Chapter 9
Actinobacteria in Agricultural and Environmental Sustainability

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Abstract The advent of green revolution or high input agrotechnologies have led to self-reliance in food production. Modern agriculture methods are getting increasingly dependent on the steady supply of synthetic inorganic fertilizers and pesticides, which are products of fossil fuels. There is an increasing concern about the excessive dependence on the supply of chemical fertilizers and pesticides, and the adverse effects of the indiscriminate use of synthetic inputs in soil productivity and environmental quality. The cumulative effect of environmental degradation due to application of agrochemicals has led to a decline in food production during the last two decades. In order to overcome these adverse effects, there is an urgent need to develop new strategies for ensuring further growth in agricultural output. By adapting a strategy involving integrated supply of nutrients from a combination of chemical fertilizers and pesticides, organic manures, and biofertilizers and biopesticides, the soil can be saved from further impoverishment and environmental degradation. The use of microbes as bioinoculants for promoting plant growth and/or bioremediation purposes gives a new dimension to agricultural and environmental biotechnology. Actinobacteria are considered as the most prominent source of bioactive compounds (antibiotics, enzymes, and plant growth modulators) facilitating plant growth promotion and plant disease suppression. Attempts are being made to utilize actinobacteria that produce antibiotics and agro-active compounds as biofertilizers and biopesticides; these aids in mitigating the use of harmful chemical fertilizers and pesticides. Besides making agriculture systems sustainable, soil inhabiting actinobacteria play important roles in various ecological processes such as organic matter decomposition and toxic pollutant and heavy metal bioremediation, thus contributing to the restoration of soil fertility and environmental sustainability.

Keywords Actinobacteria • Antibiotics • Biofertilizers • Biopesticides • Organic matter decomposition • Environmental sustainability

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9.1 Introduction

Ever increasing population and over exploitation of natural resources are the two major causes of disturbance in the structure of world economy that has resulted in drastic setbacks on overall growth and development (Bretschger 2013). The world population has already reached 6.8 billion and is estimated to cross nine billion by 2050 (Alexandratos and Bruinsma 2012). Intensive agricultural technologies have been adopted to feed the escalating population since 1960s. These conventional agricultural technologies include hybridized seed distribution, modern irrigation practices, use of improved crop varieties, synthetic fertilizers and pesticides, etc. With advances in modern technologies, crop productivity rates have increased to meet the global food demand and provide future food security through green revolution. The green revolution is an agrotechnology-based solution to the worldwide food scarcity that arose after the Second World War. It has brought tremendous breakthroughs in agricultural economy in the last few decades (Pingali 2012) and has led to a phenomenal increase in food production per capita, especially in the yield of staple foods (rice, maize, and wheat). This revolution has been successful in making many nations self-sufficient in food grains. The development of agricultural self-reliance system in many countries has ensured a long-term food production in an economically viable way (Herdt 1998). Despite impressive results, these modern practices have caused certain negative impacts on ecological units encompassing changes in physiochemical properties of soil, depletion of stratospheric ozone, and destruction of food chains. An excessive use of synthetic fertilizers and pesticides pollute land area and ultimately water resources giving rise to algal blooms, nitrate poisoning, emergence of pesticide-resistant insects and pathogenic fungi (Ntalli and Menkissoglu-Spiroudi 2011), and thereby making crop production more susceptible to abiotic and biotic stresses (Babalola 2010). Other severe repercussions include ecological infrastructure damages, unfavorable climate change, deforestation, and soil erosion (Zacharia 2011), thus disturbing the overall sustainability of agriculture system and environment, which ultimately leads to major health concerns, extinction of wildlife, and other life forms (Carson 1962).

Environmental degradation is one of the biggest concerns that must be addressed at the global level. This is mainly due to ever increasing human population, urbanization, and industrialization. The effluents from various industries contaminate the atmosphere as well as aquatic and terrestrial zones of the biosphere, thus, influencing both biotic and abiotic environmental factors. Disturbances in the environment lead to undesirable and deleterious outcomes triggering unseasonal rainfall, atmospheric pollution, soil degradation, and deterioration of soil microbiota that affect land fertility and agro-economy.

Environment and agriculture are two interlinked systems. The perturbation of environment causes negative impacts on agriculture system and vice versa. These two systems determine the economic status and progressive structure of a nation. The preservation of sustainability in agriculture and environment is an important concern in the current scenario that needs special attention. Consequently, robust organizational systems need to be developed, which control land use and coordinate soil and water management to a sustainable level. Sustainable agriculture aims primarily at making nutritious food available for the present and future generation to conserve soil fertility and natural resources. To fulfill these, sustainable soil management, development of pest-resistant crop plants, improvement in agricultural services, and search for alternatives to hazardous chemicals are the current focus.

Soil management practices increase nutrient content and water holding capacity of soil that permits proliferation of beneficial microbes and restricts the entry of toxic compounds into the food chain. Soil microbes regulate nutritive and physical status of the soil (Anderson and Domsch 1989) and make an essential contribution in humus formation and soil texture improvement, thereby making soil more suitable for sustainable cropping practices. In the present scenario, pesticide-resistant plant pathogens and abiotic stresses are emerging factors that severely affect the agricultural production. Genetically modified and improved crop varieties are being used to relieve the effects of biotic and abiotic stresses (Rai et al. 2011). On the other hand, the emergence of resistant pathogenic strains is comparably high warranting a search for an alternate solution. The application of microbial inoculants has proven to be effective for suppression of pathogenic fungal growth (Toyota and Watanabe 2013). In addition, some microbes have an inherent trait of triggering the plant immune system in order to defend herbivore insect attack (Van Wees et al. 2008). Thus, these microbes can be employed as alternatives to harmful pesticides. Some extremotolerant microbes are capable of supporting plant growth in adverse environments (Yandigeri et al. 2012; Selvakumar et al. 2015), and these could serve as suitable candidates to cope with abiotic stresses (drought, salinity, and nutrient deficiency) to enable exploitation of unsuitable soils (saline coastal sediments and desolate areas) for cultivation purposes.

Microbial flora also has a key role to play in biogeochemical cycles, which regulates recycling of principal elements (carbon, nitrogen, sulphur, and phosphorus) between biotic and abiotic factors. Recycling of essential elements facilitates growth and survival of microbes and others in the ecological niches (Rousk and Bengtson 2014). Moreover, microorganisms participate in plant growth promotion via plant–microbe associations. This association can be cooperative or antagonistic. Mutualistic association is broadly classified into two major types: bipartite communities (nitrogen-fixing nodular symbioses or arbuscular mycorrhiza) and multipartite communities (endophytes and epiphytes) (Tikhonovich and Provorov 2011). Beneficial microbes provide solubilized minerals to plants and fixed nitrogen to enhance fitness of plants, and thus, bepragmatic biofertilizers. The application of biofertilizer and biopesticide is more promising as they have negligible detrimental effects on the environment. Likewise, the multiple benefits of microbial inoculants offer an effective way for sustainable agriculture (Jha et al. 2013).

Microbes are a boon to keep the environment clean. They possess an immense tolerance to toxic environment and exhibit metabolic potential to degrade xenobiotics. They play a role in providing a cleaner and healthier environment for mankind through pollution control. They are of paramount importance in the degradation of recalcitrant organic compounds (Daubaras and Chakrabarty 1992), detoxification of heavy metals (Lovley and Coatest 1997) and waste treatment. Several microbes and their enzymes have found application in the process of bioremediation. To improve their degradation capabilities, potential microorganisms have been genetically improved for combating environmental problems (Sayler and Ripp 2000). Microbes such as bacteria, actinobacteria, fungi, and algae have been tested for their utility in agricultural and environmental sustainability. The domain bacteria include a large number of biotechnologically important strains. One such good example is of the phylum *Actinobacteria* that constitutes a large number of antibiotic producing, disease suppressing, and plant growth-promoting genera (Hamedi and Mohammadipanah 2015). Their ability to secrete a large number of bioactive compounds, high catabolic rate, and omnipresence in the environment make them potential candidates for agriculture and environmental biotechnology. Moreover, their metabolic diversity, characteristic growth pattern, and tolerance to noxious environmental pollutants enable them to remediate extremely polluted sites (http://www.biotecharticles.com/Environmental-Biotechnology-Article/Actinomycetes-and-Bioremediation-1091.html). In this chapter, an attempt has been made to describe the utility of actinobacteria in the conservation or restoration of agricultural and environmental sustainability.

9.2 Actinobacteria: Biological Properties and Prospects

Actinobacteria is an interesting prokaryotic phylum that includes physiologically, taxonomically, and morphological diverse genera (Atlas 1997). This includes a heterogeneous group of Gram-positive/Gram-variable, aerobes or anaerobes, motile/nonmotile and sporulating/non-sporulating prokaryotes. The majority of actinobacteria possess DNA with high GC content (>50 %) and a few with low GC (Ghai et al. 2012, 2013). Actinobacteria are mostly heterotrophs that thrive on complex organic matter, but the oligotrophic mode of nutrition has also been documented in a very few actinobacteria (Yoshida et al. 2014; Toth 1996). These are often regarded as the prokaryotic equivalent of fungi or filamentous bacteria as most of them grow as branched filamentous hyphae resembling fungi and show similar nutritional preferences. They also share certain characteristic features with bacteria in being unicellular and having prokaryotic nuclei, cell wall composition, and antibiotic susceptibility patterns. Genome size of actinobacteria is in the range of 0.93 Mb (*Tropheryma whipplei*) and 11.9 Mb (*Streptomyces bingchenggensis*) (Verma et al. 2013). Some actinobacteria harbor circular (*Nocardia*)/linear (*Streptomyces*) plasmids. Actinobacteria have been considered as an intermediate group between bacteria and fungi. Subsequently, the precise taxonomic status of actinobacteria had been approved and categorized as a separate phylum *Actinobacteria* within the domain Bacteria. The phylum *Actinobacteria* is one of the most dominant taxonomic units of the domain Bacteria (Ventura et al. 2007) that constitutes six major classes (*Actinobacteria, Acidimicrobiia, Coriobacteriia, Nitriliruptoria, Rubrobacteria, and Thermoleophilia*).

