We are IntechOpen, the world’s leading publisher of Open Access books
Built by scientists, for scientists

5,500 Open access books available
135,000 International authors and editors
170M Downloads

154 Countries delivered to
TOP 1% Our authors are among the most cited scientists
12.2% Contributors from top 500 universities

WEB OF SCIENCE™
Selection of our books indexed in the Book Citation Index in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?
Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected.
For more information visit www.intechopen.com
Potential Role of Rice Plant Growth Promoting Phylloplane and Rhizospheric Bacteria in Controlling Xanthomonas oryzae pv. oryzae

Md. Mahfujur Rahman, Md. Mostafa Masud, Muhammad Iqbal Hossain, Nur-E-Tajkia Islam, Md. Zahangir Alam, Md. Mamunur Rashid, Mohammad Ashik Iqbal Khan, Md. Abdul Latif, Krishna Pada Halder and Md. Rashidul Islam

Abstract

Rice is an important cereal worldwide and it occupies the top position among the cereals in Bangladesh. Rice plant suffers from around 32 diseases of which ten are major in Bangladesh at present. Among the diseases, Bacterial Blight (BB) caused by X. oryzae pv. oryzae (Xoo) considered as a most destructive disease occurs in both rainfed and irrigated seasons of Bangladesh. BB causes considerable yield loss varies from 30 to 50% depending on the outbreak. It is also an important disease in most of the South and Southeast Asian countries. To develop environment-friendly sustainable management approach against BB of rice, in total sixty three plant growth promoting bacteria were identified from rice phylloplane and rhizosphere that are antagonistic to X. oryzae pv. oryzae during boro and aman seasons 2018 and 2019. These bacterial species inhibited the growth of X. oryzae pv. oryzae in vitro by 20.83 to 76.19%. These bacterial isolates were identified by sequencing of PCR products of 16SrDNA belonging to the genera mostly Pseudomonas, Bacillus and Serratia. Out of these bacterial species, 48 bacterial species were found as positive for IAA production, all 63 bacterial species were found positive for siderophore production and 48 were found capable to solubilize insoluble phosphate. Based on growth inhibition of X. oryzae pv. oryzae in in vitro, thirty two bacterial species were selected for plant growth promotion assessment and evaluation of net house and field efficacy in controlling BB of rice. These bacterial species were formulated using talcum powder which was viable for at least three months post formulation. Assessment of plant growth promoting determinants revealed that all 32 bacterial species identified in this study enhance the growth of rice plants as measured by root and shoot length and and reduced the BB severity in susceptible rice cultivar significantly as compared with untreated control.

Keywords: Rice, Plant growth promoting phylloplane and rhizospheric bacteria, control, X. oryzae pv. oryzae
1. Introduction

Rice (*O. sativa* L.) suffers from 32 diseases of which in Bangladesh 10 has been known as dreadful diseases [1]. Among the diseases three bacterial diseases are frequently occurred in Bangladesh. Among these three diseases, Bacterial Blight (BB) caused by *X. oryzae* pv. *oryzae* (*Xoo*) considered as a most destructive disease occurs in all Agro Ecological Zones (AEZs) of Bangladesh and mostly in two rice growing seasons namely viz. raifed and irrigated [2–4] and cause severe yield loss. In Japan, India and Bangladesh due to this devastating disease around 50%, 60% and 30% yield loss was observed [5], respectively in the highly infected rice fields. It is also a crucial disease in most of the South and Southeast Asian countries [6]. Bacterial blight (BB) is disease associated with several growth phases of rice plant showing either “Kresek” (acute wilting of young plants) symptoms and “leaf blight” (straw color blighted area with weavy margin) symptoms [7]. Excess amount of nitrogenous fertilizer in rice varieties (HYV) facilitates the emergence of this disease and its severity in the field [8–12]. In Bangladesh different pathogenic [13, 14] and genetic variability [15] have been detected and those were excessively perilous for rice [16].

Chemical fungicides (copper compounds, other chemicals and antibiotics) are not effective in controlling this disease [17]. However, control measures are including chemical, cultural, host resistance, genetic modification methods, among them cultural practices are not also effective in all circumstances as well as no fruitful chemical control and commercial product was found in this tropical climatic area which can be suppressed this disease nicely [18, 19]. Moreover, using antibiotics, toxic residues and chemicals have several limitations against BB of rice [20]. Apart from that, the uses of host resistance genes are used, in case of breeding single gene (Xa4) are manifested ineffective BLB management due to sub-populations [21].

Thus, biological control alleviates costs and it also serves as an environment friendly approach to mitigate this devastating threat [22], besides, the application of biological strains of PGPB would be the fullest alternative way of minimizing chemical pesticides, fertilizer and environmental pollution [23]. PGPB plays a crucial role in developing immunization in plants body, ISR is triggered by PGPB which is a signaling pathway while SAR mainly dependent on salicylic acid triggering a induced resistance by a particular infection, However, it is observed that ISR requires salicylic acid (SA) and ISR demands ethylene (ET) and jasmonic acid (JA) signal pathways [24] and both of these are triggered latent resistance mechanism subsequently after inoculation [25]. In recent years, application of PGPB in the field has been evaluated as an inducer showing systematic resistance [26, 27, 38]. Due to fruitful leaf colonization, quick growth, normal application procedure of *L. antibioticus* have been utilized as a bio control agents against Xoo [28]. *Bacillus* spp. also found effective in quelling BLB of rice under greenhouse condition [29].

According to [30], *S. globisporus* have been effective against rice blast. Sheath blight disease was alleviated by using a few biofilm and surfactant delivering strains of *Bacillus subtilis* [31]. Amalgamation of *B. subtilis* and *Streptomycetes philanthi* were biologically effective against rice sheath blight adding with chemical fungicides [32]. HCN (Hydrogen cyanide) played an effective role inhibiting the surges of *M. oryzae* as well as developing its bio control agents against blast of rice [33]. These antagonistic bacteria have the ability to subvert plant pathogens by releasing chemicals such as glucanases, proteases and chitinases, siderophores [34]. Rice disease can be controlled by the antagonistic strains of *Bacillus* and *Pseudomonas* spp. up to 90% based on what kind of strains are used [35]. When systemic resistance is exposed is called as ISR, and conversely, by other phenomenon is called SAR [36]. No necrosis manifested while ISR developed by PGPB [36]. Last few decades, PGPB have been
showing as a systematic resistance in the field [26, 27, 37, 38]. ISR demands three systematic pathway which are jasmonic acid (JA), ethylene (ET), salicylic acid (SA) signaling pathways [24]. PGPB can induce priming by the release of volatiles. For instance, *Bacillus subtilis* GBO3 induces a signaling pathway that is independent of salicylic acid (SA), jasmonic acid (JA) and the Npr1 gene (SA insensitive or nonexpresser of PR genes), yet it requires ethylene [39]. Priming offers an energy cost efficient strategy, enabling the plant to react more effectively to any invader encountered by boosting infection induced cellular defense responses [40, 41]. The increased levels of defense related enzymes during ISR are known to play a crucial role in host resistance [42, 43], reported that *Pseudomonas fluorescens* have been used as a bacterial antagonists against BLB of rice. A plentiful of bacterial strains *B. cereus*, *B. pasteurii*, *pumilus*, *Bacillusmycoides*, *B. amyloliquifaciens*, *B. sphaericus*, *B. pumilus*, *B. cereus have been effective in reducing disease resistance upon using ASM* (acibenzolar-S-methyl) [39, 43]. Species such as *Bacillus* spp. which showed ISR are radically linked to plant growth modification promotion [39] and this strains have been manifested resistance activity against a number of plant diseases studied by several researcher [44–50]. In rice, limited number of studies found discussing on induced resistance, the main theme of PGPB also includes production of growth hormones such as IAA and IA (inorganic phosphate) (Khan et al., 1997 and [51]), and zinc solubilization [52], atmospheric nitrogen [53]. Plant health also maintained by PGPB by producing ISR, siderophores and competition [54] as well as mitigate plant pathogens by developing enzymes such as antibiotics, proteases, glucanases and chitinases [34]. In both lab and field conditions PGPB bacteria are significantly reduced plant disease incidence, among them *Bacillus* and *Pseudomonas spp*. suppressed diseases up to 90% based on rice variety and types of pathogens [35]. ISR (Induced systemic resistance) is an environment friendly option for plant disease control because it initiates defense related genes and enzymes in host plant through inoculated bacteria to reduce disease incidence [29]. Bacterial Blight pathogen, however, radical information on rice PGPB which can be used as both biopesticide and biofertilizer is not disclosed in Bangladesh. Besides, more investigation needs to be executed from other dimension to completely minimize this deadly disease.

2. Materials and methods

2.1 Isolation and identification of bacteria from rice phylloplane and rhizosphere

2.1.1 Plant sample collection

To isolate the bacteria from rice phylloplane and rhizosphere, the healthy rice plants with root system and soils of different rice cultivars were collected from 40 districts representing 30 Agroecological Zones (AEZs) of Bangladesh from the vicinity of BB infected rice plants during boro and aman season, 2018 and 2019 at maximum tillering stage to pre-ripening stage. Then the rice plant samples were brought into the laboratory in labeled polybags.

2.1.2 Isolation and purification of bacteria

The phylloplane bacteria were isolated using washing method. Freshly harvested 2nd, 3rd, 4th leaves were vortexed in sterile saline solution for 12 minutes with two or three brief intervals. Then 100 µl solution was placed at the center of Luria
Bartani (LB) or King’s B agar plate and the solution was spread with glass spreader. The inoculated plates were incubated for 3–5 days at room temperature. After incubation of the inoculated plates, bacterial colonies appeared with various types of colors. Then the bacterial colonies were selected and isolated depending on their color and were streaked on LB media separately. Again the streaked LB plates were incubated at room temperature for 2 days. For isolation of antagonistic bacteria from rhizosphere, 1 g roots with rhizospheric soils were taken and then it was shaken with 100 ml sterile water for about 10–15 min to obtain soil suspension. Isolation of bacteria were carried out from rhizospheric soil by serial dilution technique up to $10^{-5}$ to $10^{-6}$ using LB (Luria Bertani) medium. Then the solution was placed at the center of Luria Bartani (LB) or King’s B agar plate and the solution was spread with glass spreader. The inoculated plates were incubated for 3–5 days at room temperature. After incubation of the inoculated plates, bacterial colonies appeared with various types of colors. Then the bacterial colonies were selected and isolated depending on their color and were streaked on LB media separately. Again the streaked LB plates were incubated at room temperature for 2 days.

2.2 Assay of antagonism of bacterial spp. to *X. oryzae pv. oryzae* by dual culture method

Antimicrobial activity of antagonistic strains of *Pseudomonas* spp./*Bacillus* spp. were determined by agar diffusion technique method [55] with some modifications. Antagonistic bacterial suspension was spot inoculated (5 μl of $10^8$ CFU/ml) at three places on the NBY plates that were prior inoculated with *X. oryzae pv. oryzae* cell suspension ($10^8$CFU/ml ~ optical density: 0.3). The plates were incubated for 7 days post inoculation at 28°C. Then *X. oryzae pv. oryzae* growth inhibition by the antagonistic bacterial isolates indicated by clear halo zones were measured with a ruler in mm. The percent growth inhibition of *X. oryzae pv. oryzae* by bacterial isolates was calculated as follows:

$$\text{Growth inhibition} \% = \frac{\text{Total diameter} - \text{Colony diameter} + \text{clear halo zones}}{\text{Total diameter}} \times 100$$

(1)

2.3 Assessment of plant growth promoting determinants of bacteria antagonistic to *X. oryzae pv. oryzae*

Active isolates with antagonistic potential against *X. oryzae pv. oryzae* were further evaluated for their ability to produce plant growth promoting determinants viz. siderophore production, Indole acetic acid (IAA) production and phosphate solubilization capability as follows:

2.3.1 Assay for siderophore production

Siderophore productions by antagonistical bacterial isolates were tested qualitatively as described by Alexander and Zuberer [56]. 5 μl of antagonistic bacterial cell suspension ($5 \times 10^8$ CFU/mL) was spot inoculated on Chrome azurol S (CAS) agar plate. The plates were then incubated at 30°C for 5 days. Development of yellow-orange halo zone around the bacterial growth was considered as positive for siderophore production. Experiment was performed with a completely randomized design with 3 replications. CAS agar was prepared from 4 solutions. Solution 1 (Fe-CAS indicator solution) was prepared by mixing 10 mL of 1 mmol L$^{-1}$ FeCl$_3$.6H$_2$O
(in 10 mmol L\(^{-1}\) HCl) with 50 mL of an aqueous solution of CAS (1.21 g L\(^{-1}\)). The resulting dark purple mixture was added slowly with constant stirring to 40 mL of aqueous solution of hexadecyl trimethyl ammonium bromide (1.821 g L\(^{-1}\)). The yielded of dark blue solution which was autoclaved, then cooled to 50°C. The entire reagent was freshly prepared for each batch CAS agar. Solution 2 (buffer solution) was prepared by dissolving 30.24 g of piperazine-N, N-bis (2-ethane sulfonic acid) (PIPES) in 750 mL of salt solution containing 0.3 g K\(_2\)PO\(_4\), 0.5 g NaCl and 1.0 g NH\(_4\)Cl. The pH was adjusted to 6.8 with 50% (w/v) KOH, and water was added to bring the volume 800 mL. The solution was autoclaved after adding 15 g of agar then cooled to 50°C. Solution 3 contained 2 g glucose, 2 g mannitol, 493 mg MgSO\(_4\).7H\(_2\)O, 11 mg CaCl\(_2\), 1.17 mg MnSO\(_4\).2H\(_2\)O, 1.4 mg H\(_3\)BO\(_3\), 0.04 mg CuSO\(_4\).5H\(_2\)O, 1.2 mg ZnSO\(_4\).7H\(_2\)O, 1.0 mg NaMoO\(_4\).2H\(_2\)O in 70 mL water, autoclaved, cooled to 50°C. Solution 4 was 30 mL filter sterilized 10% (w/v) casamino acid. Finally, solution 3 added to solution 2 along with solution 4, solution 1 was added last, with sufficient.

