Review Article

EFFICACY OF RHIZOBACTERIA IN WEED DYNAMICS OF CROP PRODUCTION RHYTHM

ABSTRACT

Weeds plague food crop agriculture of regions of the world. This continued with no adequate and most cost-effective control measures available. Weedicides, for sure, are the leading solution to challenges posed by weeds in the food crop agriculture; however, high costs and the underlying environmental and health repercussions have prompted many works in biological strategies to tackle weeds. The current work gives an overview of rhizobacteria's (RB) efficacy evaluation in tackling weeds dynamics in the crop production system. RB, as free-living soil microorganisms detrimental to weeds in nature; colonize plant roots, suppresses and inhibits the growth of seeds and seedlings in various pathways and mechanisms involving a spectrum of biosynthesized toxins as phytogenic compounds or metabolites. However, RB's efficacy is a constraint due to many reasons such as low activity, a limited spectrum of activities, reduced survival rates, persistence of the suppressive and inhibitive compounds, and complexity of the interactions between the RB and the target weeds. It is imperative to understand the interaction between the weeds and rhizospheres ecological systems to improve the RB approach's efficacy and effectiveness. Hence, advances in microbial genetics, microorganism-plant interactions, and community-level analysis of microbial organisms, including microbe-host relationships that include various biological agents and their potential hosts with higher susceptibility virulence, are essential. Treatments that really can guarantee a longer shelf life, effectiveness, and continued existence of microbial agents, microbial population structure and function that can accelerate microbial weed suppression systems and molecular characterization are essential. Likewise, fatty acid profiling of the targeted weeds suppression strategy, nucleic acid tools, an array pyrosequencing. All these as paradigm shifts to precisely control weeds in cropping systems to increase yield and boost productivity.

Keywords: Efficacy, plant growth-promoting bacteria, IWM, rhizobacteria, weed dynamics, crop production rhythm

INTRODUCTION

Agricultural crop production for food and fiber in the current dispensation is becoming more challenging in changing and unpredictable environmental and climatic factors. Weed, as a single element in crop production, causes more significant economic losses compared to other crop pests (Kremer and Kennedy, 1996). Yield reduction in agricultural fields (Kremer and Kennedy, 1996; Fadhly and Tabri, 2009; Oerke and Dehne, 2004) with the high cost and decreased availability of herbicides coupled with the presence of nearly 300 herbicide-resistance weed species (Kao-Kniffin *et al.,* 2013) made alternative look for weed management approaches in seeded crop fields critical. Weeds mainly grow in proximity to seeded crops to create intense competition (Moenandir,1993). This undesirable competition occurs as the plants thrive for growth factors such as nutrients, water, light, air, and space (Sembodo, 2010). However, the most potent and formidable means of controlling weeds in agricultural fields are herbicides, responsible for about 60% of the pesticide application in crop production worldwide (Gianessi and Puffer, 1991). Pesticides have also been tagged as the primary cause of pollution of groundwater sources, soils, and foods with their allied products, threatening public health, safety, and wellbeing. The fear of herbicides' environmental safety with all pesticides has generated a renewed and cautious interest in advancing chemical-free weed management techniques. These non-chemical approaches and alternatives, which are frier and more environmental-friendly weed management strategies, include mechanical control in conjunction with other traditional practices like allelopathic mechanisms, effective biological control strategies, and crop rotation (Aldrich, 1984).

Organisms, such as insects and fungi, have earlier been studied as biological agents with several aspects of integrated weed strategies to control weed dynamics in crop production efforts (McWhorter, 1984; Charudattan et al., 1988; Muller-Scharer et al., 2000; Kremer et al., 1990). A paradigm shift in weed management has emerged for increased crop yields in smart agricultural production using microorganisms as biological control agents (TeBeest et al., 1992) to induce microbial associations in seed crop root rhizosphere. Rhizobacteria, especially those with higher biological control potential for controlling weed, are involved in this situation (Cherrington and Elliott, 1987; Kremer et al., 1990; Kennedy et al., 1991; Kao-Kniffin et al., 2013). Thus, this work aimed at appraising concepts and some of the relative attributes and potentials of rhizobacteria as a biological weed suppressive agent to effectively and precisely function in weed dynamics of crop production rhythm.

The Rhizosphere

The rhizosphere is considered a small region of the soil, subject to the control of roots, where exudates of roots enhance or suppress associated microorganisms and their activities (Lynch, 2012). It represents a narrow soil area surrounding the root system that is profoundly nutrient-rich due to the release of plant exudates, including sugars and amino acids, which act as a reservoir of nutrients and energy to promote the growth and development of different microorganisms. (Arrebola *et al.,* 2019). The preceding explains why there are many bacteria in the rhizosphere than in other soil areas, and these bacteria are called rhizobacteria. They can be considered symbiotic or non-symbiotic based on the way they interact with the plants. Activities of microorganisms in the rhizosphere influence the behavior of roots the availability of readily available nutrients to plants, leading to modifications in the root exudates' consistency and quantity (Azco, 2005). One of the essential lifelines for heterogeneous, involved, and active metabolization of soil species such as free-living rhizosphere bacteria, fungi, foliar and root herbivorous insects and nematodes is the Rhizospheric zone (Mhatre et al., 2019). The rhizoplane, or root surface, provides a favorable nutrient reserve for various fungi and bacteria species, giving rise to the soil-plant interface (Lynch, 2012). Thus, the rhizosphere is that part of the soil environment where the roots of plants, soil, and soil biota interact (Figure 1).

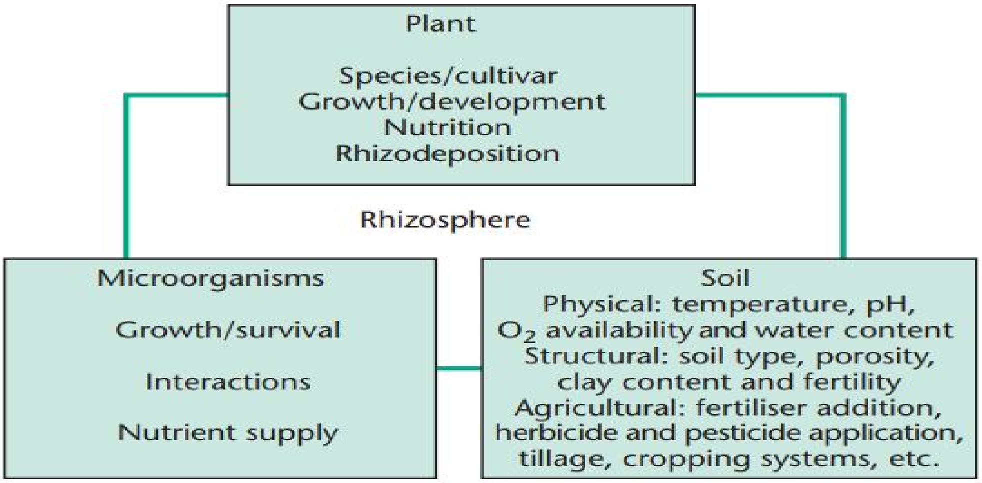

Figure 1: Factors influencing rhizosphere interactions (Source: Lynch, 2012)

The rhizosphere is that the soil region is affected by the roots, by releasing substrates that affect microbial activity. The root surface, including the soil particles, is the rhizoplane. The root itself is part of the system since some of these microorganisms commonly inhabit the root tissues, the endophytes (Azco, 2005; Bowen and Rovira, 1999). The decaying plant materials and the released root exudates provide the heterotrophic soil biota with sources of carbon compounds as either building components, growth substrates, or root-associated microorganisms (Werner, 1998). Rooting behaviors and plant supply of readily available nutrients influence microbial activity in the rhizosphere, altering the root exudates' amount and quality (Bowen and Rovira, 1999; Barea, 2000; Gryndler 2000).

Plant Growth Promoting Rhizobacteria

The rhizosphere is rich in nutrients, primarily caused by the accumulation of various organic substances that the roots release through secretion, exudation, and rhizodeposition. (Chauhan *et al.*, 2015). These same organic compounds are being utilised by microorganisms and microbial activity as carbon and energy sources. Therefore, the rhizosphere comprises a variety of root-associated bacteria widely recognized as rhizobacteria. These beneficial rhizobacteria, which positively affect plant growth, are collectively referred to as rhizobacteria promoting plant growth (PGPR). (Prigent-combaret, 2013; Chauhan *et al.*, 2015).

The term "PGPR" was first used to describe a colony of soil bacteria colonizing around or in the root surface of plants and having a various positive impact on their growth and development (Arrebola *et al.,* 2019). The most predominant of the many microbial species in the rhizosphere are bacteria. Genera of bacteria such as Enterobacteria, Pseudomonas, Bacillus, Klebsiella, Voriovorax, Azospirillum, and Azotobacter rhizosphere-colonizing PGPRs play an essential role in improving plant growth efficiency (Nadeem *et al.,* 2014). There is also a large proportion of fungi in the soil rhizosphere, which also affects plant growth. This association between the fungi and the plant roots called mycorrhizae increases the root surface area, allowing the plant to efficiently absorb nutrients and water and protect the plant from various abiotic stresses (Figure 2).