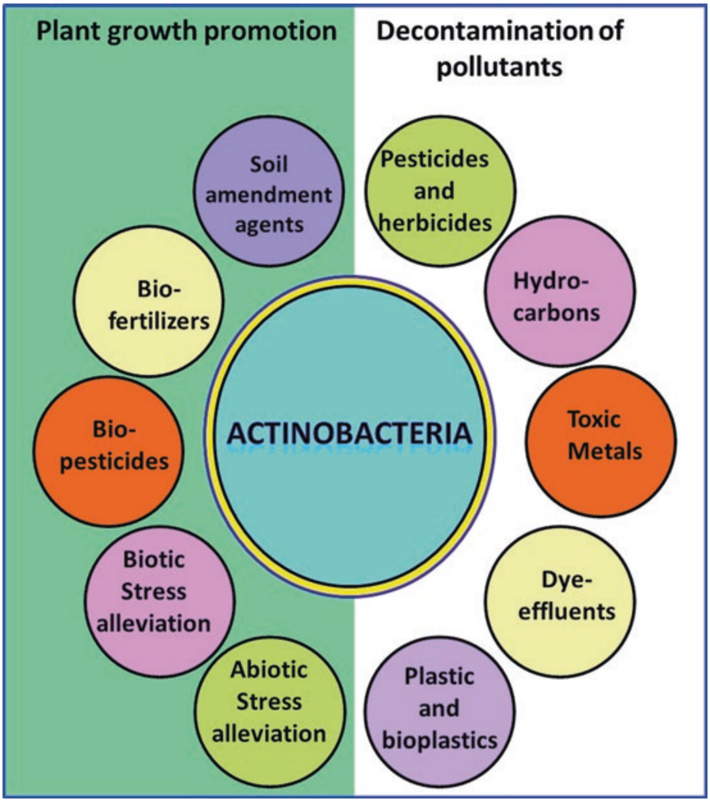

Fig. 9.1 A schematic diagram showing the role of actinobacteria in agriculture and environment sustainability

Actinobacteria encompass a large group of industrially and agriculturally significant species. They are a prolific source of novel secondary metabolites [antimicrobial, antitumor, anti-inflammatory agents (Brana et al. 2015), antioxidants (Karthik et al. 2013)], and other pharmaceutically valuable compounds. Actinobacterial species have a tremendous economic importance in both agriculture and environmental ecology (shown in Fig. 9.1). The phylum *Actinobacteria* includes a considerably high number of plant growth-promoting genera than bacteria (Hamedi and Mohammadipanah 2015). Plant growth-promoting actinobacteria secrete a vast array of chemical modulators, which either directly stimulate plant growth or act indirectly by supporting other plant beneficial microbes. Soil-dwelling actinobacteria either kill or inhibit the growth of plant pathogens via antibiotic production, thereby ensuring the good health of plants. The term “wonder drug” was proposed for antibiotics, as these diminish the threat caused by plant and animal pathogens (Demain 1999). Actinobacteria comprises the largest number of antibiotics producing genera, which produce approximately 45 % of the total antibiotics known (Raja and Prabakarana 2011). They secrete some volatile tertiary alkaloids such as geosmin

(Gerber and Lechevalier 1965) and 2-methylisoborneol (2-MIB) (Gerber 1969), which account for the earthy smell of soil (Wilkins 1996) and indicate fertility and nutrient levels of the soil to farmers. Some actinobacteria display mutualistic relationship like actinorhizal (Verghese and Misra 2002), actinolichen (Lazo and Klein 1965) and endophyte associations (Taechowisan et al. 2005) to promote plant fitness viaplant morphogenesis. Other ecophysiological roles of actinobacteria include nitrogen fixation, phosphate solubilization, and production of phytohormones (auxins and cytokinin) and siderosphores (Palaniyandi et al. 2013b), which add further value to the significance of actinobacterial taxa from the perspective of agriculture.

The effectiveness of actinobacteria is not only limited in formulation of biofertilizers or biopesticides, but they also appear ideal for myriad applications in environmental biotechnology. Their adaptive morphology as well as exceptional metabolic versatility enables them to establish their populations to all kinds of extreme environments including highly polluted locations. Pizzul et al. (2006) evaluated the significant role of actinobacteria in decontamination of polyaromatic hydrocarbons. Studies on the evaluation and characterization of pollutant degrading actinobacteria are currently increasing and these are gaining considerable attention in developing bioremediation tools because of their favorable characteristics such as filamentous structure, sporulation, drought resistance, and having an ability to secrete hydrolytic enzymes.

9.3 Role of Actinobacteria in Sustainability of Agriculture System

Besides being a potential source of antibiotics, actinobacteria are a prominent source of agro-active products (Tekaya et al. 2012). Actinobacteria are naturally associated with plants and display several beneficial effects on plant growth. Their distinctive features make them highly useful in the conservation of soil quality, control of plant diseases, and regulation of plant metabolism. The inoculants of some actinobacteria are being employed in soil amendment, biocontrol and as biofertilizers. The mechanisms and applications, through which they regulate and improve the health of plants, are described below.

9.3.1 Soil Amendments

Conventional farming practices rely on chemical inputs (fossil fuel derivatives) and highly mechanized approaches which have proven to be effective in feeding an exponentially increasing population. These rapid agricultural innovations have been successful in maximizing the crop yield though at the cost of natural ecosystems. They bring about a radical change in environmental biotic and abiotic factors that lead to soil and land degradation, water scarcity, and resource depletion. These modern practices often require high cost energy inputs and nonrenewable resources affecting the landscape economy. These concerns have prompted the agriculture policies to shift towards organic farming to preserve the ecological integrity that includes the health of soils, ecosystems, and people. Organic agriculture techniques include sustainable practices such as crop rotation, composting, and biological pest controls. Composting is microbial degradation of complex organic matter into nutrient-rich humus that nurtures plants and helps in restoration of productivity of eroded soils (Barker 1997). Humus contributes to the formation of dense aggregates by gluing soil particles together and thereby improving water retention capacity of the soil. Similarly, the filamentous structure of actinobacteria is also involved in the formation of stable soil aggregates (Barea et al. 2005). Humus results from hydrolytic microbial actions on lignocellulosic materials during the composting process. Actinobacteria secrete various types of peroxidases (le Roes-Hill et al. 2011) among which, lignin peroxidases facilitate humification and composting via hydrolysis of lignin into humic acid-like complexes. Compost not only acts as a good soil conditioner to improve soil texture, but also supplements the nutrient content of the soil. Microbes (bacteria, actinobacteria, and fungi) show cumulative actions to break down the complex organic matter during the composting process. Actinobacteria and bacteria belonging to the phylum Firmicutes (Fracchia et al. 2006) primarily dominate composts. Cultivation- dependent and -independent methods have revealed the dominant and active participation of actinobacteria in composting (Dees and Ghiorse 2001). The composition of actinobacterial community changes during various stages of composting, for example, the presence of both mesophilic (*Corynebacterium*, *Rhodococcus* and *Streptomyces*) and thermotolerant species (*Saccharomonospora viridis*, *Thermobifida fusca* and *Thermobispora bispora*) have been recorded at different phases of compost formation (Steger et al. 2007).

9.3.2 Nutrient Availability

The high metabolic rate and hydrolytic enzyme secretion (amylase, chitinase, cellulase and peroxidases) makes actinobacteria potential decomposers that mineralize complex organic matter into simpler assimilative forms. They release solubilized carbon compounds in large quantities into the soil. In addition to carbon sources, other macro- and micro-nutrients are also essential for plant growth. Agricultural practices such as irrigation and natural phenomena like rain result in unwanted washing away of essential minerals from the cropland making soil unproductive. Numerous chemical fertilizers are used to the soil directly or onto the plant foliage to improve crop yield and quality. These fertilizers get immobilized in soil (Reddy et al. 2002) or percolate into deeper soil horizons and become unavailable for plant uptake. The agricultural runoff contaminates ground water as well as fresh surface water resources such as pond and river by leaching the hazardous chemicals (Shigaki et al. 2006). Therefore, innovative agricultural research inclines towards cleaner and safer cropping practices such as utilization of microbes as biofertilizers. Several actinobacterial species with efficient biological activities such as nitrogen fixation, phosphate solubilization and siderophore production have been isolated and screened from soil, rhizosphere, roots and aerial parts of plants (Table 9.1).

9.3.2.1 Nitrogen Fixation

Nitrogen is a versatile element available in both organic and inorganic forms that play various structural and functional roles in all living organisms. It is a critical limiting factor for plant morphogenesis. Despite being a highly abundant gas (approximately 78 % of total atmospheric gases), molecular nitrogen ($N\equiv N$) is quite stable and inert which is an unsuitable form for plant use. Some microbes, known as diazotrophs, possess nitrogenase activity, and are capable of fixing the atmospheric N_2 into ammonium (NH_4^+), which is transformed into nitrate (NO_3^-) or organic nitrogen forms for their own growth or for plant assimilation. They maintain symbiotic association with plants by providing nitrogenous compounds and in turn utilizing carbon compounds like sugars of plant origin. They live as either endobionts of plants or free living. Diazotrophic growth metabolism is also displayed by some actinobacterial species. For example, *Frankia* species have been well characterized which make an association with dicot plants (belonging to 24 genera and eight families) and cause nodulation on plant roots, known as actinorhizal association (Yamaura et al. 2010). Nitrogen fixation activity has also been noticed in non-*Frankia* actinobacteria including *Arthrobacter* sp. (Cacciari et al. 1979), *Mycobacterium flavum* (Fedorov and Kalininskaya 1961), *Corynebacterium autotrophicum* (Berndt et al. 1978), *Microbacterium* isolates (Ruppel 1989), *Agromyces* and *Propionibacteria* (Sellstedt and Richau 2013). The actinobacterial species belonging to the family *Thermomonosporaceae* and *Micromonosporaceae* are also capable of fixing atmospheric nitrogen (Valdes et al. 2005). A thermophilic actinobacterium, *Streptomyces thermoautotrophicus* is an obligate chemoautotroph, which has been isolated from burning charcoal pile (Gadkari et al. 1990). This actinobacterium has a tendency to fix atmospheric nitrogen during autotrophic growth (Ribbe et al. 1997). Actinobacterial species also facilitate nitrogen availability by promoting the growth of other plant symbionts (Palaniyandi et al. 2013b). Actinobacterial species such as *Streptomyces*, *Micromonospora*, and *Actinoplanes* have been shown to promote the root nodulation of *Frankia* sp. (Solans 2007) and *Sinorhizobium meliloti* (Solans et al. 2009). Several other actinobacteria are known to colonize the mycorrhizae, and strengthen the plant mycorrhiza association (Table 9.1) by promoting the growth of fungal hyphae or germination of fungal spore. Mycorrhiza is a plant–fungal association in which fungal species mineralize the nutrients and make them available to the plant and utilize the sugars released by plant roots.

