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Streptomyces from rotten wheat straw endowed the high plant growth potential traits and agro-active compounds

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ABSTRACT

Wheat straw is a major lignocellulosic waste produced in agricultural processes and has been traditionally used as soil conditioners in the form of compost, a precursor for humus. Microorganisms play an important role in the conversion of organic waste into plant available nutrients. Thus, it is essential to isolate the potential microorganisms from rotten/decomposed agricultural waste like wheat straws and endowed the plant growth promotion (PGP) as well as antagonism behavior against phyto-pathogens. The current study was conducted to investigate the actinobacteria isolated from rotten wheat straw for PGP and antagonistic traits. Among the all isolates, three strains (UU07, UU11 and UU15) were screened and were found potential to plant growth promoting (PGP) traits (IAA, siderophore, phosphate solubilization, HCN, ammonia and AAC deaminase). Based on 16S rRNA gene sequencing, isolates were identified as *Streptomyces rochei* UU07, *Streptomyces vinaceusdrappus* UU11 and *Streptomyces* sp. UU15. Strain UU07 showed 6.0% tolerance to salt and grew well at pH 4.5–9.4, while UU11 and UU15 were moderately tolerant to salt and pH. They grew well at 28 °C but were unable to grown on temperature above 45 °C. Seedling assay and antagonism test of *S. rochei* UU07 revealed it as one of the best PGP strain and potential antagonist for *Rhizoctonia solani*. These results confirmed that rotten wheat straw can serve as a potential source for isolation of actinobacteria with PGP traits which could further be used as consortia for composting of different agriculture-waste and increase crop production.

1. Introduction

India is an agrarian country that produces a wide range of crops, including food grain, oilseed, sugarcane and other agricultural products. These crops generate significant amounts of leftover residues. The leftover residues are the noneconomical plant parts left after the harvest. Approximately 500–550 million tonnes (Mt) of crop residue is generated on-farm and off-farm annually from production of 110 Mt of wheat, 122 Mt of rice, 71 Mt of maize, 26 Mt of millets, 141 Mt of sugarcane, 8 Mt of fibre crops and 28 Mt of pulses (IARI, 2012). Wheat (*Triticum aestivum*) has been categorized as the third most widely grown cereal crop after maize and rice and covers approximately 30% of the total cereal products worldwide. Wheat crop contributes 53% of the total cereal crop residue. This huge amount of crop residue represents a potential source of renewable biomass and nutrients in agriculture.

Approximately half of the crop residue is used for feeding cattle, soil mulching, organic manure, thatching for rural homes, cooking fuel and packing material, while the other half is disposed of by burning in the field. It is estimated that about 234 million tones/year of the residue that is generated in India is available as surplus. The farmers burn the crop residues in field so that they can sow the succeeding crop on a clear land. This practice has increased in recent years because of lack of availability of low-skilled labor, mechanized farming and high costs. Burning agro-residues in the field is considered a cheap, fast and easy means of disposal of excess residues. Burning of crop residue not only results in air pollution resulting in respiratory problems, but also increases soil erosion. Further, it also increases the incidences of fog. Beri et al. (2003) estimated that 22% of rice straw and 10% of wheat straw

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are burned in-situ in Uttar Pradesh, India.

Although addition of the residue to the soil can be a solution to the problem of residue burning, long term studies have shown that it may lead to addition of toxins and allelochemicals in the soil. Therefore, it is better to use composted agricultural residue. The residue is composted by the action of lignocellulolytic microorganisms and is easier to manage. This compost is not only easier to manage, but also significantly improves soil fertility and health.

The decomposition of lignocellulosic residue is governed by physicochemical, physiological and microbiological factors. Microorganisms play an important role in composting of the residue. Wheat straw is hard due to its complicated structure and composition, which leads to a poor degradation from environment. It is less useful due to low sugar yield (Chandra et al., 2007; Kumar et al., 2009). However, several reports revealed that glycoside hydrolases (GH) enzymes are a potential tool for the processing of complex carbohydrates Lombard et al. (2005). Moreover, bacteria were more potential to decompose polysaccharides and number and diversity of GH domains in bacterial genome were reported abundantly (Medie et al., 2012; Berlemont and Martiny, 2015). So, it is important that the microbes for plant biomass degradation and composting are explored, identified and utilized. However, the information on microbes with the potential of degradation, sustainability against abiotic factors (salt, pH and temperature stress) and with PGP traits still remains scarce.