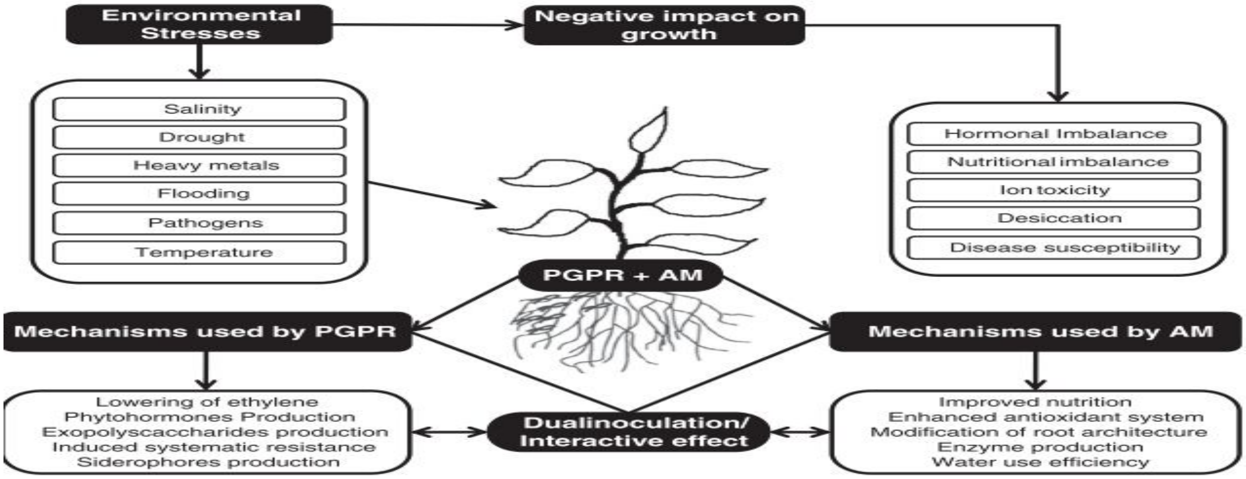

Figure 1: Mechanisms used by plant growth-promoting rhizobacteria and mycorrhizae for enhancing under stress (Source: Nadeem *et al.*, 2014)

PGPRs are categorized into two, namely: extracellular plant growth-promoting rhizobacteria (ePGPR) and intracellular plant growth-promoting rhizobacteria (iPGPR) (Viveros *et al.*, 2010;

Arrebola *et al.*, 2019). Usually, ePGPR colonizes the rhizosphere or spaces on the root cortex surface. The genera of ePGPR bacteria include *Serratia, Azospirillum, Azotobacter, Bacillus, Chromobacterium, Caulobacter, Agrobacterium, Erwinia, Pseudomonas, Flavobacterium, Micrococcus, Arthrobacteria*, and *Burkholderia*, while iPGPR exists in the specific nodules of root cells, and they include *Rhizobium*, *Bradyrhizobium, Allorhizobium, Mesorhizobium* (Bhattacharyya and Jha, 2012; Viveros *et al.*, 2010).

As shown in Figure 3, the effect of PGPRs on plant growth and development is by direct and indirect means. Plant growth is strongly stimulated by its expression in the synthesis of growth-promoting compounds such as phytohormones (cytokinin, IAA, ethylene), vitamins, enzymes, and naturally fixed nitrogen, phosphate, and iron. In contrast, plant growth is promoted indirectly by these rhizobacteria by inhibiting phytopathogens' harmful effects through the production of antagonistic substances and inducing resistance against the pathogen (Arrebola *et al.*, 2019).

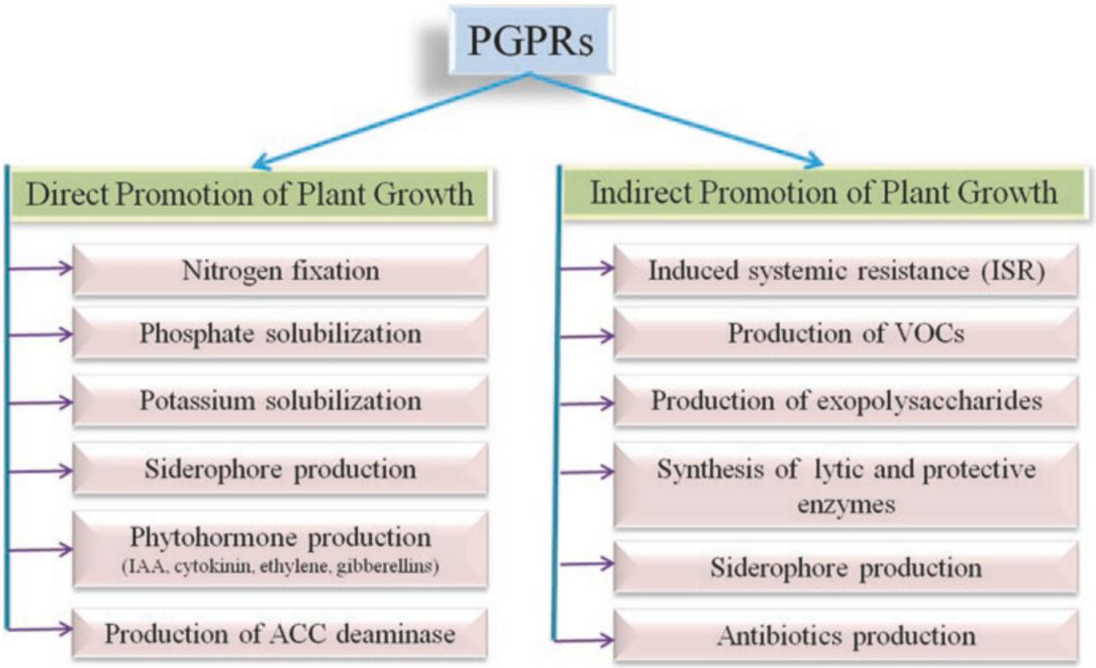

Figure 2: Direct and indirect promotion of plant growth by PGPRs (Source: Arrebola *et al.*, 2019)

The Rhizosphere of Seeded Crop

The rhizosphere is the soil zone that surrounds plant roots immediately, where the roots influence the soil's biochemistry. This zone is around 1 mm long but does not have any distinct edges. It is an environment of intensive activities dominated by substances exuded by the compounds that microorganisms feed on (Chaitanya and Meenu, 2015). Because of their enormous phenotypic and genotypic diversity, soil microbial populations are often difficult to classify. Bacterial communities in the soil's upper layers can have as many as 109 cells per gram of soil (Torsvik and Ovreas, 2002). The proportion of soil microbial biomass cells is small and mostly accounts for less than 5 % of the total population (Borneman and Triplett, 1997). The microbial community of planted crop roots inside and around the rhizosphere includes bacteria, fungi, yeasts, and protozoa. Others are free-living, while others form mutualistic associations with different crops. Microbial communities of the rhizosphere may be seen as a whole group in a given soil or a succession of communities around a particular plant species. The interaction between these microorganisms and the roots of seed crops may be advantageous, dangerous, or inactive, mediated by microorganisms, and may vary with environmental conditions (Singh and Varaprasad, 2008). There are different pathways of microbial diversity (Ahmad et al., 2008), such ways with their particular limitations and benefits revealed that rhizosphere and seed plant roots are controlled by culture-based and molecular approaches, including methods of isolation and cultivation and non-cultural DNA / RNA-based methods that investigate bacterial diversity associated with crop roots. These pathways (Imaizumi *et al.*, 1997; Scott *et al.*, 2012; Mejri *et al.*, 2013; Chaitanya and Meenu, 2015) further suggested different genera such as *Asticcacaulis, Chryseobacterium, Alcaligenes, Enterobacter, Klebsiella, Grimontella, Novosphingobium, Microbacterium, Moraxella, Acinetobacter, Pantoea, Variovorax, Herbaspirillum, Mitsuaria, Serratia, Sphingobium, Xanthomonas, Shinella,* and *Pseudomonas* as surrounding rhizosphere of seeded crop plants.

Weed Dynamics

Weed is a critical factor in crop production that must be kept under control to reduce any adverse effects that it might have on crops (Oerke and Dehne, 2004). Weed assessment in crops is so significant that 40-60% of the agrochemicals sold worldwide are herbicides. As these substances are essential for the acquisition of food and fiber as necessary items, they have some negative repercussions, as do toxic residue production costs and environmental pollution (Hoagland, 1996; McFayden, 1998; Paoletti and Pimentel, 2000) and its attendant health challenges to both humans, livestock and wildlife. Thus less expensive and dangerous solutions to weed control are also welcome. The approach used to deal with such a scenario that, of course, not be entirely unrelated to the use of rhizobacteria, significantly influences crop growth and development to a large extent as in phytopathogenic bacteria (Kremer and Kennedy, 1996). For example, Mazzola et al. (1995) and

Ahonsi et al. (2002) documented empirical works on *Pseudomonas putida*, *Stenotrophomonas maltophilia*, and *Enterobacter taylorae* to tackle typical *Bromus tectorum* [L.] weeds in wheat fields as well as *Pseudomonas spp* to test *Striga hermonthica* [Del.] activities in cornfields. More so, suppression of weeds growth and development in *Beta vulgaris* [L.] (Suslow and Schroth, 1982), *Solanum tuberosum* [L.] (Bakker and Schippers, 1987), and *Triticum aestivum* (L.) (Elliott and Lynch, 1985) are available in the literature. The measure of control exerted by bacterial pathogens is crop-specific (Kloepper,1980; Elliott and Lynch, 1985; Schippers *et al.*, 1987). Their existence and potentials as biological suppressing agents on weeds (Kremer *et al.*, 1990). Thus, illustrating how biological or ecological aspects of weeds are mediated as a strategy to reduce weeds-seeds bank in soils, prevent weeds emergence and seedling growth, and minimize intense competition for growth requirements with seeded crops (Aldrich and Kremer, 1997).

