



Isolation of Rhizospheric Bacteria from Soil and Their Antifungal Activity Against *Helminthosporium oryzae* the Causal Agent of Brown Spot of Rice

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Abstract

The brown spot of rice caused by Helminthosporium oryzae is a serious disease that affects the yield of rice crops. Brown spots of rice have been reported in almost all rice-growing countries. Therefore, the present study was to explore the management of brown spots of rice. through an antagonistic activity using rhizospheric bacteria. The method employed for soil sample collection was persuaded for bacterial isolation through the serial dilution plate technique. For the results of morphological characteristics of bacterial strain from soils of rice crop collected from Hyderabad. The results of the present study show that many colonies made by bacteria and which were consisted of different sizes, shapes, and colors. Whereas the results of the 15 isolates strains of rhizobacteria, only 06 bacterial strains IAP-1, IAP-2, IAP-04, IAP-09, IAP-12, and IAP-14 were found more effective in antagonizing *H.oryzae*, under *in-vitro* conditions. Antagonistic activity of rhizobacteria against *H. organize showed significant inhibitory* effects. The rhizobacteria showed the primordial result against against *H. oryzae* and will be helpful as a formulation not only for commercial purposes but also for beneficial biological control against the Brown spot of rice.

Keywords: Rhizospheric bacteria, antifungal, Helminthosporium oryzae

INTRODUCTION

Rice (*Oryza sativa* L.) serves humans in a variety of ways throughout the world. Rice is used by around half of the world's population, either partly or entirely. It is consumed by the vast majority 90% of the impoverished Asian populace. It also contributes to Pakistan's economy in a variety of way. It is the country's second most common food and the main sources of employment (9 percent). Unfortunately, there is a large yield gap of 1-3 t/ha between potential and actual rice output (Reni *et al.*, 2016; Sudheer *et al.*, 2018).

Ninety percent of the world rice crop is grown and consumed in Asia. On an average. each household in Pakistan spends about 3.8% of its total food expenditure on rice and rice flour in Sindh province specializes in producing long-grain white rice IRRI-6 and IRRI-9. Major verities produced in this area are IRRI-6, IRRI-9, and D-8 while minor verities including Super Basmati. Major rice-growing areas in Sindh province are Kashmore, Jacobabd, Larkana, Qambar Shahdadkot Shikarpur, and Dadu in Sindh, while Badin, Thatta, and Tando Muhammad Khan are Major ricegrowing areas in lower Sindh.

Rice is attacked by more than 50 different diseases, including six bacterial infections, 21 fungal infections, four parasitic nematodes, and 12 viral infections. The most dangerous infections are *Pyricularia oryzae* (which causes blast), *H. oryzae* (which causes brown spots), and *Xanthomonas oryzae* (which causes bacterial blight). *H.oryzae*, casual organism brown spot of rice, the pathogen responsible for brown spot disease, stands out as the most lethal infection on a global scale. *H. oryzae* was first discovered in 1942-43 in Bengal, India. During this time, the disease wiped out 50-90% of rice crops, resulting in a terrible famine that killed two million people due to malnutrition (Padmanabhan, 1973).

The pathogen responsible for brown leaf spot disease in rice is *H.oryzae* commonly known as *Bipolaris oryzae* Breda De Hann. It is a member of the family *Dematiaceae*, the order *Moniliales*, and the sub-division *Deuteromycotina* its ideal stage is known as *Cochliobolus miyabeanus*, and it belongs to the *Ascomycotina* sub-division, especially the sac fungi. Within the host plant, *H. oryzae* brown mycelium can be found intercellularly or intracellularly (Ahlawat, 2007).

Brown spot disease is caused by a fungal pathogen that can damage the rice crop at any stage of development, affecting both seedlings and adult plants. It appears as scattered brown patches on the foliage, which might coalesce and cause the leaves to wither and yellow. Furthermore, the disease inhibits seed germination, resulting in seed and root breakdown. Significant economic losses result from impaired seed development and seedling vigor (Mia & Nahar, 2001; Naeem *et al.*, 2001; Malavolta *et al.*, 2002). Brown spot disease caused by *H.oryzae* has been linked to agricultural output losses ranging 16- 43 % (Datnoff *et al.*, 1991). It is also acknowledged to be a severe problem for impoverished rice growers (Zasoks, 2002).

