<i>O. sativa</i>	IAA	15.96 µg/ml	-	-	-	-	-	-	-	-	-	-	-	-	-	√	Harikrishnan <i>et al.</i> (2014)
<i>Streptomyces</i> spp. ASU14	<i>T. aestivum</i>	IAA	22 µg/mL	-	-	-	-	-	-	-	-	-	-	-	-	-	√	Abd-Alla <i>et al.</i> (2013)
<i>S. rochei</i> IDWR19, <i>S.</i> <i>carpinensis</i> IDWR53 and <i>S.</i> <i>thermolilacinus</i> IDWR81	<i>T. aestivum</i>	IAA, SP and PS	17.81±2.1(I DWR19), 13.36±2.3(I DWR53), 11.5±2.1(ID WR81)	√	34.17±0.07 (IDWR19) , 27.63 ± 0.08 (IDWR53) , 26.9 ± 0.07(IDW R81) PS- 95.40 ± 5.1 (IDWR19) , 405.17 ± 6.2 (IDWR53) , 911.6 ± 5.3 (IDWR81)	√	-	-	-	-	-	-	-	-	-	-	√	Jog <i>et al.</i> (2012)
<i>Streptomyces</i> spp.	<i>T. aestivum</i>	Increase d uptake of N,P,Fe and Mn	2.4 µg/ml	92 mg/l	√	-	-	-	-	-	-	-	-	-	-	-	√	Sadeghi <i>et al.</i> (2012)
<i>S. hygroscopicus</i> TP-AO451	<i>Phaseolus</i> <i>vulgaris</i>	Pteridic acids A and B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Igarashi <i>et al.</i> (2002)
<i>Streptomyces</i> spp.	<i>Z. mays</i> , <i>C.</i> <i>arietinum</i>	IAA, GA,Pho sphatas	-	√	√	√	-	-	-	-	-	-	-	-	-	-	√	Radha T.K. (2016)

<i>Streptomyces</i> spp.	<i>Vigna radiata</i>	e and PS SP	√	-	√	√	-	-	-	-	-	-	-	-	-	-	√	Rungin <i>et al.</i> (2012)	
<i>Streptomyces</i> AzR-051	<i>Azadirachta indica</i> A. Juss.	IAA, SP	13.73 μmol/mL	√	√	-	-	-	√	-	-	-	-	-	-	-	√	Verma <i>et al.</i> (2011)	
<i>Streptomyces</i> CMU-H009	lemongrass (<i>Cymbopogon citratus</i>)	IAA	300 mg/mL	-	-	-	-	-	-	-	-	-	-	-	-	-	√	Khamna <i>et al.</i> (2010)	
<i>N. jiangxiensis</i>	<i>Aquilaria crassna</i> Pierre ex Lec (eaglewood)	IAA	15.14 ± 0.22 μg/mL	-	√	-	√	-	-	-	√	-	-	-	-	-	-	Nimnoi <i>et al.</i> (2010)	
<i>Streptomyces</i> ST24	<i>Heritiera fomes</i> (mangrove)	PS	-	√	-	-	-	-	-	-	-	-	-	-	-	-	-	Gupta <i>et al.</i> (2010)	
<i>Thermobifida</i> MCR24	<i>Trifolium repens</i> L	SP	-	√	√	-	-	-	-	-	√	-	-	-	-	-	√	√	Franco-Correa <i>et al.</i> (2010)
Actinomycete LSCH-10C	<i>O. sativa</i>	PS and ChP	√	√	-	-	-	-	-	-	-	√	-	-	-	-	√	Ningthoujam <i>et al.</i> (2009)	
<i>Micromonospora endolithica</i>	<i>Phaseolus vulgaris</i> L.	PS	-	√	-	-	-	-	-	-	-	-	-	-	-	-	√	El-Tarabily <i>et al.</i> (2008)	
<i>S. aureofaciens</i> CMUAc130	-	ChP	-	-	-	-	-	-	-	-	-	-	-	-	-	-	√	Taechowisan <i>et al.</i> (2003)	

<i>S.olivaceoviridis</i> , <i>S.rimnosus</i> , <i>S.</i> <i>rochei</i>	<i>T. aestivum</i>	IAA, GBs and CKs	34.19 ± 1.46 μg/mL, 39.04 ± 0.61 μg/mL, 32.75 ± 0.23 μg/mL	-	-	-	-	-	-	-	-	-	-	-	5.53±0. 16 μg/mL, 8.30 ± 0.87 μg/mL, 5.69±0. 09 μg/mL	14.88± 0.26 μg/mL, , 4.70 ± 0.08 μg/mL, , 6.73 ± 0.37 μg/mL	√	√	Aldesuquy <i>et</i> <i>al.</i> (1998)
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√: positive findings / tested, IAA: indole-3-acetic acid, PS: phosphate solubilization, SP: siderophore production, AD: ACC deaminase, AP: ammonia production, HCN: hydrogen cyanide production, NF: nitrogen fixation, CP: cellulase production, LP: lipase production, PP: protease production, β-G: β-1, 3-glucanase, ChP: chitinase production, PhP: phytase production, GBs: gibberellins, CKs: cytokinins, OA: others PGP attributes

ACTINOBACTERIA AS BIOCONTROL AGENTS FOR PLANT PROTECTION

There are several studies and trials based on the usage of biological sources of pesticides instead of chemical sources. A good alternative to chemical sources is microbial sources, which have an impact on their multifunctionality and a beneficial effect on plants and ecosystems. Actinobacteria are usually regarded as potent natural biocontrol agents in soil (Gopalakrishnan *et al.*, 2013). Actinobacteria competing with pathogens through the production of different secondary metabolites, enzymes, parasitism, and other biocontrolling activities (Hamdali *et al.*, 2008a; Goudjal *et al.*, 2014; Sreevidya *et al.*, 2016). Studies reported that the different types of plant pathogens e.g. *Alternaria* spp., *F. oxysporum*, *C. higginsianum*, *P. aphanidermatum*, *P. capsici* and *A. lactucumare* are very sensitive to the different bioactive compounds produced by *Streptomyces* spp. (Lu *et al.*, 2008; Hamdali *et al.*, 2008a; Goudjal *et al.*, 2014; Sreevidya *et al.*, 2016). Recently, Wu *et al.* (2019) reported that *Streptomyces* spp. produce a novel compound ‘Antifungalmycin N2’ which was effective against *R. solani*. De Oliveira *et al.* (2014) and Kanini *et al.* (2013) reported that *Streptomyces* spp. demonstrated antimicrobial activity against *Xylella fastidiosa* and *R. solani*. Similarly, *S. vinaceusdrappus* showed activity against rice fungal pathogens. *S. violarius* was effective against leaf blight disease pathogens (e.g. *A. alternata*). Furthermore, studies have discovered a metabolite, namely ‘A Factor’, which induced the production of other secondary metabolites in Actinobacteria (Fiebig *et al.*, 2018). Different kinds of antibacterial agents, such as lankacidin C (Lu *et al.*, 2018), lankamycin (Lu *et al.*, 2018), actinorhodin (Čihák *et al.*, 2017) and aureomycin, are synthesized by *Streptomyces* spp., including avermectins (Cheng *et al.*, 2018b). Table II shows the lists of Actinobacteria which suppress plant pathogens and their efficiency in biocontrol activity.

TABLE II

Biocontrol activity of Actinobacteria against pathogens for plant protection and disease management