Rhizobacteria and its Properties

Rhizobacteria, as has been observed, produce a host of allelopathic substances (phytotoxins) such as hydrogen cyanide [HCN] (Alstrom and Burns, 1989), phytotoxic indole-3-acetic acid [IAA] (Loper and Schroth, 1986), and haterumalide A (Gerhardson et al., 2001). In particular, HCN formed by a sizeable bacterial strain, particularly *Pseudomonas spp* and *Pseudomonas aeruginosa*, can reduce *Amaranthus spinosus*, *Portulac oleraca*, and many other weeds (Lakshmi *et al.*,2015). HCN has been considered as a significant factor in the inhibition of weed growth, since its compound exhibits enormous potential to inhibit the growth of weed, taking an active part in the metabolism process, which includes inhibiting respiratory path, CO_2 and binding plastocyanin protein to block photosynthetic electron transport and to inhibit oxygen released during electron transport. This process eventually causes cells to die back due to the total lack of oxygen supply [hypoxia] (Kremer and Souissi, 2001). Reviewed by Duke and Dayan (2011), as well as Omer and Balah (2011), of microbial phytotoxins with specific target sites in crops such as chemical herbicides, showed that many bacterial phytotoxins have unique target sites, potentially providing a new mode of action capable of inhibiting germination of weeds and growth of seedlings. Many more empirical works also showed that rhizobacteria possed phytotoxic properties avast to weeds wellbeing with multiple mechanisms (Flores-Vargas and O'Hara, 2006; Stubbs and Kennedy, 2012; Gealy *et al.*, 1996; Carvalho *et al.*, 2007) which negatively deal with cell membrane integrity, macromolecule synthesis and metabolism (Tranel *et al.,* 1993; Nehl *et al.,* 1997). However, these mechanisms depend on the specie and type of bacterial and host plant genotype (Strange, 2007; Berg *et al.,* 2002); therefore, strains with a better adaptation to a specific rhizosphere environment can be more competitive than strains without.

Phytotoxins inhibit weed growth on different growth and development; for example, germination arrest factors (GAF) suppress weeds' germination in a developmentally-specific manner (Kimbrel *et al.,* 2010; Halgren *et al.,* 2011). Also, oxyvinylglycine irreversibly arrests germination of the seeds of grassy weeds, such as annual bluegrass (*Poa annua*), without a significant effect on grass seedlings' growth and mature plants or germination of the seeds of broadleaf plant species (McPhail *et al.,* 2010). As a rhizobacteria phytotoxic metabolite, Phaseolotoxin induces the formation of chlorotic halo lesions on infected leaves and inhibits *Escherichia coli* (Tamura *et al.,* 2002). The production of phaseolotoxin is restricted to strains of *Pseudomonas syringae* pv. phaseolicola and pv. *actinidiae* (Sawada *et al.,* 1997).

Rhizobacteria Phytotoxins

Pathogenic bacteria frequently kill their host plants by producing toxins that cause chlorosis, necrosis, wilting, and water in plants that lead to death (Kremer, 2006a; Kennedy and Stubbs, 2007; Strange, 2007; Sheikh *et al.,* 2009; Dzoyem *et al.,* 2011; Carvalho *et al.,* 2011; Martínez-Mendoza and Mena-Violante, 2012; Stubbs and Kennedy, 2012; Zheng *et al.,* 2012). The phytotoxic metabolite strategy aims to circumvent many of the weed control restrictions (Boyetchko and Rosskopf, 2006). Here, the same amount of phytotoxic metabolites directly applied to the host tissue is applied to the most vulnerable plant growth (Stubbs and Kennedy, 2012). Additionally, microbial toxins by fermentation are more natural to mass-produce than spore production (Li et al., 2003). Another benefit of using phytotoxin in weed control practices is that it is easier to derive phytotoxins from bacteria for use as herbicides than to use living species with inherent issues, such as environmental sensitivity (Kremer and Kennedy, 1996). Specific knowledge of the pathogen(s) involved in virulence and the biology of the target host weed helps establish an appropriate phytotoxin for weed control. Phytotoxins are substances with a low molecular weight capable of reproducing symptoms similar to those observed in natural plant infections (Amusa, 2006; Carvalho *et al.,* 2011). A toxic metabolite should cause all the symptoms characteristic of the disease in a susceptible host to be considered a phytotoxin, which does not attack its structural integrity. They affect the metabolism subtly, so they differ from the enzymes (Strange, 2007). Microbial products can offer a readily accessible source of novel compounds with biological activity towards weeds. Therefore, phytotoxins can be used as biocontrol substances without biocontrol organisms (Duke *et al.,* 2000; Hoagland, 2009).

Mechanisms of rhizobacteria phytotoxins

Rhizobacteria, as one of the bacterial groups, have been evaluated for its metabolites in different systems (Kennedy *et al.,* 1991; Tranel *et al.,* 1993; Norman *et al.,* 1994; Mazzola *et al.,* 1995; Gealy *et al.,* 1996) to determine its mode of action. Rhizobacterial phytotoxins use various mechanisms of action to inhibits weeds growth and performance. Some of the phytotoxic metabolites function by altering the host plants' metabolism while others are once accumulated toxic to the plant tissues and kill the plant tissues. For example, a phytotoxin secreted by *Pseudomonas syringae* pv. *actinidiae* drastically modifies the plant's amino acid metabolism and causes chlorotic halo lesions on leaves, producing a toxin inhibiting ornithine carbamoyltransferase (Tamura *et al.,* 2002). Syringomycin as a peptide phytotoxin produced by *Pseudomonas syringae* pv. *syringae* induces a protein kinase-mediated phosphorylation of red beet plasma, which is extremely toxic to many weeded plants as a virulent factor. Syringomycin, in this connection, damages cell membranes, causes rapid K+ efflux and stimulates a plasmalemma ATPase (Suzuki *et al.,* 1992). Both syringomycin and syringopeptin form pores in plasma membranes, which leads to electrolyte leakage (Bender *et al.,* 1999). Coronatine functions mimic methyl jasmonate, a hormone synthesized by plants undergoing stress (Benedetti *et al.,* 1998; Uppalapati *et al.,* 2005). Tabtoxin and phaseolotoxin are strongly antimicrobial and function by inhibiting glutamine synthetase and ornithine carbamoyltransferase, respectively.

Biosynthesis of rhizobacterial phytotoxins

Genetic analysis revealed the mechanisms which are responsible for the biosynthesis of phytotoxin. Tabtoxin is derived from the biosynthetic pathway to lysine (Bender *et al.,* 1999). Activation of phytotoxin synthesis is controlled by diverse environmental factors, including plant signal molecules and temperature. A strain of *Xanthomonas campestris* pv. *poae* (strain JT-P482) (Imaizumi *et al.,* 1997) infects *Poa* plants through wounds and multiplies in the vascular system, prevents water transport via the production of a polysaccharide substance and cause wilting and death of the plants (Fujimori, 1999). Bacterial ethylene can also be considered a phytotoxin, because pathogenic bacteria produce it during pathogenesis (Durbin, 1991). The involvement of ethylene in the virulence of *Pseudomonas syringae* pv. *glycinea* and *phaseolicola* have been reported (Weingart *et al.,* 2001). These results indicated that the production of ethylene increases the virulence of phytotoxic strains. Various researches have shown a direct link between ethylene production of diseased plants and the development of chlorosis and leaf abscission in various plant species (Boller, 1991; Bent *et al.*, 1992; Broekaert *et al.,* 2006). Plant responses to ethylene are varied from chlorosis, senescence to abscission, and it promotes the predisposition of plant tissue to disease. *Pseudomonas solanacearum* and *Xanthomonas citri* are other examples of phytopathogenic bacteria producing ethylene during disease development in plant tissues (Goto *et al.,* 1980; Lund *et al.,* 1998; Weingart *et al.,* 2001). Although ethylene, as a phytohormone, influences numerous physiological processes during plant growth, its microbial synthesis causes hormonal imbalance in the infected plant tissue—this results in enhancing the extent of disease expression in various plant-pathogen interactions. Studies with ethylene showed ethylene's role in the development of foliar weakness (Weingart *et al.,* 2001). Plants without the ability to produce ethylene showed a considerable reduction in disease symptoms after inoculation with bacterial pathogens. The inhibitory effect of many microbial phytotoxic metabolites on plant growth is dose-dependent and regulated by temperature. For example, the effect of *Xanthomonas campestris* pv. *poae* (JT-P482) against annual bluegrass is significantly affected by temperature, and some studies have determined the optimum temperature for maximum control (Imaizumi *et al.,* 1999; Carvalho *et al.,* 2011). Tagetitoxin (Tgt) inhibits bacterial RNA polymerase. Cyanogenesis is widely documented (Kremer and Souissi, 2001; Owen and Zdor, 2001; Kremer, 2006a), and cyanide, as an inhibitor of enzymes involved in main plant metabolic processes (e.g., respiration, CO_2 and nitrate assimilation, and carbohydrate metabolism) can bind with the protein plastocyanin to block photosynthetic electron transport (Kremer and Souissi, 2001).