2.3.2 Assay for indole acetic acid (IAA) production

IAA production of antagonistic bacterial isolates were carried out as per the procedure described by Patten and Glick [57]. Every isolate was grown in LB media supplemented with (0.005%) L-tryptophan and incubated in shaker at 30°C with 160 rpm for 48 h. Then bacterial culture was centrifuged at 8000 rpm for 15 min and 1 mL culture filtrate was mixed with 4 mL salkowski's reagent (1.5 mL FeCl\(_3\).6H\(_2\)O 0.5 M solution in 80 mL 60% H\(_2\)SO\(_4\)) and the mixture was incubated at room temperature for 30 min, presence of pink color indicate qualitatively that isolate produced IAA. Formation of pink color indicated the presence of indoles [58].

2.3.3 Phosphate solubilization assay by antagonistic bacterial isolates

Phosphate solubilization was determined according to the method of Azman et al. [59]. Sterile filter papers (5.0 mm) were soaked in antagonistic bacterial cell suspension (5 × 108 CFU/mL) was dispensed using pipette onto sterile filter paper (6.0 mm) that was placed on National Botanical Research Institute’s phosphate (NBRIP) agar plate (Glucose (10 g/L), Ca\(_3\) (PO\(_4\))\(_2\) (5 g/L), MgCl\(_2\).6H\(_2\)O (5 g/L), MgSO\(_4\).H\(_2\)O (0.25 g/L), KCl (0.2 g/L), (NH\(_4\))\(_2\)SO\(_4\) (0.1 g/L), Bacteriological Agar (15 g/L) [60]. The plates were then incubated at 28°C for 7 days. Phosphate solubilization was assessed by observing the clear halo zone. The experiment was performed with a completely randomized design (CRD) with 3 replications.

2.4 Identification of selected plant growth promoting antagonistic bacterial isolates by sequence analyses of 16SrDNA

2.4.1 Extraction of genomic DNA

Bacterial culture from NA media was transferred in LB broth and shaken for 18 h at 28°C. Then genomic DNA of antagonistic bacteria was extracted according to Wizard® Genomic DNA purification Kit (Promega, Madison, USA). Obtaining the DNA pellet was rehydrated by adding 25 μL DNA rehydration solution and kept it overnight at 4°C. Finally the genomic DNA samples of the isolates were preserved at −20°C for further use.
2.4.2 Primers and PCR conditions

To identify the antagonistic bacterial isolates, the primer sets 27F (5'-AGA GTT TGATCM TGG CTC AG-3') and 1518R (5'-AAG GAG GTG ATC CAN CCR CA-3') specific to 16SrDNA were used for amplification of 16SrDNA from the prepared genomic DNA template [61]. The PCR conditions were as follows: initial denaturation at 95°C for 5 min, 35 cycles denaturation at 94°C for 1 min, annealing at 55°C for 1 min, extension at 72°C for 2 min and finally a 7 min extension at 72°C. PCR products were visualized by electrophoresis on 1.0% agarose gel containing 0.5% of ethidium bromide using a Gel documentation System after separating the PCR products in the agarose gel for 50 min at 80 volt.

2.4.3 Sequencing of PCR products

A partial nucleotide sequencing of 16SrDNA was performed from amplified PCR products using primers 27F (5'-AGA GTT TGATCM TGG CTC AG-3') in the Macrogen Lab, South Korea via Biotech Concern Bangladesh. The sequencing was done directly from PCR products according to the standard protocols for the ABI 3730xl DNA genetic analyzer (Applied Biosystems, Foster City, CA, USA) with BigDye® Terminator v1.1 and 3.1 Cycle Sequencing Kits.

2.4.4 Processing of sequence data

The sequencing data were processed and nucleotide sequence data was exported using Chromas software version 2.6.4. The quality of nucleic acid sequences was evaluated using Chromas (Version 2.6) software to avoid the use of low quality bases.

2.4.5 Analyses of nucleotide sequences

The nucleotide sequences were analyzed using online bioinformatics tools. The DNA sequences of 16Sr DNA of the bacterial isolates were compared with 16Sr DNA of the bacterial spp. and the sequences of ITS region of the fungal isolates were compared with ITS region of the fungal spp. that were available in the NCBI database using Basic Local Alignment Search Tool (BLAST) algorithm to identify closely related sequences (https://blast.ncbi.nlm.nih.gov/Blast.cgi).

2.5 Formulation of plant growth promoting antagonistic bacterial species

The pure cultures of thirty two selected potential bacterial antagonists were grown on LB agar medium for 24 hrs. Then the bacterial isolates were transferred in LB broth for about six hours by taking a loopful of bacteria from the LB agar plate. After that the liquid culture was then centrifuged and resuspended the pellet in previously prepared 200 ml peptone broth aimed to fortify the carrier materials. This culture broth was then grown for another two hours with shaking. After that 5 ml of sterile 100% glycerol was added to this 200 ml culture. Then the cultures of the bacterial antagonists (200 ml fortified with 1% peptone and 1% glycerol) were added to the mixture of 500 g talcum powder amended with 5 g carboxy methyl cellulose (CMC) and 7.5 g Calcium carbonate which were autoclaved for two consecutive days at 121°C under 15PSI pressure for 30 min each. The formulations were then being dried overnight in the tray. After that the formulations were powdered with hand, the formulated bacterial antagonists were packed in plastic bags. The formulated bacterial antagonists were then kept at both room and 4-8°C temperature in the refrigerator.
2.6 Assessment of viability of the formulated fungal and bacterial antagonists

The viability of the bacterial and fungal antagonists were checked by drawing 1 g of the formulated products in sterile water in every 30 days after formulation and diluted serially up to $10^{-4}$ or $10^{-5}$. The numbers of viable cells (colony forming unit) were counted per gram formulations kept at both room temperature and 4-8°C temperature in the refrigerator.

2.7 Assessment of plant growth promotion induced by antagonistic bacterial and fungal isolates

Rice seeds (cv. IR24) were surface sterilized and dried. Then the sterilized rice seeds were treated with formulated bacterial and fungal antagonists (10 g/kg seeds) and the treated seeds were left for 1 hr under shade. The rice seeds were then sown in the plastic pots previously filled with sterile soils. Fifty seeds were sown in each pot and three replications were maintained. Then the germination of seeds were recorded at 7DAS. The seedlings were uprooted at 7 DAS, 14 DAS and 28 DAS to measure the root length, shoot length and to calculate the vigor index \[ = \frac{(\text{root length} + \text{shoot length})}{\text{germination percentage}} \] were measured.

2.7.1 Seed priming, raising of seedlings and transplanting

Seeds of IR24 were treated with 32 selected formulated PGP antagonistic bacterial isolates. The treated sees were left for 1 hr. for adherence of the bacterial and fungal isolates with the treated seed surface. The treated seeds were then sown in the plastic pots filled with sterilized soils. One month old seedlings were then transplanted in the plastic pots filled with puddle soils.

2.7.2 Foliar spray of formulated PGP bacterial and fungal isolates

Formulated PGP antagonistic bacterial isolates were sprayed two times (at 50 and 55 DAS) before inoculation and two times after inoculation i.e. 65 and 70 DAS.

2.7.3 Inoculation of the rice plant with \textit{X. oryzae} pv. \textit{oryzae}

Rice plants were inoculated with a strain of \textit{X. oryzae} pv. \textit{oryzae} by Scissor clip method at 60 DAS.

3. Results

3.1 Isolation and identification of antagonistic bacteria against \textit{X. oryzae} pv. \textit{oryzae}

Rice plant samples were collected from 40 districts of Bangladesh representing 30 AEZs during boro seasons 2018–2019 and aman seasons 2018–2019. In total 300 bacterial isolates and 100 fungal isolates were isolated and purified from rice plant samples during boro season, 2018. Some selected representative bacterial species were shown in Figure 1. Out of 300 bacterial isolates, eighteen were identified as antagonist against \textit{X. oryzae} pv. \textit{oryzae} and inhibited the growth of \textit{X. oryzae} pv. \textit{oryzae in vitro} which was ranged by 28.39–76.19% (Table 1 and Figure 2). The maximum (76.14%) growth inhibition of \textit{X. oryzae} pv. \textit{oryzae in vitro} was recorded by BDISOBO5P while the minimum (28.59) growth inhibition was exhibited by
These antagonistic bacterial isolates were identified by sequencing of PCR products of 16SrDNA gene (Figure 3A). The identified bacterial species were BDISOB04P (*P. putida*), BDISOB05P (*P. putida*), BDISOB98P (*Stenotrophomonas maltophilia*), BDISOB241P (*Burkholderia* sp.), BDISOB242P (*B. gladioli*), BDISOB219R (*P. taiwanensis*), BDISOB220R (*Serratia* sp.), BDISOB221R (*Pseudomonas* sp.), BDISOB222R (*P. plecoglossicida*), BDISOB258R (*P. putida*), BDISOB272R (*Stenotrophomonas maltophilia*), BDISOB275R (*P. putida*), BDISOB186R (*Pseudomonas* sp.), BDISOB283R (*Pseudomonas fluorescens*), BDISOB306R (*P. putida*), BDISOB53R (*P. putida*), BDISOB61R (*Delftia tsuruhatensis*) (Table 1). In total 400 bacterial isolates and 40 fungal isolates were isolated and purified from rice plant samples collected in aman season, 2018. Seventeen bacterial isolates were identified as antagonist against *X. oryzae pv. oryzae* and inhibited the growth of *X. oryzae pv. oryzae in vitro* which was ranged by 38.33–60.66% (Table 2). The highest (60.66%) growth inhibition of *X. oryzae pv. oryzae* was exhibited by BDISO147P and the lowest (38.33%) growth inhibition was shown by BDISO135P. These antagonistic bacterial isolates were identified by sequencing of PCR products of 16SrDNA gene (Figure 3B) The bacterial species were BDISO04P (*P. putida*), BDISO45P (*Bacillus paramycooides*), BDISO356P (*P. hibiscicola*), BDISO198P (*Serratia plymuthica*), BDISO135P (*Bacillus* sp.), BDISO148P (*Serratia marcescens*), BDISO92P (*Serratia marcescens*), BDISO237P (*Alcaligenes faecalis*), BDISO12P (*Alcaligenes faecalis*), BDISOB272R. These antagonistic bacterial isolates were identified by sequencing of PCR products of 16SrDNA gene (Figure 3A). The identified bacterial species were BDISOB04P (*P. putida*), BDISOB05P (*P. putida*), BDISOB98P (*Stenotrophomonas maltophilia*), BDISOB241P (*Burkholderia* sp.), BDISOB242P (*B. gladioli*), BDISOB219R (*P. taiwanensis*), BDISOB220R (*Serratia* sp.), BDISOB221R (*Pseudomonas* sp.), BDISOB222R (*P. plecoglossicida*), BDISOB258R (*P. putida*), BDISOB272R (*Stenotrophomonas maltophilia*), BDISOB275R (*P. putida*), BDISOB186R (*Pseudomonas* sp.), BDISOB283R (*Pseudomonas fluorescens*), BDISOB306R (*P. putida*), BDISOB53R (*P. putida*), BDISOB61R (*Delftia tsuruhatensis*) (Table 1). In total 400 bacterial isolates and 40 fungal isolates were isolated and purified from rice plant samples collected in aman season, 2018. Seventeen bacterial isolates were identified as antagonist against *X. oryzae pv. oryzae* and inhibited the growth of *X. oryzae pv. oryzae in vitro* which was ranged by 38.33–60.66% (Table 2). The highest (60.66%) growth inhibition of *X. oryzae pv. oryzae* was exhibited by BDISO147P and the lowest (38.33%) growth inhibition was shown by BDISO135P. These antagonistic bacterial isolates were identified by sequencing of PCR products of 16SrDNA gene (Figure 3B) The bacterial species were BDISO04P (*P. putida*), BDISO45P (*Bacillus paramycooides*), BDISO356P (*P. hibiscicola*), BDISO198P (*Serratia plymuthica*), BDISO135P (*Bacillus* sp.), BDISO148P (*Serratia marcescens*), BDISO92P (*Serratia marcescens*), BDISO237P (*Alcaligenes faecalis*), BDISO12P (*Alcaligenes faecalis*),
BDISO196P (Alcaligenes faecalis), BDISO145P (Serratia marcescens), BDISO09P (Serratia marcescens), BDISO21R (Serratia marcescens), BDISO154P (P. taiwanensis), BDISO154P (P. taiwanensis), BDISO147P (Serratia marcescens), BDISO158R (Serratia marcescens), BDISO0R (B. amyloliquefaciens). In boro season 2019, 300 bacterial isolates were isolated and purified. In boro season 2019, out of 400 bacterial isolates fourteen were identified as antagonist against X. oryzae pv. oryzae and inhibited the growth of X. oryzae pv. oryzae in vitro which was ranged by 20.83–60.87% (Table 3 and Figure 3C). The maximum (60.87%) growth inhibition of X. oryzae pv. oryzae in vitro was recorded by BDISOB37R while the minimum (20.83%) growth inhibition was exhibited by BDISOB14R. The bacterial species identified were BDISOB37R [Pseudochrobactrum asaccharolyticum], BDISOB16R [Pseudochrobactrum asaccharolyticum], BDISOB98P [Stenotrophomonas maltophilia], BDISOB241P [Burkholderia sp.], BDISOB242P [B. gladioli], BDISOB219R [P. taiwanensis], BDISOB220R [Serratia sp.], BDISOB221R [Pseudomonas sp.], BDISOB222R [P. plecoglossicida], BDISOB258R [P. putida], BDISOB272R [Stenotrophomonas maltophilia], BDISOB275R [P. putida], BDISOB186R [Pseudomonas sp.], BDISOB283R [Pseudomonas fluorescens], BDISOB306R [P. putida], BDISOB53R [P. putida], BDISOB61R [Delftia tsuruhatensis] by sequencing of bacterial 16SrDNA. In aman season 2019, 400 bacterial isolates were isolated and purified. In aman season 2019, out of 400 bacterial isolates fourteen were identified as antagonist against X. oryzae pv. oryzae and inhibited the growth of X. oryzae pv. oryzae in vitro which was ranged by 20.83–60.87% (Table 3 and Figure 3C). The maximum (60.87%) growth inhibition of X. oryzae pv. oryzae in vitro was recorded by BDISOB37R while the minimum (20.83%) growth inhibition was exhibited by BDISOB14R. The bacterial species identified were BDISOB37R [Pseudochrobactrum asaccharolyticum], BDISOB16R [Pseudochrobactrum asaccharolyticum], BDISOB98P [Stenotrophomonas maltophilia], BDISOB241P [Burkholderia sp.], BDISOB242P [B. gladioli], BDISOB219R [P. taiwanensis], BDISOB220R [Serratia sp.], BDISOB221R [Pseudomonas sp.], BDISOB222R [P. plecoglossicida], BDISOB258R [P. putida], BDISOB272R [Stenotrophomonas maltophilia], BDISOB275R [P. putida], BDISOB186R [Pseudomonas sp.], BDISOB283R [Pseudomonas fluorescens], BDISOB306R [P. putida], BDISOB53R [P. putida], BDISOB61R [Delftia tsuruhatensis] by sequencing of bacterial 16SrDNA.