Table 9.1 List of plant growth-promoting actinobacteria

Actinobacteria	Inhabitation types	Host plant/ mycorrhizal association	References
Nitrogen-fixing actinobacteria			
Frankia sp.	Root colonizing or free living	Plants of families (*Betulaceae*, *Casuarinaceae*, *Coriariaceae*, *Datiscaceae*, *Elaeagnaceae*, *Myricaceae*, *Rhamnaceae*, and *Rosaceae*)	Benson and Silvester (1993)
Micromonospora sp.	Root colonizing	*Casuarina equisetifolia*	Valdes et al. (2005)
	Root nodule colonizing and rhizosphere inhabitant	*Pisum sativum*	Carro et al. (2012)
Streptomyces thermoautotrophicus	Soil inhabitant	–	Ribbe et al. (1997)
Phosphate solubilizing actinobacteria			
Streptomyces sp. CTM396	Agricultural soil and rock processing site inhabitants	–	Farhat et al. (2015)
Citricoccus zhacaiensis B-4	Rhizosphere inhabitant	Banana plant	Selvakumar et al. (2015)
Cellulosimicrobium sp. S16	Rhizosphere soil inhabitants	Potatoes plant	Nabti et al. (2014)
Streptomyces badius	Mangrove isolate	–	Bhardwaj et al. (2012)
Leifsonia soli	Rhizosphere inhabitant	Teak plant	Madhaiyan et al. (2010a)
Microbacterium azadirachtae	Rhizoplane inhabitant	Neem seeding	Madhaiyan et al. (2010b)
Thermobifida sp.	Rhizosphere inhabitant	Clover plant	Franco-Correa et al. (2010)
Kitasatospora sp.	Rhizosphere inhabitants	Maize crop	Oliveira et al. (2009)
Streptosporangium isolates	Casts isolates of tropical earthworms	–	Mba (1997)
Plant mycorrhiza growth influencing actinobacteria			
Streptomyces sp.	Mycorrhizal inhabitants	Norway spruce	Schrey et al. (2012)
Rhodococcus sp. strain EJP75	Ectomycorrhizal colonizing	*Pinus sylvestris*–*Lactarius rufus* association	Poole et al. (2001)

(continued)

Table 9.1 (continued)

Actinobacteria	Inhabitation types	Host plant/ mycorrhizal association	References
Actinomycetes	Soil inhabitant	–	Carpenter-Boggs et al. (1995)
Streptomycescoelicolor 2389	–	Sorghum–*Glomus intraradices* LAP8 association	Abdel-Fattah and Mohamedin (2000)
Streptomyces strains MCR9, MCR26 and *Thermobifida* strain MCR24	Rhizosphere inhabitant	Clover plants–*Glomus mosseae*	Franco-Correa et al. (2010)
Siderophore producing actinobacteria			
Streptomyces sp.	–	–	Imbert et al. (1995)
Rhodococcus erythropolis IGTS8	–	–	Carrano et al. (2001)
Nocardia tenerifensis NBRC 101015	–	–	Mukai et al. (2009)

9.3.2.2 Phosphate Solubilization

Like carbon and nitrogen, phosphorus is also a crucial macro-element, which is necessary for growth and development of all living organism. It is an integral part of various biological molecules such as nucleic acids, phospholipids and energy-rich compounds (ATP, NADH, and NADPH). It has an important role in numerous metabolic pathways such as cell division, signal transduction, macromolecular biosynthesis, photosynthesis (Shenoy and Kalagudi 2005; Fernandez and Schaefer 2012), and constitutes approximately 3 % of total dry cell weight (Bhardwaj et al. 2012). It is second most crucial component after nitrogen for plant growth (Donahue et al. 1990). Despite the presence of high quantity (400–1200 mg/kg) of phosphorus in soil (Fernandez and Novo 1988), only a small proportion (1 mg/kg or less) is accessible to the plant (Goldstein 1996). The availability of phosphorus is mainly limited by two processes (1) immobilization of soluble phosphorus in soil particles (2) adsorption of phosphorus onto compounds (aluminum oxide, iron oxide, and aluminum silicate) in acidic soil (Whitelaw 2000) or calcium carbonate in alkaline soil (Gyaneshwar et al. 2002). Several phosphate solubilizing microbes have been characterized which transform insoluble phosphorus into solubilized form through processes such as acidification, chelation (Delvasto et al. 2006), and hydrolytic enzyme production. Mutualistic actinobacterial species are the key participants in the biogeochemical cycling of phosphorus in marine environments (Sabarathnam et al. 2010). Various rhizosphere inhabitants and endophytic actinobacteria have phosphate solubilizing capability, among which, a comparatively high abundance of *Streptomyces* species occur in phosphate mobilizing sites (Hamdali et al. 2008; Jog et al. 2014; Franco-Correa et al. 2010). Their additional antimicrobial activities make them more competent to function as Plant

Growth-Promoting Agents (PGPA). Few other non-*Streptomyces* species have also been reported (Table 9.1) to facilitate plant growth by mineralizing insoluble phosphorus into soluble forms for plant uptake.

9.3.2.3 Enhancement of Iron Uptake

Plant growth and development also requires additional elements such as Fe, Co, Cr, Cu, Zn, Mn, and Mo in very small quantities. Iron is a major limiting element which functions as a cofactor of several enzymes and reaction center of numerous proteins involved in energy metabolism. In the soil, it mainly exists in various oxide forms such as insoluble (Fe^{+3}) and soluble (Fe^{+2}) forms. Many microbes have a tendency to catalyze the reduction of Fe^{+3} into a soluble form (Fe^{+2}) which is assimilated by plant or plant beneficial microbes (Francis et al. 2010). Actinobacteria such as *Arthrobacter* spp. (Valencia-Cantero et al. 2007) and *Kocuria rosea* HN01 (Wu et al. 2014) are capable of catalyzing the reduction of ferric iron to a soluble form and facilitate plant growth in alkaline soils. The actinobacteria enhance iron availability (listed Table 9.1) by producing siderophores. Siderophores are small organic molecules, which chelate the iron moieties and sequester them in the rhizospheric zone of the plant. Furthermore, siderophore production enables *Streptomyces* species to hinder the germination of basidiospores of pathogenic fungus, *Moniliophthora perniciosa* (Macagnan et al. 2006). Actinobacterial siderophores can also promote the proliferation of beneficial actinobacteria exhibiting antagonistic activity against pathogens (Palaniyandi et al. 2013b), thereby involving in the regulation of health of plants.

9.3.3 Alleviation of Biotic and Abiotic Stresses

Plants are constantly subjected to various biotic and abiotic stresses in their natural environment. These stresses cause severe impact on agricultural crop productivity. Biotic plant attackers include microbial pathogens (bacteria, fungi, and viruses), weed plants and insects, which lower crop yields and their market value. Abiotic stresses are due to environmental factors (drought, temperature, nutrient deficiency, and salinity). To cope up with these stresses, plants have developed various strategies such as synthesis of phytohormones (salicylic acid, jasmonic acid, abscisic acid, and ethylene). These phytohormones are involved in providing protection against both biotic and abiotic stresses (Fujita et al. 2006). A diverse array of microbes help plants to mitigate the negative impact of various stresses caused by abiotic factor (Grover et al. 2011). Actinobacteria are the prominent species that participate in providing protection to plants by killing or suppressing the growth of microbes directly via antibiosis, parasitism or in an indirect manner (induction of the plant immune system) (Palaniyandi et al. 2013b). The mechanisms, through which the actinobacteria show plant disease suppression and biotic or abiotic stress alleviation, are described below.

9.3.3.1 Biotic Stress Alleviation

Microbial pathogenicity and emergence of pesticide-resistant pathogens bring about new challenges to agro-economy. Biotic stresses, primarily plant diseases, are a significant impediment in attaining the actual potential crop yield. The incidence of several plant diseases brings nearly 9–16 % losses in total production yields of many important crops (rice, wheat, barley, maize, potato, and cotton) (Chakraborty et al. 2000). Several side effects of using chemical pesticides are prompting researchers to find eco-friendly solutions to combat the severe damages caused by plant pathogens. Actinobacteria have a great potential in controlling plant pathogens. Many genera including *Arthrobacter* (Mitchell and Hurwitz 1965) *Cellulomonas* (Wadi and Easton 1985), *Actinoplanes*, *Micromonospora* (Filnow and Lockwood 1985), and *Streptomyces* (Al-Askar et al. 2015) are capable of reducing the growth of plant pathogens. Palaniyandi et al. (2013b) described basic mechanisms of disease suppression by actinobacteria that include: (1) production of antibiotics or cell wall degrading enzymes, (2) exhibition of hyperparasitism on plant parasitic microbes as well as competition with disease causing microbes in order to colonize the plant rhizosphere, and (3) induction of plant immune system. Antibiotic production is a major mechanism that gives the actinobacterial group prominence in agricultural crop protection. Actinobacteria colonize as a major microbial population in rhizosphere of many plant species. Their high dominance has been recorded in soil amended with *Brassica* plant residues. An increased actinobacterial population had resulted in a significant suppression of *Rhizoctonia solani* damping-off disease (Ascencion et al. 2015) in the *Brassica* amended soil. Many *Streptomyces* species are known for having a pronounced competence for controlling the growth of plant pathogens (Table 9.2). For instance, *Streptomyces griseorubens* E44G showed a high antifungal effect, thus, could inhibit the mycelial growth of *Fusarium oxysporum* f. sp. *lycopersici* (Al-Askar et al. 2015) which is a seed-borne fungal species responsible for causing damages to tomato crop. The growth of another soil-borne pathogen, *Sclerotium rolfsii*, has been controlled by *Streptomyces* sp. (Errakhi et al. 2007). A novel actinobacterium, *Streptomyces* sp. N2, had a broad-spectrum inhibitory effect against various phytopathogenic fungi such as *Pyricularia grisea*, *Fusarium oxysporum* f. sp. *niveum, F. oxysporum* f. sp. *vasinfectum*, *Penicillium italicum*, *Colletotrichum gloeosporioides*, and *Rhizoctonia solani.* In vivo, this actinobacterium showed significant inhibitory action only against *Rhizoctonia solani* causing anthracnose disease of grapes (Xu et al. 2015). Li et al. (2014b) isolated a *Streptomyces* sp. strain CNS-42 from the plant *Alisma orientale,* which displayed a broad-spectrum antimicrobial activity against pathogenic bacteria and fungi. The strain CNS-42 produced a compound staurosporine that shows both antifungal and plant growth-promoting activity. Another *Streptomyces* species, *Streptomyces araujoniae* ASBV-1^T was reported to produce a multiantibiotic complex (containing monactin, dinactin, trinactin, tetranactin, and valinomycin) that eradicates fungal pathogens by disturbing the integrity of cell structure (Silva et al. 2014) via formation of ionophores in the cell membrane. Actinobacteria reported to exhibit plant disease suppression activities are listed in Table 9.2.