Actinobacteria name	Host	Pathogen name	Biocontrol activity against	References
<i>S. avermitillis</i> , <i>S. cinnamonesis</i> and <i>S. canus</i>	<i>Punica granatum</i> L.	<i>Cerotocystis fimbriata</i> , <i>Fusarium oxysporum</i> , <i>Macrophomina</i> sp. and <i>Sclerotium</i> sp.	Suppression level 58.0% to 85.0%	Panneerselvam <i>et al.</i> (2020)
<i>Streptomyces</i> spp. <i>S. rochei</i> and <i>S. sundarbansensis</i>	<i>O. sativa</i> <i>Mikania micrantha</i>	<i>Burkholderia glumae</i> <i>Fusarium graminearum</i>	Bacterial diseases Inhibit <i>F. graminearum</i> by 39.31% and 31.72%, respectively	Suarez Moreno <i>et al.</i> (2019) Han <i>et al.</i> (2018)
<i>Streptomyces</i> spp. CB-75	<i>Musa</i>	<i>F. oxysporum</i> f. sp. <i>cubense</i> Race 1, <i>F. oxysporum</i> f. sp. <i>cubense</i> Race 4, <i>C. gloeosporioides</i> (Penzig), <i>C. fragariae</i> Brooks, <i>C. acutatum</i> Simmonds, <i>Botrytis cinerea</i> Persoon, <i>C. musae</i> ; <i>Curvulatia fallax</i> , <i>C. gloeosporioides</i> , <i>A. tenuissima</i> and <i>C. gloeosporioides</i>	Against plant pathogenic fungi and highest antifungal activity against <i>C. gloeosporioides</i>	Chen <i>et al.</i> (2018b)
<i>S. vinaceusdrappus</i> <i>S. violarius</i>	<i>O. sativa</i> <i>Arachis hypogaea</i>	<i>Magnaporthe oryzae</i> (<i>Pyricularia oryzae</i>) <i>Alternaria alternata</i>	Rice fungal pathogen Biocontrol of leaf blight disease	Law <i>et al.</i> (2017) Chitraselvi and Kalidass (2016)
<i>S. globosus</i>	<i>Phoenix dactylifera</i>	<i>Thielaviopsis punctulata</i>	biocontrol of the black scorch disease	Saeed <i>et al.</i> (2017)
<i>Streptomyces</i> spp.	<i>Fragaria</i> × <i>ananassa</i>	<i>B. cinerea</i> , <i>Mucor hiemalis</i> , <i>Rhizopus stolonifer</i> , and <i>S. sclerotiorum</i>	Suppression of fruit rot pathogen	Lyu <i>et al.</i> (2017)
<i>S. rimosus</i>	<i>Cucumis sativus</i>	<i>F. oxysporum</i> f. sp. <i>cucumerinum</i>	Prevents the development of the disease caused by <i>F. oxysporum</i> <i>C. sativus</i>	Lu <i>et al.</i> (2016)
<i>Nonomuraea</i> spp. <i>Micromonospora</i>	<i>O. sativa</i> <i>Solanum lycopersicum</i>	<i>Xanthomonas oryzae</i> <i>Fusarium circinatum</i> , <i>Sclerotinia sclerotiorum</i> , <i>R. solani</i> and <i>B. cinerea</i>	Bacterial leaf blight Against <i>B. cinerea</i> (reduced leaf infection)	Ilsan <i>et al.</i> (2016) Martínez-Hidalgo <i>et al.</i> (2016)
<i>Streptomyces</i> sp. UPMRS4	-	<i>Pyricularia oryzae</i>	Highest activity against mycelial growth of <i>P. oryzae</i>	Awla <i>et al.</i> (2016)
<i>Amycolatopsis</i> spp.	<i>Malus domestica</i>	<i>Colletotrichum gloeosporioides</i>	Against bitter rot	Sadeghian <i>et al.</i> (2016)
<i>Streptomyces</i> spp. PM9	<i>Eucalyptus globulus</i>	<i>Botrytis cinerea</i>	Establishment of gray mold	Salla <i>et al.</i> (2016)
<i>S. vinaceusdrappus</i>	<i>S. lycopersicum</i>	<i>R. solani</i>	Against <i>R. solani</i>	Yandigeri <i>et al.</i> (2015)

<i>Streptomyces</i> spp.	<i>Sorghum bicolor</i>	<i>Macrophomina phaseolina</i>	Control of charcoal rot disease	Gopalakrishnan <i>et al.</i> (2015b)
<i>S. philanthi</i>	<i>O. sativa</i>	<i>Rhizoctonia solani</i>	Effectively suppressed	Boukaew and Prasertsan (2014)
<i>S. flavotricini</i>	<i>O. sativa</i>	<i>Pyricularia grisea</i>	Antifungal activity	Khalil <i>et al.</i> (2014)
<i>S. sindeneusis</i>	<i>O. sativa</i>	<i>Magnaporthe oryzae</i>	Inhibition - pathogen and suppression - leaf symptoms	Zarandi <i>et al.</i> (2009)
<i>Streptomyces</i> spp., <i>Micromonospora</i> spp., <i>Nocardia</i> spp., <i>Actinomadura</i> spp., <i>Microbispora</i> spp., and <i>Actinoplanes</i> spp.	<i>Glycine max</i>	<i>R. solani</i> , <i>F. oxysporum</i> , <i>S. rolfsii</i> , <i>C. truncatum</i> , <i>M. phaseolina</i> and <i>A. alternata</i>	For crop protection and biological control	Dalal and Kulkarni (2014)
<i>Streptomyces</i> spp.	-	<i>Aspergillus niger</i> , <i>Penicillium chrysogenum</i> and <i>Microsporium gypseum</i>	Antifungal activity	Jog <i>et al.</i> (2014)
<i>S. pluripotens</i>	-	<i>S. aureus</i>	Exhibited a broad-spectrum bacteriocin	Lee <i>et al.</i> (2014)
<i>S. fradiae</i> , <i>S. avermitilis</i> , <i>S. cinnamomensis</i> and <i>S. canus</i>	<i>Punica granatum</i> L. cv. Bhagwa	<i>Xanthomonas axonopodis</i> pv <i>punicae</i> (Xap)	Controls bacterial blight disease	Poovarasani <i>et al.</i> (2013)
<i>Streptomyces</i> spp. ASBV-1	<i>Arachis hypogaea</i>	<i>A. parasiticus</i>	Inhibits the spore viability of <i>A. parasiticus</i>	Zucchi <i>et al.</i> (2008)

PLANT GROWTH-PROMOTING TRAITS AND PLANT PROTECTION ABILITIES OF ACTINOBACTERIA

Nitrogen fixation

Nitrogen (N) has been regarded as one of the most important elements for plant and accounts for about 78% of the atmosphere. Due to the presence of stable triple bond, N remains unavailable for most of the organisms (Callaham *et al.*, 1978). N fixing bacteria convert the atmospheric N₂ into ammonical form (NH₄⁺) that becomes available for plants (Dudeja *et al.*, 2012). Plants undergoing symbiosis with N fixing bacteria generally do not experience N deficiency and their co-existence in soil decreases the rate of N application (Hurek *et al.*, 2002). Two groups of N-fixing bacteria, rhizobia and *Frankia*, form nodules, which are specialized organs, required for coexistence of microorganisms in roots of the host plant. Diazotrophy in Actinobacteria for long time has been thought to be restricted to the genus *Frankia* (Villegas *et al.*, 1997; Buckley *et al.*, 2007; Trujillo *et al.*, 2010; Gonzalez-Ruiz *et al.*, 2012; Dahal *et al.*, 2017). Molecular studies revealed the existence of *nifH* gene in numerous species of *Frankia* and this observation has brought deep insights into the origin and emergence of bacterial isotrophs among the Actinobacteria phyla (Buckley *et al.*, 2007; Trujillo *et al.*, 2010; Gonzalez-Riz, 2012). These findings on Actinobacteria have stimulated further research and inquiries on the basis of diazotrophy and *nifH* gene transfer. Studies have found *Frankia* establish symbiosis with several non-legume plant species (>200) belonging to 23 genera of 8 families called actinorhizal plants (Normand and Lalonde 1982). Additionally, several studies have been performed on non-*Frankia* N fixing Actinobacteria, and discovered new plant-Actinobacteria associations among which *Micromonospora* based N fixation has been the most prevalent one. Various species belonging to the genus *Micromonospora* have been obtained in Italy and Brazil from the root surface of plants such as maize (Carro *et al.*, 2012; Martínez-Hidalgo *et al.*, 2015). In recent years *Micromonosporae* have been reported as the major symbiont involved in N fixing in root nodules of both leguminous and actinorhizal plants (Garcia *et al.*, 2010; Carro *et al.*, 2012; Trujillo *et al.*, 2015).

Actinobacteria as a phosphate enhancer

Phosphorus (P) is one of the key plant nutrients responsible for plant growth promotion. In soil, P is mainly present in unavailable form (*i.e.* insoluble, precipitate or immobilized form), constituting 30-65% of organic P present in total soil (Shen *et al.*, 2011). Thus, it is very difficult for plants to utilize this type of P because of their association with different cations present in soil. The availability of P directly affects crop production, if the P level is low. Plant uptake of P is only in the form of soluble organic monobasic (H₂PO₄⁻) and dibasic (HPO₄²⁻) ions (Narang *et al.*, 2000). Phosphate solubilizing soil microbes have the ability to release free phosphate by mechanisms including production of organic acids such as commonly succinic acid, gluconic acid, oxalic acid and citric acid which participate in dissociation of chemical bonds of bound phosphates in soil (Verma, 2019; Rajput *et al.*, 2013). Therefore, converting the unavailable forms of P to available state by solubilization and mineralization is one of the basic criteria involved in the selection and introduction of P solubilizing microorganisms (PSM), among which Actinobacteria have been found to be important (Lunggani and Suprihadi, 2019). These bacteria are used to secrete different types of organic acids (e.g. gluconic acid and ketogluconic acid etc.) that decrease the

rhizosphere pH, thereby releasing bound forms of P, such as $\text{Ca}_3(\text{PO}_4)_2$, into calcareous soils (Farhat *et al.*, 2015).