Symptoms of *H. oryzae* infection can be seen as early as the tillering stage. They begin as tiny, spherical foliar lesions that are dark brown to purple-brown in colour. These lesions range in form from round to oval, with a light brown to grey center and a reddish-brown edge. The lesions are frequently encircled by a brown or yellow-brown halo, which is a pathogen toxin (Vidyasekaran et al., 1980). Lesions on vulnerable rice cultivars can range in length from 6 to15 mm, causing leaf wilting (Webster & Gunnel, 1992). Lesions on tolerant cultivars, on the other hand, are smaller and brown, resembling pinheads. Lesions on leaf sheaths look similar to those on leaves. In addition to damaging the leaves and plant components, the virus H. oryzae can infect the grains, causing "pecky rice." The emergence of spots and discoloration on the grains is described by this phrase (Pandy, 2003). Various techniques, including the use of fungicides, are being used to manage this fungal disease. Other management measures proposed by Ribot et al. (2008) include using bio-control agents, resistant cultivars, agronomic practices, and biotechnology technologies. These alternate treatments can also be used to address brown spot disease in rice.

When it comes to chemical control, using pesticides to manage H. oryzae is seen to be the most effective method. However, it is crucial to remember that attaining effective management under high disease pressure might be difficult (Lore et al., 2007). Furthermore, the usage of fungicides might lead to contamination of the environment. While fungicide application is still a low-cost control tool for brown spot caused by H.oryzae management, depending only on host plant tolerance is a more cost-effective technique. Unfortunately, due to the establishment of new or more virulent races of the virus, host plant tolerance is limited and unstable (Katasntone et al., 2007). As a result of these conditions, there has been a change in emphasis towards investigating alternate management practices.

According to Harpyaree *et al.* (2010), the relevance of plant compounds discovered in medicinal plants has received substantial attention, particularly in terms of their potential in disease

Materials And Methods

Isolation and identification of the fungal pathogen: The collected samples consisted of rice leaves of DR -82, DR-83, DR-59, and IR-8, which were collected from the district of Hyderabad

prevention. According to Karuppusamy et al. (2009), botanical extracts have been widely examined for their antibacterial activity and have been used in a variety of applications such as disease management, food preservation. and pharmaceuticals, medications, natural treatments. According to Philip et al. (2009), researchers are increasingly focused on natural products as a source of fresh leads for generating superior medications against microbial diseases. Numerous angiosperm plants contain useful chemotherapeutic chemicals, and biological utilisation of these plants has showed promise in treating diseases, as demonstrated by Tewari et al. (1988). Microorganisms colonising plant roots, such as Streptomyces griseoviridis, have showed potential as a bio-control technique for soil-borne diseases. S. griseoviridis is an antagonistic microbe renowned for colonising the rhizosphere and efficiently controlling disease such as H.oryzae (Tahvonen, 1988). Furthermore, Pseudomonas aeruginosa-induced peroxidases in rice have been shown to have antifungal action against *H. oryzae* (Saikia et al., 2006). These findings emphasize the possibility of antagonistic microorganisms to improve plant health and disease resistance. It is a new field in agriculture that can potentially improve crop fitness. Commercially available antagonistic microorganisms, generally belonging to the Pseudomonas genus, have been found to significantly minimize pathogen impacts via processes such as mycoparasitism, antibiosis, iron competition, and plant resistance induction (Singh et al., 2005). Direct antagonism is efficient in reducing multiple pathogens, whereas induced resistance (IR) is effective against a variety of foliar pathogens, including both bacteria and fungi, conjunction frequently in with other microorganisms (Shoresh et al., 2010). Therefore, the present studies were designed to explore rhizospheric bacteria from Sindh soil that are antagonistic to brown spot fungus H.oryzae The present studies were conducted on the following objectives. Objectives

- Sampling of rice crops for the isolation and identification of the causal fungus *Helminthosporium oryzae* from the vicinity of Tandojam
- Isolation and identification of bacteria from rhizospheric soils of rice
- To screen potential biocontrol agents against the *Helminthosporium oryzae* under *in-vitro* condition

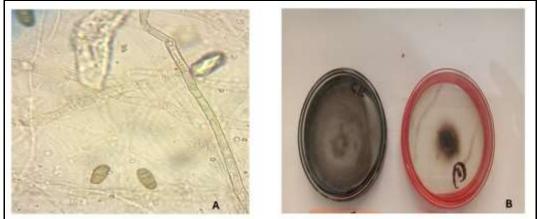
surrounding areas. These rice verities are commonly cultivated in different districts of Sindh province, These samples were brought to the Laboratory, Department of Plant Pathology, FCPT, SAU Tando jam for the isolation and identification of the casual fungus of brown leaf spot of rice. These sample placed in standard blotter paper method was used for the isolation and identification of fungi with help of key as described by Mew and Gonzales (2002).