### Table 1.
List of antagonistic bacterial isolates identified by homology search of sequences of 16SrDNA by BLAST program obtained from plant samples collected in boro season 2018.

| Isolates    | Closest relatives                  | Accession no. | Alignment | Homology | Growth inhibition of X. oryzae pv. oryzae (%) |
|-------------|-----------------------------------|---------------|-----------|----------|-----------------------------------------------|
| BDISOB04P   | P. putida strain                  | MF838698.1    | 968/1086  | 89       | 61.67                                         |
| BDISOB05P   | P. putida strain                  | MH085459.1    | 931/1140  | 82       | 76.14                                         |
| BDISOB16P   | Bacillus sp.                      | MH819972.1    | 702/738   | 95       | 59.94                                         |
| BDISOB98P   | Stenotrophomonas maltophilia     | AY486381.1    | 1224/1271 | 96       | 33.04                                         |
| BDISOB241P  | Burkholderia sp.                 | GU979224.1    | 1154/1222 | 94       | 63.64                                         |
| BDISOB242P  | B. gladioli                      | MH748602.1    | 1186/1239 | 96       | 51.18                                         |
| BDISOB219R  | P. taiwanensis                    | KC293831.1    | 913/969   | 94       | 63.12                                         |
| BDISOB220R  | Serratia sp.                     | FM875872.1    | 150/186   | 81       | 61.77                                         |
| BDISOB221R  | Pseudomonas sp.                  | MG021242.1    | 303/341   | 89       | 68.33                                         |
| BDISOB222R  | P. plecoglossicida               | KC864769.1    | 614/751   | 82       | 64.79                                         |
| BDISOB258R  | P. putida                        | MF417798.1    | 917/1050  | 87       | 64.40                                         |
| BDISOB272R  | Stenotrophomonas maltophilia     | KJ534495.1    | 794/923   | 86       | 28.59                                         |
| BDISOB275R  | P. putida                        | KT984874.1    | 1201/1229 | 98       | 71.86                                         |
| BDISOB186R  | Pseudomonas sp.                  | JQ977022.1    | 29/29     | 100      | 64.43                                         |
| BDISOB283R  | Pseudomonas fluorescens          | KF010368.1    | 969/1006  | 96       | 66.04                                         |
| BDISOB306R  | P. putida                        | KF030905.1    | 1298/1374 | 94       | 44.97                                         |
| BDISOB53R   | P. putida                        | JQ833720.1    | 53/60     | 88       | 48.19                                         |
| BDISOB61R   | Delftia tsuruhatensis            | MF353931.1    | 976/1168  | 84       | 38.54                                         |
The maximum (61.54%) growth inhibition of *X. oryzae* pv. *oryzae* in *vitro* was recorded by BDISOB54R while the minimum (50.93%) growth inhibition was exhibited by BDISOB12R. These antagonistic bacterial isolates were identified by sequencing of 16SrDNA gene (*Figure 3D*). The bacterial species were BDISOB70R [*Serratia marcescens*], BDISOB54R [*B. gladioli*], BDISOB08R [*Serratia marcescens*], BDISOB31R [*Serratia marcescens*], BDISOB06R [*Serratia marcescens*], BDISOB171R [*Alcaligenes faecalis*], BDISOB46R [*Serratia marcescens*], BDISOB09R [*Serratia marcescens*], BDISOB33R [*Serratia marcescens*], BDISOB11R [*Serratia marcescens*], BDISOB36R [*Serratia marcescens*], BDISOB07R [*Serratia nematodiphila*], BDISOB172R [*B. aerophilus*] and BDISOB12R [*Serratia marcescens*] by sequencing of bacterial 16SrDNA.

### 3.2 Assessment of plant growth promoting determinants

Three plant growth promoting determinants viz. siderophore and IAA production as well as phosphate solubilization capability were assessed. The results revealed that the development of yellow-orange halo zone around the bacterial growth on chrome azurol S agar plates was considered as positive (+) for siderophore production, formation of pink color by the culture supernatant of the bacterial isolates in presence of Salkowski’s reagent confirmed IAA production which was indicated by ‘+’ sign and observation of clear halo zone in National Botanical Research Institute’s phosphate (NBRIP) agar plates indicated the bacterial
isolates are capable of phosphate solubilization which was denoted by “+” sign (Figure 3). Out of these bacterial species, 48 bacterial species were found as positive for IAA production, all 63 bacterial species were found positive for siderophore production and 48 were found capable to solubilize insoluble phosphate. In case of Indole Acetic Acid (IAA), BDISOB92FarR (Pseudomonas fluorescens), BDISOB172ThaR (B. aerophilus), BDISOB45PanP (Bacillus paramycoides), BDISOB01MymR (Bacillus amyloliquefaciens) showed highest IAA production. Whereas, BDISOB186KusR (Bacillus paramycoides) showed lowest IAA production. BDISOB54KhuR (B. gladioli) and BDISOB21ChaR (S. maltophilia) indicated moderate IAA production. BDISOB198HabP (Seratiaplymuthica), BDISOB148JoyP (Seratia marcescens), BDISOB145JoyP (Seratia marcescens), BDISOB07FarR (Seratiinematodiphilia), BDISOB12FarR (Seratia marcescens), BDISOB31MagR (Seratia marcescens), BDISOB46GopR (Seratia marcescens) and BDISOB70KusR (Seratia marcescens) were statistically similar. The bacterial isolates BDISOB222GaiR (P. plecoglossicida), BDISOB45PanP (Bacillus paramycoides) BDISOB01MymR (B. amyloliquefaciens) BDISOB04KhaP (P. putida), BDISOB05MymP (P. putida), BDISOB221GaiR (Pseudomonas sp.) showed highest siderophore production. Whereas, BDISOB135SerP (Bacillus sp.), BDISOB145JoyP (Seratia marcescens) and BDISOB21ChaR (Stenotrophomonas maltophilia) showed

Figure 3. PCR confirmation of the antagonistic bacterial isolates by amplification of 16S rDNA using primers 27F and 1518R obtained from plant samples collected in irrigated and rainfed seasons. These PCR products were then used for sequencing. Bacterial isolates obtained from (A) irrigated: BDISOB04P, BDISOB05P, BDISOB16P, BDISOB89P, BDISOB241P, BDISOB242P, BDISOB221R, BDISOB219R, BDISOB220R, BDISOB222R, BDISOB258R, BDISOB272R, BDISOB275R, BDISOB186R, BDISOB283R, BDISOB316R, BDISOB313R and BDISOB65R. (B) Rainfed: BDISOB04P, BDISOB45P, BDISOB53P, BDISO156P, BDISO198P, BDISO215P, BDISO237P, BDISO192P, BDISO147P, BDISO145P, BDISO158R, BDISO192R, BDISO115R, BDISO125R, BDISO126R, BDISO135R, BDISO306R, BDISO178R, BDISO12R, BDISO117R, BDISO154R, BDISO158R, BDISO11R, BDISO158R, BDISO12R, BDISO124R, BDISO172R, BDISO145P, BDISO117R, BDISO124R, BDISO172R and BDISO12R.
lowest siderophore production. The Siderophore production found in BDISOB219GaIR (P. taiwanensis), BDISOB5KusR (Sierratosiobacteria sp.), BDISOB283KisR (P. fluorescens), BDISOB219HabP (Serratia plymuthica), BDISOB35P (Bacillus sp.), BDISOB21ChaR (Serratia plymuthica), BDISOB148JoyP (Seratia marcescens), BDISOB12FarR (Seratia marcescens), BDISOB31MagR (Seratia marcescens), BDISOB46GopR (Seratia marcescens) and BDISOB70KusR (Seratia marcescens) were statistically similar. The bacterial isolates BDISOB05MymP (P. putida), BDISOB45PanP (Bacillus paramycoides) and BDISOB01MymR (Bacillus amyloliquefaciens) showed highest siderophore production. Whereas, BDISOB186KusR (Pseudomonas sp.), BDISOB258GaiR (P. putida) and BDISOB70KusR (Serratia marcescens) showed lowest phosphate solubilization activity. The others bacteria in case of phosphate solubilization were statistically similar.

3.2.1 IAA production

In case of Indole Acetic Acid (IAA), four isolates those were BDISOB92FarR (Pseudomonas fluorescens), BDISOB172ThaR (B. aerophilus), BDISOB45PanP (Bacillus paramycoides), and BDISOB01MymR (Bacillus amyloliquefaciens) revealed highest IAA production. Conversely, only one BDISOB186KusR (Bacillus paramycoides) depicted lowest IAA production. Around, twelve isolates exhibited upper-moderate IAA production, besides, seven showed lower and lower-moderate IAA production. BDISOB198HabP (Serratia plymuthica), BDISOB148JoyP (Seratia marcescens), BDISOB219GaIR (P. taiwanensis), BDISOB5KusR (Sierratosiobacteria sp.), BDISOB283KisR (P. fluorescens), BDISOB219HabP (Serratia plymuthica), BDISOB35P (Bacillus sp.), BDISOB21ChaR (Serratia plymuthica), BDISOB148JoyP (Seratia marcescens), BDISOB12FarR (Seratia marcescens), BDISOB31MagR (Seratia marcescens), BDISOB46GopR (Seratia marcescens) and BDISOB70KusR (Seratia marcescens) were statistically similar. Bacterial isolates BDISOB05MymP (P. putida), BDISOB45PanP (Bacillus paramycoides) and BDISOB01MymR (Bacillus amyloliquefaciens) exhibited upper-moderate siderophore production. Whereas, BDISOB186KusR (Pseudomonas sp.), BDISOB258GaiR (P. putida) and BDISOB70KusR (Seratia marcescens) showed lowest phosphate solubilization activity. The others bacteria in case of phosphate solubilization were statistically similar.