Table 9.2 Biocontrol of plant pathogens by actinobacterial species

Actinobacteria	Bioactive compounds/enzymes	Plant pathogen	Economic plant	References
Streptomyces sp.	Antifungal agent	*Sclerotium rolfsii*	Sugar beet	Errakhi et al. (2007)
Streptomyces sp. N2	Antifungal metabolite (3-methyl-3,5-amino-4-vinyl-2--pyrone, $C_6H_7O_2N$)	*Colletotrichum gloeosporioides*	Grape fruits	Xu et al. (2015)
Streptomyces ambofaciens S2	Antifungal compounds	*Colletotrichum gleosporioides*	Red Chilli fruits	Heng et al. (2015)
Streptomyces sp. strain CNS-42	Antifungal agents (staurosporine)	*Fusarium oxysporum* f. sp. *cucumerinum*	Cucumber	Li et al. (2014b)
Streptomyces (*S. canus, S. fradiae, S. avermitilis,* and *S. cinnamonensis*) and non-*Streptomyces* sp. (*Leifsonia poae*)	–	*Xanthomonas axonopodis*	Pomegranate	Poovarasan et al. (2013)
	Antifungal compounds	*Fusarium oxysporum* and *Alternaria solani*	Guava	Mohandas et al. (2013)
Propionicimonas sp. ENT-18	Albocycline	*Sclerotinia sclerotiorum*	–	Zucchi et al. (2014)
Streptomyces hygroscopicus	–	*Colletotrichum acutatum, C. gloeosporioides and Fusarium avenaceum*	Apple	Grahovac et al. (2014)
Streptomyces araujoniae ASBV-1 T	Multiantibiotic complex	*Botrytis cinerea*	Strawberry pseudofruit	Silva et al. (2014)
Production of cell wall degrading and other antagonistic enzymes				
Streptomyces sp.	Chitinase	*Lasiodiplodia theobromae*	Rubberwood	Sajitha and Florence (2013)
Streptomyces sp. 9p	Chitinase and β-1,3-glucanase	*Alternaria brassiceae* OCA3	Chilli	Srividya et al. (2012)
Streptomyces sp. PTK19	Chitinase	*Fusarium oxysporum* PTK2	–	Thiagarajan et al. (2011)
Streptomyces vinaceusdrappus S5 MW2	Chitinase	*Rhizoctonia solani*	Tomato	Yandigeri et al. (2015)
Streptomyces goshikiensis YCXU	Volatile antifungal compounds and enzymes (β-1,3-glucanase, chitinase, and urease)	A broad range of phytopathogenic fungi and in vivo suppression of *Fusarium* sp.	Watermelon	Faheem et al. (2015)

(continued)

Table 9.2 (continued)

Actinobacteria	Bioactive compounds/enzymes	Plant pathogen	Economic plant	References
Streptomyces phaeopurpureus ExPro138	Proteases	*Colletotrichum coccodes*	Tomato	Palaniyandi et al. (2013a)
Streptomyces sp.	Chitinase, phosphatase, and siderophores	*Xanthomonas oryzae* pv.*oryzae*	Rice	Hastuti et al. (2012)

EL-Tarabily et al. (1997) screened 45 *Streptomyces* and non-*Streptomyces* sp. for their in vitro and in vivo fungal inhibition activity. Among them, seven species (*Streptomyces janthinus*, *Streptomyces cinerochromogenes*, *Streptoverticillium netropsis*, *Actinomadura ruhra*, *Actinoplanes philippinensis*, *Streptosporangium albidum*, and *Micromonospora carbonaceae*) showed inhibitory action against fungal pathogens (*Pythium* sp.) by producing non-volatile metabolites. *Pythium* species are widely known as causative agents of disease cavity spot in carrots, which decrease the quality of carrots resulting in substantial economic losses. *Actinoplanes philippinensis* and *Micromonospora carbonaceae* showed hyperparasitism on growing hyphae and oospores of *Pythium coloratum.* They colonized heavily on the outer surface of mycelium and resulted in cytoplasmic collapses of oospores. In another report, 64 out of total 317 actinobacterial cultures (isolated from roots and rhizospheric soils of leguminous plants) were reported to exhibit antagonism against soybean pathogen *Xanthomonas campestris* pv. *glycine* (Mingma et al. 2014) causing bacterial pustule. Among them, *Streptomyces* sp. RM 365 showed highest inhibition rate against *Xanthomonas campestris* pv. *glycine*. This actinobacterium did not display any antagonistic activity against *Rhizobium* sp. (plant growth-promoting bacterial species), thus, can be a potential candidate for the development of a biocontrol agent (BCA) to control the plant bacterial pustule. *Streptomyces phaeopurpureus* ExPro138, isolated from rhizosphere of yam plant, was shown to produce multiple proteases and inhibit the growth of foliar fungal pathogen (*Colletotrichum coccodes*) in early stage by disrupting various processes such as spore germination, spore adhesion, and appressorium formation (Palaniyandi et al. 2013a). Marine isolates belonging to the genera *Streptomyces*, *Nocardiopsis*, and *Saccharopolyspora* also displayed antagonism against phytopathogens like *Colletotrichum falcatum*, *Thielaviopsis paradoxa,* and *Fusarium semitectum* (Vijayakumar et al. 2012). *Streptomyces* sp. PM9 was effective candidate for controlling microbial disease in forest plants (Salla et al. 2014). This actinobacterium brought changes in the secondary metabolism of economically valuable plants (*Eucalyptus grandis* and *Eucalyptus globulus*) by (1) boosting up the plant immune system by triggering the enhanced production of key enzymes (polyphenol oxidase and peroxidase) of plant defense mechanism and (2) inducing synthesis of total phenolic and quercetinic flavonoid fraction. The strain PM9 also produces indole-3-acetic acid to stimulate high rooting of plants. Mohamed et al. (2013) reported that *Streptomyces noboritoensis* produces bioactive compounds and their usefulness was assessed for suppressing the growth of bacterial or fungal contaminants during in vitro micropropagation of banana. The two actinobacterial species, *Curtobacterium flaccumfaciens* and *Rhodococcus* sp., were isolated from ascocarps of *Tuber magnatum* collected from a natural truffle ground in Western Serbia (Pavic et al. 2013). Both showed β-glucanase activity, siderophore production, and ammonification of organic matter. Besides enhancing the nutrition content of soil, they were also capable of promoting growth of other plant beneficial fungal species such as *Trichoderma* species. Valois et al. (1996) showed that multiple glucanases (β-1,3-, β-1,4-, and β-1,6-glucanases) producing actinobacteria triggered lysis of the cell wall of *Phytophthora fragariae* and reduced root rot when co-inoculated with raspberry plantlets. *Streptomyces* species (*Streptomyces canus, S. fradiae, S. avermitilis,* and *S. cinnamonensis*) and non-*Streptomyces* species (*Leifsonia poae*) colonizing the mycorrhizae (*Glomus mosseae*) of plant pomegranate (*Punica granatum* L. cv *Bhagwa*) were shown to exhibit antibacterial activity against *Xanthomonas axonopodis* which causes bacterial blight of pomegranate and decreases its export drastically (Poovarasan et al. 2013). Among them, *Streptomyces canus* was capable of promoting the plant growth by producing gibberellic acid (GA3) and auxin (indole 3-acetic acid). Mohandas et al. (2013) isolated same *Streptomyces* and non-*Streptomyces* species from the mycorrhizal (*Glomus mosseae*–guava plant association) zone. Out of five, *S. canus*, *S. avermitilis*, and *L. poae* exhibited higher activity of siderophore production and phosphate solubilization. All isolates possessed chitin degradation activity. Chitinase producing actinobacteria mainly provide protection against fungal pathogen because chitinase breaks down chitin, a major component of fungal cell wall. Some endophytic *Streptomyces* species provide protection to plants against pathogenic actinobacterial species such *Streptomyces scabies* by activating the salicylic acid (SA)-mediated plant defense system (Lin et al. 2012). Besides the above, an unusual plant protecting mechanism was identified in an actinobacterium (*Rhodococcus erythropolis*) which was capable of degrading the signaling molecules such as *N*-acyl-homoserine lactone, and thus disturbed quorum sensing-based communication of Gram-negative soft-rot bacteria, thereby providing protection against Gram-negative bacterial pathogens (Latour et al. 2013). In this actinobacterium, the degradation of signaling molecules is stimulated upon activation of γ-lactone degradation pathway that generally requires the presence of incuder (γ-lactone) or cheap stimulating compounds such as γ-caprolactone. The biocontrol system of *R. erythropolis* could be activated by using a stimulator in order to guard crop plants from microbial attack.

Priyadharsini and Dhanasekaran (2015) reported that some actinobacterial species exhibit allelopathic activity against weed plants such as *Cyperus rotundus*. Other reports also suggested that *Streptomyces* species are a potent source of herbicide and inhibit the growth of *Echinochilora crusgalli* (Dhanasekaran et al. 2010) as well as *Cyperus rotundus* (Dhanasekaran et al. 2012). Many *Streptomyces* species exhibit insecticidal or pesticidal activity. For instance, *Streptomyces hydrogenans* DH16 exhibited antifeedant, pupicidal, larvicidal, and growth inhibitory effects against pest, *Spodoptera litura.* This pest causes defoliation in plants and damages crop yield severely (Kaur et al. 2014). *Streptomyces* species also displayed insecticidal activity against lepidopteran insects (*Helicoverpa armigera*, *Spodoptera litura,* and *Chilo partellus*) (Vijayabharathi et al. 2014). A compound with antibacterial and insecticidal properties was purified from *Streptomyces bikiniensis* A11 (El-khawaga and Megahed 2012). This compound belonging to the class of aminoglycoside antibiotics was found to be very effective against cotton leaf worm *Spodoptera littoralis*, which is one of the most destructive agricultural lepidopteran pests.

9.3.3.2 Abiotic Stress Mitigation

In addition to soil topology, other abiotic factors such as nutrient content, temperature, and moisture are also key determinants influencing global crop productivity. For example, drought has an immense impact on agriculture crop yield, and has generally been considered as one of the major destruction factors of the entire crop system. Actinobacterial species such as *Citricoccus zhacaiensis* B-4 (MTCC 12119) was reported to show plant growth modulation. The strainB-4 (MTCC 12119) enhanced biopriming of onion seeds even under water stress conditions (Selvakumar et al. 2015). This actinobacterium showed other activities such as IAA and GA3 production, phosphate and zinc solubilization, NH_3 production, and 1-aminocyclopropane-1-carboxylate (ACC) deaminase activity to assist the plant growth by alleviating stress caused by water deficit condition. ACC deaminase activity has been reported from a number of plant growth-promoting actinobacteria. The enzyme ACC deaminase hydrolyzes a substrate (ACC) that is a precursor of ethylene. Ethylene is a well-known stress hormone, which negatively modulates the plant growth during stress conditions (Glick 2005). The concentration of ethylene increases during both biotic and abiotic stresses, which shrinks plant growth and activates other stress alleviating mechanisms. ACC producing actinobacteria therefore enhance plant growth by reducing the effect of stress environment. *Streptomyces* sp. strain PGPA39 isolated from agriculture soil was found to produce ACC deaminase and endorse the growth of “MicroTom” tomato plants under salt stress (Palaniyandi et al. 2014). Besides ACC deaminase activity, this strain produced indole 3-acetic acid (IAA) and was also capable of solubilizing tricalcium phosphate, thus, enhancing both nutrient availability and plant tolerance capacity. El-Tarabily (2008) isolated 64 *Streptomyces* isolates from rhizosphere of tomato plant, which were screened for evaluating their ACC deaminase and plant growth modulation. Among them, two strains *S. filipinensis* no. 15 and *S. atrovirens* no. 26 showed both ACC deaminase activity and high rhizosphere competence. However, an increased plant growth promotion was observed in the plants co-cultured with *S. filipinensis* no. 15 as compared to *S. atrovirens* no. 26. Since the former strain also produces the phytohormone IAA that gives an additional benefit to the plants for their growth.