Groups of rhizobacteria phytotoxins

Pseudomonas

Pseudomonas spp has been described as the leading group of rhizobacteria that decreases typically or inhibits weeds' growth (Whipps, 2001). They are rhizosphere species that can be adapted to rhizosphere life, and their characterization shows that they are fast-growing, simple to cultivate, and genetically manipulate in the laboratory. Moreover, they can utilize a variety of metabolizable organic compounds, which make them amenable to experimentation. Two harmful strains of *Pseudomonas* isolated from the rhizosphere of *Elytrigia repens* (L.) have decreased this abundant weed -couch-grass growth. The deleterious strain of *Ps. fluorescens* D7 isolated from winter wheat root suppresses the growth of root and seedling development of cheatgrass (*Bromus tectorum*) (Kennedy *et al.,* 1991) via the production of a phytotoxin (Tranel *et al.*, 1993). This bacterium acts relatively specific to cheatgrass and does not have considerable effects on non-target species (Kennedy *et al.,* 2001). Several reports are available on the production of phytotoxic metabolites by species of *Ps. syringae* pv. *phaseolicola* identified as phaseolotoxin. *Pseudomonas* species produce a variety of potent phytotoxins, such as syringomycins and syringopeptins. Members of the syringomycins class are pore-forming cytotoxins that act by promoting passive transmembrane ion flux (Hutchison and Gross, 1997).

The work is done by Kennedy *et al.* (1991), and Kremer (2006b) has shown that *Ps. syringae* strain 3366 reduced the root growth of weed in controlled-environments and field studies. A study on rhizobacteria has shown that genus *Pseudomonas members* with highest similarity to *Ps. koreensis* Ps 9-14T can inhibit indicator plants by producing phytotoxic metabolites. The *Pseudomonas syringae* pv. *tagetis* (PST) causes apical chlorosis on several members of *Asteraceae* (Johnson and Wyse, 1991; Sciegienka *et al.*, 2011). It has been demonstrated to control several weeds outside the *Asteraceae* family (Johnson *et al.*, 1996).

Bacillus

Bacillus genus; *B. cereus* (Karadeniz *et al.,* 2006; Carvalho *et al.*, 2007), *B. safensis* (Karadeniz *et al.*, 2006), *B. pumilus* (Kang *et al.,* 2006; Carvalho *et al.*, 2007), and *B. megaterium* (Shirdashtzadeh, 2014) are widely identified as powerful agents having a broad spectrum of the host with the ability to form endospores and produces phytotoxins with a wide range of activity, the properties that make them useful weed control agents (Kremer *et al.,* 1990; Saharan and Nehra, 2011). Preliminary work on rhizobacterial strains reported by Shirdashtzadeh (2014) showed that metabolites produced by genus *Bacillus* regarding *B. cereus, B. pumilus,* and *B. safensis* appreciably arrest weeds seeds from germination and reduced weed growths and infestation in *Cucumis sativus* [L.], *Lepidiumus sativum* [L.] and *Raphanus sativus* [L.].

Xanthomonas

A strain of *Xanthomonas campestris* pv. *poae* (strain JT-P482) as a viable bacterium decrease annual bluegrass (ABG) and cutgrass (Imaizumi *et al.*, 1997). This strain causes significant wilting in ABG without a detrimental effect on other plants growing together via the production of a polysaccharide substance that prevents water transport (Fujimori, 1999). This bacterium infects and suppresses plants by wounds in the stem and leaf tissues and increases in the vascular system, causing the ABG's wilting and death without affecting the developing plant species.

Arthrobacter

Arthrobacter genus; *A. globiformis* suppressed weeds seeds germination and weakened the general performances of weeds seedlings through tumor and gall formation (Sneh, 1981; Suslow and Schroth, 1982) due to production and exertion of secondary phytotoxic metabolites such as IAA (Mazzola *et al.,* 1995; Spaepen and Vanderleyden, 2011; Carvalho *et al.,* 2011; Shirdashtzadeh, 2014).

Efficacy of Rhizobacteria in Weeds Suppression

The effectiveness of rhizobacteria as a single-tactical weed-suppressing inundative strategy in crop production is described as the ability to provide an adequate measure of weed control at an appropriate rate and encourage fitting into best practices for pest control [BPCPs]. (Cardina, 1995; Charudattan,1989). Thus efficacy in this wise is a function of several characteristics of rhizobacteria, including weeds roots-or seeds colonizing abilities and adaptations and extent and rate of weeds emergence, growth, and development suppression toxigenic ones through manipulation of rhizosphere ecosystems (Kremer and Kennedy, 1996). Conventional approaches elucidate on absolute elimination of competition from weeds growing in association with field crops by total eradication of the weeds. Rhizobacteria are considerably less successful in this vein as it is successful solely by growth inhibition or reduction and weed suppression. Works on crop yields were substantially higher in fields where rhizobacteria suppressed weed growth than in healthy weeds (Kennedy et al., 1991). Thus, the strategy's profitability does not rely on the complete kill of weeds but on reducing the competitiveness of weeds growing with field crops.

The efficacy of rhizobacteria is not only in reducing weeds' competitive abilities but also in inhibiting biomass accumulation, reduced densities, and seeds production by weeds, including a very weak-seeds bank strength. Advance crop production and management strategies on the specificity of rhizobacteria in contribution to its natural weed suppression or inhibitory effects include reduced weed-seeds germination, seedlings growth inhibition, reduced roots elongation, roots deformation or discoloration, and elicit increased roots-injury by a root-colonizing pathogen (Li and Kremer, 2000; Kremer and Li, 2003 and 2006).

Be it as it may, rhizobacteria's efficacy in suppressing or inhibiting weeds plants is species-specific- or cultivar-specific mediated (Mazzola *et al.,* 1995; Kennedy *et al.,* 2001; Kremer, 2002). Only those phytotoxic metabolites that specifically colonize and inhibits the growth of weeds functions in this repute (Boyetchko, 1997; Kremer, 2002). Many studies (Kennedy *et al.,* 1991; Kremer and Kennedy, 1996; Kremer, 2006a; Carvalho *et al.,* 2007) acknowledged that efficacies in rhizobacteria to mar weeds' developmental processes in field crops agriculture is a novelty, and its deleterious effect is highly hosted specific-centered with a magnitude of suppressiveness correlating perfectly with a concentration of host-specific phytotoxic metabolites available (Boyetchko, 1997).

Constraints to rhizobacteria efficacies in weeds suppression

Omer and Balah (2011), however, revealed that efficacies of rhizobacteria in weed suppression are limited due to many reasons such as low activity due to a limited spectrum of activities, reduced survival rates, persistence of the suppressive and inhibitive compounds, large-scale production, storage, formulation, shelflife of the organism, delivery systems, avoiding injury to non-target organisms, interactions with chemical herbicides, regulations, commercialization, economic feasibility stabilization of high titers the following fermentation, shelflife of formulations, the achievement of a viable delivery system and obtaining virulence of the product before reaching the target. All these factors are essential in efficacy and reliability tests. However, despite the microbial candidates, little has been successful and persisted in the marketplace due to the mentioned problems

(Van Elsas *et al.*, 1992). The main challenge is the practical possibilities of reproducing en masse the empirical works done in laboratories or screen and greenhouses. The potential phytotoxins responsible for weeds suppression or inhibition must survive unpredictable field conditions as a test of feat in rhizobacterial efficacy. Following this carefully is the inherent complexity of the rhizosphere of seeded crops earlier discussed as an essential ecological complex that interface in nature with millions of genomes within a single gram of rhizosphere soil rhizosphere to provide productivity functions for the plant symptoms becomes very challenging. Also, diversity in rhizobacteria species can cause a high degree of inconsistency in outcomes (Bailey, 2004; Ward *et al.*, 2008). More so, weeds accessions, age, and competitiveness may influence rhizobacteria's efficaciousness (Abu-Dieyeh and Watson, 2007). The complexity of the interactions between the rhizobacteria and the target weeds is another reason that can cause unpredictable and inconsistency in outputs. Furthermore, the mode of action and active ingredients reactions of the different phytotoxins of the rhizobacteria can be affected by environmental conditions to cause constraints further.

Way out of constraints

Continuous research efforts are needed to improve the efficacy of the rhizobacteria. Rhizobacteria should possess root colonizing attributes of soil and rhizosphere-ecosystem survival and competition, active colonization of the rhizosphere, ability to convey inhibitory traits on the rhizoplane, and adaptability to specific delivery systems (Bolton et al., 1992). Observations indicated a relationship between colonization of rhizoplanes by rhizobacteria and the suppression of weeds (Begonia, 1989). Nonetheless, in soil-rhizosphere systems, root colonization's fundamental mechanisms require further evaluation (Kloepper, 1992). Protocols for selecting successful rhizobacteria should be based on essential ecological features required to convey behavior against the target weeds (Nijhuis et al., 1993; Skipper et al., 1996). It should accurately explain the reasoning for selecting particular weeds as the target for a search using rhizobacteria. Such selection should identify weeds with high potential for tolerance or resistance growth, and weeds that are problematic in shifts due to cultural practices changes. Based on these traits and their relative economic value, a list of weeds could be ranked and assigned indices based on their occurrence and significance in crop production regions (Schroeder et al., 1993). The top-scoring weeds will be prime targets for such control in each cropping scheme. Rhizobacteria's harmful activity is caused by phytotoxin production (Tranel et al., 1993; Souissi and Kremer, 1994).

Rhizobacteria produce phytotoxins on root surfaces, where the plant readily absorbs them. There is currently some doubt about whether these phytotoxins produced in culture and used alone are as successful in comparison with the intact organism's application. Durbin (1983) points out that such rhizobacterial pathogens cannot produce phytotoxins in vitro but only in animals.

A thorough understanding of the conditions needed for optimum and effective development of phytotoxin is therefore necessary. This will result in the successful establishment of rhizobacteria developing high rhizosphere levels of phytotoxins, which would be more economical and rational (Arshad and Frankenberger, 1991). The application of rhizobacteria in weed suppression and inhibition is primarily an inundative strategy; thus, formulating a delivery system that promotes the survival and colonization of seeds and roots of weeds in the field is critical to achieving a high degree of effectiveness.