Recent research has established the P-solubilizing activity of Actinobacteria has role in sustainable agriculture (Hozzein *et al.*, 2019). It has been found that about 20% of Actinobacteria, such as *Streptomyces* and *Micromonospora*, have high P solubilization potential (Barreto *et al.*, 2008). Jog *et al.*, (2014) reported that highest malate amount was recorded for a P solubilizing Actinobacteria, *Streptomyces mhcr0816*. Malate synthesis may be performed by glyoxalate by-pass that was proved among relative expression of isocitrate dehydrogenase (IDH), malate synthase (MS) and isocitrate lyase (ICL) using specifically designed enzymes and primers activities. Some studies have shown that N-fixing Actinobacteria also have present P solubilization activity (Sahu *et al.*, 2007; Gangwar *et al.*, 2012; Salcedo *et al.*, 2014). Actinobacteria with P solubilization potential increase plant growth due to their ability to produce active metabolites such as phytohormones, siderophores and antibiotics, as well as their ability to withstand stressful conditions (Hamdali *et al.*, 2008c; Tanvir *et al.*, 2018). A study found that 44% of all Actinobacteria isolated from the rice rhizosphere had P solubilization activity in which the actinobacterium, *S. lavendulae* R22, showed the highest amount of P solubilization (265 mg/l) (Gangwar *et al.*, 2012). In one experiment, it was reported that from all the Actinobacteria isolated from the rhizosphere of *Trifolium repens*, Actinobacteria exhibited 20% inorganic P dissolution activity. In that experiment, all isolates were capable of producing acid phosphatase, and 43% produced alkaline phosphatase, which showed the higher potential of Actinobacteria to mineralize organic P (Richardson *et al.*, 2009). In addition, Actinobacteria have been also reported producing phosphatases (Franco-Correa *et al.*, 2010; Pragya *et al.*, 2012).

The rate of solubilization of P by Actinobacteria depends on: (i) the type of insoluble inorganic phosphorus sources, (ii) the intrinsic phosphorus solubilization ability of the Actinobacteria species and (iii) the amount and types of photosynthetic compounds present in the rhizosphere (Banik and Dey, 1982). It has been observed that a single Actinobacteria species can have the capacity to dissolve both inorganic and organic P (Guang-Can *et al.*, 2008; Asadu *et al.*, 2018). Actinobacteria have also been reported to produce the extracellular enzyme phytase in addition to phosphatase. The phytate mineralized through phytase is known as a predominant form of phosphorus but unavailable to plant hosts. Phytate is produced by sporulating *Streptomyces*, *Bacillus* and several other Actinobacteria (Richardson and Simpson, 2011; Jog *et al.*, 2012). Ghorbani-Nasrabadi *et al.* (2012) reported the isolation of phytate-degrading Actinobacteria (*S. alboniger* and *S. venezuelae*) from arable soil with the highest activity at 46.30%. In another study, P-soluble Actinobacteria isolated from Moroccan P mines were tested on the wheat crop, and the results implied an increase in wheat plant biomass. The highest P solubilizer, which was Actinobacteria strain BH7, produced the highest biomass in wheat under *in-vitro* conditions. An increase in plant yield of 70% was observed in test tubes and of more than 30% in soil with rock P. Similarly, Jog *et al.* (2014) reported Actinobacteria isolated from soil with P solubilization (1.916 mg l^{-1}) and production of phytase (0.68 U ml^{-1}), auxin (136.50 mg l^{-1}), siderophore (47.40 mg l^{-1}) and chitinase (6.20 U ml^{-1}). Inoculation of this Actinobacteria (*Streptomyces mhcr0816*) with the wheat plant not only increased the biomass and yield but also enhanced the contents of potassium, iron and zinc. If applied as bio-fertilizers, efficient strains of Actinobacteria can reduce the use of chemical fertilizers (Sahu *et al.*, 2007; Hozzein *et al.*, 2019). PSM has been found as an alternative biotechnology solution for sustainable agriculture, including the heterogeneous and naturally abundant rhizosphere microbes, whose participation *in-toto* fulfills phosphate demands of the plant (Richardson and Simpson, 2011).

Phytohormone production by Actinobacteria and their role in plant growth

Plant hormones perform an essential role in controlling plant cell physiological processes (Le Bris, 2017) and also in plant-microbial interactions (Solans *et al.*, 2011). The effects of plant hormones (e.g. auxins, abscisic acid, ethylene, cytokines and gibberellins) on plant growth depend upon the hormone levels (Passari *et al.*, 2016). Some microorganisms (including fungi and bacteria) are capable of synthesizing these phytohormones (Shutsrirung *et al.*, 2013). The synthesis of *in vitro* phytohormones including gibberellic acid, auxins and cytokinins from Actinobacteria, which support in plant growth, has been documented by several researchers (Mahadevan and Crawford, 1997; Ghodhbane-Gtari *et al.*, 2010; Gopalakrishnan *et al.*, 2014; Anwar *et al.*, 2016; Solá *et al.*, 2019).

The primary type of auxin is IAA, which controls many fundamental cellular mechanisms including cell division, differentiation and elongation (Le Bris, 2017). It also results in enhanced formation of root hair, which improves the rhizospheric area and nutrient absorption capacity from soil. Auxins also play an integral role in several developmental processes, like the development of embryos and fruit, vascular tissue differentiation, elongation, organogenesis, root patterning, tropic growth, apical dominance and apical hook formation (Dobbelaere *et al.*, 1999). Farina *et al.* (2012) reported that five isolates of Actinobacteria produced high amount of IAA when grown on tryptophan supplemented medium. Several reports have suggested that the application or treatment with Actinobacteria in plant or seeds induces seed germination, seedling growth, rooting and cell elongation etc. (El-Tarabily, 2008 ; Goudjal *et al.*, 2013). Radha T.K. (2016) reported improvement of growth and yield parameters of maize and chickpea with Actinobacterial strains inoculation. Meguro *et al.* (2006) reported that plant inoculated with *Streptomyces* sp. MBR52 (IAA producer), improved emergence and elongation of new roots within a few days. Goudjal *et al.*, (2013) reported *S. rochei* strain PTL2 isolated from Algerian native plants showed IAA was of 127 $\mu\text{g mL}^{-1}$. Inoculation of this isolate in the tomato plant resulted in a significant increase in seed germination and root elongation rates, respectively. In a similar experiment, inoculation of tomato with auxin phytohormones producing *S. caeruleatus* ZL2 strain significantly increased dry weight and root length of the plant (Zamoum *et al.*, 2017). Inoculation of plants with an auxin and gibberellin-producing actinobacterium, *Streptomyces* sp. IA1, isolated from field soil, was also found to increase both tomato (Goudjal *et al.*, 2016) and wheat growth (Toumatia *et al.*, 2016). El-Tarabily *et al.* (2008) reported that the inoculation of cucumber plants with endophytic Actinobacteria significantly increased growth of the plant due to the production of IAA, indole-3-pyruvic acid, and gibberellic acid. Shutsrirung *et al.* (2013) reported that 64 isolates from mandarin (*Citrus reticulata* L.) were found to belong to *Nocardopsis*, *Streptomyces*, *Spirillospora*, *Microbispora*, *Nocardia*, and *Micromonospora* genera, from which 85.3% belonged to the *Streptomyces* genus. From these 64 isolates, the top 12 auxin-producing isolates were inoculated into the mandarin plant, which resulted in increased shoot - root fresh weight and height. Cytokinin production in the rhizosphere has been reported in plant-associated Actinobacteria (Khamna *et al.*, 2010; Patel and Saraf, 2017), such as *S. flavousare* (Coppola and Giannattasio 1968). Actinobacteria isolated from *Ochetophila trinervis* have been reported to have the potential for auxin (IAA), cytokinin and gibberellic acid production (Solans *et al.*, 2011). Based on reports and reviews, it is seen that the phytohormone-producing Actinobacteria play a superior role in plant-microbe interactions and act as an effective plant growth regulator that can be used for rhizospheric engineering purposes (Khamna *et al.*, 2010; Solans *et al.*, 2011; AbdElgawad *et al.*, 2019).