High salt concentration is another growth limiting factor, which disrupts plant metabolism leading to crop destruction. Basic mechanisms of alleviation of saline stress are production of IAA, secretion of siderophore and ACC deaminase activity. For instance, *Streptomyces* isolate (C) exhibited high IAA production, siderophore biosynthesis, and phosphate solubilization under high salt environment (Sadeghi et al. 2012), which makes it a good candidate as a bioinoculant for enhancing nutrient content in saline crop field. A rhizosphere inhabitant, *Kocuria turfanensis* strain 2 M4 produces IAA and was isolated from rhizospheric soil of the halotolerant plant *Suaeda fruticosa*, colonizing in the saline desert of Little Rann of Kutch, Gujarat, India (Goswami et al. 2014). Srivastava et al. (2014) demonstrated that *Streptomyces rochei* SM3 activates ethelyne-mediated defense pathway and phenylpropanoid pathway in chickpea and therefore discharged stresses caused by both biotic (*Sclerotinia sclerotiorum*) and abiotic (NaCl) factors. Hence, this could be a potential candidate for the development of a plant growth-promoting agent (PGPA).

9.4 Bioformulation of Actinobacteria Inoculant as Biofertilizer and Biopesticide

Bioformulation is a preparation of microbial cell inoculants or microbe-derived products with economical carrier materials (Arora et al. 2010). The use of a suitable carrier material improves shelf-life and stability of microbes and their bioactive compounds during storage and field implementation. Several plant growth-promoting microorganisms including bacteria, actinobacteria, and fungi have been formulated and tested in crop fields. Microbes with multiple mechanisms of disease suppression and plant growth promotion are better candidates for the development of biofertilizers and biopesticides. It is obvious from the foregoing discussion that actinobacteria have several attributes useful for biocontrol and plant growth promotion. Many *Streptomyces* species and their bioactive compounds have, therefore, been formulated and commercialized as biofertilizers and biopesticides for crop protection and enhancing yield (Table 9.3).

9.5 Role of Actinobacteria in Environment Sustainability

Besides plant growth promotion and disease suppression, actinobacteria play a vital role in various biological degradation processes. They have a high competence for degrading recalcitrant polymers such as toxic chemicals (pesticides, insecticides, and herbicides), dyes, bioplastics, and oil and petroleum products. Their imperative role in heavy metal detoxification has also been documented. In general, laboratory studies related to microbial degradation are not always successful during in situ bioremediation, since microbial cells used are subjected to both biotic and abiotic

Table 9.3 Commercially available bioformulants of actinobacteria (adapted from Palaniyandi et al. (2013b).

Commercialized product name	Actinobacterium and/or bioactive compounds	Applications
Actinovate® AG	*Streptomyces lydicus* WYEC108	BCA
Micro108® soluble	*S. lydicus* WYEC108	BCA
Action Iron®	*S. lydicus* WYEC108	BCA and PGPA
Thatch Control	*S. violaceusniger* strain YCED 9	BCA
Mycostop®	*S. griseoviridis* strain K61	BCA
YAN TEN *Streptomyces saraceticus*	*S. saraceticus* KH400	BCA
AFFIRM$^{\text{WDG}}$	Polyoxin D (*S. cacoi* var. *asoensis*)	BCA
PH-D® Fungicide	Polyoxin D (*S. cacoi* var. *asoensis*)	BCA
Keystrepto™	Streptomycin (*S. griseus*)	BCA
Agri-Mycin 17 WP	Streptomycin (*S. griseus*)	BCA
Strepto	Streptomycin (*S. griseus*)	BCA
Plantomycin WG	Streptomycin (*S. griseus*)	BCA
Ag-Streptomycin	Streptomycin (*S. griseus*)	BCA
Plantomycin	Streptomycin (*S. griseus*)	BCA
Kasumin™	Kasugamycin (*S. kasugaensis*)	BCA
Biomycin	Kasugamycin (*S. kasugaensis*)	BCA
Omycin	Kasugamycin (*S. kasugaensis*)	BCA

environmental challenges that may decrease their survival rate and degradation efficiency. Therefore, microbes isolated from polluted sites are better candidates for bioremediation. Many investigations support the fact that actinobacterial species show supremacy in heavily contaminated zones (Gremion et al. 2003; Chikere et al. 2009). Actinobacteria have considerable tolerance or acclimatization potential for the toxic compounds or metals, which help them to grow in highly polluted sites as well as to clean the environment. The use of actinobacteria and their enzymes as a bioremediation tool may thus provide an effective gateway to the field of environmental biotechnology.

9.5.1 Bioremediation of Pesticides/Insecticide-Polluted Sites

Cultivable land area and water resources are becoming scarce in modern industrial times, which drastically affect the world agro-economy. The new challenges of modern agricultural system include producing more and more food commodities to feed the ever increasing population with limited resources. Considering the agricultural intensification aspects, the use of various organic or inorganic agrochemicals has been allowed for cropping. Most chemical compounds are hazardous and persist for longer in the environment raising serious concerns such as their toxicity to nontarget organisms. This creates a need to decontaminate toxic pollutants and restore the environmental sustainability. A high catabolic rate, adaptability, rapid germination of spores, and fast-growing hyphae make actinobacteria potent candidates to remediate polluted sites (Fuentes et al. 2010). Their filamentous structures penetrate and facilitate colonization into the deep soil horizon, therefore, minimizes the mixing step of bioremediation process (Ensign 1992), which is an advantage for using actinobacteria in bioremediation. In addition, the indigenous actinobacterial population is comparatively high (10^4–10^6 per gram of soil) and has been enumerated as the second most abundant inhabitants after bacteria in soil (Goodfellow and Williams 1983). In general, indigenous microbes of contaminated environment are considered as good candidates for bioremediation (El Fantroussi and Agathos 2005) since they are already acclimatized to tolerate (Shelton et al. 1996). The actinobacteria isolated from a polluted site are capable of secreting a large number of extracellular enzymes such as monooxygenase and dioxygenase that catalyze the mineralization of xenobiotic pesticides with diverse chemical compounds. A large group of actinobacterial species was observed as the active participants of biodegradation processes in freshwater and marine sediments. They constitute an approximately 21.7 % fraction of the total genera identified by a metagenomic approach (Fang et al. 2014). Actinobacteria utilize pesticides either as a carbon and energy source or co-metabolize the harmful chemicals without gaining any advantage. Co-metabolism is the degradation of toxic chemicals by hydrolytic enzymes produced by microbes for metabolism of other energy yielding biomolecules. *Brevibacterium linens* DSM20425 was shown to co-metabolize the toxic pesticide 2,4,5-T into 3,5-dichlorocatechol (Horvath 1971). Pesticide degradation is most often completed through synergistic actions of microbial consortia than via a single isolate. In mixed microbial populations, microorganisms either directly degrade toxic compounds or hasten the biotransformation efficiency of other microbes. Byss et al. (2008) showed the synergistic action between actinobacteria and *Pleurotus ostreatus* in bioremediation.

Organophosphate pesticides (OP) are chemicals with O-P bonds, used worldwide as pesticide, insecticide, and herbicide accounting for more than 34 % of the total world market (Singh and Walker 2006). It includes chlorpyrifos (*O*,*O*-diethyl *O*-(3,5,6-trichloro-2-pyridinyl) phosphorothioate), parathion (*O*,*O*-diethyl *O*-4-nitrophenyl phosphorothioate), malathion (*O*,*O*-dimethyl *S*-1,2-di(ethoxycarbonyl), ethyl phosphorodithionate), and diazinon (*O*,*O*-diethyl *O*-(2-isopropyl-6-methylpyrimidine-4-yl(phosphorothioate)). Most of them have been found to interfere with the function of acetylcholinesterase (a key enzyme of neurotransmission) (Hassall 1990), thus act as broad-spectrum insecticides. However, only <0.1 % fraction of total employed pesticide is used up in killing or suppression of growth of the target organisms (Pimentel 1995), while the rest remains in the environment and contaminates both soil and water ecosystems, leading to major environmental and human health problems. The extensive use of OP has become a major cause of over 2,00,000 deaths annually worldwide (Singh et al. 2009). These polluted sites require to be decontaminated by chemical, physical, and biological methods. Microbial degradation is considered as a better option to clean up the polluted sites since microbes can detect even the presence of small quantity of pesticides and detoxify them.

Chlorpyrifos (CP) is a broad-spectrum chlorinated organophosphorus insecticide that has been used for over 40 years to increase crop productivity. According to the statistics data of the Committee of the Ministry of Agriculture and Land Reclamation (2011), approximately 1280 tons of CP is consumed annually in agriculture fields in Egypt. Persistence of CP is between 10 and 120 days in soil, but can extend up to 1 year in some environmental conditions. CP residues have been detected in various ecosystems, which led to disturbance in biogeochemical cycles (Chishti et al. 2013). They need to be completely detoxified as soon as possible after their application. Briceno et al. (2012) isolated two potent *Streptomyces* strains, which could metabolize up to 90 % of toxic CP within 24 h of incubation, and yield 3,5,6-trichloro-2-pyridinol (TCP). However, the release of TCP into environment is another major ecological problem because of its higher solubility and mobility than the parent compound (CP). It exhibits antimicrobial activity inhibiting the proliferation of CP degrading bacteria (Singh and Walker 2006), thus the complete degradation of CP is required. An actinobacterium, *Gordonia* sp. JAAS1 capable of degrading the CP and its hydrolytic metabolite such as TCP into diethylthiophosphoric acid (DETP) was isolated from a paddy field (previously exposed to CP treatment) (Abraham et al. 2013). Recently, a kinetic study of parathion degradation by *Streptomyces venezuelae* ACT 1 has been done, which revealed that the actinobacterium strain ACT 1 has a high ratio of degradation and chemical oxygen degradation (COD) reduction rate (Naveena et al. 2013). The high biodegradability enhances industrial importance of this strain, especially in the treatment of pesticide-contaminated wastewater. Conversion of methyl parathion into PNP has been achieved by using *Nocardiopsis* sp. DD2, isolated from the coastal area, Gujarat, India (Pravin et al. 2012). The strain DD2 showed a broad catabolic activity and was capable of degrading other organophosphate pesticides such as endosulfan (6,7,8,9,10,10-hexachloro-1,5,5a,6,9,9 a-hexahydro-6,M9-methano-2,4,3-benzo-dioxathiepine-3-oxide). A constitutive expression of enzymes degrading parathion has been observed in *Arthrobacter* sp. (Nelson 1982) that utilizes parathion as a sole source of carbon and energy. *Arthrobacter* species are also capable of degrading another OP such as diazinon, but it requires the process of cometabolism by *Streptomyces* species to initiate the degradation process (Gunner and Zuckerman 1968).

