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Antagonistic Potential of *Bacillus* and *Pseudomonas* Isolates from Wheat Rhizosphere against *Gaeumannomyces graminis* var. *tritici* and *Bipolaris sorokiniana*

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ABSTRACT

Take-all and common root rot diseases are the important diseases of wheat that are caused by two fungi, *Gaeumannomyces graminis* var. *tritici* and *Bipolaris sorokiniana*, respectively. In this study, we aimed to isolate rhizobacteria *Bacillus* and *Pseudomonas* from wheat rhizosphere and evaluate their antagonistic effect against *G. graminis* var. *tritici* and *B. sorokiniana*. Thirty six soil samples from wheat rhizosphere were cultured and isolates were identified by bacteriological and biochemical tests. Using the dual culture method antagonistic effects of all the *Bacillus* and *Pseudomonas* isolates were tested against the target fungal pathogens. The isolates were also evaluated for volatile metabolites and siderophore production. The polymerase chain reaction assay was performed for accurate identification of the isolates. Fifty seven *Bacillus* and *Pseudomonas* strains were isolated. Of the isolates, 19 strains had antagonistic effect against the tested pathogens. *Bacillus* isolates had a greater antagonistic effect against the tested fungi than *Pseudomonas* isolates. In addition, *Bacillus* isolates showed a greater antagonistic effect against *B. sorokiniana* than *G. graminis* var. *tritici*. In this study, only 7 isolates were able to produce volatile metabolites. Siderophore production was detected in 3 strains of *Pseudomonas* isolates. Based on the 16S rRNA analysis, the 3 strains of *Bacillus* and *Pseudomonas* were identified as *Bacillus megatrium*, *Bacillus subtilis* and *Pseudomonas aeruginosa*. According to majority of the isolates belonged to the *Bacillus* strains and some of them had a good antagonistic activity against *G. graminis* var. *tritici* and *B. sorokiniana*, they are promising for biocontrol of these important pathogens.

1. Introduction

Wheat is the most abundant crop in the world and is the staple food of many countries (Delcour and Hosney, 2010). Every year, a significant amount of this crop is lost in the field and storage due to various factors, including diseases. About 200 diseases of wheat have been

reported that the most important causes of these diseases are fungi (Akbarpour & behbodi, 2019).

Among the important diseases of wheat are take-all and common root rot diseases, caused by two fungi, *Gaeumannomyces graminis* var. *tritici* and *Bipolaris sorokiniana*, respectively. The common root rot disease causes severe

damage to wheat and barley crops in hot and humid regions of the world every year (Gupta et al., 2018). In recent years, this disease has become one of the most important factors limiting wheat production in various parts of Asia. It is observed in countries such as Pakistan, India and Central Asia with an area of 12 million hectares and the global area of infection of wheat fields with this disease is estimated about 25 million hectares (Acharya et al., 2011).

The take-all is a root and crown rot disease of wheat that has been reported from warm regions of the world such as Australia, Japan, parts of Europe, North and South America, as well as temperate regions, the Middle East and warm tropical heights (Khezri, 2017) and is referred to as the global wheat disease (Kwak & Weller, 2013). In Iran, the disease was first reported in the spring of 1989 from wheat fields in Dasht-e Naz, Sari and other areas of Mazandaran province and Gorgan by Forootan et al. After that, wheat Take-all disease has been reported from most provinces of the country (Rajabi & Behrozin, 2003).

The primary approach for control of plant fungal diseases is use of chemical fungicides but they increase the cost of production, promote resistance, and lead to environmental pollution (Wang et al., 2018). These days due to the lack of public acceptance of these chemicals, resistance of some fungal pathogens and the high cost of producing new chemicals, they are being phased out from use (Heydari & Pessarakli, 2010). *Rhizobacteria* are an alternative to chemical fungicides because of playing a key role in crop production by means of siderophore and antibiotic production, antagonism to soilborne root pathogens, phosphate and potassium solubilization (Wang et al., 2018). There have been many reports of promising biocontrol potentials of *rhizobacteria* such as *Bacillus subtilis*, *Pseudomonas fluorescens* and *Streptomyces* spp. (Quecine et al., 2008, Khezri, 2017, Lagzian et al., 2013). Therefore, according to Golestan province is one of the most important areas for wheat cultivation and common root rot and take-all diseases are problems of wheat growers in this region, in this study, we aimed to isolate rhizobacteria *Bacillus* and *Pseudomonas* from wheat rhizosphere and evaluate their antagonistic effect against *G. graminis* var. *tritici* and *B. sorokiniana*.