Integrated weed management (IWM)

Herbicides are the primary method used in modern agriculture for weed control; they are highly successful on most weeds but are not a complete solution to the complex challenge that weeds pose (Harker *et al.,* 2013). The heavy reliance on synthetic herbicides to combat weeds has been questioned for several decades and is still being questioned, as today's problems are much more severe (Triolet *et al.,* 2016). Embracing herbicides at a broader scale has dramatically affected the environment, raising questions about natural stability and environmental health. Its continued use has resulted in herbicide resistance in many plant species (Bajwa, 2014; Harker *et al.,* 2013). Specific practices are performed to limit the weed population below the economic threshold point, which can not significantly affect crop growth and yield. Those management techniques are recommended for economically viable and environmentally sustainable weed control. None of the single practices will regulate the cannabis population to an appropriate level within cannabis management strategies. Therefore, some management methods are used to best manage the weed population to reduce the weed population below the economic threshold and increase the yield (Hasanuzzaman and Practices, 2019). Integrated weed management (IWM) provides an excellent chance of growing weed production, density, and population.

In order to control weeds, IWM has been viewed as a collection of mutually supportive technologies. It is a multidisciplinary weed management strategy involving various alternative prevention steps (Knezevic *et al.*, 2017). It is an approach to weed management by cropping systems that rely on essential information for its implementation and focuses sincerely on crop health (Swanton *et al.*, 2008) and keeping weed populations below the threshold level by optimizing the control measures in an organized way (Bajwa, 2014). IWM at its center is the perception that several different weed management techniques can be used to control weeds in a more coordinated manner, and this can be conceptualized as combining the four ways (physical, chemical, biological and ecological) of weed management (Figure 4) expressed by Merfield (2018).

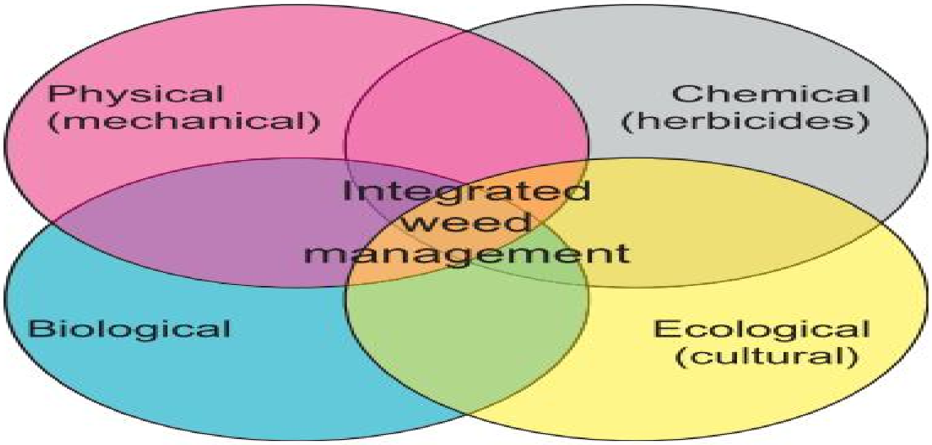

Figure 3: Integrating the four means of managing weeds (Source: Merfield, 2018)

IWM is about assembling the components, not removing them. It is about combining components instead of reducing weed management to unnecessary reliance on a single method or technique (Swanton *et al.*, 2008).

These four approaches are briefly described below:

i. Physical approaches to weed control which involve activities such as tillage and flame weeding.

ii. Synthetic herbicides dominate chemical weed control while "human" (eobiotic) herbicides still exist.

iii. Biological weed control measures which involve understanding the biology of plants to help in managing weeds.

v. Cultural weed management (ecological) which includes processes like crop-weed competition, allelopathy, and crop rotations.

Prospects and perspective

Rather than employing singly or two methods of weed control strategies, the efficient approach will combine various methods. However, weed check with the best fit is adopted, regardless of cropping situations, location, or season. Applications of desirable rhizobacterial populations in rhizosphere-soils of crops have established considerable promises in all aspects (laboratory, screen, or greenhouse and field conditions) of crop production. Another promising research area is an enhanced understanding of how rhizobacteria can lead to expanded exploitation to reduce the possible negative environmental effects associated with food and fiber production. A concerted effort to apply genetically engineered rhizobacteria (i.e., *gene*Rhizobacteria) to remediate complex scenes in marginalized soils (Denton, 2007), especially in fields infested with weeds and invasive plants, is another attractive area of interest. This development is conceptualized under the broader knowledge of yield gap, characterized as the difference between the yield performance that could be achieved under ideal production and the yield obtained under current production (Lobell et al., 2009). Closing the yield gap in a real sense contributes to the meeting- up with the food and fiber needs of our teeming and ever-increasing global population. Therefore, specific weed management culture with precision as in *gene*Rhizobacteria has the basis and withal to solve the yield gap challenge. Weeds contest with crops for space, light, nutrients, and water, which affects field-grown crops' health in many ways. Growing weed in a field, for example, absorbs water and nutrients that could be used by crops planted. The rhizobacterial community is scientifically engineered (*gene*Rhizobacteria) to focus on various weeds and invasive plant species, which easily colonized and infests crop fields to develop customized- environmentally friendly rhizobacterial systems (Wu *et al.,* 2006) that remediates challenges on the spot. Principles, theories, and practices in this sphere (customized-environmentally friendly rhizobacterial systems) to handle weed dynamics in the crop production rythm requires more knowledge of crops, soils, and climatic conditions with their relative interactions and how to smartly adjusts to varying soil conditions. Agricultural farmers also faced challenges from both the climate and the use of suitable techniques to different production scales and complexities that occur locally, nationally, and even globally. Many regions of the world have recently been severely threatened by soil loss, droughts, floods, crop-related diseases, and plagues of unpalatable weedy conditions that have adversely affected crop production. Crop producers also faced challenges of high input costs, particularly agrochemicals, as nutrient expenses to promote yield development and forms of pesticide costs to reduce losses due to weeds and many other crop production vagaries. Therefore, with perspective *gene*Rhizobacteria, comes the need for gathering the crop, soil, and environmental information to put definite and precise checks in place. The future typical paradigm shifts in crop production focus on the status and health of individual crop plants. However, numerous other considerations must be accounted for, to come up with the techniques that would precisely address individual plants, both crops, and weeds, notwithstanding the possible difficulty that can be created by environmental elements such as the wind, rain, and other factors, including terrain and spatial distribution of crops and weeds which are independent of weather and climate. These challenges currently might not have a simple answer, especially with limited funding for perceived high-risk research projects. Therefore, if solutions to the limited world food supply are obtained, the view of national and foreign agricultural policy managers, many in industries, and financial investors who regulate investment capital needs to shift. Crop agriculture is immensely contributing to meeting the needs of a growing population, but methods for growing food crops must get better and faster to avoid a major and significant shortfall, especially in the face of pandemics such as COVID-19, that would never make the world to remain the same again. One way to do this is by being more precise in managing crop pests, principally weeds and invasive plants. Precision weed management (PWM) described above which results in increased production, lowered inputs, and reduced environmental contamination as well as in many ways moves closer to more sustainable and enduring systems, refers simply to placing the right quantity of inputs (*gene*Rhizobacteria) on the right target (weeds) at the right time. The approach is better for the environment and better for the greater farmers who mostly are poor resource persons, as it leads to a reduction of inputs without decreasing weed control efficacies. The approach is also a novel contribution to improved handling and controlling weeds in any cropping regime. Weeds are a major problem in cropping systems throughout the world. Weedy and invasive plant species cost the world economy billions of dollars annually in crop damage and lost earnings (Grube *et al.,* 2011).

Recent progress in understanding rhizosphere interactions with crop nodules supports a crucial area of study for mechanisms linked to colonization. Studies are now available from genetically modified *Arabidopsis thaliana* plants (i.e., geneArabidopsis thaliana) to increase efficacy after inoculation with the rhizobacterial population (Ali and Hj, 2010).

Transgenic plants have endured efforts (Zhuang et al., 2007). Farwell et al. (2007) compared geneBrassica napus inoculated with rhizobacterial strain to transgenic canola development. Wu et al. (2006) has studied the symbiotic relationship between Pseudomonas putida and sunflower seeds with synthetic phytochelatins. They found the gene-engineered strain can cover the sunflower plants. Genomic tinkering of naturally occurring PGPR strains with useful genes (Nakkeeran et al., 2005) may lead to an amplified representation of genomic products, thereby ameliorating the attacks on crop plants of both pests and diseases, thus facilitating the better introduction of a single bacterium with multiple modes of action to the benefit of farmers.

Cook et al. (2014) identified four possible harmful, non-target effects of microbes used as biological disease and pest control agents (e.g., weeds). Those are competitive replacement, allergenicity, toxigenicity, and pathogenicity of a beneficial microorganism. Those are the possible non-target consequences, whether the strain is local, imported, human, or gene-engineered. They further concluded that horizontal gene transfer of a biological control trait would only become a safety issue if the transferred trait led to another microorganism possessing the ability to produce one or more of these four harmful, non-target effects. For the four possible non-target effects, all but allergenicity, depending on the biological control mechanisms, are also desirable target effects. Since the possible non-target effects for all categories of microbial biocontrol agents have been established, it is vital to investigate those effects specifically for plant pathogen antagonists. Competitive disruption may become a problem for an adversary that has been introduced into the rhizosphere if, in addition to the displacement of a pathogen, rhizobia, or mycorrhizal fungus that is essential to the health of that crop.