Actinobacteria are well recognized for their importance during composting. They are extensively abundant in soil and occasionally constitute a larger part of the soil microbial population. They are dominant in dry, humic and calcareous type of soil. The soil type and particularly some of the soil physical characteristics shape the population size and genus composition (Araragi, 1979). The soil organic matter content may be one of the utmost vital factors that influence the presence of actinobacteria population in soil. Actinobacteria are Gram-positive, aerobic and myceliated bacteria, specially known for nutrient cycling, PGP traits and secondary metabolites production ability. There are few reports regarding their ability of phosphate solubilization, organic acid production, siderophore production and secretion of large number of enzymes, which directly or indirectly help plant growth (Doumbou et al., 2002; Al-Aksar, 2012; Sadeghi et al., 2012). Actinobacteria can produce phytohormones (IAA) and siderophore as well as solubilize phosphate and support plant growth (Jeon et al., 2009). Their main use have been in pharmaceutical industry since 1940s but limited to PGP traits and application in agriculture (Minuto et al., 2006).

Hence, the main objectives of present study was to isolate and identify actinobacteria from rotten wheat straw and further characterize these bacteria for tolerance to environmental factors (salt, pH and temperature), PGP traits (phosphate solubilization, siderophore and indole acetic acid (IAA) production) potential.

2. Methodology

2.1. Actinobacteria isolation

Rotten wheat straw sample were collected from straw dumping site from Agethuwa (26.6999°N, 81.9388°E), Surwari (26.7060°N, 81.9630°E) and Kuchera (26.6507°N, 81.9944°E) village of Uttar Pradesh, India and processed it for actinobacteria isolation with partial modification of (Jog et al., 2012). Briefly, samples were enriched with 0.1% of Sodium dodecyl sulphate (SDS) and 2.5% of yeast extract. Then, it has been incubated for 30 min at 30 °C temperature to cultivate most abundant actinomycetes.

Further, samples were suspended in sterile dH_2O and vortexed for 10 min in 50 ml falcon tube. This was followed by centrifugation at 1000 rpm to separate the supernatant from straw. Desired dilutions of suspension (100 µl) were spread onto Humic acid Vitamin agar (pH 7.2) (gl^{-1}: Humic acid 1.2, Na_2HPO_4 0.6, KCl 2.052, $MgSO_4{\cdot}7H_2O$ 0.6, $FeSO_4{\cdot}7H_2O$ 0.012, $CaCO_3$ 0.024, agar 15). Filtered sterile Nalidixic acid ($10\,mg\,l^{-1}$), Tri- methoprim ($20\,mg\,l^{-1}$) and Cycloheximide ($20\,mg\,l^{-1}$) antibiotics were added to autoclaved media so as to eliminate the bacterial contamination and incubated it at 30 °C for 7–15 days. After that, pure actinobacterial colonies were selected morphologically and were maintained on actinobacteria agar (Hi-media) slant at 28 °C for 12–15 days. All the media and antibiotics were supplied by Hi-media, India.

2.2. Morpho-phenotypic characterization

The selected Actinobacteria morpho-phenotype characters were observed on to the following growth media: tryptone yeast medium (ISP1); yeast malt-extract medium (ISP2); oat meal medium (ISP3); inorganic salt starch medium (ISP4); glycerol asparagine medium (ISP5); pep- tone yeast iron medium (ISP6) and tyrosine medium (ISP7); and observed for their substrate utilization, colony morphology, mycelia colour, pigmentation as well as microscopic characteristics (Rungin et al., 2012).

Tolerance to pH (4.5–10) and NaCl (4.5–6.0% w/v) was examined according to Singh et al. (2015). Briefly, ISP1 broth was inoculated with 5 µl of log phase culture of tested strain and was incubated at 28 °C in orbitary shaker at 120 rpm for 5–10 days. Further, growth was measured at spectrophotometer and compared with positive control (without pH and NaCl) and negative control (un-inoculated broth). Temperature tolerance was estimated by incubation of culture inoculated actinobacteria agar plate at 28–45 °C in incubator and growth was measured for 14 days.

2.3. PGP attributes and cellulose degradation

Selected actinobacteria were tested for P-solubilizing activity on Pikovskaya agar (Pikovskaya, 1948) based on the formation of halo zone. Quantitative estimation of P-solubilization was done by using National Botanical Research Institute Phosphate broth (Farhat et al., 2015). IAA production was estimated according to Brick et al. (1991). Briefly, pure culture of selected isolates were grown in ISP1 broth with and without L-Tryptophan for 10 days at 30 °C and culture supernatant was collected at 4000 rpm by centrifugation of grown cell broth. Further, Salkowski reagent (50 ml, 35% of perchloric acid, 1 ml 0.5 M $FeCl_3$ solution) was added separately and estimated spectrophotometrically. IAA concentration in the culture supernatant was measured through extrapolate against standard curve of pure IAA (10–100 $\mu g ml^{-1}$). Production assay of Ammonia, HCN and Siderophore was carried out according to Cappuccino and Sherman (1992), Lorck (1948) and Alexander and Zuberer (1991), respectively.