PNP is another environmental pollutant, extensively used as a raw material in the manufacturing of dyes, explosives, drugs, and herbicides. It is also released as an end product of microbial degradation of pesticides such as parathion and methyl parathion (Ningthoujam et al. 2012). A comparatively high solubility of PNP (16 g/L) in water enhances its infiltration through soil strata, leading to the contamination of both surface and ground water (Kulkarni and Chaudhari 2006). High concentration of PNP is extremely hazardous to human health and affects severely both microbial flora and fauna (PAN 2008). It has been listed as a major pollutant by the U.S. Environmental Protection Agency (EPA) (http://www.epa.gov/waterscience/methods/pollutants.htm). Several actinobacterial species such as *Citricoccus nitrophenolicus* (Nielsen et al. 2011), *Rhodococcus* sp. HS6-1 and *Brevibacterium* sp. (Ningthoujam 2012) have been reported to metabolize PNP and lower its toxicity. The last two actinobacterial strains were shown to degrade up to 350 and 270 mg/L PNP, respectively. Hanne et al. (1993) isolated two PNP degrading soil actinobacteria (*Arthrobacter aurescens* TW17 and *Nocardia* sp. strain TW2). *Arthrobacter* strain harbors genes, which encode enzymes involved in biodegradation on an extrachromosomal plasmid. The enzyme production in both strains is inducible and requires the presence of pesticides.

Glyphosate is a well-known organophosphonate herbicide (Pn) with C-P linkage which inhibits the function of a critical enzyme (5-enolpyruvyl shikimic acid-3-phosphate synthase) of the biosynthetic pathway of aromatic amino acids (Steinrucken and Amrhein 1980). The C-P bond makes glyphosate more stable and resistant to the microbial degradation. Only two *Arthrobacter* species had been reported to utilize glyphosate as the sole source of phosphorus (listed in Table 9.4). Metabolic pathways of glyphosate differ in both the actinobacteria. *Arthrobacter* sp. GLP-1 produces two distinct C-P lyases, which act on glyphosate to yield sarcosine. Sarcosine is further degraded to glycine (incorporated in purine and pyrimidine) and C_1-unit (utilized for the synthesis of aminoacids) (Kertesz et al. 1991). A very dissimilar glyphosate metabolism was observed in *A. atrocyaneus* ATCC 13752 that catabolizes glyphosate into aminomethylphosphonic acid (AMPA) and C_2-units (Pipke and Amrhein 1988). Complete degradation of AMPA to CO_2 occurs in this actinobacterium.

Organochlorine pesticides such as Endosulfan (6,7,8,9,10,10-Hexachloro-1,5,5a,6,9,9a-hexahydro-6,9-methano-2,4,3-benzodioxathiepine-3-oxide), Lindane (gamma-hexachlorocyclohexane (γ-HCH)), Chlordane (1,2,4,5,6,7,8,8-Octachloro-3a,4,7,7a-tetrahydro-4,7-methanoindane), Metolachlor [(RS)-2-Chloro-*N*-(2-ethyl-6-methyl-phenyl)-*N*-(1-methoxypropan-2-yl)acetamide],atrazine(2-chloro-4-isopropylamino-6-ethylamino-*s*-triazine), Methoxychlor [1,1,1-Trichloro-2,2-bis(4-methoxyphenyl) ethane], DDT (Dichloro diphenyl trichloroethane), PCNB (pentachloronitrobenzene), 2,4-D [(2,4-Dichlorophenoxy)acetic acid], 2,4,5-T [(2,4,5-Trichlorophenoxy)-acetic acid], and pentachlorophenol are the most toxic and environmentally destructive synthetic chemicals. Most of them have been banned in many countries because of their long lasting persistence, high toxicity and ability to bioaccumulate in the living tissues (Hirano et al. 2007). Actinobacteria have a good potential to detoxify or feed on the hazardous organochlorine pesticides (listed in Table 9.4). Martens (1976) had isolated several endosulfan degrading actinobacteria. The detailed investigations on actinobacteria confirmed that the genus *Streptomyces*is capable of catabolizing a wide range of organochlorine pesticides, specifically, DDT, PCNB (Chacko et al. 1966), metolachlor (Liu et al. 1990), Dalapon (Kaufman 1964), diuron (Castillo et al. 2006), atrazine (Fadullon et al. 1998), lindane, chlordane, and methoxychlor (Fuentes et al. 2010).

The degradation of mono-, di-, and tri-chlorinated pesticides is commonly observed among actinobacteria. The enzymatic system involved in biodegradation of 2,4-D has been extensively studied in two actinobacterial strains including *Nocardioides simplex* 3E (Kozyreva and Golovleva 1993) and *Arthrobacter* strain

Table 9.4 List of actinobacteria degrading pesticide and insecticide

Chemicals	Actinobacteria	Site of isolation	Pesticide degradation capacity	References
Organophosphorus pesticides				
Chlorpyrifos	*Streptomyces* sp. strain AC5	Soil samples, southern Chile	90 % of 25 mg/L or 50 mg/L	Briceno et al. (2012)
	Streptomyces sp. strain AC7			
	Streptomyces thermocarboxydus strain A-B	Agricultural wastewater, Egypt	77.57 % in 28 days	Eissa et al. (2014)
	Gordonia sp. JAAS1	Agricultural soil	110 mg/L	Abraham et al. (2013)
Parathion	*Streptomyces venezuelae* ACT 1	Marine water sample	Hydrolase activity rate as 0.273/h	Naveena et al. (2013)
Methyl parathion	*Nocardiopsis* sp.	Coastal area, India	–	Pravin et al. (2012)
Diazinon	*Streptomyces* sp. AC1–6	Agricultural soil	40–50 % and 70–90 % after 24 and 96 h of incubation, respectively	Briceno et al. (2015)
	Streptomyces sp. ISP4			
	Arthrobacter sp. and Streptomyces	–	84 % in 7 days	Gunner and Zuckerman (1968)
Organophosphonate pesticides				
Glyphosate	*Arthrobacter* sp. GLP-1	–	–	Pipke et al. (1987)
	Arthrobacter atrocyaneus ATCC 13752	–	–	Pipke and Amrhein (1988)
Organochlorine pesticides				
Chlordane	*Streptomyces* sp. A5	Contaminated environment, Argentina	56 % in 28 days	Cuozzo et al. (2012)
Lindane	*Streptomyces*sp. M7	Pesticide-contaminated sediments, Argentina	50 % in 3 days	Benimeli et al. (2007)
	Streptomyces strain PS1/5	–	–	Speedie et al. (1987)
Metolachlor	*Streptomyces* sp.	Soil	70 %	Liu et al. (1990)

Atrazine	*Streptomyces* sp. PS1/5	Soil, Beltsville	~70 %	Fadullon et al. (1998)
	Frankia alni ACN14a	–	–	Rehan et al. (2014)
2,4-D and 2,4,5-T	*Nocardioides simplex* 3E	–	100 %	Kozyreva and Golovleva (1993)
DDT and PCNB	*Nocardia* and *Streptomyces* species	–	–	Chacko et al. (1966)
Dalapon	*Arthrobacter*, *Nocardia*, and *Streptomyces* species	–	–	Kaufman (1964)
Aldrin	*Mycobacterium, Nocardia, Streptomyces*, and *Micromonospora* species	–	–	Ferguson and Korte (1981)
Pentachlorophenol (PCP)	*Janibacter* sp. FAS23	Saline sediment of arid land, southern Tunisia	300 mg/L	Khessairi et al. (2014)
	Mycobacterium chlorophenolicum PCP-1	–	40 μmol (g of dry cells)$^{-1}$ h^{-1}	Wittmann et al. (1998)
	Rhodococcus chlorophenolicus PCP-I	Biofilter filled with soft wood bark chips	–	Apajalahti et al. (1986) and Apajalahti and Salkinoja-Salonen (1984)
	Arthrobacter strain ATCC 33790	–	–	Edgehill (1994)
	Kocuria sp. CL2	Secondary sludge of pulp and papermill, India	58.64 % of sludge (>100 mg/L)	Karn et al. (2011)
	Saccharomonospora viridis	Mushroom compost	100 %	Webb et al. (2001)
Diuron	Actinomycete strain CCT	Soil	–	Esposito et al. (1998)
Polychlorinated biphenyls	*Janibacter* sp. MS3–02	Soil sample, Spain	70–100 % in 7 days	Sierra et al. (2003)
Monochlorinated dibenzo-*p*-dioxin	*Janibacter* sp. strain YA	River sediment	>90 % in 18 h	Iwai et al. (2005)

(continued)

Table 9.4 (continued)

Chemicals	Actinobacteria	Site of isolation	Pesticide degradation capacity	References
Chlorinated dibenzo-*p*-dioxin	*Terrabacter* sp. strain DBF63	–	–	Habe et al. (2001)
	Rhodococcus opacus SAO 101	Forest soil, Japan	–	Kimura and Urushigawa (2001)
Benzonitrile herbicides				
Bromoxynil	*Aminobacter* sp. MSH1	Plant nursery	20–30 %	Frkova et al. (2014)
Ioxynil				
Dichlobenil				
Synthetic pyrethroid insecticides				
Deltamethrin	*Streptomyces aureus* strain HP-S-01	Activated sludge, China	50–300 mg/L deltamethrin in 7 days	Chen et al. (2011)
Cypermethrin	*Streptomyces* sp. HU-S-01	Wastewater sludge, China	1.236 μmol/min	Lin et al. (2011)

(Loos et al. 1967). The former actinobacterium was also found to degrade another pesticide 2,4,5-T (Golovleva et al. 1990). The *Arthrobacter* strain was also capable of utilizing two other organochlorine pesticides, viz. 4-CPA (4-chlorophenoxyacetate) and MCPA (2-methyl-4-chlorophenoxyacetate) as the sole source of carbon and energy. Stability of organochlorine compounds depends on the degree of chlorination. The polychlorinated compound, pentachlorophenol (PCP), is a highly stable compound, widely used as biocide (bactericide, fungicide, and algaecide), wood and leather preservative (Kao et al. 2004). PCP acts as an inhibitor of oxidative phosphorylation, therefore, is toxic to almost all living organisms (Shen et al. 2005) causing severe disease symptoms in humans. This compound has also been listed as a toxic pollutant (EPA 1987). Aerobic degradation of this recalcitrant chemical by diverse genera of actinobacteria has been confirmed (listed in Table 9.4). *Streptomyces rochei* 303 is the only actinobacterium reported till date that can metabolize a broad spectrum of chlorophenols ranging from mono- to pentachlorophenols (Golovleva et al. 1992). Mono- and polychlorinated dibenzo-p-dioxin degradation is known to be catalyzed by *Janibacter*, *Rhodococcus*, and *Terrabacter* species (shown in Table 9.4). They metabolize and incorporate the carbon moieties of the toxic compounds into their cell biomass.