Siderophore production by Actinobacteria for nutrient acquisition

Actinobacteria are a versatile group of soil bacteria as far as their metabolic activity is concerned. They can produce different types of substances, including siderophores, which are low-molecular-weight iron-chelating [ferric iron {Fe (III)}] compounds (Walsh and Marshall, 2004; Oves-Costales *et al.*, 2009). Siderophores are generally produced by microorganisms under iron-deficient conditions, and they include phenolate hydroxamates, catecholate, salicylates and carboxylates compounds (Kannahi and Senbagam, 2014). Wittenwiler (2007) suggested that iron bioavailability is enhanced by siderophores through influencing the low mobility and solubility of iron. This atom is coordinated in a soluble complex through siderophores which facilitate dissolution and attach on the mineral surface. The main function of these compounds is the utilization and acquisition of the insoluble form of iron (Fe^{+3}) in available form. Siderophores can supply the iron nutrient during iron deficiency periods of plant development, which have generally been observed in alkaline soils with $\text{pH} > 7.5$ (Vansuyt *et al.*, 2007). Siderophores have been referred to as micronutrient fertilizers because they improve nutrient availability of minerals by chelating those which are required in a very small amount (Ahmed and Holmström, 2014). Sathya *et al.* (2017) suggested that the siderophores can also improve rhizosphere colonization of bacteria. *A. madurae*, *N. asteroides*, and *S. griseus* are among these siderophore-producing Actinobacteria (Kannahi and Senbagam 2014). Actinobacteria produce mainly hydroxamate and salicylate types of siderophores. Desferrioxamine E, a siderophore, has been reported to be produced by *S. griseus* (Yamanaka *et al.*, 2005). Similarly, coelichelin (Lautru *et al.*, 2005; Challis and Ravel, 2000) and griseobactin (Patzner and Braun 2010) are different types of siderophores produced by *Streptomyces* spp. A new class of siderophores such as heterobactin (hydroxamate and catecholate type) have been found to be produced by *Rhodococcus* (Carrano *et al.*, 2001).

1-aminocyclopropane-1-carboxylic acid (ACC) deaminase activity

When the plant is under stress, ethylene is a phytohormone that is evolved through its roots, limiting the growth and development of the plant's roots and further decaying the plant's overall growth (Pandey and Gupta, 2019). Under stress conditions, the production of ethylene phytohormone is mediated by the ACC precursor. A wide variety of microbes are able to separate the amine group from the ACC by the enzyme ACC demaminase (ACCd), and convert it into two ammonia (as a source of N) and α -ketobutyrate. Therefore, these bacteria in stressful conditions, by reducing the level of ethylene, lead to increased growth and elongation of the plant root and its development, and therefore these plants will have a better and more favorable general condition under stress situation (Misra *et al.*, 2017). Many bacteria including the genera *Enterobacter* (Sarkar *et al.*, 2018) and *Bacillus* (Ghosh *et al.*, 2003) produced ACCd, and reduce ACC content in plant tissues. It has been reported that in Actinobacteria, the genera *Streptomyces* spp. has the ACCd activity (El-Tarabily, 2008).

Role of Actinobacteria in decomposition by the production of degrading enzymes

Enzymes play a catalytic role in all biosynthetic and decomposition processes. Actinobacteria play a significant role in decomposition (Tiwari *et al.*, 2019), due to their saprophytic nature and production of different types of plant cell wall degrading enzymes (Ramírez and Calzadiaz, 2016). These enzymes can help to degrade various complex polymers, such as lignin, hemicellulose, laccase, xylanase and cellulose. Ventorino *et al.* (2016) reported that important lignocellulose degrading enzymes are produced by *Streptomyces* spp. The degrading enzymes which are produced by Actinobacteria (Gupta *et al.*, 1995; Fodil *et al.*, 2011) for decomposition provide organic nutrients to plants and are shown in Fig. 3. Apart from the lignocellulolytic enzymes, chitinase produced by Actinobacteria has shown potential for biocontrol activity of several phytopathogens, including fungal and insect pests. The fungal cell wall and insect cell wall contain chitin, which can be degraded by chitinase enzyme (Yandigeri *et al.*, 2015). In this way, Actinobacteria (*Streptomyces* spp.) inhibit the growth of phytopathogens and protect the plant.

Fig. 3 Different enzymes produced by Actinobacteria for increased organic matter decomposition and crop productivity

Actinobacteria as metabolite and antibiotic producers for protection

Actinobacteria are known for production of different secondary metabolites like antibiotics (low molecular weight secondary metabolites that can exterminate or inhibit the growth of other organisms) that can indirectly help plant growth by reducing the incidences of phytopathogenic bacteria and fungal species (Table III; Fig. 4). A variety of antibiotics such as polyketides, peptide β -lactams in addition to other secondary metabolites, are responsible for antifungal, immunosuppressive and antitumor activity (Behal, 2000). Liu *et al.* (2012) reported that 45 % of all antibiotics were produced from Actinobacteria. Among these, *Streptomyces* spp. was dominant as it was capable of producing a wide spectrum of antibiotics (Toumatia *et al.*, 2015). Streptomycin, discovered by Selman A. Waksman in 1943 (Woodruff, 2014), was the first antibiotic to be effective against tuberculosis, and it was produced from *S. griseus*. *Streptomyces* spp. are clearly capable of producing bioactive secondary metabolites with antimicrobial (Singh *et al.*, 2016), antifungal and antiviral activities (Maldonado *et al.*, 2010). Molano *et al.*, (2000) reported that the antibiotic actinomycin, produced by *Nocardia* spp., strongly inhibited *Fusarium oxysporum*. Similarly, *S. avermitilis* produced avermectins, which acts as a potent antimicrobial as well as antiparasitic agent (Cheng *et al.*, 2018b). Actinobacteria also produce VOCs (low molecular weight carbon-containing compounds) which are easily evaporated under normal temperature and help to reduce the pathogenic infestation (Wang *et al.*, 2013). In addition, Quecine *et al.* (2008) reported that *Streptomyces* endophytes with chitinolytic activity significantly reduce pathogenic infection besides plant growth promotion.

Secondary metabolites synthesized by Actinobacteria are not only involved in plant growth promotion and control of pathogens but are also effective against major insect pests of agricultural crops and disease treatments or control (Table III; Fig. 4). The antibiotic avermectin produced by *S. avermitilis* was found to stimulate the gamma amino butyric acid (GABA) system and disrupt nicotinic acetylcholine receptors (Adhya *et al.*, 2018) of the parasite. Nikkomycins, a class of nucleoside peptide antibiotics produced by *S. tendae*, inhibit chitin synthesis of fungi and insects. Similarly, milbemycin, a class of macrocyclic lactone derivatives produced by *S. Hygroscopicus*, showed a broad spectrum of activity

against agricultural pests such as aphids, mites, caterpillars, intestinal worms and other parasites that prey on crops and livestock. Tetranectin, a pesticidal macrotetrolide antibiotic produced by *S. aureus*, has been used as an agricultural miticide in Japan since 1973. Spinosyn A and Spinosyn D, produced by *Saccharopolyspora spinosa*, were found to be active against lepidopteran and Dipteran pests (Snyder *et al.*, 2007). Chen *et al.* (2018a) isolated 85 actinomycetes strains from the *Azadiachta indica* tree and tested them for their insecticidal action against *Myzus persicae*. The results revealed that crude extracts from 24 strains were highly effective against *M. persicae* with above 60% of insecticidal activity. El-khawaga and Megahed (2012) screened the antibacterial and insecticidal activities of crude extract of 20 actinomycetes isolates from desert soil samples collected from different locations of Cairo, Egypt. *S. bikiniensis* A11 was found to be the most active actinomycetes isolate against Gram positive and negative bacteria as well as against 2nd instar larvae of cotton leaf worm *Spodoptera littoralis*. The Actinobacteria genome sequencing have provided insights into the production of the secondary metabolites found the gene clusters responsible for biosynthesis of secondary metabolites are arranged as genomic islands and are dynamic entities transferred from one actinomycete to other through horizontal gene transfer (HGT) (Penn *et al.*, 2009). ActDES (Actinobacterial Database for Evolutionary Studies) is a curated database developed using high-quality genetic sequences of 612 genomes of Actinobacteria covering 80 genera, primarily aimed at understanding the genetic architecture of Actinobacteria and designing a metabolic engineering framework (Schniete *et al.*, 2020). HGT has been mainly found in prokaryotes and contributes to the evolution of new metabolites and pathways of degradation, such as the transfer of Nsar (N-succinylamino acid racemization) and osbs (o-succinylbenzoate synthase) from Firmicutes to Actinobacteria using HGT that required for menaquinone biosynthesis (Bar-Even *et al.*, 2011; Odokonyero *et al.*, 2018).