ACC deaminase production was estimated by the partial modified method of Li et al. (2011). Briefly, Actinobacteria medium (HiMedia) was inoculated with tested isolates and were incubated for 7–10 days at 28 °C with 200 rpm. Further, grown culture was pellet out by centrifugation at 10,000 rpm for 10 min and washed with 2 ml of liquid DF-medium. After that, washed pellet was mixed with 2 ml DF mineral medium containing ACC substrate whereas without pellets was obliged as control and all were incubated at 28 °C with 200 rpm for 6 days. Afterward, 100 µl of supernatant from each sample was taken after harvesting at 12,000 rpm for 10 min and diluted again with 1 ml of liquid DF medium. In 96-well tissue culture plate (BRAND™), 60 µl each of diluted supernatant was mixed with 120 µl of ninhydrin reagent, covered the plated and placed in to water bath (110 °C) for 30 min. Liquid DF medium filled well was used as a blank. Further, colour change (dark purple) was recorded as ACC deaminase positive. Quantification of ACC deaminase was done by the measurement of absorbance at 570 nm with spectrophotometer. Isolates with perceptibly reduced colour depth and lower absorbance was compared to DF-ACC medium without inoculation were considered as ACC utilizing isolates.

Confirmation of cellulose-degrading ability of bacterial isolates was performed according to Lu et al. (2006) with partial modification.

Briefly, 5 µl of log phase culture of tested strain were spotted on to cellulose Congo-Red agar media with the following composition: KH_2PO_4 0.5 g, $MgSO_4$ 0.25 g, cellulose 2 g, agar 15 g, Congo-Red 0.2 g, and glycerol 10 ml; distilled water 1 L and at pH 6.8–7.2. Discoloration of congo-Red was showed as an indicator for cellulose degradation in growth media which provides the basis for degradation of cellulose.

2.4. Molecular Identification

Genomic DNA of tested strains were isolated through Wizard® Genomic DNA Purification Kit (Promega) and visualized on 0.8% horizontal agarose gel by gel electrophoresis. Nearly full-length 16S rRNA gene was amplified using actinobacteria specific primer pair, 243 f (5′-GGATGAGCCCGCGGCCTA-3′) and 1378r (5′-CGGTGTGTACAAGGC CCGGGAACG-3′) (Heuer et al., 1997). Amplified gene product was examined in 1.2% agarose and further PCR products were purified by gel-elution method (Nucleo-Pore gel elution kit). Obtained PCR products were further sequenced with the same primers and data was curated at Bioedit software version 7.2.1. Similarity search and annotation of sequence was carried out by NCBI-$BLAST_N$ program and was deposited in to NCBI data base. Further, tested sequence was aligned with reference sequences (downloaded from NCBI data base) by ClustalW program in the software MEGA version 5.0 (Tamura et al., 2011). Phylogenetic study of tested strain was done by Maximum Composite Likelihood model and tree topology was analysed at 1000 bootstrap replication and 64238 seed value.

2.5. Seedling assay

PGP potential of strain *S. rochei* UU07 was evaluated by seedling assay of wheat (*Triticum aestivum*) with and without inoculation. Briefly, surface sterilized, healthy wheat seeds were inoculated with log phase liquid culture of UU07 and placed in sterilized petri-plate containing 0.5% water based agarose and covered with sterilized blotting paper sheet. Untreated seeds (without culture) were used as control. After that, experimental petri-plates were incubated in laboratory at room temperature. After 16 days, root numbers, root length, shoot length and plant weight was observed and compared with control to estimate the PGP potential of UU07. Total 15 seeds were placed in each plate and experiment was carried out in three replicates.

2.6. Antagonism effect assay

A round mycelial plug (5 mm) of soil-borne fungi, *Rhizoctonia solani* (Taken from Dr. Alok R. Rai, Kamptee college, Nagpur) was placed on one side of a potato dextrose agar (PDA, HiMedia) and 5 µl of UU07 cultured broth was spread on the other side of the medium. Plate was incubated at 28 °C for 7–12 days. 100 µl of Cell-free culture supernatant (CFCS) was also dropped nearby (2.0 cm) fungal disc into wells (0.5 mm) and incubated at above given conditions. During the growth, antagonism behavior of tested strains as well as CFCS was confirmed by zone of inhibition formed along with the cultivation of mycelia. All the experiments were performed in triplicate.