Table 2.
List of antagonistic bacterial isolates identified by homology search of sequences of 16SrDNA by BLAST program obtained from plant samples collected in aman season 2018.
| Isolate ID | Closest relatives | Accession no. | Alignment | Homology (%) | Growth inhibition of X. oryzae pv. oryzae (%) |
|------------|------------------|--------------|-----------|--------------|---------------------------------------------|
| BDISOB37R  | *Pseudochrobactrum asaccharolyticum* | KC456599.1 | 275/298   | 92           | 60.87                                       |
| BDISOB16R  | *Pseudochrobactrum asaccharolyticum* | KC456599.1 | 275/298   | 92           | 57.09                                       |
| BDISOB91R  | *Pseudochrobactrum asaccharolyticum* | KC456543.1 | 748/841   | 89           | 56.55                                       |
| BDISOB17R  | *Limnosyngibacter circumcreta*       | KR697754.1  | 86/105    | 82           | 43.42                                       |
| BDISOB15R  | *Pseudochrobactrum asaccharolyticum* | KM921740.1  | 399/535   | 75           | 49.94                                       |
| BDISOB86R  | *Enterobacter aerogenes*              | KM503142.1  | 444/483   | 92           | 45.75                                       |
| BDISOB30R  | *Pseudochrobactrum asaccharolyticum* | MK100767.1  | 166/177   | 94           | 47.73                                       |
| BDISOB92R  | *Pseudomonas fluorescens*             | KJ027533.1  | 29/29     | 100          | 45.44                                       |
| BDISOB178R | *Serratia marcescens*                 | MN691653.1  | 635/679   | 94           | 45.91                                       |
| BDISOB11R  | *Pseudochrobactrum asaccharolyticum* | MK377096.1  | 770/827   | 93           | 40.00                                       |
| BDISOB21R  | *Stenotrophomonas maltophilia*        | MN173472.1  | 994/1084  | 92           | 38.42                                       |
| BDISOB24R  | *Pseudochrobactrum asaccharolyticum* | FJ950551.1  | 994/1084  | 92           | 36.55                                       |
| BDISOB23R  | *Pseudochrobactrum asaccharolyticum* | KC456600.1  | 1082/1122 | 96           | 32.46                                       |
| BDISOB14R  | *Pseudochrobactrum asaccharolyticum* | KC456600.1  | 535/541   | 99           | 20.83                                       |

Table 3.
List of antagonistic bacterial isolates identified by homology search of sequences of 16SrDNA by BLAST program obtained from plant samples collected in boro season 2019.
BDISOB145JoyP (Seratia marcescens), BDISOB07FarR (Seratia nematodiphilia), BDISOB12FarR (Seratia marcescens), BDISOB31MagR (Seratia marcescens), BDISOB46GopR (Seratia marcescens) and BDISOB70KusR (Seratia marcescens) were statistically similar as well as BDISOB172ThaR, BDISO1MymR, BDISO45PanP and BDISOB92FarR were statistically similar, apart from these all were under the group of statistically dissimilar (Table 5 and Figure 3).

### 3.2.2 Siderophore production

Six bacterial isolates BDISOB222GaiR (P. plecoglossicida), BDISOB45PanP (Bacillus paramycoides), BDISOB01MymR (B. amyloliquefaciens), BDISOB04KhaP (P. putida), BDISOB05MymP (P. putida), BDISOB221GaiR (Pseudomonas sp.) exposed highest siderophore production. On the opposite, three of them which were BDISOB135SerP (Bacillus sp.), BDISOB172ThaR (B. aerophilus) and BDISOB45JoyP (Seratia marcescens) were statistically similar and rest of them were statistically dissimilar (Table 5 and Figure 3).

| Isolate ID | Closest relatives | Accession no. | Alignment Homology Growth inhibition of X. oryzae pv. oryzae (%) |
|------------|-------------------|---------------|---------------------------------------------------------------|
| BDISOB70R  | Serratia marcescens | MG571677.1     | 239/300 80 52.38                                             |
| BDISOB54R  | B. gladioli        | MH748601.1     | 1050/1108 95 61.54                                           |
| BDISOB08R  | Serratia marcescens | KU963569.1     | 100/114 88 59.31                                             |
| BDISOB31R  | Serratia marcescens | MN691926.1     | 929/990 94 59.17                                             |
| BDISOB06R  | Serratia marcescens | MG571677.1     | 111/127 87 59.26                                             |
| BDISOB171R | Alcaligenes faecalis | MN53225.1     | 927/1094 85 57.37                                            |
| BDISOB46R  | Serratia marcescens | MF360051.1     | 545/630 87 55.53                                             |
| BDISOB09R  | Serratia marcescens | MN252007.1     | 171/185 92 55.92                                             |
| BDISOB33R  | Serratia marcescens | KJ535346.1     | 127/143 89 52.27                                             |
| BDISOB11R  | Serratia marcescens | MK806681.1     | 88/98 90 53.57                                               |
| BDISOB36R  | Serratia marcescens | MK961214.1     | 787/910 86 58.33                                             |
| BDISOB07R  | Serratia nematodiphila | MN691930.1 | 572/639 90 52.00                                             |
| BDISOB172R | B. aerophilus      | KY307912.1     | 874/1043 84 51.19                                            |
| BDISOB12R  | Serratia marcescens | MH074778.1     | 780/841 93 50.93                                             |

Table 4. List of antagonistic bacterial isolates identified by homology search of sequences of 16SrDNA by BLAST program obtained from plant samples collected in aman season 2019.
### Table 5.
Growth promoting determinants produced by different bacterial isolates antagonistic to X. oryzae pv. oryzae.

| Treatments/ bacterial isolates | Name of bacteria | Indole acetic acid (IAA) (ng/ml) | Siderophore production (orange color halo zone) (mm) | Phosphate solubilization (clear halo zone) (mm) |
|-------------------------------|------------------|---------------------------------|-----------------------------------------------|-----------------------------------------------|
| Control                       | —                | 0.00 a                          | 0.00 h                                         | 0.00f                                         |
| BDISOB04KhaP                  | *P. putida*      | 44.88d                          | 28.67a                                         | 8.17c-e                                      |
| BDISOB05MymP                  | *P. putida*      | 44.54 l                         | 29.00a                                         | 14.33a                                        |
| BDISOB219GaiR                 | *P. taiwanensis* | 70.98c-g                        | 20.13b                                         | 7.83 c-e                                      |
| BDISOB221GaiR                 | *Pseudomonas sp.*| 42.93 l                         | 28.00a                                         | 8.67c                                         |
| BDISOB222GaiR                 | *P. plecoglossicida* | 41.46 m                     | 29.83a                                         | 11.67b                                        |
| BDISOB258GaiR                 | *P. putida*      | 49.27j                          | 14.50d-f                                      | 6.83de                                        |
| BDISOB186KusR                 | *Pseudomonas sp.*| 36.83n                          | 39.50bc                                        | 6.50e                                         |
| BDISOB283KisR                 | *Pseudomonas fluorescens* | 43.90 l          | 18.38bc                                        | 6.83 cd                                       |
| BDISO44DinP                   | *P. putida*      | 46.59 k                          | 13.00 fg                                       | 8.17 c-e                                      |
| BDISO45PanP                   | *Bacillus paronymosoides* | 81.46a                        | 28.17a                                         | 8.83 c-e                                      |
| BDISO198HabP                  | *S. plymanthia*  | 71.22c-f                        | 20.00b                                         | 7.50 c-e                                      |
| BDISO135SerP                  | *Bacillus sp.*   | 67.80 h                          | 10.83 g                                        | 8.33 cd                                       |
| BDISO148JoyP                  | *S. marcescens*  | 71.22c-f                        | 20.00b                                         | 7.50 c-e                                      |
| BDISO1MymR                    | *B. amylophilopfaciens* | 81.46a                        | 29.83a                                         | 14.17a                                       |
| BDISO145JoyP                  | *S. marcescens*  | 71.71c-e                        | 13.17 fg                                       | 6.83de                                        |
| BDISO158ChaR                  | *S. marcescens*  | 69.60a-h                        | 20.00b                                         | 7.50 c-e                                      |
| BDISO137KhaR                  | *Pseudochrobactrum asaccharolyticum* | 69.93d-g                      | 14.33d-f                                      | 8.33 cd                                       |
| BDISO166CumR                  | *Pseudochrobactrum asaccharolyticum* | 61.46l                         | 16.50c-e                                      | 8.17 c-e                                      |
| BDISO892FarR                  | *Pseudomonas fluorescens* | 82.68a                        | 0.00 h                                         | 7.50 c-e                                      |
| BDISO21ChaR                   | *S. maltophilia* | 78.78b                           | 11.17 g                                       | 7.00 c-e                                      |
| BDISO17CumR                   | *Limnolyngya circumcreta* | 68.93gh                        | 18.33bc                                        | 7.67 c-e                                      |
| BDISO15CumR                   | *Pseudochrobactrum asaccharolyticum* | 70.27c-g                      | 18.06bc                                        | 8.17 c-e                                      |
| BDISO86FarR                   | *E. aerogenes*   | 68.93 h                          | 18.33bc                                        | 7.33 c-e                                      |
| BDISO30ChaR                   | *Pseudochrobactrum asaccharolyticum* | 69.27a-h                      | 18.06c                                        | 8.17 c-e                                      |
| BDISO87FarR                   | *S. nemaotrophila* | 71.22c-f                        | 13.50e-g                                       | 7.50 c-e                                      |
| BDISO12FarR                   | *S. marcescens*  | 72.22c                          | 20.17b                                         | 6.83de                                        |
| BDISO31MagR                   | *S. marcescens*  | 70.89-c-g                       | 17.50b-d                                      | 7.50 c-e                                      |
| BDISO36MagR                   | *S. marcescens*  | 71.55c-e                        | 20.00b                                         | 7.33 c-e                                      |
| BDISO46GopR                   | *S. marcescens*  | 71.89 cd                         | 20.00b                                         | 7.17 c-e                                      |
| BDISO54KhuR                   | *B. gladioli*    | 77.56b                          | 18.33bc                                        | 7.33 c-e                                      |
| BDISO70KusR                   | *S. marcescens*  | 71.22-c-f                       | 20.00b                                         | 6.83de                                        |
| BDISO172ThaR                  | *B. aerophilus*  | 81.71a                          | 20.17b                                         | 8.00 c-e                                      |

**Level of significance**

* LSD — 1.839 3.101 1.702
* CV (%) — 1.78 10.34 12.88

* indicated 5% level of significance.

Values in columns followed by the same letters indicate no significant differences.
3.2.3 Phosphate solubilization

Among all bacterial isolates three of them those were BDISOB05MymP (P. putida), BDISOB45PanP (Bacillus paramycoides) and BDISOB01MymR (B. amyloliquefaciens) manifested supreme amount of phosphate solubilization activity. Whereas, another three of them which were BDISOB186KusR (Pseudomonas sp.), BDISOB258GaiR (P. putida) and BDISOB70KusR (Seratia marcescens) showed lowest phosphate solubilization activity. Except highest and lowest phosphate solubilization producing isolates rest of them were showed moderate type activity. In this case, a noticeable differences were observed that except two isolates BDISOB221GaiR and BDISOB222GaiR all other isolates are statistically similar. The others bacteria in case of phosphate solubilization were statistically similar (Table 5 and Figure 4).

3.3 Plant growth promotion by bacterial isolates antagonistic to X. oryzae pv. oryzae

Based on the growth inhibition of X. oryzae pv. oryzae by these antagonistic bacterial species, 32 bacterial isolates were selected for plant growth promotion assay and for subsequent assessment of their net house and field performances. Different plant growth promoting bacterial antagonists enhanced the root length, shoot length and vigor index at 14, 21 and 28 DAS (Table 6). Among 32 bacterial isolates, BDISOB05MymP showed the highest growth promotion activity.
| Treatments       | Root length (cm) | % Increase of vigor index over control | Shoot length (cm) | % Increase of root length over control | Vigor index | % Increase of shoot length over control |
|------------------|------------------|----------------------------------------|-------------------|----------------------------------------|-------------|----------------------------------------|
| Days after sowing (DAS) | 14 | 21 | 28 | 14 | 21 | 28 | 14 | 21 | 28 | 14 | 21 | 28 | 14 | 21 | 28 |
| Control          | 6.76 | 9.20 | 11.28 | 0 | 0.00 | 0.00 | 10.72 | 11.97 | 17.23 | 0.00 | 0.00 | 0.00 | 1316.32 | 2046.56 | 2449.34 |
| BDISOB04P        | 9.12 | 12.31 | 13.20 | 34.93 | 33.77 | 17.05 | 12.37 | 16.77 | 23.07 | 15.40 | 40.11 | 33.89 | 1697.18 | 2306.48 | 2877.95 |
| P. putida        | 8.13 | 12.92 | 12.84 | 21.85 | 32.83 | 13.80 | 12.37 | 16.53 | 18.32 | 15.40 | 38.16 | 6.29 | 1634.27 | 2549.46 | 2688.42 |
| BDISOB05P        | 8.69 | 12.22 | 12.58 | 28.56 | 32.83 | 11.55 | 12.40 | 16.53 | 18.88 | 15.71 | 38.16 | 9.57 | 1869.68 | 2549.46 | 2790.04 |
| P. taiwanensis    | 8.43 | 11.13 | 13.30 | 24.81 | 21.01 | 0.18 | 11.90 | 15.65 | 19.53 | 11.04 | 30.78 | 13.35 | 1647.00 | 2169.45 | 2497.50 |
| BDISOB221R       | 10.63 | 14.95 | 16.23 | 57.38 | 62.50 | 43.91 | 15.12 | 21.15 | 27.85 | 21.06 | 74.67 | 28.79 | 2360.42 | 3309.17 | 4048.97 |
| Pseudomonas sp.  | 9.12 | 13.04 | 13.37 | 34.93 | 41.78 | 18.56 | 12.37 | 17.60 | 23.42 | 15.40 | 47.08 | 35.88 | 1697.18 | 2420.82 | 2906.41 |
| BDISOB222R       | 10.12 | 14.95 | 16.23 | 57.38 | 62.50 | 43.91 | 15.12 | 21.15 | 27.85 | 21.06 | 74.67 | 28.79 | 2360.42 | 3309.17 | 4048.97 |
| P. plecoglossicida | 8.12 | 11.75 | 13.50 | 20.13 | 27.75 | 19.68 | 12.00 | 17.38 | 22.32 | 11.98 | 45.82 | 29.52 | 1634.27 | 2549.46 | 2658.42 |
| BDISOB258R       | 8.69 | 12.22 | 12.58 | 28.56 | 32.83 | 11.55 | 12.40 | 16.53 | 18.88 | 15.71 | 38.16 | 9.57 | 1869.68 | 2549.46 | 2790.04 |
| P. putida        | 8.12 | 11.75 | 13.50 | 20.13 | 27.75 | 19.68 | 12.00 | 17.38 | 22.32 | 11.98 | 45.82 | 29.52 | 1634.27 | 2549.46 | 2658.42 |
| BDISOB258R       | 10.32 | 14.25 | 15.63 | 52.69 | 54.89 | 38.59 | 14.18 | 21.73 | 30.33 | 32.35 | 81.62 | 76.02 | 2327.67 | 3286.48 | 4198.29 |
| Bacillus paramyces | 10.32 | 14.25 | 15.63 | 52.69 | 54.89 | 38.59 | 14.18 | 21.73 | 30.33 | 32.35 | 81.62 | 76.02 | 2327.67 | 3286.48 | 4198.29 |
| BDISOB198P       | 10.32 | 14.25 | 15.63 | 52.69 | 54.89 | 38.59 | 14.18 | 21.73 | 30.33 | 32.35 | 81.62 | 76.02 | 2327.67 | 3286.48 | 4198.29 |
| S. plymuthica    | 8.65 | 11.38 | 13.42 | 23.33 | 23.73 | 9.34 | 11.43 | 13.35 | 20.07 | 6.69 | 15.66 | 1644.00 | 2127.07 | 2689.20 |
| BDISOB135P       | 7.82 | 11.45 | 12.05 | 15.69 | 24.46 | 6.83 | 12.90 | 15.35 | 20.05 | 20.37 | 29.81 | 16.34 | 1788.54 | 2329.56 | 2418.03 |
| Bacillus sp.     | 7.82 | 11.45 | 12.05 | 15.69 | 24.46 | 6.83 | 12.90 | 15.35 | 20.05 | 20.37 | 29.81 | 16.34 | 1788.54 | 2329.56 | 2418.03 |
| BDISOB148P       | 8.65 | 11.38 | 13.36 | 28.02 | 23.73 | 18.41 | 11.43 | 13.35 | 20.57 | 6.69 | 15.66 | 1644.00 | 2127.07 | 2689.20 |
| S. marcescens    | 8.65 | 11.38 | 13.36 | 28.02 | 23.73 | 18.41 | 11.43 | 13.35 | 20.57 | 6.69 | 15.66 | 1644.00 | 2127.07 | 2689.20 |
| BDISOB37R        | 8.13 | 12.66 | 12.33 | 20.37 | 37.61 | 9.34 | 12.18 | 16.52 | 20.07 | 13.69 | 38.02 | 16.44 | 1632.11 | 2324.41 | 2689.20 |
| P. asaccharolyticum | 8.13 | 12.66 | 12.33 | 20.37 | 37.61 | 9.34 | 12.18 | 16.52 | 20.07 | 13.69 | 38.02 | 16.44 | 1632.11 | 2324.41 | 2689.20 |