Fig. 4 Actinobacteria: secondary metabolites and antibiotic production for plant protection and disease control

TABLE III

Metabolites and antibiotics produced by Actinobacteria and their activities

Actinobacteria name	Metabolites / Antibiotic names	Mode of action	References
<i>S. avermitilis</i>	Avermectins	Antiparasitic, antimicrobial, pesticide	Rath <i>et al.</i> (2019); Cheng <i>et al.</i> (2018b); Choi <i>et al.</i> (2018); Zhang <i>et al.</i> (2015)
<i>S. griseus</i> , <i>S. tinghiriensis</i> and <i>S. rimosus</i>	-	Antimicrobial	Ouchari <i>et al.</i> (2019)
<i>Micromonospora</i> spp., <i>Salinispora</i> spp. and <i>Streptomyces</i> spp.	-	Antimicrobial	Phongsopitanun <i>et al.</i> (2019)
<i>S. griseus</i> , <i>S. flavovirens</i> , <i>Kocuria kristinae</i> and <i>K. rósea</i>	Bioactive substance	Antimicrobial	Elbendary <i>et al.</i> (2018)
<i>S. rochei</i>	Lankacidin C and Lankamycin	Antibacterial	Lu <i>et al.</i> (2018)
<i>S. clavuligelus</i>	Cephamycin C	-	Romero-Rodríguez <i>et al.</i> (2018)
<i>S. coelicolor</i>	Dihydrogranticin	Novel antibiotics	Hasani <i>et al.</i> (2014)
<i>S. sannanensis</i>	Bioactive compound	Antimicrobial	Singh <i>et al.</i> (2014)
<i>S. coelicolor</i>	Prodiginines	-	Moore <i>et al.</i> (2012)
<i>Actinoplanes philippinensis</i>	Chitinase	Pesticidal	Gadelhak <i>et al.</i> (2005)
<i>Streptomyces</i> sp. 8E-12	Methoxyhygromycin	Herbicidal	Lee <i>et al.</i> (2003)
<i>Streptomyces</i> spp.	UN	Antiviral	Mohamed and Galal (2005)
<i>Streptomyces avermitilis</i>	Avermectin	Nematicidal	Jayakumar (2009)
<i>Streptomyces</i> spp.	UN	Fungicidal	Baharlouei <i>et al.</i> (2011)
<i>Streptomyces</i> sp RK-1051	Enopeptin A	Antiviral	Osada (1995)
<i>Streptomyces</i> AzR-051	-	Antifungal	Verma <i>et al.</i> (2011)
<i>Streptomyces</i> sp.	-	Antifungal	Sangmanee <i>et al.</i> (2009)
<i>Streptomyces</i> sp.	-	Antifungal and Antibacterial	Oskay M (2009)
<i>Streptomyces hygrosopicus</i>	-	Antifungal	Prapagdee <i>et al.</i> (2008)
<i>Streptomyces</i> spp.	-	Antifungal	Errakhi <i>et al.</i> (2007)
<i>S. sannanensis</i> RJT-1	-	Antibacterial	Vasavada <i>et al.</i> (2006)
<i>Streptomyces halstedii</i>	-	Antifungal	Joo (2005)
<i>S. rochei</i> F20	Streptothricin	-	Anukool <i>et al.</i> (2004)
<i>Streptomyces</i> sp. AP77	Anti- <i>Pythium</i> protein (SAP)	Antifungal	Woo and Kamei (2003)
<i>Streptomyces</i> sp.	-	Antifungal	Samac <i>et al.</i> (2003)
<i>Streptomyces</i> sp.KH-614	cyclo(L-leucyl-L-prolyl)	Antifungal	Rhee (2003)
<i>S. violaceusniger</i> G10	-	Antifungal	Getha and Vikineswary (2002)
<i>Streptomyces viridodiasticus</i>	-	Antifungal	El-Tarabily <i>et al.</i> (2000)

<i>S. violaceusniger</i> YCED-9	AFA (Anti-Fusarium Activity), Nigericin, Geldanamycin	Antifungal	Trejo-Estrada <i>et al.</i> (1998)
<i>S. violaceonige</i>	Tubercidin	Antifungal	Hwang <i>et al.</i> (1994)
<i>S. hygrosopicus</i> AM-3672	Herbimycin	Herbicide	Omura <i>et al.</i> (1979)

ACTINOBACTERIAL MEDIATED REGULATION OF PLANT STRESS

Achieving the expanding (about 1.05% each year) global food demand is a massive problem for the agriculture sector (World Population Prospects, 2019). Global agricultural productivity, quality has been regulated by biotic (infection of the plant due to various pests and pathogens) and abiotic stress (salt concentration, water content, and nutrient level in soil, etc.) (Atkinson and Urwin 2012, Kumar *et al.*, 2020). Actinobacterial mediated biotic stress regulation in the plant has been fulfilled by the production of different antimicrobial substances. Salinity and drought are the most devastating abiotic stresses that cause a decrease in plant productivity. Salinity stress caused by the high concentrations of mineral elements (such as Na^+ , Ca^+ , Mg^+ , K^+ , Cl^- , SO_4^{2-} , CO_3^{2-} , HCO_3^- and 468NO_3^-) in the soil. Soil salinity resulted in detrimental effects *i.e.* osmotic stress, oxidative stress, nutrient (N, Ca, K, P, Fe, and Zn) deficiency, ion toxicity, etc. in plants (Grover *et al.*, 2016). Drought is another important environmental stress, that happens due to the absence of an adequate level of soil moisture content. In the drought stress conditions, the growing Plants have water limitation and nutrient deficiencies (Grover *et al.*, 2016). To overcome this environmental stress, soil Actinobacteria plays a critical role by synthesizing different phytohormones, siderophores, phosphate solubilization, ACC deaminase activity, secondary metabolites, extracellular polysaccharides (EPS) production, regulation of stress-responsive genes in the plant, etc. (Table IV) (Grover *et al.*, 2016).

TABLE IV

Actinobacterial mediated alleviation of abiotic stress in plant

Actinobacteria name	Host/Plant	Attributes	Reference
Salinity Stress			
<i>Nocardioides</i> sp. NIMMe6	Wheat	IAA	Meena <i>et al.</i> (2020)
<i>Streptomyces</i> sp. GMKU 336	Rice	Reduction of ethylene by the action of ACCd	Jaensaeng <i>et al.</i> (2018)
<i>Arthrobacter</i> sp.	Maize	IAA, ACCd, biofilm formation	Aslam and Ali (2018)
<i>Arthrobacter protophormiae</i> (SA3)	Wheat	Enhancing IAA, reducing ABA/ACC content, modulating expression of a regulatory component (CTR1) of the ethylene signaling pathway and DREB2 transcription factor	Barnawal <i>et al.</i> (2017)
<i>A. pascens</i>	Maize	The accumulation of osmolytes, including sugar and proline, and the elevation of antioxidant enzymes activity	Ullah and Bano (2015)
<i>S. rochei</i> SM3	Chickpea	Increased biomass accumulation, antioxidant activities	Srivastava <i>et al.</i> (2015)
<i>Streptomyces</i> sp. strain PGPA39	Tomato	IAA, P solubilization, ACCd	Palaniyandi <i>et al.</i> (2014)
Drought Stress			
<i>S. pseudovenezuelae</i> and <i>A. arilaitensis</i>	Maize	IAA and ACCd	Chukwuneme <i>et al.</i> (2020)
<i>Streptomyces</i> sp. Ac3	Maize	Flavonoid, antioxidant, phytohormones and Siderophores production and	Warrad <i>et al.</i> (2020)

<i>Streptomyces</i> sp. Ac5	Maize	improved the photosynthesis rate Flavonoid, phytohormones and siderophores production and improved the photosynthesis rate	Selim <i>et al.</i> (2019)
<i>Citricoccus zhacaiensis</i> B-4 (MTCC 12119)	Onion	Increased the germination rate	Selvakumar <i>et al.</i> (2015)

ROLE OF ACTINOBACTERIA IN SOIL HEALTH AND NUTRIENT MOBILIZATION

Soils contain a huge population of living microorganisms that derive their energy by oxidizing organic residues (OR) which are generally left behind after harvesting crops, growth on the soil, or by livestock feeding on these crops. Beneficial soil microorganisms can be classified into four major divisions, which are bacteria, fungi, Actinobacteria, and algae. Bacteria and fungi are the first to act upon OR added to the soil, followed by Actinobacteria, because of their slow activity and growth. In soil they decompose the OR which are more resistant and indecomposable and also generate numerous dark brown to black pigments that add to the dark color of soil humus. They are also liable for further decomposition of humus.