3. Results

Based on the phenotypic characteristics, 17 actinobacteria were isolated from rotten wheat straw of three different dumping sites (Fig. 1). All of them were found to be Gram-positive, filamentous rods and pigment producers. The morphological and cultural characteristics of the isolates were examined using different culture media and three distinct isolates UU07, UU11 and UU15 were selected for further study (Fig. 2). Interestingly, all the three isolates grew well on ISP1 and ISP2 medium while slow growth was observed at ISP3 and ISP4. ISP5 and ISP6 showed fast growth (5 days) but colonies dried after 12 days, In ISP7, dried colonies were observed after 8 days. All were able to produce the diffusible pigment after 8–10 days after incubation at 30 °C.

Sampling of rotten wheat straw

Fig. 1. Sampling of rotten wheat straw.

Tolerance to abiotic stress was evaluated based on the growth condition. Strain UU07 showed salt tolerance. It grew well with a NaCl concentration range of 2–6%, while UU07, UU11 and UU15 showed moderate response at 6% and failed to grow on 8% (Table 1). UU07 showed high growth at pH range 4.5–8.5 but moderate and slow growth at pH 9.5 and 10 respectively. Strain UU11 and UU15 revealed the similar tolerance to pH as they grew well with pH 4.5–8.5 while showed slow growth and failed to grow at pH 9.5 and 10 respectively (Table 1). Temperature tolerance was measured by plate growth assay on to actinobacteria agar. All isolates were able to grow at temperature 28–40 °C except for the isolate UU11 (Table 1).

Qualitative analysis of culture supernatant revealed that selected actinobacteria were able to produce significant IAA with tryptophan but failed to produce in the absence of L-tryptophan. Quantification assay of IAA showed that UU07, UU15 and UU11 produced $74.13 \pm 1.32\ \mu g\ ml^{-1}$, $68.05 \pm 1.14\ \mu g\ ml^{-1}$ and $70.12 \pm 1.07\ \mu g\ ml^{-1}$, respectively. Moreover, qualitative and quantitative assay of phosphate solubilization represented the similar pattern of IAA trait and quantified as 89.98 ± 1.41, 76.72 ± 1.32, $81.54 \pm 1.14\ mg^{-100\ ml}$ in UU07, UU11 and UU15 respectively. Siderophore, HCN and ammonia production was high in all the tested isolates. Siderophore production was detected by forming clear orange halo zone around the colonies on CAS agar media. All the three isolates showed the efficient HCN production as illustrated by a deep red colour on the filter paper. Ammonia positive characteristics were displayed potentially by UU07 followed by UU11 and UU 15 after conversion of brown to yellow colour of culture filtrate, peptone water and Nessler's reagent mixture. Overall, the selected actinomycete isolates reveled strengthened survival against different stress conditions as well as had PGP traits (Table 1). All the tested strains were found positive and variable to ACC deaminase test. UU07 was noticeable to ACC deaminase production ($1.47\ mmol^{-1}$) while other 2 strains UU11 and UU15 were moderate ($1.03\ mmol^{-1}$ and $0.94\ mmol^{-1}$).

Cellulose degradation test of screened isolates showed high potentiality against cellulose during the incubation of spotted culture on minimal growth medium supplemented with synthetic cellulose. Decolorizing zone of congo-red was found in UU15, UU07 and UU11.

The BLAST annotation results of 16S rRNA gene sequence of strain UU07, UU11 and UU15 designated the strains as *Streptomyces rochei*, *Streptomyces vinaceusdrappus*, and *Streptomyces sp.*, respectively. Curated sequences of UU07, UU11 and UU15 were deposited to the NCBI GenBank under the accession number MH890455, MH890456 and MH890457. Phylogenetic tree was generated on Neighbour-Joining method for selected strains along with the closest lineages of the genus *Streptomyces* (Fig. 3). The constructed phylogenetic tree for partial 16S rRNA (> 1400pb) gene sequence of UU07, UU11 and UU15, clustered with the same clade. UU07 revealed highest closeness to *S. rochei* NR116078 followed by *S. plicatus* NR112357 and *S. geysiriensis* NR 112459. Though, UU11 and UU15 grouped in to subclade with *S.*