2. Materials and Methods

2.1. Sample Collection

Thirty six soil samples from wheat rhizosphere of farming fields around Kalaleh, Gulikesh, Minoodasht, Gonbad Kavous, Azadshahr, Khanbebein, Aliabad and Fazelabad (located in Golestan province) were collected randomly and transferred to a sterile zip lock bag. The samples were labeled and sent to laboratory of Gorgan Branch of Islamic Azad University.

2.2. Bacterial isolation and identification

Then 100 g of each soil sample was poured into 200 cc of sterile distilled water and placed on a shaker for 15 min with a slow motion, then left motionless for 5 min and after the sediments rest, 100 µl of the suspension was cultured on nutrient agar medium containing 1% sucrose and King B. The plates were incubated at 25°C for 5 days (Schaad et al., 2001). All isolates were evaluated by Gram staining, oxidase, sporulation and examined also for fluorescence under UV light. Standard biochemical tests given in Bergey's manual of determinative bacteriology and laboratory guide by Schaad et al. were used to identify the bacterial isolates (Bergey's Manual of Determinative Bacteriology, 2000, Schaad et al., 2001).

2.3. Detection of Antagonistic Effect

2.3.1 Dual Culture Method

Antagonistic effects of all the *Bacillus* and *Pseudomonas* isolates were tested against *G. graminis* var. *tritici* and *B. sorokiniana* using the dual culture method. The isolates were streaked as a streak line with a loopfull of 2 day-old culture on potato dextrose agar (PDA) plates, and incubated for 48 h. A mycelial disc (5 mm in diameter) of the tested fungus was placed at a distance close the other edge of the plate and incubated at 30°C for 5 days. After that, inhibition zones (the distance among the edge of antagonistic bacterial growth and the edge of fungal growth) were measured. The experiment was repeated three times for each fungus (Abo-Zaid et al., 2020) (Figure 1).

2.3.2. Screening for volatile metabolites production

The bacterial isolate was cultured uniformly on PDA plate. A mycelial disc (5 mm in diameter) of the tested fungus was placed in another plate containing the PDA medium. Under sterile condition, the plates containing bacteria and fungi were placed on top of each other in such a way that the plate containing the fungus is placed on top. The area around the plates is completely surrounded by parafilm. In the control plate instead of bacteria, a drop of sterile distilled water was placed. The plates were incubated at 25° C for 7 days, after that the fungal colony in control and treatment petri dishes were compared (Fiddaman & Rossal, 1993) (Figure 2).

2.4. Screening for Sidrophore production

To perform this test, all *Pseudomonas* isolates were checked for their ability to produce siderophores. Detection of siderophores was achieved on CAS agar plates, the color changes from greenish blue to orange indicated a positive siderophore production. The *Pseudomonas* isolates were grown in succinic medium contained 4 g succinic acid; 6 g KH₂PO₄; 4 g K₂HPO₄; 0.2 g MgSO₄·7H₂O; 1 g (NH₄)₂SO₄ and dH₂O up to 1000 mL for 24 h at 200 rpm and 30 °C. After that, 10 mL of each culture was centrifuged at 10,000 rpm for 10 min and then the supernatant was filtrated throughout a 0.2 μ syringe filter. Then, 80 μL of the culture filtrate was poured in each 5-mm-deep wells punched into CAS agar plate. The plates were incubated at 30 °C for 24 h and the presence of siderophores was detected visually (Abo-Zaid et al., 2020) (Figure 3).