Actinobacteria are an intermediate group between bacteria and fungi, and 70% of soil Actinobacteria have been identified as *Streptomyces*. In general, Actinobacteria may have a positive role in nutrition mobilization, which is associated with the capacity to mobilize nitrogen and metal-containing mineral nutrients such as Zn, Fe and Se (Sathya *et al.*, 2017). Actinobacteria such as *Streptomyces* spp. are involved in nutrient management and thus affect soil fertility and serve as nutrient enhancers (Jog *et al.*, 2014). They play a critical role in soil health through many mechanisms, such as organic acid production (Rozycki and Strzelczyk, 1986), P solubilization (Salcedo *et al.*, 2014; Farhat *et al.*, 2015), solubilization of K (Nafis *et al.*, 2019), N₂ fixation (Kucho *et al.*, 2017), decomposition of organic matter (Das *et al.*, 2007), production of plant growth-promoting hormones (Solá *et al.*, 2019), as plant growth regulators, producing siderophores (Lee *et al.*, 2012), plant protection against biotic stress, bio-corrosion, and biodegradation/bioremediation (Limaye *et al.*, 2017). Actinobacteria can also be a source of metabolites that encourage or enhance the growth and development of host plants, as well as decreasing symptoms of disease induced by plant pathogens or many environmental stresses. Radha (2016) reported improvement of soil chemical properties, nutrient mobilization, soil biological activities *i.e.*, beneficial microbial populations and soil enzyme activities (dehydrogenase, acid and alkaline phosphatase) with the inoculation of Actinobacteria on maize and chickpea. Viaene *et al.* (2016) recently emphasized the contribution of *Streptomyces* to growth and nutrient management of plants. In plants, Actinobacteria play a major role in shaping the root micro-biome by modulating the composition of root exudates (chemotaxis) and nutritional exchanges. Plant root exudates are the source of metabolic signals (such as strigolactones, flavonoids and terpenoids) which participate in shaping the rhizosphere microbial communities. The signals that attract *Streptomyces* into the rhizosphere of plants are not clearly understood. *Streptomyces* colonize the root tissues by entering the root from the rhizosphere (Coombs and Franco, 2003). Actinobacteria, such as *Streptomyces* spp., influence soil fertility through the involvement of many components and serve as nutrient enhancers. They play a critical role in maintaining soil fertility and make the complex nutrients into simple mineral forms by secreting hydrolytic enzymes-including amylase, chitinase, cellulase, invertase, lipase, keratinase, peroxidase, pectinase, protease, phytase and xylanase (Ramírez and Calzadiaz, 2016).

IMPROVEMENT OF PLANT RESIDUE DECOMPOSITION BY ACTINOBACTERIA

Lignin degradation potential in *Streptomyces* species is higher than any other species of bacteria (Janusz *et al.*, 2017). Molecular insights into the role played by Actinobacteria during plant residues decomposition have found the reason for predominance of actinobacteria throughout the decomposition process particularly during degradation of crop residues (Wei *et al.*, 2018). Lignocellulose decomposition in soil proceeds through an array of oxidative biochemical reactions caused by series of enzymes secreted by different groups of microorganisms (Kumar and Chandra, 2020), which have definite succession orders depending upon the type of plant residue as found in wheat crop residue (Zhong *et al.*, 2020) and rice residue decomposition (Bao *et al.*, 2020) in soil. Lignin is an important polymer of lignocellulose present in the plant cell wall, that provides strength to the plant residue requires coordinated actions of different lignin degrading catabolic enzymes. Kraft lignin (KL) decomposition studies using gel permeation chromatography coupled with mass spectrometry, have revealed *Streptomyces* sp. S6 produces an array of lignin degrading enzymes including laccases, lignin peroxidases, dye-decolorizing peroxidases and aryl-alcohol oxidases, resulting in reduction of 2115.7 Da of KL in seven days with release of at least eight types of aromatic compounds (Riyadi *et al.*, 2020). Recent advancements have revealed those cryptic pathways involved in metabolism of aromatic compounds generated as by-products during microbial lignin degradation. Most of the microbial degraded lignin by-products include vanillate, cumarate and other lignin aromatic hydrocarbons which are referred to as protocatechuate and phenylacetate are converted into succinyl-CoA and acetyl-CoA using the β -keto adipate pathway using *pca* (protocatechuate) and *paa* (phenylacetate) genes, whereas the phenol derivatives of homoprotocatechuate enters the meta-cleavage pathway leading to production of succinyl-CoA regulated by *Gab* (succinate semialdehyde dehydrogenase) gene, which enter the TCA (trichloroacetic acid) cycle completing oxidation of lignin to CO₂ and H₂O as found in the soil Actinobacteria *Kocuria rhizophila* (Takarada *et al.*, 2008). Genome sequencing have revealed the presence of other different catabolic pathways apart from those discussed above *viz.* 2-hydroxypentadienoate pathway, gentisate pathway, homogentisate pathway and hydroxyquinol pathway as found in the nocardioform Actinobacteria *Rhodococcus ruber* strain Chol-4 (Guevara *et al.*, 2019). Further insights into the genome of *Arthrobacter* sp. strain Rue61a revealed presence of meta cleavage pathway wherein 4-hydroxyphenylacetate catabolism was found to support the growth of this Gram positive bacteria, whereas phenylacetate could not, demonstrating presence of incomplete set of *paa* genes (Niewerth *et al.*, 2012). Actinobacteria have a different type of Type VII secretion system known as WXG100 secretion system for secreting larger protein molecules and found to share homology with similar secretion systems found in some members of other phyla including Proteobacteria, Firmicutes, Cyanobacteria and Lentisphaerae (Sutcliffe, 2011). The presence of competent enzymatic machinery and robust secretion system available for complete catabolism of lignin polymers make Actinobacteria as last successors during decomposition of plant residues. Among the other lignocellulose degrading enzymes produced by actinomycete are auxiliary members of glycoside hydrolases (GHs) including Lytic polysaccharide monoxygenases (LPMOs) as found in the Actinobacteria *Jonesia denitrificans* (Mekasha *et al.*, 2020), *Kitasatospora papulosa* (Corrêa *et al.*, 2019) which are capable of enhancing the rate of lignocelluloses degradation particularly affecting the crystalline cellulose polymers. The first representative of bacterial LPMO was found in the cellulose binding module CBH1 of *Streptomyces olivaceoviridis* (Schnellmann *et al.*, 1994). Later AA10 type LPMO such as CelS2 was identified in *S. coelicolor* (Forsberg *et al.*,

2011), *Streptomyces* sp. SirexAA-E (Takasuka *et al.*, 2013), suggesting that the AA10 group of LPMO are predominantly present in the Actinobacteria *Streptomyces* species (Book *et al.*, 2014). Moreover recent genome sequencing of the Actinobacteria *Streptomyces albus* CAS922 provided insights into the vast lignocellulolytic enzymes repertoire including 232 GHs with 3 belonging to AA10 family identified as LPMO (Tippelt *et al.*, 2020). Earlier reports found some members of *Streptomyces* such as *S. flavovirens* produces lignin degrading enzymes and cause decay of thick vascular tissue walls as in Douglas-fir (Sutherland *et al.*, 1979) and *S. viridosporus* T7A which being found as potent lignin depolymeriser due to secretion of higher amount of extracellular esterases was also found to be a potent phytopathogen (Donnelly and Crawford, 1988). Presently, several nonpathogenic beneficial Actinobacteria have been known among which some lignocellulose degrading Actinobacteria species have been classified as probiotic entites for plants which includes *Actinoplanes*, *Agromyces*, *Arthrobacter*, *Curtobacterium*, *Frankia*, *Kocuria*, *Microbacterium*, *Microbispora*, *Micromonospora*, *Nocardia*, *Streptomyces* and *Rhodococcus* through different PGPR traits including as mentioned above through production of phytohormones, P solubilization, siderophore production, antimicrobial and antagonistic activities suggested by Menendez and Carro (2019).

IMPACT OF FARMING PRACTICES ON ACTINOBACTERIA DIVERSITY IN SOIL

Cultural independent studies have revealed the population of Actinobacteria to be higher in non-cultivated soil rather than cultivated soil (Wolińska *et al.*, 2019). The finding suggested, Actinobacteria are sensitive to physical disturbances in soil, which breaks the actinomycetal hyphae that are difficult to repair. The cell diameter of *S. coelicolor* although less than 1 μm but can reach 100 μm through hyphal extensions occurring at the tips by using membrane vesicles transporter, which can become perturbed by tangential forces in soil acting on the hyphae resulting in mechanical disruption of hyphae (Goriely and Tabor, 2003). Therefore, soil texture plays an important role in determining the dominance of soil bacterial species and such studies have found conservation tillage practices to improve abundance of functional bacteria population in soil (Wang *et al.* 2016). Actinobacteria plays an important role in carbon biogeochemical cycle, whose cellulose catabolism rate seems to be controlled by the C/N ratio of soil (de Menezes *et al.*, 2015). Although research have found the application of inorganic fertilizers to have impact the spatial community structure of Actinobacteria (Piao *et al.*, 2008), there are evidences which suggests improvement of relative abundances of Actinobacteria population under long term doses of only N fertilization as compared to combination with P and K (Dai *et al.*, 2018). Studies have also found a certain Actinobacteria consortium comprising four *Streptomyces* sp. strains A2, A5, A11, and M7 had demonstrated capability to remove 70.3% of recalcitrant insecticide lindane from contaminated soil, which showed the Actinobacteria to act as promising tools for restoring soil types contaminated with agrochemicals and thereby help in reclamation of soil arability (Raimondo *et al.*, 2019). Moreover, metagenomic studies have confirmed that the Actinobacteria have higher diversity in organic soil as compared to conventional modern agricultural soil (Sharma *et al.*, 2019). The association of Actinobacteria with AM fungi is quite intriguing since the close association of *Arthrobacter* with the arbuscular mycorrhizae fungi (AMF) *Rhizophagus intraradices*, absorbed cadmium from soil, making it unavailable to plants, as reported for reducing the Cd toxicity in rice (Chen *et al.*, 2019). Because of the high price of chemical fertilizers and the widening gap between supply and demand, the solubilization of nutrients by microorganisms has been seen to be useful and economical. Microbial inoculants are eco-friendly and environmentally secure with low-cost technology, so productivity can

be enhanced and environmental problems can be decreased. They play a vital role in sustainable development by controlling physical, chemical and biological components (Fig. 5).