CONCLUSION

The usefulness of the rhizobacteria in the crop production rhythm dynamics of weeds is in the offing. It will evolve as intensive and fundamental ecological research works, and biological activity of bacteria-plant relationships and phytotoxin selection continue to progress. The ideas, values, and theories of rhizobacteria, including constraints and their way out, depending on a better perception and understanding of efficacy-based mechanisms and the creation of suitable formulations for crop field delivery. As more successful rhizobacteria-based strategies are developed for consistent suppression and inhibition of weed growth, the prospects for accepting and using crop production systems in the field and subsequent development for mass production for commercial purposes should be vigorously pursued. The rhizobacteria approach provides both a strategy and an alternative that supplements and increases weed control options as conventional methods are increasingly limited due to environmental and health concerns. It is essential to understand the relationship between the ecological processes of weeds and rhizospheres (Boyetchko, 1999; Boyetchko and Rosskopf, 2006) to enhance the new approach's feasibility and efficacy as it is a priority to reduce the negative experiences of traditional methods. The more biologically mediated strategy of weed suppression and inhibition strategy is particularly important for areas with problematic infestations of higher and multiple weeds; Areas of low-value land where weeds have become resistant to weedicides and pesticides; and areas where labor shortages and prescribed topography constraints hinder best practices, and small rowed crops. Microbe-host relationships that involve a match of biological agents and their potential hosts with a greater sensitivity to virulence become a significant interest. Likewise, solutions that can ensure more excellent shelf life, efficacy, and survival of microbial agents and microbial group structure and function investigations can advance microbial weed suppression systems.

Control measures currently employed in managing weeds are not efficient, and most times comes with adverse side effects on the environment and humans. Hence, the need for microbial inoculant producing industries. In particular, PGPRs should rely on creative business management, product development, extension training, and comprehensive testing. Further optimization of the capable PGPR strains to be implemented in agriculture, there is a need for better fermentation and formulation processes. The majority of weed control activities would be less than adequate without recognizing plant growth and development phases. Today's transmission of herbicides impacts our habitats (e.g., erosion, drift, groundwater contamination) and triggers the breakdown of entire crop systems, signaling the need for improved efforts among scientists. With the increasing number of people on this planet earth and the little time required to reconcile how to feed them all, we can not afford to have our existing systems collapse, let alone neglect what is required. Hence, a paradigm shift involving rhizobacteria is required to precisely monitor weeds in crop systems, from the crop farmer's doorpost to the consultant and the laboratories, screens, greenhouses, and the researchers' open fields.

REFERENCES

Abu-Dieyeh, M. H and Watson, A. K (2007). Population dynamics of broadleaf weeds in turfgrass as influenced by chemical and biological control methods. *Weed science.* **55**:371-380.

Ahmad, F., Ahmad, I and Khan, M.S (2008). Screening of free-living rhizospheric bacteria for their multiple plant growth promoting activities. *Microbiol Res.* **163** (2):173–181.

Ahonsi, M.O., Berner, D.K., Emechebe, A.M and Lagoke, S.T (2002). Selection of rhizobacterial strains for suppression of germination of *Striga hermonthica* (Del.) Benth. seeds. *Biol. Control*. **24** :142-152.

Aldrich, R.J and Kremer, R.J (1997). Principles in weed management. Iowa State University Press, Ames, Iowa.

Aldrich, R. J (1984). Weed-Crop Ecology: Principles in Weed Management. New Breton Publ., North Scituate, Mass. 465pp.

Alstrom, S and Burns, R.G (1989). Cyanide production by rhizobacteria as a possible mechanism of plant growth inhibition. *Biol. Fert. Soils.* **7**: 232- 238.

Ali, K and Hj, S.Z (2010). Phytoremediation of heavy metals with several efficiency enhancer methods. *Afr J. Biotechnol.* **9** (25):3689–3698

Amusa, N (2006). Microbially produced phytotoxins and plant disease management. *African Journal of Biotechnology.* **5**: 405-414.

Arshad, M and Frankenberger, W. T., Jr (1991). Microbial production of plant hormones. *Plant Soil*. **133**:1-8.

Bailey, K. L (2004). Microbial weed control: an off-beat application of plant pathology. *Canadian Journal of Plant Pathology.* **26**: 239-244.

Bakker, A. W and Schippers, B (1987). Microbial cyanide production in the rhizosphere in relation to potato yield reduction and *Pseudomonas spp.*-mediated plant growth reduction. *Soil Biol. Biochem.* **19**:452-458.

Begonia, M.F.T (1989). Characterization of attraction of rhizobacteria to weed seeds and seedlings. Ph.D. Diss. Univ. of Missouri, Columbia, MO. 165pp.

Bender, C. L., Alarcón-Chaidez, F and Gross, D. C (1999). Pseudomonas syringae phytotoxins: mode of action, regulation, and biosynthesis by peptide and polyketide synthetases. *Microbiology and Molecular Biology Reviews.* **63**:266-292.

Benedetti, C. E., Costa, C. L., Turcinelli, S. R and Arruda, P (1998). Differential expression of a novel gene in response to coronatine, methyl jasmonate, and wounding in the coil mutant of *Arabidopsis*. *Plant Physiology.* **116**:1037-1042.

Bent, A. F., Innes, R. W., Ecker, J. R and Staskawicz, B. J (1992). Disease development in ethylene-insensitive Arabidopsis thaliana infected with virulent and avirulent *Pseudomonas* and *Xanthomonas* pathogens. *Molecular Plant Microbe Interactions.* **5**:372-372.

Berg, G., Roskot, N., Steidle, A., Eberl, L., Zock, A and Smalla, K (2002). Plant-dependent genotypic and phenotypic diversity of antagonistic rhizobacteria isolated from different *Verticillium* host plants. *Applied and Environmental Microbiology.* **68**:3328-3338.

Boller, T (1991). Ethylene in pathogenesis and disease resistance. *The plant hormone ethylene*. 293-314.

Bolton, J. H., Fredrickson, J. K and Elliott, L. F (1992). Microbial ecology of the rhizosphere. p. 27-63 **In:** F. B. Metting, Jr., ed. Soil Microbial Ecology. Marcel Dekker, New York.

Borneman, J and Triplett, E.W (1997). Molecular microbial diversity in soils from eastern Amazonia: evidence for unusal microorganisms and microbial population shifts associated with deforestation. *Appl Environ Microbiol.* **63**: 2647–2653

Boyetchko, S and Rosskopf, E (2006). Strategies for developing bioherbicides for sustainable weed management. *Handbook for Sustainable Weed Management, Singh, HP, DR Batish and RK Kohli (Eds.). Haworth Press, Inc., New York, USA.*

Boyetchko, S and Rosskopf, E., Caesar, A., Charudattan, R., Khachatourians, G and Arora, D (2002). Biological weed control with pathogens: search for candidates to applications. *Applied mycology and biotechnology. Volume 2: Agriculture and Food Production***.** 239-274.

Boyetchko, S. M (1997). Principles of biological weed control with microorganisms. *HortScience.* 32: 201-205.

Boyetchko, S. M. (1999). Innovative applications of microbial agents for biological weed control. *Biotechnological approaches in biocontrol of plant pathogens.* Springer.

Broekaert, W. F., Delauré, S. L., De Bolle, M. F and Cammue, B. P (2006). The role of ethylene in host-pathogen interactions. *Annu. Rev. Phytopathol.* **44**:393-416.

Cardina, J (1995). Biological weed management, pp. 279-341. *In* A.E. Smith [ed.], Handbook of weed management systems. Marcel Dekker, Inc., New York.

Carvalho, D. D., Oliveira, D. F., Corrêa, R. S., Campos, V. P., Guimarães, R. M and Coimbra, J. L (2007). Rhizobacteria able to produce phytotoxic metabolites. *Brazilian Journal of Microbiology.* **38** :759-765.

Carvalho, D. D., Oliveira, D. F., Corrêa, R. S., Campos, V. P and Pasqual, M (2011). Selection of phytotoxin producing rhizobacteria. *Anais da Academia Brasileira de Ciências.* **83** :1091-1096.

Chaitanya, K. J and Meenu, S (2015). Plant growth promoting Rhizobacteria (PGPR): a review. *Journal of Agricultural Research and Development.* **5**(2):0108-0119. http://www.e3journals.org

Charudattan, R., Deloach Jr., J and Liebman, M (1988). Management of pathogens and insects for weed control in agroecosystems. *Weed Management in Agroecosystems: Ecological Approaches.* 245-264.

Charudattan, R (1989). Assessment of efficacy of mycoherbicide candidates. p. 455-464 **In:** E. S. Delfosse, ed. *Proc. VII Int. Symp. Biol. Control Weeds*. 1st. Sper. Patol. Veg. (MAF), Rome, Italy.

Cherrington, C and Elliott, L (1987). Incidence of inhibitory pseudomonads in the Pacific Northwest. *Plant and Soil.* 101:159-165.

Cook, R. J., Bruckart, W. L and Coulson, J. R (1996). Safety of microorganisms intended for pest and plant disease control: Framework for scientific evaluation. *Biol. Control* **7**:333-351.

Denton, B (2007). Advances in phytoremediation of heavy metals using plant growth promoting bacteria and fungi. MMG 445 *Basic Biotechnol.* **3**:1–5.

Duke, S. O and Dayan, F. E (2011). Modes of action of microbially-produced phytotoxins. *Toxins.***3**: 1038-1064.