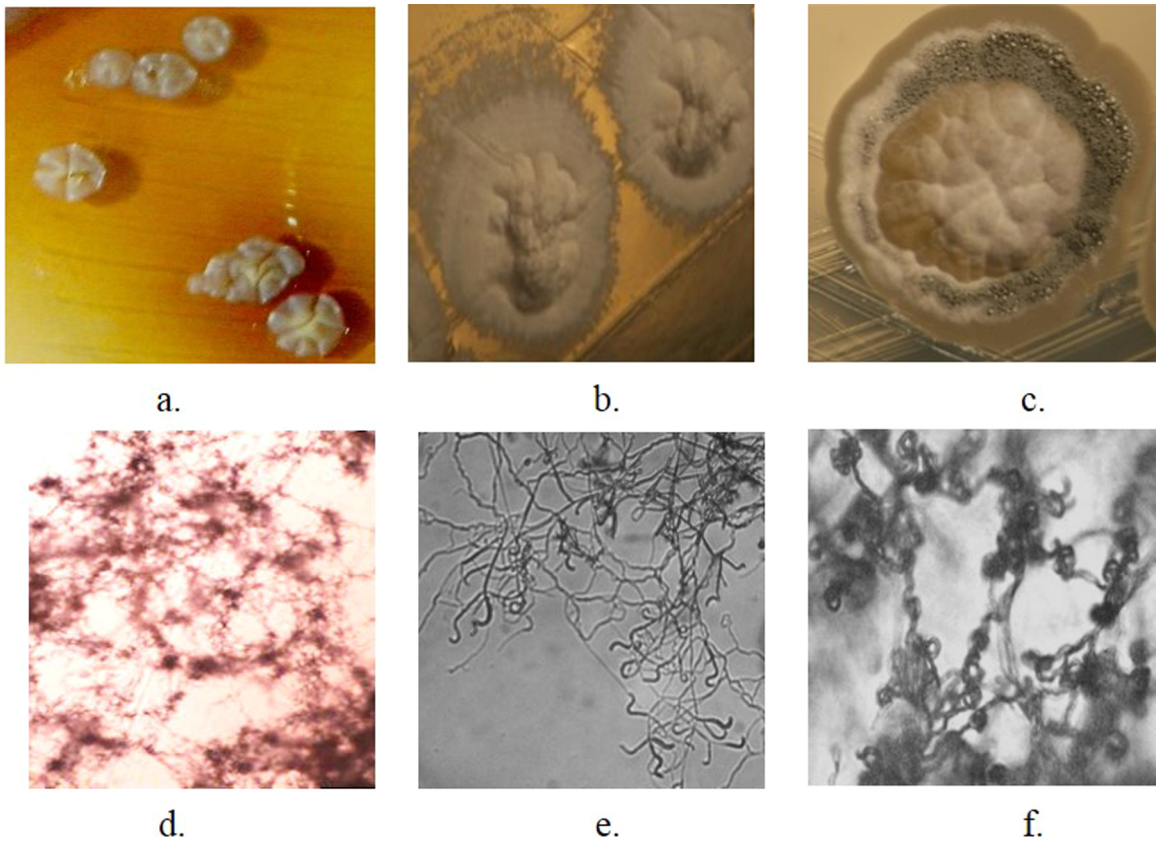

Fig. 2. (a, b, c, d, e and f). Colony morphology of tested strains: UU07 (a & d), UU11 (b & e) and UU15 (c & f).

Table 1
Physiological and Plant growth Promotion Characteristics.

Characteristics	*S. rochei* UU07	*S. vinaceusdrappus* UU11	*Streptomyces sp.* UU15
Salinity (% NaCl)			
2	+ + +	+ +	+ +
4	+ + +	+ +	+ +
6	+ +	+	+
8	–	–	–
pH Level			
4.5	+ + +	+ +	+ +
5.5	+ + +	+ +	+ +
6.5	+ + +	+ + +	+ + +
7.5	+ + +	+ + +	+ + +
8.5	+ + +	+ +	+ +
9.5	+ +	+	+
10.0	+	–	–
Temp. Level (°C)			
25	+ +	+	+
28	+ + +	+ +	+ +
30	+ + +	+ + +	+ + +
35	+ + +	+ + +	+ + +
38	+ +	+ +	+ +
40	+ +	–	+
IAA (μg ml^{-1})	74.13 ± 1.32	68.05 ± 1.07	70.12 ± 1.28
P-solubilization ($mg^{-100\ ml}$)	89.98 ± 1.41	76.72 ± 1.32	81.54 ± 1.14
Siderophore production	+ + +	+ +	+ + +
HCN production	+ +	+ +	+ + +
Ammonia production	+ + +	+ +	+ +
Cellulase production	+ + +	+ +	+ + +
ACC Deaminase $mmol^{l}$	1.47 ± 0.18	1.03 ± 0.09	0.942 ± 0.04