DOI: http://dx.doi.org/10.5772/intechopen.99854
| Treatments                  | Root length (cm) | % Increase of vigor index over control | Shoot length (cm) | % Increase of root length over control | Vigor index | % Increase of shoot length over control |
|-----------------------------|------------------|----------------------------------------|-------------------|----------------------------------------|-------------|----------------------------------------|
|                            | Days after sowing (DAS)                                                                 |
| BDISOB16R                  | Pseudochractrum asaccharolyticum          | 8.34  | 11.95  | 12.12  | 23.38  | 29.89  | 7.42  | 11.57  | 18.52  | 24.45  | 7.93  | 54.74  | 41.88  | 1585.63  | 2528.73  | 3071.60  | 20.46  | 23.56  | 25.41  |
| BDISOB92R                  | Pseudomonas fluorescens                     | 7.10  | 13.06  | 12.38  | 5.08   | 41.92  | 9.78  | 12.02  | 15.87  | 20.28  | 12.19  | 32.59  | 17.70  | 1587.24  | 2429.56  | 2613.33  | 20.58  | 18.71  | 6.70   |
| BDISOB21R                  | S. marcescens                                 | 8.65  | 11.62  | 13.52  | 28.02  | 26.30  | 19.86 | 11.43  | 12.50  | 19.43  | 6.69   | 4.46   | 12.77  | 1687.00  | 1792.92  | 2449.53  | 28.16  | -12.39 | 0.01   |
| BDISOB17R                  | Limnolyngbya circumcreta                           | 7.10  | 11.45  | 13.36  | 5.08   | 24.46  | 18.41 | 12.02  | 15.53  | 20.57  | 12.19  | 29.81  | 19.38  | 1587.24  | 2329.56  | 2567.37  | 20.58  | 13.83  | 4.82   |
| BDISOB15R                  | P. asaccharolyticum                           | 8.13  | 12.66  | 12.33  | 20.37  | 37.61  | 9.34  | 12.18  | 16.52  | 20.07  | 13.69  | 38.02  | 16.44  | 1632.11  | 2324.41  | 2689.20  | 23.99  | 13.58  | 9.79   |
| BDISOB172R                 | B. aerophilus                                  | 8.40  | 12.35  | 12.84  | 24.32  | 34.24  | 13.80 | 13.00  | 16.92  | 22.92  | 21.31  | 41.36  | 32.98  | 1719.13  | 2351.09  | 2872.18  | 30.60  | 14.88  | 17.26  |

Table 6. Effect of different antagonistic bacteria on plant growth promotion of rice (cv. IR24).
isolates, the maximum vigor index (4198.29) was recorded in seedlings raised from seeds treated with BDISOB45PanR (*Bacillus paramycoidei*) followed by BDISOB283R (*Pseudomonas fluorescens*) (4087.60), BDISOB222R (*P. plecoglossicida*) (4040.97) while the minimum (2418.03) vigor index was obtained in BDISOB135SheR (*Bacillus* sp.) followed by BDISOBP (*S. marcescens*) (2449.53) and BDISOB54R (*B. gladioli*) (2449.53) at 30 DAS. However, all the antagonistic bacterial isolates exhibited the increase of vigor index ranged by 0.01 to 71.41. This result implies that some of the selected antagonistic bacterial isolates have the potentiality in enhancing plant growth.

### 3.4 Plant growth promotion by different bacterial isolates antagonistic to *Xanthomonas oryzae* pv. *oryzae*

#### 3.4.1 Fresh shoot weight

At 28 days after sowing the highest shoot weight (2260 mg) was recorded in plants raised from the seed treated with the bacterial isolate BDISOB01MymR followed by the bacterial isolates BDISOB05MymP (2250 mg), BDISOB45PanP (2173 mg), BDISOB04DinP (2033 mg), BDISOB86FarR (2033 mg), BDISOB07FarR (2033 mg) BDISOB283KisR (1950 mg). But the lowest shoot weight was observed in control (untreated seed) (933 mg) Rest of the isolates were showed moderate fresh shoot weight. Among all bacterial isolates seventeen were statistically similar and others denoted statistically dissimilar ([Table 7](#table7)).

#### 3.4.2 Dry shoot weight

At 28 days after sowing the highest shoot weight (546 mg) was recorded in plants raised from the seed treated with the bacterial isolate BDISOB01Mym followed by the bacterial isolates BDISOB04DinP (473mgmg), BDISOB04KhaP (470 mg), BDISOB92Far (466 mg), BDISOB222GaiR (443 mg) were statistically similar Whereas, the lowest (260 mg) was recorded in the plants raised from untreated seed followed by the plants sprayed with [Bactroban (inducer) + SICOGREEN® (nutrient and hormonal solution) + Hemoxy (Copper fungicide)] (313 mg), BDISOB172ThaR (266 mg), BDISOB07FarR (270 mg), BDISOB86FarR (273 mg), BDISOB70KusR (276 mg), BDISOB54KhuRwere statistically similar. On the other hand, the plants raised from the seed treated with the bacterial isolates BDISOB21ChaR (376 mg), BDISOB186KusR (330 mg), BDISOB219GaiR (373 mg), BDISOB21ChaR (376 mg) were statistically similar ([Table 7](#table7)).

#### 3.4.3 Fresh root weight

At 28 days after sowing the highest rootweight (1350 mg) was recorded in plants raised from the seed treated with the bacterial isolate BDISOB45PanP followed by the bacterial isolates BDISOB05MymP (1316 mg), BDISOB21ChaR (1306 mg) BDISOB15CumR (1256 mg), BDISOB01MymR (1253 mg), BDISOB92Far (1246 mg), BDISOB16CumR (1213 mg) were statistically similar Whereas, the lowest (830 mg) was recorded in the plants raised from untreated seed followed by the bacterial isolate BDISOB219GaiR (983 mg), plants sprayed with [Bactroban (inducer) + SICOGREEN® (nutrient and hormonal solution) + Hemoxy (Copper fungicide)] (1016 mg), BDISOB30ChaR (1080 mg). Other bacterial isolates were statistically similar ([Table 7](#table7)).
| Treatment | Isolate ID     | Fresh shoot weight (mg) | Dry shoot weight (mg) | Fresh root weight (mg) | Dry root weight (mg) |
|-----------|----------------|-------------------------|-----------------------|------------------------|---------------------|
| To        | Control        | 933.33 k                | 333.33d-g             | 830.00 g               | 170.00 l            |
| T1        | Positive control | 1300.00j               | 360.00 cd             | 1016.67ef              | 220.00jk            |
| T2        | BDISOB04KhaP  | P. putida 1693.33f-i   | 470.00a               | 1166.67a-f             | 403.33b             |
| T3        | BDISOB05MymP  | P. putida 2250.00ab    | 450.00a               | 1316.67ab              | 416.67b             |
| T4        | BDISOB219GaiR | P. taiwanensis 1816.67d-i | 410.00b              | 983.33 fg              | 246.67 hi            |
| T5        | BDISOB221GaizR | Pseudomonas sp. 1533.33ij | 293.33 h             | 1113.33c-f             | 240.00ij            |
| T6        | BDISOB222GaizR | P. pectangicida 1883.33c-h | 443.33a              | 1116.67c-f             | 440.00a             |
| T7        | BDISOB258GaizR | P. putida 1666.67i-i   | 323.33e-h             | 1166.67a-f             | 220.00jk            |
| T8        | BDISOB186KusR | Pseudomonas sp. 1633.33f-i | 330.00d-g            | 1133.33b-f             | 233.33i-k           |
| T9        | BDISOB283KisR | Pseudomonas fluorescens 1950.00a-f | 320.00e-h          | 1116.67c-f             | 266.67 h            |
| T10       | BDISO04DinP   | P. putida 2033.33a-e    | 473.33a               | 1120.00b-f             | 246.67 hi            |
| T11       | BDISO45PanP   | Bacillus pannonycides 2173.33a-c | 326.67e-g          | 1350.00a               | 343.33d-f           |
| T12       | BDISO198HabP | S. plymatherica 1660.00f-i | 350.00c-f            | 1093.33d-f             | 326.67 fg            |
| T13       | BDISO135SerP | Bacillus sp. 1766.67d-i | 336.67d-g             | 1133.33b-f             | 323.33 fg            |
| T14       | BDISO148JoyP | S. marcescens 1693.33f-i | 320.00e-h             | 1100.00f-f             | 313.33 g            |
| T15       | BDISO1MymR   | B. amyloliquefaciens 2260.00a | 346.67c-g          | 1253.33a-d             | 450.00a             |
| T16       | BDISO145JoyP | S. marcescens 1950.00a-f | 313.33 gh            | 1136.67b-f             | 240.00ij            |
| T17       | BDISO158ChaR | S. marcescens 1763.33d-i | 293.33 h             | 1180.00a-f             | 246.67 hi            |
| T18       | BDISOB37KhaR | P. asaccharolyticum 1686.67f-i | 363.33 cd          | 1190.00a-e             | 226.67i-k           |
| T19       | BDISOB16CumR | P. asaccharolyticum 1730.00e-i | 406.67b            | 1213.33a-e             | 230.00i-k           |
| T20       | BDISOB92FarR | Pseudomonas fluorescens 1933.33b-g | 466.67a            | 1246.67a-d             | 326.67 fg            |
| T21       | BDISOB21ChaR | S. maltophilia 1800.00d-i | 376.67c            | 1306.67a-c             | 336.67ef            |
| Treatment | Isolate ID | Species                        | Fresh shoot weight (mg) | Dry shoot weight (mg) | Fresh root weight (mg) | Dry root weight (mg) |
|-----------|------------|--------------------------------|--------------------------|-----------------------|------------------------|----------------------|
| T22       | BDISOB17CumR | *Limnolyngbya circumcreta*       | 2066.67a-d                | 363.33 cd             | 1220.00a-d             | 310.00 g             |
| T23       | BDISOB15CumR | *P. asaccharolyticum*            | 1866.67c-h                | 346.67c-g             | 1256.67a-d             | 363.33 cd            |
| T24       | BDISOB86FarR | *E. aerogenes*                   | 2033.33c-e                | 326.67e-g             | 1170.00a-f             | 353.33c-e            |
| T25       | BDISOB30ChaR | *P. asaccharolyticum*            | 1733.33e-i                | 363.33 cd             | 1080.00d-f             | 266.67 h             |
| T26       | BDISOB07FarR | *S. nematodiphila*               | 2033.33a-e                | 316.67f-h             | 1146.67b-f             | 373.33c              |
| T27       | BDISOB12FarR | *S. marcescens*                  | 1816.67d-l                | 320.00e-h             | 1113.33c-f             | 310.00 g             |
| T28       | BDISOB31MagR | *S. marcescens*                  | 1580.00 h-j               | 323.33e-h             | 1116.67c-f             | 236.67i-k            |
| T29       | BDISOB36MagR | *S. marcescens*                  | 1613.33 g-i               | 376.67c               | 1120.00b-f             | 230.00i-k            |
| T30       | BDISOB46GopR | *S. marcescens*                  | 1700.00f-i                | 353.33c-e             | 1123.33b-f             | 246.67 hi            |
| T31       | BDISOB54KhuR | *B. gladioli*                    | 1513.33j                  | 353.33c-e             | 1126.67b-f             | 213.33 k             |
| T32       | BDISOB70KusR | *S. marcescens*                  | 1566.67 h-j               | 363.33 cd             | 1113.33c-f             | 233.33i-k            |
| T33       | BDISOB172ThaR | *B. aerophilus*                  | 1510.00ij                 | 360.00 cd             | 1160.00a-f             | 246.67 hi            |

Level of significance

| LSD       | CV         |
|-----------|------------|
| 270.7     | 9.39       |
| 27.85     | 4.73       |
| 161.9     | 8.65       |
| 20.58     | 4.36       |

* indicated 5% level of significance.