Isolation and identification of bacterial isolates: Isolation, purification, identification and morphological characterization of Rhizosphoric bacteria rice soils which were collected rice grown in the vicinity of Hyderabad, For the isolation, dilution plate techniques was used and morphological characterization was done by light microscopy. Rhizobacteria were recovered from rice soil samples obtained from vicinity Hyderabad. Kasimpur et al. (2004) described an isolation approach that was used. In this approach, one gramme of soil was mixed in the 20ml 0.9y Nacl solution. The suspension was carefully mixed, and diluted up to 10⁻⁸ were made. 0.1 ml of each dilution was spread on the nutrient agar (NA) plates for further process. The plates were then incubated at 28+2°C. The obtained bacterial colonies were purified the streaking using technique rhizobacterial isolates were 0.3/.KOH test and visual inspection of colonies, morphology

Antagonistic activity of rhizosphoeric bacteria against *H.oryzae* using dual culture method: We followed the procedure mentioned by Montensnos *et al.* (1996) with slight modification for observing the antagonistic action of 15 selected strains against *H.oryzae* casual organisam of brown spot of rice on, Potato Dextrose Agar (PDA) were kept for 7-10 days. Old culture (at least 1 week old) of *H. oryzae* was placed in the center of Petri dishes for streaking of bacterial strain around. All these were incubated at 28°C, whereas the data were collected after 3 days and last for 7 days.

RESULTS

Identification of fungul pathogen: The fungul pathogen was identified based on cultural and morphological characteristic. The mycelial colony on PDA was smooth, and the color was dark black. In addition, microscopic examinations of the conidia were slightly curved,widest at the middle and tapering towards the hemispherical apex,where their width approximate half the median width of mature conidia are brownish with a moderately thin peripheral wall Figure 1.



Figur.1. Helminthosporium oryzae isolated from rice seed



Figure. 2. Cultural characteristics of *rhizospheric* bacteria Cultural and morphological characteristics of *H.oryzaee*

Tentative identification of bacterial isolates: Based on visual inspection, all strains were rodshaped, with varying textures. Most were off-white to cream-coloured and smooth. However, two

S.No Str IA

IA IAP7

IAP8

IAP9

IAP10

IAP11

IAP12

IAP13

IAP14

IAP15

1 2

3

4

5

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7 8

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11

12

13

14

15

strains (IAP-14 and IAP-15) were domed-shaped. In addition, the KOH test result revealed that all

strains were gram-positive, as no bacterial mixture became gummy in Figure 2 (Table.1).

Bacillus sp.

+

 $^+$

+

+

+

+

+

Tentative identification Bacillus spp					
Strains	Elevation	Shape	color	КОН	Tentative identification
IAP1	Smooth	Round	Off-white	+	Bacillus sp.
IAP2	Smooth	Round	Off-white	+	Bacillus sp.
IAP3	Smooth	Round	Off-white	+	Bacillus sp.
IAP4	Smooth	Round	Off-white	+	Bacillus sp.
IAP5	Smooth	Round	Off-white	+	Bacillus sp.
IAP6	Smooth	Round	Off-white	+	Bacillus sp.

Off-white

Off-white

Off-white

Off-white

Off-white

Off-white

Off-white

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creamy

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Table 1 Ten

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Domed

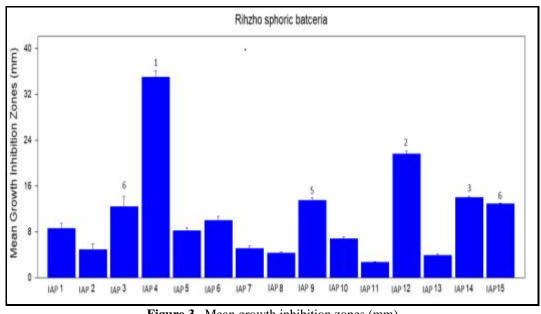


Figure 3. Mean growth inhibition zones (mm)