Note: (+) production in normal level (+ +) production in medium level, (+ + +) production in high level.
Values are expressed as Mean ± Standard Error.

vinaceusdrappus NR043383 and *S.mulabilis* NR044139 but were distant from other *Streptomyces* like *S. griseus* ATCC10137 (Y15501), *S. lydicus* ATCC21437 (X79853), *S. virginieae* etc. (Fig. 3).

Based on above results, *S. rochei* UU07 was found most promising with respect to phenotypic a well as PGP traits. Hence, UU07 was employed for antagonism assay against *R. solani,* a very common soil born fungal pathogen. Formation of clear zones between the *S. rochei* UU07 and *R. solani* fungal isolate revealed it potential for antagonism (Fig. 4).

T. aestivum seedling assay revealed that selected strain had capabilities to enhance the plant growth and development of treated seed with respect to control (Fig. 5). After 16 days, the value of root length (cm), shoot length (cm), root numbers and fresh weight (gram) of control was 3.72, 8.76, 4.17 and 10.74 respectively while the value of seeds treated with the UU07 was 4.72, 12.94, 4.82 and 14.55, with respect to control. Antagonism effects (*in vitro*) of log phase UU07 culture against soil pathogenic fungi *R. solani* was confirmed by the formation of inhibition zones between the isolate and the fungi (Fig. 5) while, CFCS was not pronounced for antagonism effects. Fungal inhibition increased with the period of incubation.

4. Discussion

Wheat straw biomass is made up of complex lignocellulosic materials in which rhamnose, fucose, arabinose, xylose, mannose, galactose, glucose, uronic acid (as anhydro sugar equivalents) and various important cell wall phenolics with a range of diferulic acids, coumaric acid and lignin are present which make it difficult to decompose (Collins et al., 2014). Thus, the need to decipher the hidden bacterial treasure for the composting it has made this study vital. A total of 17 isolates were detected and recognized as actinobacteria by morphological and microscopic examinations. Morphologically, 3 distinct types of strains, UU07, UU11 and UU15 were procured and identified as *Streptomyces*

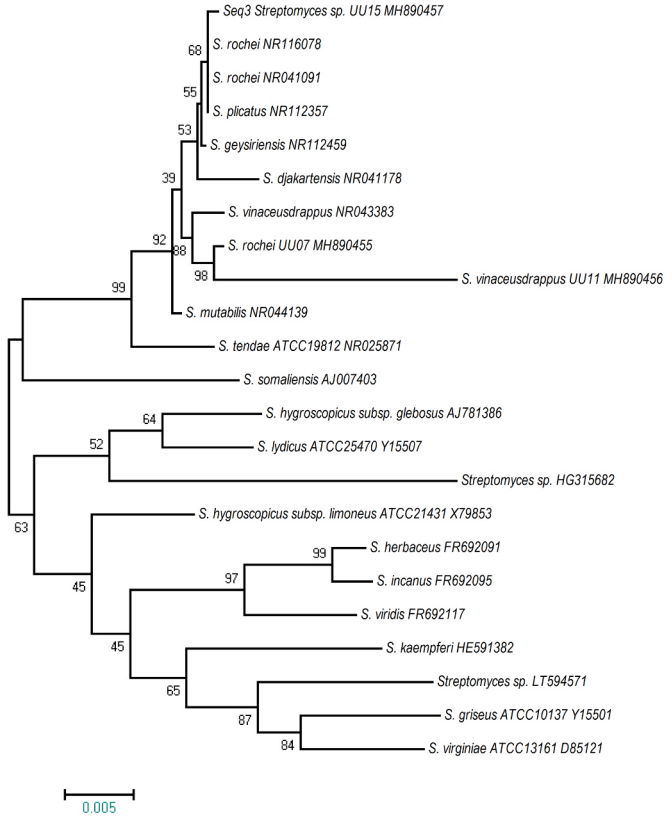

Fig. 3. Phylogeny showing the relationships between strains UU07, UU11 and UU15 and related *Streptomyces* based on 16S rRNA gene sequences alignment. Scale bars represent 0.1 substitutions per site. Significant bootstrap probability values are indicated at the branching points (only values greater than 80% over 1000 replicates are shown).