Values in columns followed by the same letters indicate no significant differences.

Table 7.
Plant growth promotion by different bacterial isolates antagonistic to *X. oryzae* pv. *oryzae*.  
DOI: http://dx.doi.org/10.5772/intechopen.99854
| Isolate ID | Name of bacteria       | Lesion length* (mm) | Reduction of lesion length (%) |
|------------|------------------------|---------------------|-------------------------------|
| Control    | —                      | 23.67a              | 0                             |
| Positive control | —                  | 6.33b-d             | 73.31                         |
| BDISOB04P  | *P. putida*            | 1.50ij              | 92.61                         |
| BDISOB05P  | *P. putida*            | 1.00j               | 95.71                         |
| BDISOB219R | *P. taiwanensis*       | 5.67c-f             | 76.04                         |
| BDISOB221R | *Pseudomonas sp.*      | 5.00d-g             | 78.85                         |
| BDISOB222R | *P. plecoglossicida*   | 0.83j               | 96.56                         |
| BDISOB258R | *P. putida*            | 1.50j               | 93.61                         |
| BDISOB186R | *Pseudomonas sp.*      | 5.33c-g             | 77.38                         |
| BDISOB283R | *Pseudomonas fluorescens* | 1.33ij            | 94.38                         |
| BDISOB04P  | *P. putida*            | 5.83c-e             | 75.25                         |
| BDISOB45R  | *Bacillus paramycoides*| 2.00ij              | 91.55                         |
| BDISOB198P | *S. plymuthica*        | 5.83c-e             | 52.36                         |
| BDISOB135R | *Bacillus sp.*         | 2.83hi              | 88.08                         |
| BDISOB148P | *Serratia marcescens*  | 5.83c-e             | 75.69                         |
| BDISOB11R  | *B. amyloliquifaciens* | 2.33ij              | 90.16                         |
| BDISOB145P | *S. marcescens*        | 6.83bc              | 71.12                         |
| BDISOB158R | *S. marcescens*        | 6.83bc              | 50.14                         |
| BDISOB37R  | *P. asaccharolyticum*  | 5.33c-g             | 77.44                         |
| BDISOB16R  | *P. asaccharolyticum*  | 5.17d-g             | 78.01                         |
| BDISOB92R  | *Pseudomonas fluorescens* | 4.50e-g           | 80.85                         |
| BDISOB21R  | *S. marcescens*        | 2.17ij              | 93.80                         |
| BDISOB17R  | *Limonolyngbya curvata* | 4.00 gh             | 83.33                         |
| BDISOB15R  | *P. asaccharolyticum*  | 5.33c-g             | 54.03                         |
| BDISOB86R  | *E. aerogenes*         | 4.00 gh              | 83.33                         |
| BDISOB30R  | *P. asaccharolyticum*  | 4.33h               | 81.64                         |
| BDISOB07R  | *S. nematodiphila*     | 4.00 gh              | 83.33                         |
| BDISOB12R  | *S. marcescens*        | 4.00 gh              | 83.06                         |
| BDISOB31R  | *S. marcescens*        | 5.00d-g             | 78.97                         |
| BDISOB36R  | *S. marcescens*        | 5.83c-e             | 75.49                         |
| BDISOB46R  | *S. marcescens*        | 4.17f-h             | 82.28                         |
| BDISOB54R  | *B. gladioli*          | 4.17f-h             | 82.41                         |
| BDISOB70R  | *S. marcescens*        | 2.83hi              | 87.96                         |
| BDISOB172R | *B. aerophilus*        | 7.50b               | 68.21                         |

| Level of significance | CV (%) |
|-----------------------|--------|
| *                      | 16.80  |

* indicated 5% level of significance.

Values in columns followed by the same letters indicate no significant differences.

Table 8.
Effect of some selected antagonistic bacterial isolates on the reduction of lesion length in susceptible check cultivar (IR24) caused by *X. oryzae pv. oryzae.*
Figure 5. 
Reduction of lesion length by some selected antagonistic bacterial in susceptible check cultivar (IR24). Photographs were taken at 14 days after inoculation. BDISOB04P (P. putida), BDISOB05P (P. putida), BDISOB219R (P. taiwanensis), BDISOB221R (Pseudomonas sp.), BDISOB222R (P. plecoglossicida), BDISOB258R (P. putida), BDISOB186R (Pseudomonas sp.), BDISOB283R (Pseudomonas fluorescens), BDISOB284P (P. putida), BDISOB45R (Bacillus paramyroides), BDISOB48P (S. plymuthica), BDISOB135R (Bacillus sp.), BDISOB48P (S. marcescens), BDISOB01R (B. amyloliquefaciens), BDISOB45P (S. marcescens), BDISOB38R (S. marcescens), BDISOB17R (Limnothelya circumcreta), BDISOB15R (P. asaccharolyticum), BDISOB16R (P. asaccharolyticum), BDISOB132R (Pseudomonas fluorescens), BDISOB12R (S. maltophilia), BDISOB17R (Limnothelya circumcreta), BDISOB15R (P. asaccharolyticum), BDISOB16R (E. aerogenes), BDISOB10R (P. asaccharolyticum), BDISOB67R (Serratia nematodiphila), BDISOB12R (Serratia marcescens), BDISOB11R (Serratia marcescens), BDISOB68R (Serratia marcescens), BDISOB46R (Serratia marcescens), BDISOB54R (B. gladioli), BDISOB70R (Serratia marcescens) and BDISOB172R (B. aerophilus).
3.4.4 Dry root weight

At 28 days after sowing the highest dry root weight (450 mg) was recorded in plants raised from the seed treated with the bacterial isolate BDISOB01MymR, BDISOB22GaiR (440 mg) followed by the bacterial isolates BDISOB05MymP (413 mg), BDISOB04KhaP (403 mg). Whereas, the lowest (170 mg) was recorded in the plants raised from untreated seed followed by the plants sprayed with [Bactroban (inducer) + SICOGREEN® (nutrient and hormonal solution) + Hemoxy (Copper fungicide)] (220 mg), BDISOB54KhuR (213 mg). Other bacterial isolates were statistically similar (Table 7).

3.5 Effect of some selected antagonistic bacterial isolates on the reduction of lesion length in susceptible check cultivar (IR24) caused by X. oryzae pv. oryzae

To evaluate the mechanisms of BB severity reduction by plant growth promoting antagonistic bacteria, susceptible check variety IR24 was used. The results of plant inoculation showed a significant reduction of lesion length in plants sprayed with formulated bacterial bioagents as compared with untreated control. (Table 8). 96.56% reduction of lesion length was marked as highest spraying with BDISOB222R followed by BDISOB05P (95.71%), BDISOB283R (94.38%), BDISOB21R (93.80%), BDISOB258R (93.61%), BDISOB04P (92.61%), BDISOB45P (91.55%) and BDISO1R (90.16%). The minimum (50.145%) reduction of lesion length were observed in plants sprayed with BDISO198P followed by BDISO158R (52.36%) and BDISOB15R (54.03%). Ten bacterial isolates were revealed upper-moderate level of lesion length reduction and eleven isolates were marked their place at lower-moderate level of lesion length reduction. However, all other bacterial isolates reduced lesion length significantly as compared with the untreated plants (Table 8 and Figure 5).

4. Discussion

Antagonistic bacterial isolates were identified mostly as different species of *Pseudomonas*, *Bacillus*, *Serratia* and *Delftia*. In a previous study, frequency of antagonistic bacteria on LB medium was low [62], but another study revealed that using different growth media such as King’s B, and Gould’s S1 and Nutrient Agar were effective for the isolation of higher number of antagonistic bacteria [63]. It was reported that some antagonistic bacteria such as *B. subtilis*, *B. amyloliquefaciens*, *B. valismortis*, *Streptomyces* sp., *P. chlororaphis* and *Acinetobacter baumannii* were identified based on 16S rRNA sequence analysis [64]. A number of bacteria from species *Alcaligenes*, *Arthrobacter*, *Burkholderia*, *Alcaligenes*, *Arthrobacter*, *Burkholderia*, *Bacillus*, *Azospirillum*, *Azotobacter*, *Klebsiella*, *Enterobacter* and *Serratia* have been observed to develop plant growth. However, as bio control agents, isolates of *fluorescens*, *Pseudomonas*, and *Bacillus* have been the most exploited and studied [65–68]. Nowadays, antagonistic bacteria were also used for plant roots as a biological control infecting by numerous plant pathogens [26, 69]. Out of 300 bacterial isolates sixteen isolates of several species were evaluated *in vitro* and they exposed antagonistic activity to *X. oryzae* pv. *oryzae*. It was observed that 54.03% to 96.56% of lesion length was diminished when treating with antagonistic bacteria. These findings were identical to the reported by Monteiro *et al.* [63] because they also showed that BB pathogen was suppressed by antagonistic bacteria. According to Ranjbariyan *et al.* [70] who also experimented that three bacterial isolates...
significantly acted higher growth inhibition of *X. oryzae pv. oryzae*. Antibiotics, enzymes like chitinases, glucanases, proteases, and siderophore produce directly or indirect mechanisms in which the antagonistic bacteria compete with the pathogen for a niche or nutrient sites [34].

Out of the 63 bacterial isolates, 48 bacterial species were found as positive for IAA (Indole Acetic Acid) production, all 63 bacterial species were found positive for siderophore production and 48 were found capable to solubilize insoluble phosphate. IAA also has been speculated to fasten the overall fitness of plant-microbe associations [57]. It was proved that numerous plant-associated bacteria have the ability to produce IAA by stimulating plant roots development and improving absorption of water and nutrients from soil [71, 72]. The IAA producing bacteria encouraged adventitious root formation, produced the greatest roots and shoots weight [73]. All 63 bacterial isolates were found to produce siderophore. When iron availability is in stress microorganism those who produce siderophore supplied Fe nutrition to enhance plant growth [74]. Siderophore also assists when it comes to the growth condition of shoots, roots as well as nutrition in plants [75]. Siderophore plays a crucial role in selecting a potential bioagent [76], besides, it has been considered as an alternative to ruinous pesticides effects [77]. The biological control mechanism depended on the role of siderophore as competitors for Fe in order to reduce Fe availability for the phytopathogen [78]. Siderophores produced by numerous bacteria had a significant role in the biocontrol and negatively affected the growth of several pathogen [78, 79]. Forty eight bacterial isolates showed the capability of phosphate solubilization. It has been also experimented that phosphate solubilizing bacteria (PSB) can also triggered plant growth promotion [80]. This PSB inoculants have been exploited as a possible alternative for phosphate fertilizers which is inorganic [81] and it also influences phosphate uptake and plant growth [82, 83]. It has also been documented that the application rates of phosphate fertilizers reduced to 50% by inoculating phosphate solubilizing microbes (PSM) added phosphate fertilizers reduced the disease incidence up to 50% [84].

Among the bacterial isolates, 32 were selected based on their antagonistic capability and growth promoting determinants. PGPB have significant impact in surging root length, vigor index and shoot length. Sakthivel *et al.* [85] and Mishra and Sinha [86] reported to enhance growth of rice seedling with bioagent application. Van Peer and Schippers [87] stated that shoot, root and fresh weight was raised for cucumber, lettuce, tomatoad potato as a result of bacterization with *Pseudomonas* strains. The results of the present study depicts that the effect of plant growth promoting bacterial isolates on growth and vigor of rice plants was significantly higher than control. It has been reported that *P. fluorescens* and other plant growth promoting rhizobacteria can show antagonisms to potentially harmful bacterial pathogens and eventually those bacteria contribute to enhance plant growth [88]. Biological agents like plant growth promoting bacteria (PGPB) can be used as bio-fertilizer [89].