Benzonitrile herbicides include dichlobenil (2,6-dichlorobenzonitrile), ioxynil (3,5-diiodo-5-hydroxybenzonitrile), and bromoxynil (3,5-dibromo-5-hydroxybenzonitrile). The massive use of these chemicals contaminates soil and ground water (US-EPA, Herbicide Report, 1974). The use of dichlobenil is restricted in the European Union since its hydrolytic metabolite [2,6-dichlorobenzamide (BAM)] is highly toxic. The complete degradation of dichlobenil by *Aminobacter* MSH1 was reported (Frkova et al. 2014). However, the use of this actinobacterium in bioremediation application is limited because it can only partially hydrolyze the other two benzonitrile herbicides (ioxynil and bromoxynil) and yields toxic end products which may pose an environmental risk.

Streptomyces sp. has also been found to metabolize the synthetic pyrethroid insecticides (shown in Table 9.4). Synthetic pyrethroid insecticides are pyrethrin analogues derived from plants (Laffin et al. 2010). Their photostability, low mammalian toxicity, and quick insecticidal capability enhanced their market value (approximately 25 % of the total world insecticide market) and replaced toxic organophosphate pesticides (Katsuda 1999; Zhang et al. 2010). Synthetic pyrethroid insecticides were earlier considered as thenontoxic insecticides (Dorman and Beasley 1991). According to recent studies, these have been found to be carcinogenic and a major causative agents of chronic diseases (Wang et al. 2009). For instance, cypermethrin was found to disturb the food chain of aquatic ecosystem (Pearce 1997). *Streptomyces aureus* strain HP-S-01 isolated from activated sludge is capable of degrading deltamethrin and its toxic metabolite (3-phenoxybenzaldehyde) (Chen et al. 2011). 3-phenoxybenzaldehyde possesses antimicrobial activity and hinders further biodegradation (Laffin et al. 2010). This actinobacterium can also efficiently degrade other synthetic pyrethroids such as cyfluthrin, bifenthrin, cypermethrin, fenvalerate, fenpropathrin, and permethrin.

9.5.2 Biodegradation of Hydrocarbon Containing Contaminants

As compared to bacteria and fungi, actinobacteria exhibit greater potential for degradation of hydrocarbons (Idemudia et al. 2014). The concentration of hydrocarbon pollutants including complex organic compounds, petroleum and oil products are steadily increasing in the environment due to their excessive use. Hydrocarbons are toxic to microbes, plants, and other living organisms (Andreoni et al. 2004) causing a potential risk to the environment. Bioremediation and phytoremediation, the use of microbes or plants to remove toxic hydrocarbon compounds, are getting attention in the recent years (Chibuike and Obiora 2014; Arthur et al. 2005). Phytoremediation method relies on a mutualistic relationship between plants and microbes. Actinobacterial species (showing close similarities with *Arthrobacter* species) form a dynamic part of microbial communities associated with phytoremediation of hydrocarbon-polluted sites (Phillips et al. 2008). The taxonomically diverse actinobacterial genera colonize as dominant populations in hydrocarbon-polluted sites. They constitute antimicrobial group capable of degrading a wide range of hydrocarbons (listed in Table 9.5). Hydrocarbonoclastic bacterial communities isolated from mangrove sediment, Guanabara Bay (Brazil) include bacterial species as well as actinobacterial species (belonging to the genera *Micrococcus, Cellulomonas*, *Dietzia*, and *Gordonia*) (Brito et al. 2006). These are capable of degrading an assortment of hydrocarbon pollutants. Hydrocarbon degrading microorganisms have also been isolated from seawater, Semarang port, Indonesia. This microbial community consisted of approximately 23 % of actinobacterial species (Harwati et al. 2007). Culture-dependent microbial diversity analysis revealed that actinobacterial species (*Micrococcus, Nocardia, Gordonia, Micromonospora*, and *Rhodococcus*) and bacterial species form a potential microbial group for degrading spent lubricating oil (Idemudia et al. 2014). These actinobacterial species showed approximately 1.035–7.53 % degradation of oil. Actinobacterial isolates belonging to the genera *Rhodococcus* and *Gordonia* were capable of degrading both long chain *n*-alkanes and *c*-alkanes of petroleum compounds (Kubota et al. 2008). Diverse salt-tolerant actinobacterial species, *Streptomyces albiaxialis* (Kuznetsov et al. 1992), *Rhodococcus erythropolis* and *Dietzia maris* (Zvyagintseva et al. 2001), *Rhodococcus* sp. and *Gordonia* sp. (Borzenkov et al. 2006), *Dietzia* sp. and *Actinopolyspora* sp. DPD1 (Al-Mueini et al. 2007) were documented to possess an efficiency to degrade crude oils under moderate to high saline environment. Bjorklof et al. (2009) reported that *Mycobacterium* species were a dominant population in the hydrocarbon-contaminated soil. Actinobacterial species (*Rhodococcus* sp., *Nocardia* sp., *Arthrobacter* sp., *Gordonia* sp., *Mycobacterium* sp., *Corynebacterium* sp., and *Micrococus* sp.) contributed significantly to the biodegradation of crude oil (Chikere et al. 2009). A high potential for biodegradation makes actinobacteria a prospective clean-up solution for remediation of hydrocarbon-contaminated sites.

Table 9.5 List of hydrocarbons degrading actinobacteria

Actinobacteria	Hydrocarbons	Site of isolation	References
Janibacter anophelis strain JY11	Phenanthrene, anthracene, and pyrene	Polluted soil sample, Jinan Oil Refinery Factory, China	Zhang et al. (2009)
Streptomyces sp., *Rhodococcus* sp., and *Nocardia* sp.	Crude oil, Anthracene, Coronene, Napthacene, Acenapthene	Soil samples, Mathura Oil Refinery, Lucknow	Shekhar et al. (2014)
Rhodococcus erythropolis BZ4, *R. cercidiphyllus* BZ22, *Arthrobacter sulfureus* BZ73, *Pimelobacter simplex* BZ91	*n*-alkanes, phenol, anthracene, pyrene	Petroleum hydrocarbon-contaminated alpine soil, Italy	Margesin et al. (2013)
Dietzia strain DQ12-45-1b	Petroleum hydrocarbons (C6–C40) and crude oil	Oil production water sample, China	Wang et al. (2011)
Micrococcus luteus GPM2603 and *Cellulomonas variformis* GPM2609	Pristine and pyrene, respectively	Mangrove sediments, Brazil	Brito et al. (2006)
Gordonia alkanivorans HKI 0136T	Hexadecane	Tar-contaminated soil, Rositz	Kummer et al. (1996)
Micrococcus luteus	Naphthalene and benzene	Oil-contaminated tropical marine sediments, south Singapore	Zhuang et al. (2003)
Dietzia sp. strain GS-1	Disodium terephthalate	Soil sample	Sugimori et al. (2000)
D. maris and *Rhodococcus erythropolis*	*n*-alkane and *iso*-alkanes	–	Zvyagintseva et al. (2001)

9.5.3 *Detoxification of Heavy Metals*

All living organisms require a small quantity of heavy metals including iron, zinc, copper, manganese, cobalt, and nickel for their physiological growth and development (Park et al. 2006), but these metals become toxic at higher concentrations. The presence of very small quantity of other heavy metals causes toxic effects on both prokaryotes and eukaryotes. On the basis of physiological viewpoints, heavy metals are classified into two major categories (1) harmful at high concentrations (e.g., Fe, Zn, Cu, Mn, Co, Ni, and Cr) (2) highly toxic or nonessential (Hg, Cd and Pb) (Valls and Lorenzo 2002). Industrial activities and abandoned mining represent major sources of discharge of copious amounts of heavy metals into the environment leading to human health risks and serious ecological complications. At present, environmental metal-toxicity is increasing alarmingly which calls for an immediate action. Currently, development of phytoextraction (Gremion et al. 2003) and microorganism-based remediation methods (Colin et al. 2012) have been in focus for toxic metal detoxification as they are cost-effective and efficient. Actinobacteria is an ecologically important group that is conferred with specific cellular machinery to respond to both metal deprived and overloaded condition. The exact mechanisms for metal homeostasis by actinobacteria have not been adequately understood. In southwest Slovakia, a heavy metal-contaminated farmland was predominantly colonized by actinobacterial species after proteobacteria (Karelova et al. 2011). High dominance of actinobacterial species occurs in heavy metal-contaminated bulk and rhizospheric zone of many metal accumulating plant species (Gremion et al. 2003). In general, microbial populations isolated from metal-contaminated sites are preferred for the development of metal remediating tools. Actinobacteria includes a number of heavy metal-resistant species (Table 9.6) that are capable of bioaccumulation of toxic elements and decontamination of metal-polluted sites. The species of *Streptomyces* has been considered as potential sources for remediating sites that were co-polluted with Cr and lindane (Aparicio et al. 2015). *Frankia* species show an elevated level of tolerance to several metals and metalloids (Pb^{2+}, Al^{3+}, SeO_2^{3-}, Cu^{2+}, AsO_4, and Zn^{2+}) (Richards et al. 2002). Metal resistance in *Frankia* species aids colonization of actinorhizal host plants in highly contaminated or nutrient-poor soils (Schwencke and Caru 2001). *Arthrobacter* sp. U3 isolated from metal-contaminated environment was capable of detoxifying a hazardous metal (Hg) up to 80 % in a bioremediation site (Giovanella et al. 2015). The soil inhabiting and nonpathogenic *Arthrobacter* species offer their exploitation in environment cleanup and remediation process.