Duke, S., Dayan, F., Romagni, J and Rimando, A (2000). Natural products as sources of herbicides: current status and future trends. *Weed Research-Oxford-* 4**0**:99-112.

Durbin, R. D (1983). The biochemistry of fungal and bacterial toxins and their modes of action. p. 137-162 *in* J. A. Callow, ed. Biochemical Plant Pathology. John Wiley and Sons, New York.

Durbin, R (1991). Bacterial phytotoxins: Mechanisms of action. *Experientia*. **47**:776-783.

Dzoyem, J., Kechia, F., Kuete, V., Pieme, A., Akak, C., Tangmouo, J and Lohoue, P (2011). Phytotoxic, antifungal activities and acute toxicity studies of the crude extract and compounds from *Diospyros canaliculata*. *Natural Product Research*. **25** :741-749.

Elliott, L. F and Lynch, J. M (1985). *Pseudomonads* as a factor in the growth of winter wheat (*Triticum aestivum* [L.]). *Soil Biol. Biochem*. **16**:69-71.

Fadhly, A.F and Tabri, dan F (2009). Pengendalian Gulma pada Pertanaman Jagung. Balai Penelitian Tanaman Serealia.Maros. [*Indonesia*].

Farwell, A.J *et al.* (2007). Tolerance of transgenic canola plants (Brassica napus) amended with plant growth-promoting bacteria to flooding stress at a metal-contaminated field site. *Environ Pollution*. **147**:540–545.

Flores-Vargas, R. and O'hara, G (2006). Isolation and characterization of rhizosphere bacteria with potential for biological control of weeds in vineyards. *Journal of Applied Microbiology*. **100**:946-954.

Fujimori, T (1999). New developments in plant pathology in Japan. *Australasian Plant Pathology*. **28**: 292-297.

Gealy, D. R., Gurusiddaiah, S and Ogg Jr, A. G (1996). Isolation and characterization of metabolites from Pseudomonas syringae-strain 3366 and their phytotoxicity against certain weed and crop species. *Weed science*. 383-392.

Gerhardson, B.; Thaning, C.; Weissmann, R.; Borowicz, J.; Welch, C.; Hedman, R. (2001). New bacterial isolate and its active metabolites, including new compound Haterumalide X, useful for controlling weeds and treating fungal diseases in plants, human and animals. *S.E. Pat. 9904334-A*. Jul. 26, 2001

Grube, J., Donaldson, D., Kiely, T and Wu, L (2011). Pesticides industry sales and usage-2006 and 2007 market estimates. US Environmental Protection Agency, EPA 733-R-11-001. http://www.epa.gov/pesticides/pestsales/07pestsales/market_estimates2007.pdf

Gianessi, L. P and Puffer, C (1991). Herbicide use in the United States: National summary report. Resources for the Future, Washington, D.C. 128pp.

Goto, M., Yaguchi, Y and Hyodo, H (1980). Ethylene production in citrus leaves infected with *Xanthomonas citri* and its relation to defoliation. *Physiological Plant Pathology*.

16:343-350.

Halgren, A., Azevedo, M., Mills, D., Armstrong, D., Thimmaiah, M., Mcphail, K and Banowetz, G (2011). Selective inhibition of *Erwinia amylovora* by the herbicidally active germination-arrest factor (GAF) produced by *Pseudomonas* bacteria. *Journal of Applied Microbiology.* **111** :949-959.

Hoagland, R. E (1996). Chemical interactions with bioherbicides to improve efficacy. *Weed Technology.* 651-674.

Hoagland, R. E (2009). Microbial Allelochemicals and Pathogens as Bioherbicidal Agents1.

Hutchison, M. L and Gross, D. C (1997). Lipopeptide phytotoxins produced by *Pseudomonas syringae* pv. *syringae*: comparison of the biosurfactant and ion channel-forming activities of syringopeptin and syringomycin. *Molecular Plant-Microbe Interactions.* **10**:347-354.

Imaizumi, S., Nishino, T., Miyabe, K., Fujimori, T and Yamada, M (1997). Biological Control of Annual Bluegrass (*Poa annua* [L.]) with a Japanese Isolate of *Xanthomonas campestris* pv. *poae* (JT-P482). *Biological Control.* **8**:7-14.

Johnson, D and Wyse, D (1991). Use of *Pseudomonas syringae* pv. *tagetis* for control of Canada thistle. *Proc. N. Cent. Weed Sci. Soc.* pp.14-15.

Johnson, D. R., Wyse, D. L and Jones, K. J (1996). Controlling weeds with phytopathogenic bacteria. *Weed Technology.* 621-624.

Kang, B. R., Yang, K. Y., Cho, B. H., Han, T. H., Kim, I. S., Lee, M. C., Anderson, A. J and Kim, Y. C (2006). Production of indole-3-acetic acid in the plant-beneficial strain *Pseudomonas chlororaphis* O6 is negatively regulated by the global sensor kinase GacS. *Current Microbiology.* **52**:473-476.

Kao-Kniffin, J., Carver, S. M and Ditommaso, A (2013). Advancing weed management strategies using metagenomic techniques. *Weed Science.* **61**:171-184.

Karadeniz, A., Topcuoğlu, Ş and Inan, S (2006). Auxin, gibberellin, cytokinin and abscisic acid production in some bacteria. *World Journal of Microbiology and Biotechnology.* **22**:1061-1064.

Kennedy, A and Stubbs, T (2007). Management effects on the incidence of jointed goatgrass inhibitory rhizobacteria. *Biological Control.* **40** :213-221.

Kennedy, A. C., Elliott, L. F., Young, F. L and Douglas, C. L (1991). Rhizobacteria suppressive to the weed downy brome. *Soil Sci. Soc. Am. J.* **55**:722-727.

Kennedy, A., Johnson, B and Stubbs, T (2001). Host range of a deleterious rhizobacterium for biological control of downy brome. *Weed Science.* **49** (6): 792-797.

Kimbrel, J. A., Givan, S. A., Halgren, A. B., Creason, A. L., Mills, D. I., Banowetz, G. M., Armstrong, D. J and Chang, J. H (2010). An improved, high-quality draft genome sequence of the Germination-Arrest Factor-producing *Pseudomonas fluorescens* WH6. *BMC Genomics.* **11**:522.

Kloepper, J. W (1992). Plant growth-promoting rhizobacteria as biological control agents. pp. 255-274 **In:** F. B. Metting, Jr., ed. Soil Microbial Ecology. Marcel Dekker, Inc., New York.

Kloepper, J.W(1980). Enhanced plant growth by siderophore production production by plant growth promoting rhizobacteria. *Nature.* **286**:885-886.

Kremer, R (2006a). Deleterious Rhizobacteria. *In:* Gnanamanickam, S. (ed.) *Plant-Associated Bacteria.* Springer Netherlands.

Kremer, R.J. (2006b). The role of allelopathic bacteria in weed management. *Allelochemicals: Biological Control of Plant Pathogens and Diseases.* Springer.

Kremer, R.J and Kennedy, A.C (1996). Rhizobacteria as biological control agents of weeds. *Weed Technol.* **10**:601-609.

Kremer, R.J and Li, J (2003). Developing weed-suppressive soils through improved soil quality management. *Soil Till. Res.* **72** :193–202

Kremer, R.J and Li, J (2006). Growth response of weed and crop seedlings to deleterious rhizobacteria. *Biological Control.* **39**:58–65

Kremer, R. J and Souissi, T (2001). Cyanide production by rhizobacteria and potential for suppression of weed seedling growth. *Current Microbiology.* **43**:182-186.

Kremer, R. J., Begonia, M.F.T., Stanley, L and Lanham, E. T (1990). Characterization of rhizobacteria associated with weed seedlings. *Appl. Environ. Microbiol.* **56**:1649-1655.

Kremer, R.J (2002). Bioherbicides: potential successful strategies for weed control. In: Koul, O., Dhaliwal, G. (Eds.), Microbial Biopesticides. Taylor and Francis, London, pp. 307–323

Lakshmi, V., Kumari, S., Singh, A and Chander, C (2015). Isolation and characterization of deleterious *Pseudomonas aeruginosa* KC1 from rhizospheric soils and its interaction with weed seedlings. *Journal of King Saud University- Science.* **27**:113-119.

Li, J and Kremer, R.J (2000). Rhizobacteria associated with weed seedlings in different cropping systems. *Weed Science.* **48**:734–741.

Li, Y., Sun, Z., Zhuang, X., Xu, L., Chen, S and Li, M (2003). Research progress on microbial herbicides. *Crop Protection.* **22**:247-252.

Lobell, D.B., Cassman, K.G and Field, C.B (2009). Crop yield gaps: Their importance, magnitudes and causes. *Annu Rev Environ Resour.* **334**:1–26.

Loper, J.E and Schroth, M.N (1986). Influence of bacteria sources of Indole-3-acetic acid on root elongation of sugarbeet. *Phytopathol.*, **76**:386-389

Lund, S. T., Stall, R. E and Klee, H. J (1998). Ethylene regulates the susceptible response to pathogen infection in tomato. *The Plant Cell Online.* **10**:371-382.

Martínez-Mendoza, E and Mena-Violante, H (2012). Effects of Bacillus subtilis extracts on weed seed germination of Sorghum halepense and Amaranthus hybridus. *African Journal of Microbiology Research.* **6**:1887-1892.

Mazzola, M., Stahlman, P. W and Leach, J. E (1995). Application method affects the distribution and efficacy of rhizobacteria suppressive of downy brome (*Bromus tectorum*). *Soil Biology and Biochemistry.* **27** :1271-1278.