Forty eight bacterial species were found positive for phosphate solubilization out of 63 antagonistic bacterial species identified in this study. It has been reported that phosphate solubilizing bacteria (PSB) induced plant growth promotion [80]. Plant roots-associated PSB have been considered as one of the possible alternatives for inorganic phosphate fertilizers for promoting plant growth and yield [81]. Plant growth and phosphate uptake have increased in many crop species due to the results of PSB inoculants [82, 83]. It has also been documented that the application rates of phosphate fertilizers reduced to 50% by inoculating phosphate solubilizing microbes (PSM) in crops without significantly reducing crop yield [84]. In sustainable agriculture, specific plant pathogens can be supressed by biological agents such as plant growth promoting bacteria (PGPB) which can also be used as bio-fertilizer [89]. There are a plenty of PGPB strains that reported to suppress numerous of
plant pathogen, reduced disease incidence, triggered plant growth factor and provides nutrition for the growth of the plant [63, 90]. Thus, it has been considerable research interest in the potential use of antagonistic bacteria as PGPB [91, 92]. To evaluate plant-interaction with bacteria, such as endophytes, biocontrol agents, phytopathogens, and symbionts needs to be re-infection and development of those experimental strains in or on field grown plants [93]. Effective root colonization by fluorescent *Pseudomonas* spp. has been manifested to take an inevitable part in controlling plant pathogens as a biocontrol agent [94]. The significance of this study is that functionally characterized all antagonistic bacteria may be used for biocontrol of BB along with enhanced rice growth. Even though, *Pseudomonas* spp. are indigenous and involve in various rhizomicrobiomes but few of them have the ability to grow above 37°C and become opportunistic pathogens, thus predictable biosafety regulations are needed to implement this technology practically for field application [95]. In a nutshell, based on all results achieved from during this study, bacterial strains may be an effective bio-inoculant for controlling BB of rice by ensuring its biosafety aspects.

5. Conclusion

Thirty two potential bacterial isolates were identified belong to the genera mostly *Pseudomonas*, *Bacillus* and *Serratia* from rice phylloplane and rhizosphere among sixty three that inhibited the growth of *X. oryzae pv. oryzae* in *in vitro* significantly and were found positive for enhancing plant growth promotion by the production of plant growth promoting determinants viz. IAA, siderophore and phosphate solubilization. Formulated bacterial isolates can be viable in talcum powder for at least three months post formulation. Reduction of lesion length caused by *X. oryzae pv. oryzae* on susceptible cultivar IR24 by the formulated bacterial isolates primarily indicates their potentiality in controlling BB of rice. Patenting, registration, large scale formulation and commercialization of these PGP bacteria would be the next step of this work.

Acknowledgements

This research work was carried out with the financial support from National Agricultural Technology (NATP), Phase-2, under Program Based Research Grant (PBRG), Bangladesh Agricultural Research Council (BARC), Farmgate, Dhaka, Bangladesh to Dr. Md. Rashidul Isalm (Grant ID No.: 091).

Conflict of interest

There is no conflict of interest among the authors.
Potential Role of Rice Plant Growth Promoting Phylloplane and Rhizospheric Bacteria...

DOI: http://dx.doi.org/10.5772/intechopen.99854

Author details

Md. Mahfujur Rahman¹, Md. Mostafa Masud¹, Muhammad Iqbal Hossain¹, Nur-E-Tajkia Islam¹, Md. Zahangir Alam¹, Md. Mamunur Rashid³, Mohammad Ashik Iqbal Khan⁴, Md. Abdul Latif², Krishna Pada Halder⁴ and Md. Rashidul Islam*¹

1 Department of Plant Pathology, Bangladesh Agricultural University, Mymensingh, Bangladesh

2 Plant Pathology Division, Bangladesh Rice Research Institute (BRRI), Joydebpur, Gazipur, Bangladesh

3 Plant Pathology Division, BRRI Regional Station, Cumilla, Bangladesh

4 Director Research, Bangladesh Rice Research Institute (BRRI), Joydebpur, Gazipur, Bangladesh

*Address all correspondence to: rashidul.islam@bau.edu.bd

© 2021 The Author(s). Licensee IntechOpen. This chapter is distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/3.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
References

[1] Latif MA, Kabir MS, Sharma NR and Hossain MA. 2007: Integrated management of five major diseases of rice. (Dhaner pachti prodhan roger somonitto babostapona- in Bangla). 1st edition, published by Bangladesh Rice Research Institute (BRRI), Gazipur 1701, Bangladesh. BRRI Press.

[2] Latif MA, Rafii MY, Rahman MM, Talukdar MRB. 2011: Microsatellite and minisatellite markers based DNA fingerprinting and Genetic diversity of blast and ufra resistant genotypes. Comptes Rendus Biologies. 334: 282-289.

[3] Miah SA. 1973: Recent research results on rice diseases in Bangladesh. A paper presented at the Annual International Rice Conference held at IRRI, Los Baños, Philippines, during April 1973.

[4] Miah SA, Shahjahan AKM, Hossain MA and NR Sharma 1985: A survey of rice diseases in Bangladesh. Tropical Pest Management 31(3): 208-213.

[5] Shahjahan AKM. 1993: Practical approaches to crop pest and disease management in Bangladesh. Bangladesh Agriculture Research Council. P.168.

[6] Sharma NR, Hossain MA, Haque MA, Mondal AH and Rahman MM. 1991: Effect of rate and split application of nitrogen on bacterial leaf blight incidence in rice. Bangladesh J. Plant Pathology.7 (1 & 2): 17-20.

[7] Nino-Liu, D., Ronald, P., and Bogdanove, A. (2006). Xanthomonas oryzae pathovars: model pathogens of a model crop. Mol. Plant Pathol. 7, 303–324. doi: 10.1111/j.1364-3703.2006.00344.x.

[8] Chattopadhyay SB and Mukherjee N. 1973. Progress of two pathogenic diseases on rice crop grown under high nitrogen fertilized and intensive rice cropping condition. Int. Rice Comm. NewsL. 22(2): 43-48.

[9] Devadath S, Dath AP and Jain RK. 1987. Effect of shade, nitrogen fertilization, waterlogging and inoculum concentration on the incidence of bacterial leaf blight of rice. Indian Phytopathology. 40: 529-530.

[10] Kim CH and Cho YS. 1970: Effect of NPK fertilizer levels and growth condition on the development of bacterial blight in rice plants. Kor. J. Plant Prot 9(1): 7-13.

[11] Kauffman HE and Rao PS. 1972: Resistance to bacterial leaf blight-India. In Rice Breeding. IRRI, Los Banos, Laguna, Philippines. 283-287.

[12] Mohanty SK, Reddy PR and Sridhar R. 1983: Effect of major nutrients on the susceptibility of rice plants to bacterial leaf blight. Z. Pflanzenkr. Pflanzensch. J. Plant Dis. Prot. 90: 50-54.

[13] Rashid, M. M; Nihad, S. A. I.; Khan, M. A. I.; Haque, A.l; Ara, A.; Ferdous, T.; Hasan, M.A.; Latif, M. A. (2021). Pathotype profiling, distribution and virulence analysis of Xanthomonas oryzae pv. oryzae causing bacterial blight disease of rice in Bangladesh, J. Phytopathol. 169 (7-8); 438-446.

[14] Alam, S, Islam, R., Hossain, I., Bhuiany, M. R. (2016). Pathotypic variation of X. oryzae pv. oryzae in Bangladesh. Archives of Phytopathology and Plant Protection, 323, 1477-2906

[15] Islam, M. R., Alam, M. S., Khan, A. I., Hossain, I., Adam, L. R., Daayf, F. (2016). Analyses of genetic diversity of bacterial blight pathogen, X. oryzae pv. oryzae using IS1112 in Bangladesh. Comptes Rendus Biologies, 339(9-10), 399-407
[16] Brar, D.S., Khush, G.S. (1997). Alien introgression in rice. *Plant Molecular Biology*, 35, 35-47.

[17] Jalaluddin M and Kashem MA. 1999: Pathogenic variability in *Xanthomomasoryzae pv oryzae* in Bangladesh. *Indian J. Agril. Sci.* 69: 25-27.

[18] Noda T, Yamamoto T, Ogawa T and Kaku H. 1996. Pathogenic races of *Xanthomomas oryzae pv. oryzae* in South and East Asia. *JIRCAS J.* 3: 9-15.

[19] Webster RK and Gunnel PS. 1992: *Compendium of Rice Disease*. p. 62.

[20] Lee KS, Rasabandith S, Angeles ER and Khush GS. 2003: Inheritance of resistance to bacterial blight in 21 cultivars of rice. *Phytopathology*. 93: 147-152.

[22] Ou 1973: *A Handbook of Rice Diseases in the Tropics*. Los Baños: International Rice Research Institute.

[23] Gnanamanickam, S. S. 2009. An overview of progress in biological control. In: Biological control of rice diseases: Progress in biological control Series, ed. by S. S. Gnanamanickam, pp. 43-51. Springer, Dordrecht, Netherlands.

[24] MacManus, P. S., Stockwell, V. O., Sundin, G. W., and Jones, A. L. (2002). Antibiotic use in plant agriculture. *Ann. Rev. Phytopathol.* 40, 443–465. doi: 10.1146/annurev.phyto.40.120301.093927

[25] Shanti ML, Shenoy VV, Lalitha Devi G, Mohan Kumar V, Premalatha P, Naveen Kumar G, Shashidhar HE, Zehr UB and Freeman WH. 2010: Marker-assisted breeding for resistance to bacterial blight in popular cultivar and parental lines of hybrid rice. *J Plant Pathol.* 92: 495-501.

[26] Kloepper, J.W., Tuzun, S., Liu, L., Wei, G., 1993: Plant growth promoting rhizobacteria as inducers of systemic disease resistance. In: Lumsden, R.D., Waughn, J.L. (Eds.), *Pest Management: Biologically Based Technologies*. American Chemical Society Books, Washington, DC, pp. 156-165.

[27] Van Loon, L.C., 1997: Induced resistance in plants and the role of pathogenesis related proteins. *Eur. J. Plant Pathol.* 103, 753-765.

[28] Viswanathan, R., 1999: Induction of systemic resistance against red rot disease in sugarcane by plant growth promoting rhizobacteria. Ph.D. Thesis, TNAU, Coimbatore, India, 175 p.

[29] Wei G, Kloepper JW, Tuzun S, 1991. Induction of systemic resistance of cucumber to *Colletotrichum orbiculare* by select strains of plant growth-promoting rhizobacteria. *Phytopathology* 81, 1508–1512.

[30] Viswanathan, R., Samiyappan, R., 1999: Induction of systemic resistance by plant growth promoting rhizobacteria against red rot disease caused by *Colletotrichum falcatum* went in sugarcane. *Proceedings of Sugar Technology Association of India*, 61 24-39.

[31] Ji, G.-H., Lan-Fang, W., Yue-Qiu, H., Ya-Peng, W., and Xue-Hui, B. (2008). Biological control of rice bacterial blight by *Lysobacter antibioticus* strain 13-1. *Biol. Control* 45, 288–296. doi: 10.1016/j.biocontrol.2008.01.004.

[32] Chithrashree, Udayashankar, A. C., Chandra, N. S., Reddy, M. S., and Srinivas, C. (2011). Plant growth-promoting rhizobacteria mediate induced systemic resistance in rice against bacterial leaf blight caused by *X. oryzae pv*.
[33] Li, Q., Jiang, Y., Ning, P., Zheng, L., Huang, J., Li, G., et al. (2011). Suppression of Magnaporthe oryzae by culture filtrates of Streptomyces globisporus JK-1. Biol. Control 58, 139–148. doi: 10.1016/j.biocontrol.2011.04.013

[34] Mousivand, M., Jouzani, G. S., Monazah, M., and Kowsari, M. (2012). Characterization and antagonistic potential of some native biofilm forming and surfactant producing Bacillus subtilis strains against six pathotypes of Rhizoctonia solani. J. Plant Pathol. 94, 171–180. doi: 10.4454/jpp.v94i1.017

[35] Boukaew, S., Chanasirin, K., and Poonsuk, P. (2013). Potential for the integration of biological and chemical control of sheath blight disease caused by Rhizoctonia solani on rice. World J. Microbiol. Biotechnol. 10, 1885–1893. doi: 10.1007/s11274-013-1353-x

[36] Spence, C. A., Raman, V., Donofrio, N. M., and Bais, H. P. (2014). Global gene expression in rice blast pathogen Magnaporthe oryzae treated with a natural rice soil isolate. Planta 239, 171–185. doi: 10.1007/s11274-013-1353-x

[37] Wei G, Kloepper JW, Tuzun S. 1996. Induced systemic resistance to cucumber diseases and increased plant growth by plant growth promoting rhizobacteria under field condition. Phytopathology 86:221224

[38] P. Vidhyasekaran and M. Muthamillian (1999) Evaluation of a Powder Formulation of Pseudomonas fluorescens Pf1 for Control of Rice Sheath Blight, Biocontrol Science and Technology, 9:1, 67-74, DOI: 10.1080/09583159929910

[39] Bardin M, Ajouz S, Comby M, Lopez-Ferber M, Grallot B, Siegwart M, Nicot PC. 2015. Is the efficacy of biological control against plant diseases likely to be more durable than that of chemical pesticides? Frontiers in Plant Science 6. doi: 10.3389/fpls.2015.00566.

[40] Montano, P. F., Alias-Villegas, C., Bellogin, R. A., del-Cerro, P., Espuny, M. R., Jimenez-Guerrero, I., et al. (2014). Plant growth promotion in cereal and leguminous agricultural important plants: from microorganism capacities to crop production. Microbiol. Res. 169, 325–336. doi: 10.1016/j.micres.2013.09.011

[41] Van Loon LC, Bakker PAHM and Pieterse CMJ. 1998: Systemic resistance induced by rhizosphere bacteria. Annu Rev Phytopathol 36 453-483.

[42] Kloepper JW, Ryu C-M and Zhang SA 2004: Induced systemic resistance and promotion of plant growth by Bacillus spp. Phytopathology 94: 1259-1266.