2.5. Molecular Identification of Bacterial Isolates

Preliminary identification of the isolates was carried out according to standard cultural and biochemical tests. The PCR assay was used for accurate identification of the isolates possessing higher antagonistic activity. To do PCR, the bacterial isolate was cultured in nutrient broth overnight. Then, the genomic DNA from overnight culture of the isolate was extracted using Geno Plus™ Genomic DNA Extraction Miniprep System (Viogene, China). The qualification and quantity of the extracted DNA was determined by agarose gel electrophoresis (1%). The genomic DNA was used as a template for 16S rDNA gene amplification using universal primers. Amplification was carried out in 25 μL volumes consisting of 0.5-μL Taq DNA polymerase, 5 μL of × 5 reaction buffer (Bioline, UK), 1 μL of each primer, 1 μL of template DNA, and 16.5 μL of DEPC water. The PCR amplification was performed with 30 cycles of denaturation at 94°C for 30 s, annealing at 56 °C for 30s, and extension at 72°C for 30 s. The initial denaturation and final extension were 94 °C for 3min and 72°C for 10min respectively. The primers used in this study are summarized in Table 1. The 16S rDNA genes were successfully amplified with universal primers and expected fragments with 1500 bp were observed on 1% agarose gel. Then, the purified PCR products were sent to Macrogen (South Korea) for sequencing. The obtained nucleotide sequences were searched for homology in the NCBI nucleotide database using BLAST tool. The 16S rRNA gene sequences were aligned against the reference nucleotide sequences retrieved from GenBank (Ebrahimi and Ahani Azari, 2016).



Figure 1. Inhibitory effect of the antagonistic isolate against *B. sorokiniana*

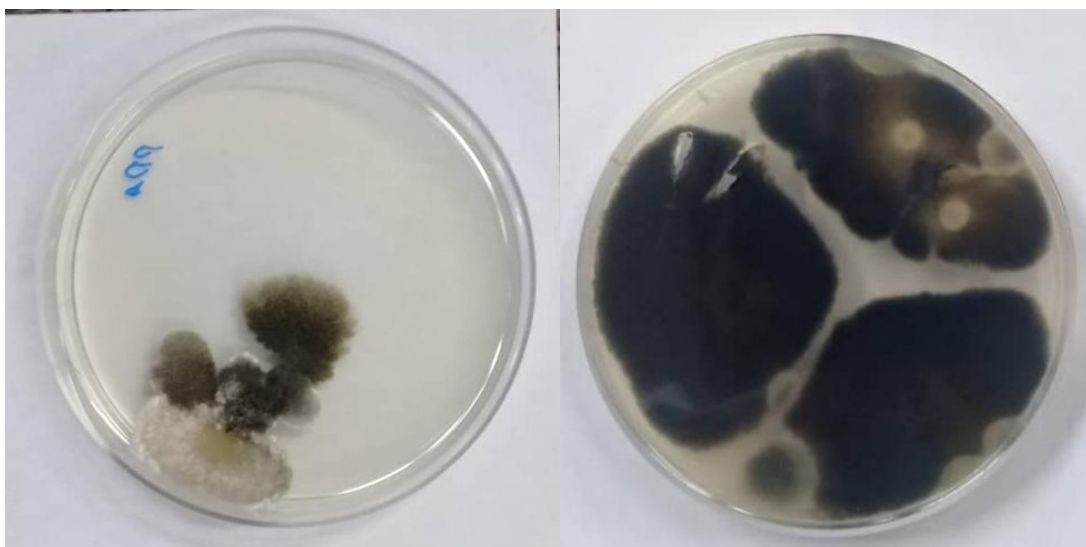


Figure 2. Qualitative assay of volatile metabolites production of the isolates. Right: control, Left: treatment petri

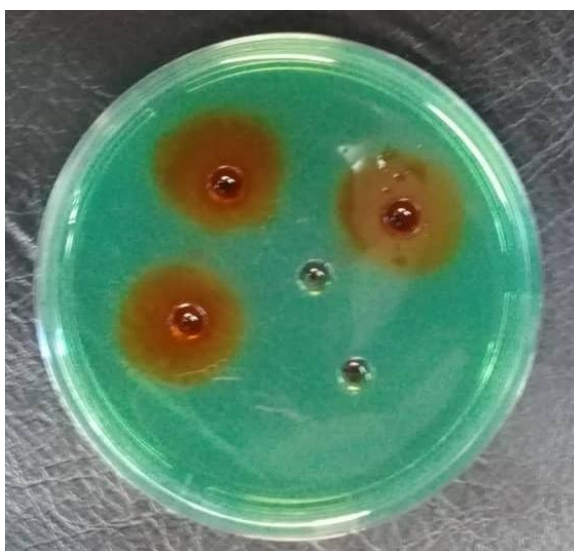


Figure 3. Qualitative assay of siderophore production on CAS agar plates using supernatant of *Pseudomonas* isolates

Table 1. Primers used in this study (Weisburg et al., 1991).