Fig. 5 Actinobacteria help to manage the availability of nutrients in plants and rhizosphere.

CONCLUSION

In this highly demanding era, the scarcity of food and scientific ability to face new challenges have led to the introduction of novel agricultural tools and chemicals. Indiscriminate use of various chemicals have decreased soil quality, including soil fertility, texture etc. An alternative way to sustain crop yield is by focusing on some biological sources. Actinobacteria are a special and proven group of bacteria that can easily troubleshoot several soil-related problems. These special bacteria participate in different plant growth promoting activities, such as IAA production, enzyme production, hormone production, P solubilization, siderophore production, N fixation and secretion of other useful metabolites. Moreover, their strong biocontrol activities, such as competition with other microorganisms, parasitism, antibiosis and volatile organic compound production, provide additional traits for Actinobacteria along with plant growth promotion activities, which have made these bacteria a good alternative for replacing chemical fertilizers and pesticides. Therefore, taking into consideration all these factors, we can affirm that Actinobacteria are a very promising group of soil microbes with proven records for agricultural practices and can help to maintain ecofriendly crop outputs.

PROSPECTS AND CHALLENGES FOR THE FUTURE

The large and diverse group of Actinobacteria has become widely known primarily for its contribution to the production of different types of metabolites, which have a tremendous impact on agriculture. However, continuous research allows us to discover more and more properties of Actinobacteria that are useful for improving agricultural productivity and maintaining agricultural sustainability. The findings and discoveries of new members of Actinobacteria will generate new challenges and changes, not only in taxonomic reclassification but also in the potential discoveries of many more plant-beneficial properties that would have important biotechnological applications to meet future needs.

ABBREVIATIONS

PGPMs: Plant growth-promoting microorganisms; PGPR: plant growth-promoting rhizobacteria; HYVs: high yielding varieties; PSM: phosphate-solubilizing microorganisms; PSB: phosphate-solubilizing bacteria; PGPS: plant growth-promoting *Streptomyces*; G: guanine; C: cytosine; CP: cellulase production; LP: lipase production; PP: protease production; β -G: β -1,3-glucanase; ChP: chitinase production; PhP: phytase production; GBs: gibberellins; CKs: cytokinins; IAA: indole-3-acetic acid; PS: phosphate solubilization; SP: siderophore production; AP: ammonia production; GABA: gamma amino butyric acid; HCN: hydrogen cyanide production; NF: nitrogen fixation; VOC: volatile organic compound; OR: organic residues; KL: Kraft lignin; TCA: trichloroacetic acid; GHs: glycoside hydrolases; LPMOs: lytic polysaccharide monooxygenases.

CONTRIBUTION OF AUTHORS

DM, RM and BK contributed equally as first authors. DM, RM, BK, AS, NU, EMM, BM, HB, BEG, TKR was involved in the review writing; PKDM, AR, TV, SA, PP, ANG, SD was involved in manuscript refinement and important intellectual content discussion; BK, DM, NU, RM was involved in manuscript figure and table preparation and DM, RM, BK initiated the idea of the review.

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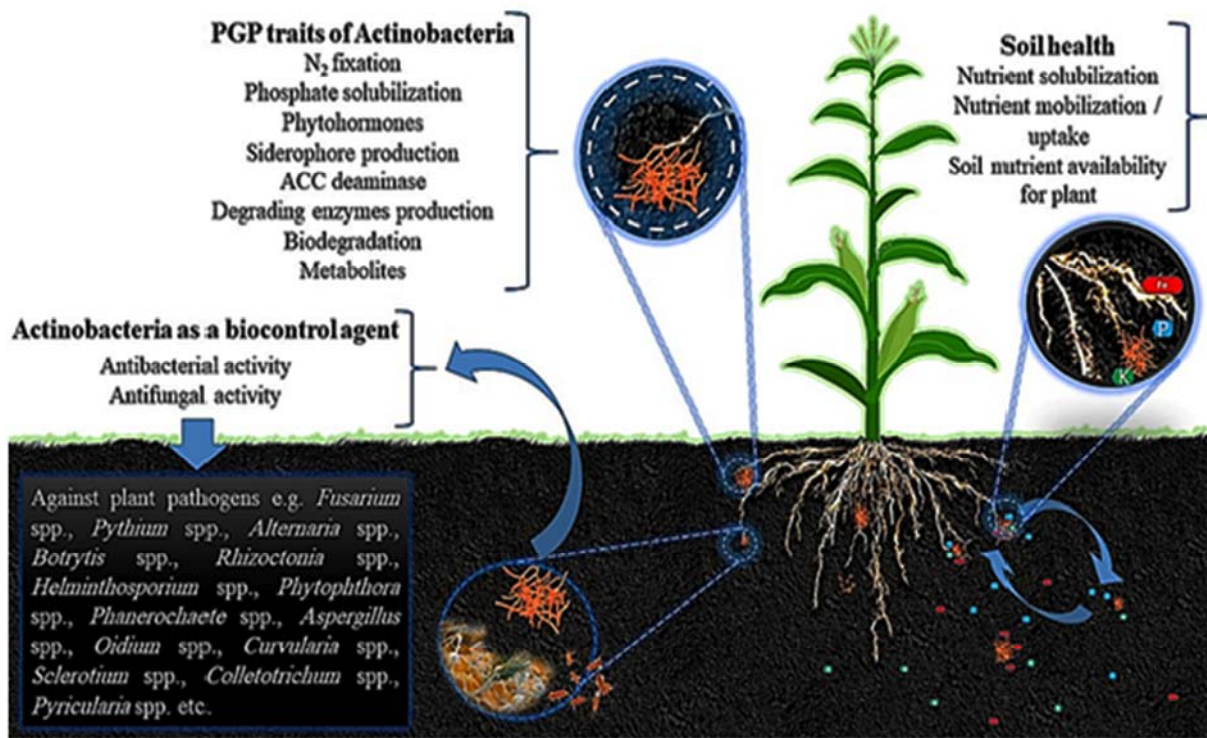


Fig. 1 Beneficial impacts and interaction of Actinobacteria with plant and rhizosphere to imply the acquisition of nutrients, growth promotion and plant protection

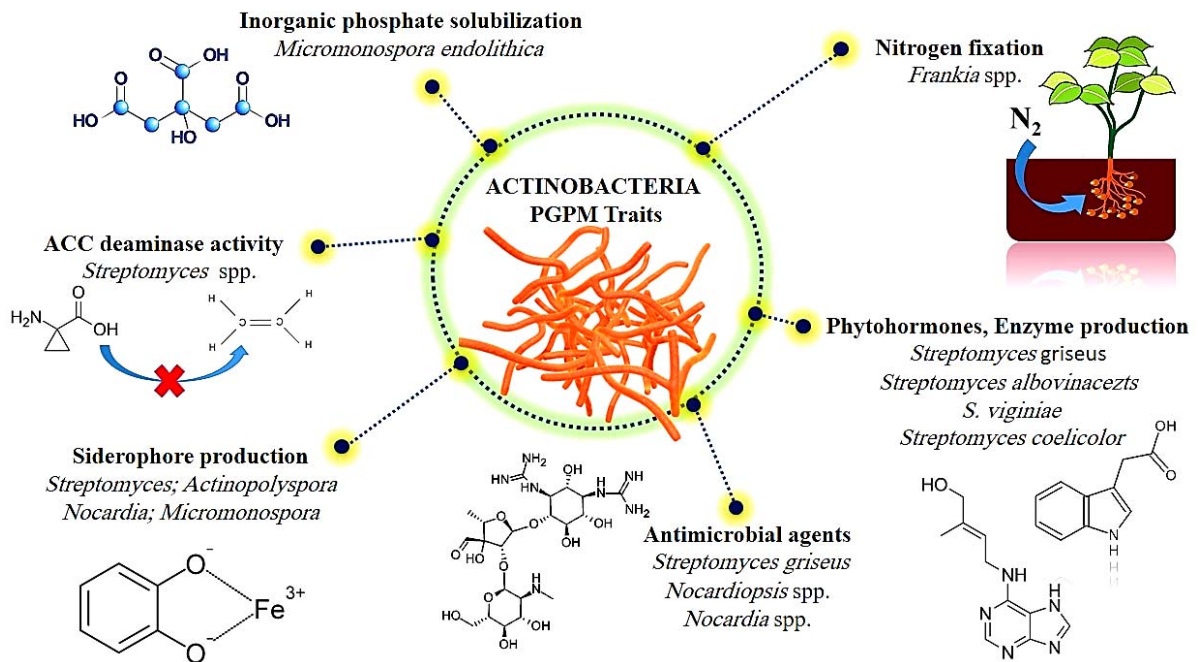


Fig. 2 Major PGP attributes of Actinobacteria.