[43] Becker, G.J., Conrath, U., 2007. Priming for stress resistance; from the lab to field. Current Opinion in Plant Biology 10, 425–431

[44] Conrath, U. et al. (2002) Priming in plant–pathogen interactions. Trends Plant Sci. 7, 210–216

[45] Chen S, Xu CG, Lin XH, Zhang Q. 2001. Improving bacterial blight resistance of ‘6078’, an elite restorer line of hybrid rice, by molecular marker-assisted selection. Plant Breeding. 120: 133-137.

[46] Ramamoorthy, V., Raghuchander, T., Samiyappan, R., 2002. Induction of defence- related proteins in tomato roots treated with Pseudomonas fluorescens Pf1 and Fusarium oxysporum f. sp. lycopersici. Plant and Soil 239, 55–68.

[47] Schneider, S., Ullrich, W.R., 1994. Differential induction of resistance and enhanced enzyme activities in cucumber and tobacco caused by treatment with abiotic and biotic
inducers. Physiological and Molecular Plant Pathology 45, 291–304.

[48] Babul RM, Sajeena A, Samundeeswari AM, Sreedhar A, Vidhyasekaran P, Seetharaman K, Reddy, M. S., 2003: Induction of systemic resistance to Xanthomonas oryzae pv. oryzae by salicylic acid in O. sativa (L.). Journal of Plant Diseases and Protection110 (5), 419–431.

[49] Choong-Min, R., Murphy, J.F., Reddy, M.S., Kloepper, J.W., 2007. A two-strain mixture of rhizobacteria elicits induction of systemic resistance against Pseudomonas syringae and Cucumber mosaic virus coupled to promotion of plant growth on Arabidopsis thaliana. World Journal of Microbiology and Biotechnology 17, 280–286.

[50] Jetiyanon, K., Kloepper, J.W., 2002. Mixtures of plant growth promoting rhizobacteria for induction of systemic resistance against multiple plant diseases. Biological Control 24, 285–291.

[51] Murphy, J.F., Reddy, M.S., Choong-Min, R., Kloepper, J.W., Li, R., 2003. Rhizobacteria mediated growth promotion of tomato leads to protection against cucumber mosaic virus. Phytopathology 93, 1301–1307.

[52] Niranjan-Raj, S., Chaluvaraju, G., Amruthesh, K.N., Shetty, H.S., Reddy, M.S., Kloepper, J.W., 2003a. Induction of growth promotion and resistance against downy mildew on pearl millet (Pennisetum glaucum) by rhizobacteria. Plant Disease 87, 380–384.

[53] Niranjan-Raj, S., Deepak, S.A., Basavaraju, P., Shetty, H.S., Reddy, M.S., Kloepper, J.W., 2003b. Comparative performance of formulations of plant growth promoting rhizobacteria in growth promotion and suppression of downy mildew in pearl millet. Crop Protection 22, 579–588.

[54] Raupach, G.S., Kloepper, J.W., 2000. Biocontrol of cucumber diseases in the field by plant growth-promoting rhizobacteria with and without methyl bromide fumigation. Plant Disease 84, 1073–1075

[55] Udayashankar, A.C., Nayaka, C.S., Niranjan-Raj, S., Kumar, B.H., Reddy, M.S., Niranana, S.R., Prakash, H.S., 2009. Rhizobacteria mediated resistance against Bean common mosaic virus strain blackeye cowpea mosaic in cowpea. Pest Management Science 65, 1059–1106

[56] Panhwar QA, Radziah O, Zaharah AR, Sariah M, Mohd Razi I (2012) Isolation and characterization of Pseudomonas syringae pv. phaseolicola from cowpea mosaic virus. J Microb Biochem Technol 7:096-102.

[57] Gupta G, Parihar SS, Ahirwar NK, Snehi SK, Singh V. 2015. Plant Growth Promoting Rhizobacteria (PGPR): Current and Future Prospects for Development of Sustainable Agriculture. J Microb Biochem Technol 7:096-102.

[58] Gordon SA, Weber RP. 1951. Colorimetric estimation of indoleacetic acid. Plant Physiology 26:192-195. doi: 10.1104/pp.26.1.192

[59] Azman NA, Sijamk, Hata EM, Othman R and Saud HM. 2017. Screening of Bacteria as Antagonist against Xanthomonas oryzae pv. oryzae, the Causal Agent of Bacterial Leaf Blight of Paddy and as Plant Growth Promoter Journal of Experimental Agriculture International 16(4): 1-15.

[60] Nautiyal, C.S. (1999) An efficient microbiological growth medium for screening phosphate solubilizing microorganisms. FEMS Microbiol. Lett. 170, 265-270

[61] Giovannoni JJ, DellaPenna D, Bennett A and Fischer R (1991).
Polygalacturonase and tomato fruit ripening. Hort. Rev. 13: 67-103

[62] Wang W, Chen LN, Wu H, Zang H, Gao S, Yang Y, Xie S and Gao X. 2013: Comparative Proteomic Analysis of Rice Seedlings in Response to Inoculation with Bacillus cereus. Letters in Applied Microbiology. 56: 208-215.

[63] Gomez LCC, Schiliro E, Valverde CA, Mercado BJ. The biocontrol endophytic bacterium Pseudomonas fluorescens PICF7 induces systemic defense responses in aerial tissues upon colonization of olive roots. Front Microbiol. 2014; 5: 427. doi: 10.3389/fmicb.2014.00427 PMID: 25250017

[64] Monteiro L, Mariano RdLR and Souto-Maior AM. 2005: “Antagonism of Bacillus spp. Against X. campestris pv. campestris.” Brazilian Archives of Biology and Technology 48: 23-29.

[65] Alexander DB and Zuberer DA. 1991. Use of chrome azurol S reagents to evaluate siderophore production by rhizosphere bacteria. Biology and Fertilization of Soil. 12: 39-45.

[66] Patten CL, Glick BR. 2002. Role of Pseudomonas putida indoleacetic acid in development of the host plant root system. Applied and Environmental Microbiology 68:3795–3801. doi: 10.1128/aem.68.8.3795-3801.2002.

[67] Yasmin S, Zaka A, Imran A, Zahid MA, Yousaf S and Rasul G. 2016: Plant Growth Promotion and Suppression of Bacterial Leaf Blight in Rice by Inoculated Bacteria. PLoS ONE 11(8): e0160688.

[68] Yasmin S, Hafeez FY, Mirza MS, Rasul M, Arshad HMI, Zubair M and Iqbal M. 2017. Biocontrol of Bacterial Leaf Blight of Rice and Profiling of Secondary Metabolites Produced by Rhizospheric Pseudomonas aeruginosa BRp3. Front. Microbiol. 8: 1895.

[69] Van Peer R, Schippers B. 1991. Plant growth responses to bacterization with selected Pseudomonas spp. strains and rhizosphere microbial development in hydroponic cultures. Canadian Journal of Microbiology 35:456-463. doi: 10.1139/m89-070.

[70] Ranjbariyan AR, Shams-Ghahtfarokhi M, Kalantari S, Razzaghi-Abyaneh M. 2011. Molecular identification of antagonistic bacteria from Tehran soils and evaluation of their inhibitory activities toward pathogenic fungi. Iranian journal of microbiology 3: 140–146.

[71] Fuhrmann, J., Wollum, A.G. Nodulation competition among Bradyrhizobium japonicum strains as influenced by rhizosphere bacteria and iron availability. Biol Fert Soils 7, 108–112 (1989). https://doi.org/10.1007/BF00292567

[72] Glick, B. R. 1995. The enhancement of plant growth by free-living bacteria. Can. J. Microbiol. 41:109-117.

[73] Kloepper JW, Lifshitz R, Zablотовicz RM. 1989. Freeling bacterial inocula for enhancing crop productivity. Trends in Biotechnology 7: 39–44. doi: 10.1016/0167-7799(89)90057-7.

[74] Okon Y, Labandera-Gonzalez CA. 1994. Improving Plant Productivity with Rhizosphere Bacteria. Commonwealth Scientific and Industrial Research Organization, Adelaide, Australia. Agronomic Applications of Azospirill.

[75] Rahman MA, Kadir J, Mahmud TMM, Rahman RA, Begum MM. 2007. Screening of antagonistic bacteria for biocontrol activities on Colletotrichum gloeosporioides in papaya. Asian Journal
of Plant Sciences 6:12–20. doi: 10.3923/ajps.2007.12.20.

[76] Aslantaş R, Çakmakçı R, Şahin F. 2007. Effect of plant growth promoting rhizobacteria on young apple tree growth and fruit yield under orchard conditions. Scientia Horticulturae 111:371–377. doi: 10.1016/j.scienta.2006.12.016

[77] Wu SC, Cao ZH, Li ZG, Cheung KC, Wong MH. 2005. Effects of biofertilizer containing N-fixer, P and K solubilizers and AM fungi on maize growth: a greenhouse trial. Geoderma 125:155–166. doi: 10.1016/j.geoderma.2004.07.003.

[78] Cakmakci R, Dönmez MF, Erdoğan Ü. 2007. The effect of plant growth promoting rhizobacteria on barley seedling growth, nutrient uptake, some soil properties, and bacterial counts. Turkish Journal of Agriculture and Forestry 31:189–199.

[79] Crowley DE (2006) Microbial siderophores in the plant rhizosphere. In: Barton LL and Abadía J (eds) Iron Nutrition in Plants and Rhizospheric Microorganisms. Springer, Dordrecht, pp 169-198.

[80] Verma VC, Singh SK, Prakash S 2011: Bio-control and plant growth promotion potential of siderophore producing endophytic Streptomyces from Azadirachta indica Juss. J Basic Microbiol 51:550–555.

[81] Manninen M, Mattila-Sandholm T. 1994. Methods for the detection of Pseudomonas siderophores. Journal of Microbiological Methods 19:223–234. doi: 10.1016/0167-7012(94)90073-6.

[82] Schenk PM, Carvalhais LC, Kazan K 2012: Unraveling plant-microbe interactions: can multi-species transcriptomics help? Trends Biotechnol 30: 177–184.

[83] Beneduzzi A, Ambrosini A, Passaglia LM. 2012. Plant growth-promoting rhizobacteria (PGPR): their potential as antagonists and biocontrol agents. Genetics and Molecular Biology 35:1044–1051. doi: 10.1590/ s1415-4757201200600020.

[84] Yu X, Ai C, Xin L, Zhou G. 2011. The siderophore-producing bacterium, bacillus subtilis CAS15, has a biocontrol effect on fusarium wilt and promotes the growth of pepper. European Journal of Soil Biology 47:138–145. doi: 10.1016/ j.ejsobi.2010.11.001.

[85] Oteino N, Lally RD, Kiwanuka S, Lloyd A, Ryan D, Germaine KJ, Dowling DN. 2015. Plant growth promotion induced by phosphate solubilizing endophytic Pseudomonas isolates. Frontiers in Microbiology 6: 745. doi: 10.3389/fmicb.2015.00745.

[86] Thakuria D, Talukdar N, Goswami C, Hazarika S, Boror R, Khan M. 2004. Characterization and screening of bacteria from rhizosphere of rice grown in acidic soils of Assam. Current Science :978–985.

[87] Fankem H, TChakounte G, Nkot L, Mafokoua H, Dowling DN, Nwaga D, Etoa FX, et al. 2015. Common bean (Phaseolus vulgaris L.) and soya bean (Glycine max) growth and nodulation as influenced by rock phosphate solubilizing bacteria under pot growth conditions. International Journal of Agricultural Policy and Research 5:242–250.

[88] Gusain YS, Kamal R, Mehta CM, Singh US, Sharma AK. 2015. Phosphate solubilizing and indole-3-acetic acid producing bacteria from the soil of Garhwal Himalaya aimed to improve the growth of rice. Journal of environmental biology 36:301–307.

[89] Yazdani M, Bahmanyar MA, Pirdashht H, Esmaili MA. 2009. Effect of phosphate solubilization microorganisms (PSM) and plant growth promoting rhizobacteria (PGPR) on yield and yield...
components of corn (Zea mays L.). World Academy of Science, Engineering and Technology 49:90–92.

[90] Sakthivel N, Sivamani E, Unnamalai N, Gnanamanickam SS. 1986. Plant growth-promoting rhizobacteria in enhancing plant growth and suppressing plant pathogens. Current Science 22–25.

[91] Mishra DS, Sinha AP. 1998. Plant growth promotion by some biocontrol agents. In: Fiftieth Annual Meeting of Indian Phytopathological Society and National Symposium on “Present Scenario in Diseases of Oilseeds and Pulses”, Maharashtra, India.

[92] Van Peer R, Schippers B. 1989. Plant growth responses to bacterization with selected Pseudomonas spp. strains and rhizosphere microbial development in hydroponic cultures. Canadian Journal of Microbiology 35:456–463. doi: 10.1139/m89-070.

[93] Kloepper JW, Leong J, Teintze M, Schiroth MN 1980: Enhanced plant growth by siderophores produced by plant growth promoting Rhizobacteria. Nature 286: 885–886.

[94] Bonaldi, M., Chen, X., Kunova, A., Pizzatti, C., Saracchi, M., and Cortesi, P. (2015). Colonization of lettuce rhizosphere and roots by tagged Streptomyces. Front. Microbiol. 6:25. doi: 10.3389/fmicb.2015.00025

[95] Shanthi AT, Vittal RR. 2013. Biocontrol potentials of plant growth promoting rhizobacteria against Fusarium wilt disease of cucurbit. ESci Journal of Plant Pathology 2:156–161.