Primer name	Primer sequence	PCR product
16S-Forward	5'-AGAGTTTGATCCTGGCTCAG 3'	1500bp
16S-Reverse	5'-ACGGCTACCTTGTTACGACTT3'	

3. Results

Based on the preliminary identification, 57 *Bacillus* (43) and *Pseudomonas* (14) strains were isolated from the samples. Of the isolates, 19 strains (12 *Bacillus* and 7 *Pseudomonas*) showed inhibition zones and had antagonistic effect against the *G. graminis* var. *tritici* and *B. sorokiniana*. Overall, *Bacillus* isolates had a greater antagonistic effect against the tested fungi than *Pseudomonas* isolates. In addition, *Bacillus* isolates showed a greater antagonistic effect against *B. sorokiniana* than *G. graminis* var. *tritici*. In this study, only 7 isolates (2 *Bacillus* and 5 *Pseudomonas* strains) were able to produce volatile metabolites and inhibit the growth of fungi by this mechanism. In addition,

sidrophore production was detected in 3 strains of *Pseudomonas* isolates (A1, A2 and A3) that showed a higher antagonistic effect against each of the target fungal pathogens.

Among the isolates, the 3 strains of *Bacillus* (R1 and R10) and *Pseudomonas* (A2) with a higher antagonistic effect against each of the tested fungus were selected and identified based on the 16S rRNA gene sequence. After sequencing of 16S rRNA gene, isolates R1, R10 and A2 were identified as *Bacillus megatrium*, *Bacillus subtilis* and *Pseudomonas aeruginosa* strains, respectively.

Table 1. Characteristics and mean diameter of growth inhibition zone (mm)

Location	Isolates	<i>G. graminis</i> var. <i>tritici</i>	<i>B. sorokiniana</i>
Kalaleh	<i>Bacillus</i> spp. R1	19.8	22.5
Kalaleh	<i>Bacillus</i> spp. R2	16.5	17.2
Azadshahr	<i>Bacillus</i> spp. R3	16.6	17.5
Aliabad	<i>Bacillus</i> spp. R4	17.4	19.2
Aliabad	<i>Bacillus</i> spp. R5	19.6	20.7
Minoodasht	<i>Bacillus</i> spp. R6	14.4	15.2
Fazelabad	<i>Bacillus</i> spp. R7	12.4	13.8
Gulikesh	<i>Bacillus</i> spp. R8	14.7	15.4
Gonbad Kavous	<i>Bacillus</i> spp. R9	18.7	19.6
Gonbad Kavous	<i>Bacillus</i> spp. R10	20.3	22.1
Gonbad Kavous	<i>Bacillus</i> spp. R11	17.1	18.2
Khanbebein	<i>Bacillus</i> spp. R12	16.2	16.8
Gonbad Kavous	<i>Pseudomonas</i> spp. A1	13.5	13.8
Gonbad Kavous	<i>Pseudomonas</i> spp. A2	15.6	15.1
Gonbad Kavous	<i>Pseudomonas</i> spp. A3	13.6	14
Kalaleh	<i>Pseudomonas</i> spp. A4	12.8	13.2
Fazelabad	<i>Pseudomonas</i> spp. A5	12.4	12.6
Minoodasht	<i>Pseudomonas</i> spp. A6	11.6	12.9
Gulikesh	<i>Pseudomonas</i> spp. A7	11.8	12.4