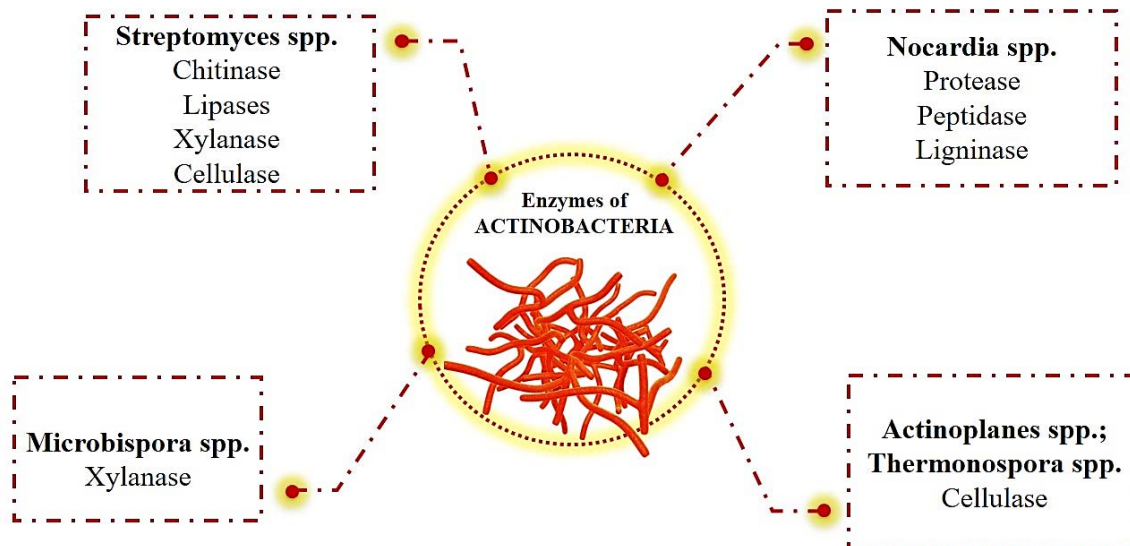


Fig. 3 Different enzymes produced by Actinobacteria for increased organic matter decomposition and crop productivity

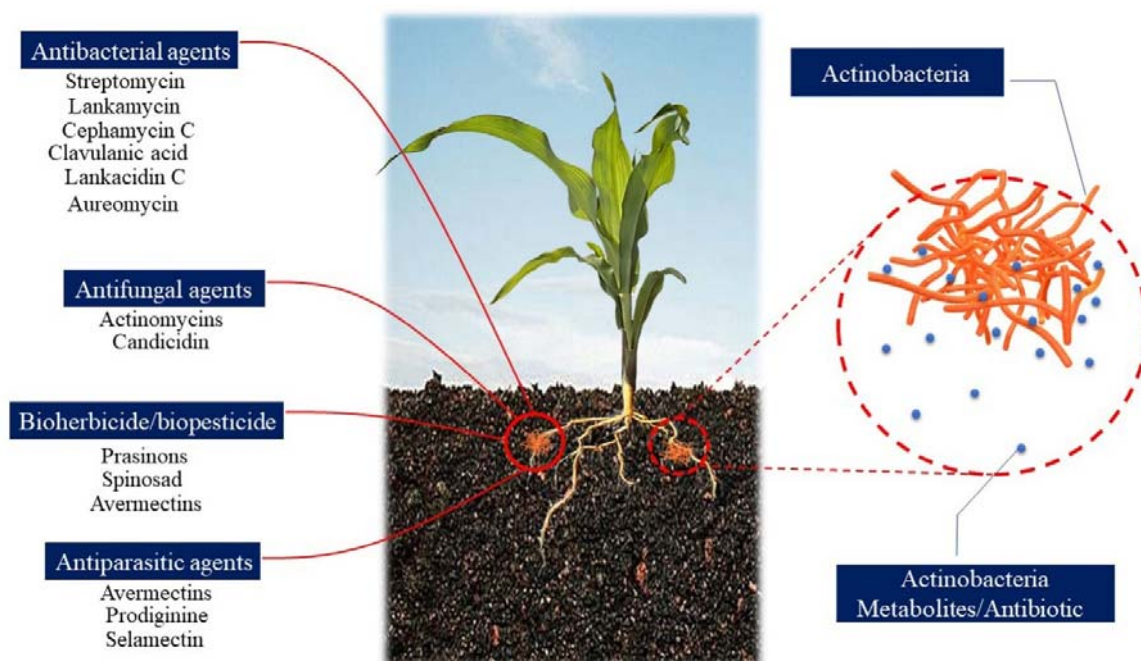


Fig. 4 Actinobacteria: secondary metabolites and antibiotic production for plant protection and disease control.

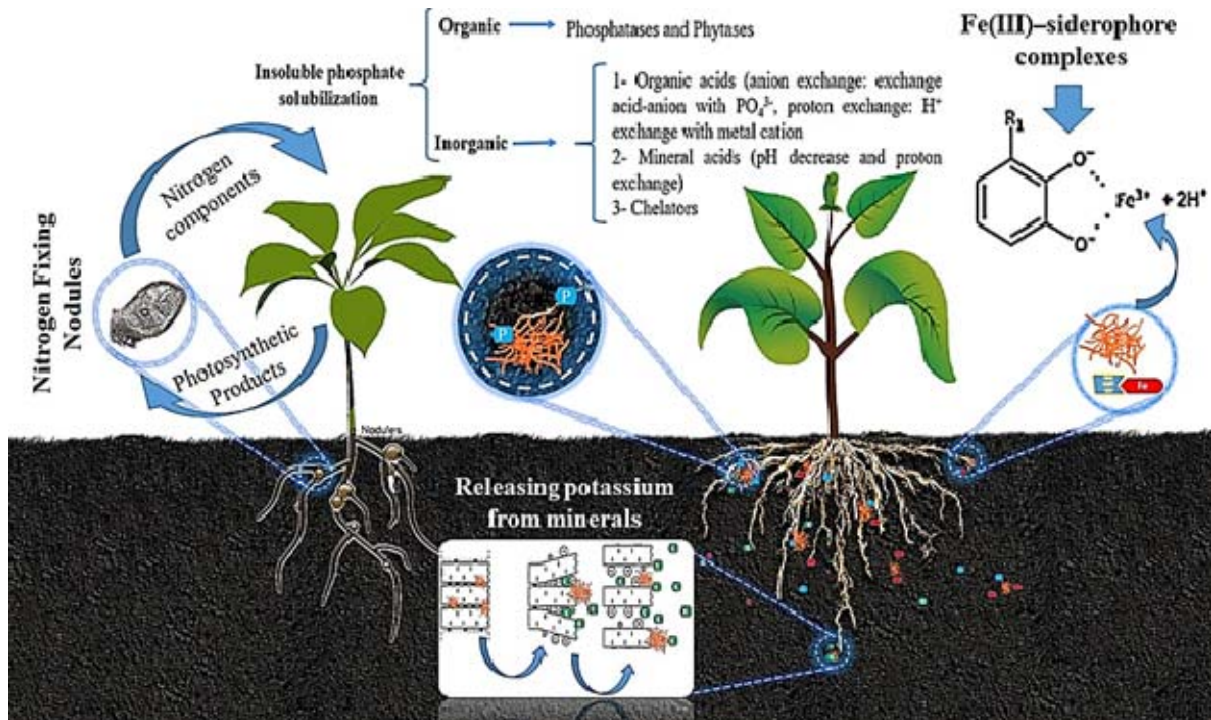


Fig. 5 Actinobacteria help to manage the availability of nutrients in plants and rhizosphere.