9.5.4 Biodegradation of Plastics/Bioplastics

The term “white pollution” refers to solid waste including polythene and plastic bags, disposed into the environment, which affect the soil ecosystem adversely. These plastic products are made of polystyrene, polypropylene, polyvinyl chloride, and other polymers that are highly resistant to microbial degradation, thereby leading to severe urban environmental consequences. The problems related to white pollution have encouraged research into finding or developing biodegradable plastics (Steinbuchel 2001). Several microbes synthesize biopolymers in the form of intracellular storage granules (Luengo et al. 2003). These have been explored for the manufacturing of biodegradable plastics. Microbe-derived biopolymers are majorly poly (3-hydroxyalkanoate) (PHA) and poly (3-hydroxybutyrate) (PHB) (Bugnicourt et al. 2014). Bioplastics are receiving considerable attention since they can easily be degraded by microbes in the environment. Diverse thermophilic and thermotolerant actinobacterial species have been reported with the capability to degrade bioplastics and rubbers (Shivlata and Satyanarayana 2015). Several mesophilic *Streptomyces* species producing polyhydroxyalkanoate and poly (3-hydroxybutyrate) depolymerases and other non-*Streptomyces* species have been shown to degrade bioplastics

Table 9.6 List of metal detoxifying, dye decolorizing, and bioplastic degrading actinobacteria

Actinobacteria	Toxic metal or effluents	Site of isolation/ collection	References
Metal detoxifying actinobacteria			
Streptomyces roseisederoticus (V5)	Cr, Cd, Zn, and Pb	Rhizosphere region of *Casuarina equisetifolia*	Vinod et al. (2014)
S. flavochromogenes (V6)			
S. vastus (V7)			
S. praguaeneses (V8)			
Streptomyces and *Amycolatopsis* species	Cr, Cd, Zn, and Pb	Abandoned mining areas	El Baz et al. (2015)
Streptomyces werraensis LD22	Cr, Pb, Ni, and Zn	Chicken and goat feces	Latha et al. (2015)
Actinobacteria including both *Streptomyces* and non-*Streptomyces* species (*Micromonospora*, *Actinoplanes*, *Norcardia* and other rare genera)	Hg, Cd, Cu, Pb, As, Ni, and Zn	Tin tailings and forest soil	Hema et al. (2014)
Arthrobacter sp. U3	Hg	Metal-contaminated industrial effluents	Giovanella et al. (2015)
Bioplastic degrading actinobacteria			
Streptomyces roseolus SL3, *Streptomyces pulveraceus, Streptomyces atratus, Streptomyces anulatus, Streptomyces beijiangensis,* and *Streptomyces omiyaensis*	Polyesters including P(3HP), P(3HB), P(HB-HV), and PCL	Soil, sludge, and water sample	Gangoiti et al. (2012)
Streptomyces venezuelae SO1	Medium-chain-length PHA	Soil sample	Santos et al. (2013)
Arthrobacter globiformis SBI-5	Polyurethane	Oil-contaminated connecticut soil	El-Sayed et al. (1996)
Corynebacterium sp.	Polyurethane	Degraded polyester polyurethane samples	Kay et al. (1991)
Rhodococcus equi TB-60	Urethane	Soil samples	Akutsu-Shigeno et al. (2006)
Actinomadura sp. AF-555	P(HB-HV)	Soil sample	Shah et al. (2010)
Kibdelosporangium aridum JCM 7912	Poly(L-lactide)	Japan collection of microorganisms	Jarerat et al. (2003)
Amycolatopsis orientalis IFO 12362	Poly(L-lactide)	Institute for Fermentation, Osaka	Jarerat et al. (2006)
Saccharothrix waywayandensis JCM 9114	Poly(L-lactide)	Japan collection of microorganisms	Jarerat and Tokiwa (2003)
Dyes decolorizing actinobacteria			
Saccharothrix aerocolonigenes TE5	Reactive azo dyes	Soil contaminated with textile effluents	Rizwana and Palempalle (2015)

(continued)

Table 9.6 (continued)

Actinobacteria	Toxic metal or effluents	Site of isolation/ collection	References
*Micrococcus glutamicus*NCIM 2168	Reactive green 19A	Culture Collection Center, National Chemical Laboratory, Pune	Saratale et al. (2009)
Streptomyces species	Azo blue and azo orange dyes	Textile industry effluent, Kerala	Pillai et al. (2014)
Rhodococcus qingshengii JB301	Triphenyl methane dyes	Sawdust	Li et al. (2014a)
Amycolatopsis orientalis	Amido black	Soil sample	Chengalroyen and Dabbs (2013)
Streptomyces chromofuscus A11	Azo dye isomers	American type culture collection	Pasti-Grigsby et al. (1996)
Dietzia sp. PD1	Congo red and indigo carmine	Textile effluent, Kolkata	Das et al. (2016)

P(3HP) poly(3-hydroxypropionate), *P(3HB)* poly(3-hydroxybutyrate), *P(HB-HV)* poly(3-hydroxybutyrate-co-3-hydroxyvalerate), *PCL* poly-ε-caprolactone

(Table 9.6). Bioplastics are also derived from renewable resources including vegetables, cornstarch, and agricultural by-products. Synthesis of bioplastics from green renewable resources is of current interest. Recently, a mesophilic actinobacterium, *Streptomyces coelicolor* CH13 degraded a blended cassava starch/natural rubber biopolymer (Watcharakul et al. 2012). An endophytic actinobacterium, *Nocardiopsis* sp. mrinalini9 capable of degrading polythene, plastic and diesel, was isolated from leaves of *Hibiscus rosasinensis* (Singh and Sedhuraman 2015). *Rothia* sp. belonging to the phylum *Actinobacteria* was isolated from a deteriorating epoxy resin statue (Pangallo et al. 2015). A chemical compound dibutylin (DBT) is a most widely used plastic stabilizer, which causes neurotoxic, hepatotoxic, and immunotoxic effect on humans. It is also released into the environment as a by-product of degradation of tributylin (used as antifouling agent in boat paints) (Antizar-Ladislao 2008). *Streptomyces* spp. isolated from plant waste composting heaps have been shown to be capable of degrading up to 90 % of DBT (added at 20 mg/L) after 1 day of incubation (Bernat and Dlugonski 2009).

9.5.5 *Decolorization of Dyes*

After the discovery and successful commercialization of the world's first synthetic dye (mauevin), more than 10,000 synthetic dyes have been developed and are being used in textile and dyestuff manufacturing (Robinson et al. 2001). Other applications of synthetic dyes include paper printing, manufacturing of food coloring additives and cosmetics. More than 7 × 10^5 metric tons of synthetic dyes are produced annually (Zollinger 1987). In general, complete utilization of coloring dyes does not occur during the dyeing processes. Approximately 10–15 % of total dyes used are lost as effluent from industries due to inefficiency of the processing operation. Dye-containing effluents discharged from industries enter into water bodies and disturb the aquatic ecosystem. Textile industries consume a substantial amount of water for wet processing of textiles and release a large quantity of liquid effluent pollutants into the environment. Approximately 2.8 × 10^5 tons of dye effluents are discharged from textile industries per annum (Jin et al. 2007), representing the largest source of water pollution. Consumption of dye-polluted water causes toxicity and carcinogenicity in all living beings (Ratna and Padhi 2012). The presence of colored dye molecules in water bodies reduces the penetration of sunlight and decreases photosynthetic activity of aquatic flora, thereby deteriorating water quality such as decreasing the dissolved oxygen concentration (Vandevivere et al. 1998). In addition, their acute toxic effects on aquatic fauna have also been demonstrated (Olaganathan and Patterson 2013). The presence of toxic dyes in the environments everly damages economically important plants growing in the vicinity of such polluted areas (Kapustka and Reporter 1993). Therefore, there is an urgent requirement of proper treatment of industrial effluents prior to their discharge into the environment. Several physical and chemical methods have been used for the treatment of wastewater effluent. Physiochemical methods are too expensive and inefficient to perform complete removal of dyes from wastewater (Saratale et al. 2011). These limitations inspire to search for an alternate effective way to decontaminate the water resources. Microbial or enzymatic decolorization methods are therefore being developed, as these are economic and eco-friendly as opposed to physiochemical decomposition methods (Rai et al. 2005). Actinobacteria are considered as potent decomposers, and they mineralize a diverse array of recalcitrant pollutants including toxic dyes (shown in Table 9.6). Ball et al. (1989) reported that three actinobacterial species, *Streptomyces badius* 252, *Streptomyces* sp. strain EC22, and *Thermomonospora fusca* MT800, have the ability to decolorize the polymeric dye Poly R. Fourteen lignocellulolytic *Streptomyces* species were screened for their ability to decolorize dyes (Poly B-411, Poly R-478 and Remazol Brilliant Blue R). A strong positive correlation was found between ligninolytic capability and dye decolorization of two dyes (Poly B-411 and Remazol Brilliant Blue R). *Streptomyces* species produced extracellular peroxidases involved in decolorization of dyes (Pasti and Crawford 1991). There is another report that also supports the fact that lignin solubilizing *Streptomyces* species, *S. violaceoruber*, decolorized 63 % of Poly R-478 after 24 h of incubation (Abou-Dobara and Omar 2014). Zhou and Zimmermann (1993) demonstrated that actinobacteria removed dyes from effluents through either adsorption or degradation process. Actinobacteria catalyzing the reactions of hydroxylation, dealkylation, and oxidation were able to degrade the xenobiotic pollutants (Goszczynski et al. 1994).

Complete degradation of Reactive Green 19A (50 mg/L) was achieved by using *Micrococcus glutamicus* NCIM 2168 within 48 h of incubation (Saratale et al. 2009). Actinobacteria are known to decolorize dyes in all states as in pure culture or co-culture or mixed culture. Saratale et al. (2010) developed a bacterial consortium by co-culturing two pure cultures of *Proteus vulgaris* NCIM-2027 and *Micrococcus glutamicus* NCIM-2168. This consortium degraded azo dyes more efficiently than the individual strains. Another actinobacterium *Rhodococcus globerulus* capable of decolorizing azo dyes was found to be an active participant in the microbial consortium with two bacterial strains (Joshi et al. 2008). *Streptomyces* sp. C1 isolated from thermophilic phase of composting showed decolorizing activity by producing an enzyme known as laccase-like multicopper oxidase (Lu et al. 2013). *Streptomyces psammoticus* was also shown to secrete an extracellular laccase that finds application in decolorization of dyes (Niladevi and Prema 2008). Therefore, whole cells of actinobacteria or their enzymes can be used for decolorization of dye-contaminated effluents.

9.6 Conclusions and Future Perspectives

Actinobacteria have potential applications in both agricultural economy and environmental biotechnology. Use of actinobacteria as microbial inoculants for enhancing crop productivity and environmental pollution control would be a beneficial approach to keep both agriculture and environment clean and safe. In order to exploit actinobacteria, there is a need to carry out detailed investigations on their physiology and molecular mechanisms. Detailed investigations are called for understanding the physiological and molecular basis of plant–actinobacteria interactions. In view of the major impact of actinobacteria in environmental sustainability, the elucidation of metabolic pathways involved in the biodegradation of toxic pollutants would be useful.

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