4. Discussion

According to take-all and common root rot diseases are the main diseases of wheat and many wheat fields are affected by these diseases in the country, we aimed to isolate and identify *Bacillus* and *Pseudomonas* from wheat rhizosphere in Golestan province and evaluate their potential for antifungal activity against *G. graminis* var. *tritici* and *B. sorokiniana*. Nineteen *Bacillus* and *Pseudomonas* isolates showed antagonistic effect that further examined for volatile metabolites and siderophore production. Among the isolates, the 3 strains of *Bacillus* (2) and *Pseudomonas* (1) with a higher antagonistic effect against each of the tested fungus were analyzed based on the 16S rRNA and showed more than 90% relatedness to *Bacillus megaterium*, *Bacillus subtilis* and *Pseudomonas aeruginosa*.

In consistent with our study, Joulideh et al. reported that the strong antagonist bacteria against *G. graminis* var. *tritici* mainly belonged to the genera *Erwinia* and *Bacillus*, *Pseudomonas* (Joulideh et al., 2012). In addition, in Khezri research all 27 studied strains of *Bacillus subtilis* were able to inhibit the growth of *G. graminis* var. *tritici* (Khezri, 2017). In a research by Babaeipour et al. antagonistic effect of *Bacillus* (*B. subtilis* and *B. pumilus*), *Pseudomonas* (*P. fluorescent*, *P. putida* and *P. aeruginosa*) and *Chromobacterium* sp., separated from wheat rhizosphere against *G. graminis* var. *tritici* was reported that is in line with the present study (Babaeipour et al. 2011). Alvani et al. isolated 130 strains of *Pseudomonas fluorescent* from wheat rhizosphere in different parts of Khorasan province, of which 21 isolates were growth inhibitors of *G. graminis* var. *tritici* (Alvani et al., 2012). Gajari Mohammad Abadi et al. showed biological control of take-all disease under greenhouse condition by *Pseudomonas* sp, *Xanthomonas* sp, *Ralstonia* sp and *Pseudomonas fluorescens* (Gajari Mohammad Abadi et al. 2016). Akbarpour and Behboudi also reported the antagonistic effect of wheat rhizosphere *Streptomyces* on *B. sorokiniana* (Akbarpour and Behboudi, 2019).

There are similar studies about antifungal effect of rhizospheric *Bacillus* and *Pseudomonas* in and out of the country. In agreement with our

study, Ehab saleh et al. reported biological control activity of *Bacillus megaterium* BM344-1 against toxigenic fungi (Ehab saleh et al., 2021). In a study from Bangladesh, biocontrol potential of rhizospheric *Pseudomonas aeruginosa* against *Fusarium oxysporum* f. sp. *Cucumerinum* was reported (Ariful Islam et al., 2018). Zhang et al. also reported antifungal effects of *Bacillus subtilis* against *Alternaria solani* in potato (Zhang et al., 2020). In similar studies, antifungal activity of *Bacillus* species against *Fusarium* and other phytopathogenic fungi has been reported (Khan et al., 2018, Mokabber & Ahani Azari, 2021). In a study by Abo-Zaid et al. antagonistic activity of *Pseudomonas aeruginosa* F2 and *Pseudomonas fluorescens* JY3 on the in vitro growth of *Fusarium oxysporum* and *Rhizoctonia solani* was shown (Abo-Zaid et al., 2020).

Consistent with the results of Jolideh et al. in this study, 7 isolates (2 *Bacillus* and 5 *Pseudomonas* strains) produced volatile metabolites and their inhibitory effect was more pronounced with the *Pseudomonas* strains than with the *Bacillus* strains (Joulideh et al., 2012). Siderophore production was detected in 3 strains of *Pseudomonas* isolates that were more effective in inhibiting the mycelial growth of the tested fungi compared to the other isolates. Similar to our findings, in a study by Abo-Zaid the isolates with high siderophore production had a more inhibitory effects against the tested fungi (Abo-Zaid et al., 2020).

Based on the result of the present study and other researches rhizospheric *Bacillus* and *Pseudomonas* strains have a potential to produce antifungal metabolites against fungal pathogens and may be used as a biological control of plant diseases. However, for better conclusions about the antagonistic activity of *Rhizobacteria*, it is recommended to perform experiments in laboratory and greenhouse conditions.

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