rochei, *Streptomyces vinaceusdrappus*, and *Streptomyces spp*., by 16S rRNA sequencing, respectively. Further, they were assessed for sustainability against the abiotic factors (salt, pH and temperature). Growth and

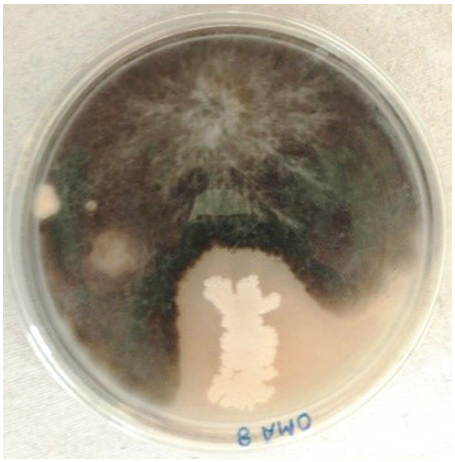

Fig. 5. Antagonism effect of *S. rochei* UU07 against *R. solani*.

survival of bacteria were also greatly influenced by the pH of the environment.

Streptomyces are neutrophilic and are grew well between pH 6.0 and 8.0 (Kim et al., 1992). In our study, all three isolates displayed normal to moderate growth on pH 8.5–9.5 while at 10.0 only UU07 survived. Kontro et al. reported that *Streptomyces spp.* grew and sporulated between pH 4.0 and 11.5. Also, highly alkaline and thermotolerant novel xylanase from *Streptomyces spp.* was identified and characterized by Thomas et al. (2013). The temperature tolerance of tested strain were 28–38 °C while at 40 °C UU11 and UU15 failed to grow and UU07 moderately survived. On the contradictory, James et al. (1991) reported that 45 °C was optimum temperature of *Streptomyces thermoviolacus.* However, Islam et al. (2009) found that *Streptomyces* grew well only at 30 °C. Halo-tolerance traits of tested strains indicated that they profoundly flourished at 4% NaCl. However, their growth was moderate at 6.0%. Prasad et al. (2013) reported that *Streptomyces* isolated from India failed of grow beyond 6.0% NaCl concentration, just in line with our study. Moreover, the preferential NaCl concentration for *Streptomyces* was 3.0% was reported from Malaysia (Hamid et al., 2015).

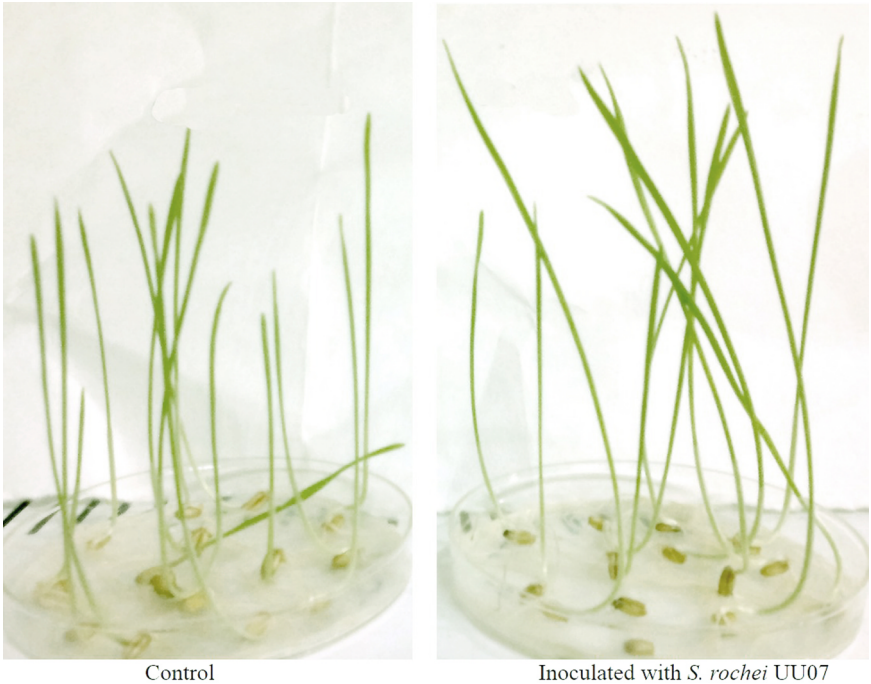

Fig. 4. Seedling assay of Wheat, inoculated with *S. rochei* UU07.