McFayden, R.E.C (1998). Biological control of weeds. *Ann. Rev. Entomol.*, **43**:369-393.

Mcphail, K. L., Armstrong, D. J., Azevedo, M. D., Banowetz, G. M and Mills, D. I (2010). 4-Formylaminooxyvinylglycine, an herbicidal germination-arrest factor from *Pseudomonas* rhizosphere bacteria. *Journal of natural products,* **73**:1853-1857.

McWhorter, C (1984). Future needs in weed science. *Weed Science*. 850-855.

Mejri, D., Gamalero, E and Souissi, T (2013). Formulation development of the deleterious rhizobacterium *Pseudomonas trivialis* X33d for biocontrol of brome (*Bromus diandrus*) in durum wheat. *Journal of Applied Microbiology.* **114**:219-228.

Moenandir, J (1993). Persaingan tanaman budidaya dengan gulma. Cetakan kedua. Rajawali Press, Jakarta [*Indonesia*].

Muller-Scharer, H., Scheepens, P and Greaves, M (2000). Biological control of weeds in European crops: recent achievements and future work. *Weed Research-Oxford.* **40**:83-98.

Nakkeeran, S., Fernando, W.G.D and Siddiqui, Z.A (2005). Plant growth promoting rhizobacteria formulations and its scope in commercialization for the management of pests and diseases. **In**: Siddiqui ZA (ed) PGPR: biocontrol and biofertilization. Springer, *Dordrecht*. 257–296.

Nijhuis, E. H., Maat, M. J. I., Zeegers, W.E., Waalwijk, C and Van Veen, J. A (1993). Selection of bacteria suitable for introduction into the rhizosphere of grass. *Soil Biol. Biochem.* **25**:885-895.

Norman, M. A., Patten, K. D and Gurusiddaiah, S (1994). Evaluation of a phytotoxin (s) from *Pseudomonas syringae* for weed control in cranberries. *HortScience.* **29**:1475-1477.

Oerke, E.C and Dahne, H.W (2004). Safeguarding production-losses in major crops and the role of crop protection. Crop Protection. **23**: 275- 285.

Omer, A.M and Balah, M.A (2011). Using of Rhizo-Microbes as Bioherbicides for Weeds. *Global Journal of Biotechnology and Biochemistry.* **6** (3): 102-111.

Owen, A and Zdor, R (2001). Effect of cyanogenic rhizobacteria on the growth of velvetleaf (*Abutilon theophrasti*) and corn (*Zea mays*) in autoclaved soil and the influence of supplemental glycine.

Soil Biology and Biochemistry. **33**:801-809.

Paoletti, M.G and Pimentel, D (2000). Environmental risks of pesticides versus genetic engineering for agricultural pest control. *J. Agr. Environ. Ethics.* **12**:279-303.

Saharan, B and Nehra, V (2011). Plant growth promoting rhizobacteria: a critical review. *Life Sci Med Res.* **21**:1-30.

Sawada, H., Takeuchi, T and Matsuda, I (1997). Comparative analysis of *Pseudomonas syringae* pv. *actinidiae* and pv. *phaseolicola* based on phaseolotoxin-resistant ornithine carbamoyltransferase gene (argK) and 16S-23S rRNA intergenic spacer sequences. *Applied and Environmental Microbiology*. **63**: 282-288.

Schippers, B., Bakker, A.W and Bakker, P.A (1987). Interaction of deleterious and beneficial rhizosphere microorganisms and the effect of cropping practices. *Annu. Rev. Phytopathol*., **25**:339-358.

Schroeder, D., H. Mueller-Schaerer, H and Stinson, C.S.A (1993). A European weed survey in 10 major crop systems to identify targets for biological control. *Weed Res*. **33**:449-458.

Sciegienka, J.K., Kareen, E.N and Menalled, F.D (2011). Interactions between two biological control agents and an herbicide for Canada thistle (*Cirsium arvense*) suppression. *Invasive Plant Science and Management*. **4** (1):151-158.
DOI: http://dx.doi.org/10.1614/IPSM-D-10-00061.1
URL: http://www.bioone.org/doi/full/10.1614/IPSM-D-10-00061.1

Scott, J., Cullen, J., Julien, M and McFadyen, R (2012). *Raphanus raphanistrum* (L.) -Wild radish. Biological control of weeds in Australia. (Eds.). pp: 486-493. CSIRO Publishing. Melbourn.

Sembodo, D.R.J (2010). Gulma dan Pengelolaannya. Graha Ilmu. Yogyakarta.

Sheikh, T., Wheeler, T. A., Dotray, P. A and Zak, J. C (2009). Biological Control of Woollyleaf Bursage (*Ambrosia grayi*) with *Pseudomonas syringae* pv. *tagetis*1.

Shirdashtzadeh, M (2014). Deleterious rhizobacteria as weed biological control agent: development and constraints. *Asian Journal of Microbiology, Biotechnology and Environmental Sciences*. **16** (3):561-574. https://www.researchgate.net/publication/271447167

Singh, A.K and Varaprasad, K.S (2008). Criteria for identification and assessment of agro-biodiversity heritage sites: Evolving sustainable agriculture. *Curr Sci*. **94**: 1131-1138

Skipper, H. D., Ogg, Jr. A. G and Kennedy, A. C (1996). Root biology of grasses and ecology of Rhizobacteria for biological control. *Weed Technol*. **10**:610-620.

Sneh, B (1981). Use of rhizosphere chitinolytic bacteria for biological control of *Fusarium oxysporum* f.sp. dianthi in carnation. *Journal of Phytopathology*. **100**: 251-256.

Souissi, T and Kremer, R. J (1994). Leafy spurge (*Euphorbia esula*) cell cultures for screening deleterious rhizobacteria. *Weed Sci*. **42**:310-315.

Spaepen, S and Vanderleyden, J (2011). Auxin and Plant-microbe interactions *Cold Spring Harb Perspect Biol* **3**: a001438

Strange, R. N (2007). Phytotoxins produced by microbial plant pathogens. *Natural Product Reports*. **24**:127-144.

Stubbs, T. L and Kennedy, A. C (2012). Microbial weed control and microbial herbicides. *Herbicides—Environmental Impact Studies and Management Approaches*. InTech, Rijeka, Croatia**,** 135-166.

Suslow, T. V and Schroth, M. N (1982). Role of deleterious rhizobacteria as minor pathogens in reducing crop growth. *Phytopathology*. **72**:111-115.

Suzuki, Y. S., Wang, Y and Takemoto, J. Y (1992). Syringomycin-stimulated phosphorylation of the plasma membrane H+-ATPase from red beet storage tissue. *Plant Physiology*. **99**:1314-1320.

Tamura, K., Imamura, M., Yoneyama, K., Kohno, Y., Takikawa, Y., Yamaguchi, I and Takahashi, H (2002). Role of phaseolotoxin production by *Pseudomonas syringae pv. actinidiae* in the formation of halo lesions of kiwifruit canker disease. *Physiological and Molecular Plant Pathology*. **60**:207-214.

TeBeest, D. O., Chang, X. B and Cisar, C. R (1992). The status of biological control of weeds with fungal pathogens. *Annu. Rev. Phytopathol.* **30**:637-657.

Torsvik, V and Ovreas, L (2002). Microbial diversity and function in soils: from genes to ecosystems. *Curr Opin Microbiol.* **5**: 240–245.

Tranel, P. J., Gealy, D. R and Kennedy, A. C (1993). Inhibition of downy brome (*Bromus tectorum*) root growth by a phytotoxin from *Pseudomonas fluorescens* strain D7. *Weed Technol.* **7**:134- 139.

Uppalapati, S. R., Ayoubi, P., Weng, H., Palmer, D. A., Mitchell, R. E., Jones, W and Bender, C. L (2005). The phytotoxin coronatine and methyl jasmonate impact multiple phytohormone pathways in tomato. *The Plant Journal.* **42**:201-217.

Van Elsas, J., Trevors, J., Jain, D., Wolters, A., Heijnen, C and Van Overbeek, L (1992). Survival of, and root colonization by, alginate-encapsulated *Pseudomonas fluorescens* cells following introduction into soil. *Biology and Fertility of Soils.* **14**:14-22.

Ward, D. M., Cohan, F. M., Bhaya, D., Heidelberg, J. F., Kühl, M and Grossman, A (2008). Genomics, environmental genomics and the issue of microbial species. *Heredity.***100**:207-219.

Weingart, H., Ullrich, H., Geider, K and Völksch, B (2001). The role of ethylene production in virulence of *Pseudomonas syringae* pvs. *glycinea* and *phaseolicola*. *Phytopathology.* **91**: 511-518.

Whipps, J. M (2001). Microbial interactions and biocontrol in the rhizosphere. *Journal of Experimental Botany.* **52**:487-511.

Wu, C.H., Wood, T.K., Mulchandani, A and Chen, W (2006). Engineering plant-microbe symbiosis for rhizoremediation of heavy metals. *Appl Environ Microbiol*. **72** (2):1129–1134. doi:10.1128/AEM.72.2.1129-1134

Zheng, X.Y., Spivey, N. W., Zeng, W., Liu, P.P., Fu, Z. Q., Klessig, D. F., He, S. Y and Dong, X (2012). Coronatine Promotes *Pseudomonas syringae* virulence in Plants by activating a signaling cascade that inhibits salicylic acid accumulation. *Cell Host and Microbe.* **11** :587-596.

Zhuang, X., Chen, J., Shim, H and Bai, Z (2007). New advances in plant growth-promoting rhizobacteria for bioremediation. *Environ Int.* **33**(3):406–413.