PGP effects including root development by soil microbes were reported by many researchers (Yang et al., 2018; Yuan et al., 2018; Singh et al., 2015). El-Tarabily (2008) reported that actinobacteria synthesize IAA which helps in adventitious root growth and facilitates to absorb the large volume of nutrients and water. Here, the selected isolates efficiently produced IAA (Table 1). Phosphate solubilization is a common and most promising traits for soil fortification. The phosphate solubilization activity was reported as 83.3, 58.9, and 39 mg/100 ml by *Streptomyces cavourensis*, *Streptomyces griseus*, and *Micromonospora aurantiaca*, respectively which is similar to our finding (Table 1). Production of ammonia and hydrogen cyanide has been reported in several actinobacteria (Marques et al., 2010; Yandigeri et al., 2012; Kaur et al., 2013). In this study, all the selected isolates were able to produce ammonia and HCN which makes these more beneficial for PGP application because synthesized ammonia can helps in protein synthesis and it supplied the nitrogen to the host plant. Moreover, production of ammonia can serve as a stimulating factor for the virulence of opportunistic pathogens. Tan et al. (2010) reported that plant growth development and phytopathogen antagonism can be directly influenced by siderophore. The studied strains were very good producers of siderophore. It is well established that plant growth promotes by lowering the ethylene levels of plant through ACC deaminase (Hardoim et al., 2008; Glick, 2014) and mainly bacteria played the main role in decreasing the ethylene inhibition of numerous plant processes (Husen et al., 2011). Glick (2005), also reported that bacteria can increase root growth by lowering endogenous ACC levels. Remarkably, all the strains were found positive to ACC deaminase, while previous reports revealed the high amount of ACC-D production as $4.483 \pm 2.91\ mmol^{-1}$, $3.42\ mmol^{-1}$ by *Pseudomonas fluorescens*, (Glick et al., 2007) and $1.81\ mmol^{-1}$ by *Streptomyces djakartensis* TB4 (Anwar et al., 2016a, 2016b) with respect to studied isolates.

Facilitation of plant growth by soil bacteria is well known (Glick, 2014) and application of PGP bacteria for crops growth enhancement, including increased seed emergence, yields, stress tolerance and disease control have been widely studied (Kloepper et al., 1991; Gururani et al., 2013; Singh et al., 2015; Anwar et al., 2016a, 2016b). Further, *Streptomyces* strains have been widely described for their PGP potential (El-Tarabily, 2008; Yandigeri et al., 2012; Anwar et al., 2016a, 2016b). Similarly, our seedling assay results of inoculated wheat seeds with selected strain of *Streptomyces* revealed elevated significant plant growth by increased plant root length, root numbers, plant shoot length, and fresh plant weight with respect to un-inoculated control seeds. PGP microbes also have the potential to interfere the plant pathogen growth. *S. rochei* UU07 has been employed against the most communal soil born fungal pathogen *R. solani* and found to be antagonistic positive which could be due to the secretion of some antimicrobial substances like chitinolytic enzymes, cellulase, HCN, siderophore (Chung et al., 2008; Kunova et al., 2016; Tian et al., 2017).

Lignocellulose degradation is essential for maintaining high ability of decomposition of wheat straw and other agri-wastes as well as in biogas digesters. The tested strains were found highly efficient in cellulose degradation which indicated the presence of functional genes and gene clusters of dominant cellulose degradation. Liang et al. (2014) also reported that *Paenibacillus terrae* is capable of Cellulase enzyme production. Presence of glycoside hydrolases (GH) gene in the bacterial genomes for targeting cellulose, xylan, and chitin was also review profoundly by Talamantes et al. (2016).

5. Conclusion

We have isolated actinobacteria, which have potential PGP and antagonistic activity. Out of all isolates, the three stains namely UU07, UU11 and UU15 showed several beneficial PGP properties (i.e., IAA, siderophore, phosphate solubilization, HCN, ammonia and AAC deaminase). Further, we have done molecular characterization of these three strains based on 16S rRNA gene. Moreover, among three isolates, *S. rochei* (UU07) have shown the best PGP performance and found potential antagonist against *R. solani*. The seedling result supports the *S. rochei* UU07 as a notable PGP strain with antagonism potential that might be referred it as bioinoculant for wheat and other poaceae family.

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Conflict of interest statement

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Author contributions

RPS, GM and IL conceived and designed the experiments. RPS, GM, IKM, AKR and PKT performed the experiments. RPS, GM, IKM and AKR analyzed the data RPS, GM, and NKM prepared the figures and wrote the paper. All authors reviewed the manuscript.

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