Potential antagonistic activity of selected strains: Out of 15, 6 strains such as IAP 04,(36.2) IAP 12,(22.5) IAP 03,(15.8) IAP 14, (14.9) IAP 09(14.0), IAP14 (13.0) were able to antagonize H.oryzae with mean growth inhibition zones of strains with IAP 04, (36.2) by the strain followed IAP 12, (22.5), IAP 03, (15.8), IAP 14, (14.9), IAP 09 (14.0), IAP14 (13.0) respectively. (Figure.3)

Discussion

In the present study, total 15 strain of bactertia were isolated, purified and identified the rice crop as investigated by Ashrafuzzaman et al. (2009) who successfully isolated ten bacteria from rice crop rhizosphoric bacteria which were designated as PGB1, PGB2, PGB3, PGB4, PGB5, PGT-1, PGT-2, PGT-3, PGG-1 and PGG-2. Rice roots are thought to be an excellent source of bio-control agents for soil-borne disease. Streptomyces griseoviridis, an actinomycete that colonises the rhizosphere of plants, is one example. S. griseoviridis has antagonistic qualities and is useful

in the bio-control of plant diseases such as H.oryzae casual organism brown spot of rice (Tahvonen, 1988). Furthermore, Pseudomonas aeruginosa-induced peroxidases in rice have been isolated and shown to exhibit antifungal activity against H.oryzae (Saikia et al., 2006). These findings show the potential for using microbial agents and their enzymatic capabilities to manage plant diseases, notably in rice agriculture. In recent years, the use of antagonistic microorganisms to improve plant fitness has emerged as a potential subject of study. Commercially accessible antagonistic microorganisms, generally belonging

to the Pseudomonas genus, have demonstrated efficacy in minimizing pathogen-caused harm. They do this through a variety of methods, including mycoparasitism, antibiosis, iron competition, and plant resistance induction (Singh et al., 2005). Many pathogens are suppressed by direct antagonism, but induced resistance (IR) has shown efficiency against a wide range of foliar pathogens, sometimes in conjunction with other bacteria and fungi (Shoresh et al., 2010). These findings emphasize the possibility of using microorganisms antagonistic in agricultural practices as a feasible technique for plant protection and disease management.

From samples taken in Hyderabad, 15 bacterial strains were isolated and purified. These strains took on a variety of forms, including round and smooth. The colonies' height were elevated and convex, and their colors ranged from creamy and white to off-white. These features offer a preliminary description of the isolated bacterial colonies from the various locales. Whereas, shape was round, Out of 15 bacterial strains isolated found all strains were +ve They exert antagonistic effects by producing a variety of antimicrobial chemicals, including antibiotics such as bacilysin and siderophores. Several investigations, including those by Jabeen (2012), Arshad et al. (2015), and Kala (2015), have identified bacteria isolated from rice fields as X. oryzae causes bacterial blight However, additional biochemical tests or molecular analyses utilising PCR are needed to identify whether these bacteria are X. oryzae causes bacterial blight the causative agent of bacterial blight in rice. X. oryzae is one of the most deadly viruses infecting rice crops globally, wreaking havoc on rice-growing regions all over the world (Ishiyama, 1990; Swing et al., 1992). There has recently been an increase in the occurrence of bacterial leaf blight caused by X. oryzae causes bacterial blight in all rice-growing regions of Pakistan. Japanese farmers initially recorded the disease in 1884-85 and has subsequently been detected in other rice-growing locations across the world, including Australia, Bangladesh, India, Sri Lanka, Thailand, the Philippines, the United States, West Africa, and Vietnam (Ezaku & Kuka, 2006). Mew and Majid (1977) first recorded the disease's existence in Pakistan, and later investigations have proven its presence on a larger scale throughout the country (Akhtar et al., 2003). The disease poses a severe danger to rice farming in Pakistan's different rice-growing zones.

Conclusions

Helminthosporium .oryzae casual organism brown spot of rice was found to be most predominate fungus among rice associated fungi. From the 15 strain isolates of rhizobacteria, only 06 bacterial strains , IAP-4, IAP-12, IAP-14, IAP-3, and IAP-9, were found more effective to antagonize

in-vitro conditions. Rhizospheric H. oryzae bacteria's antagonistic activity against H. oryzae casual organism brown spot of rice has yielded good results in Hyderabad. These Rhizospheric strains have shown tolerance to environmental conditions. making them appropriate for commercial product development. Because of their antagonistic qualities, they are efficient biological control agents against Brown leaf spot disease in rice, which is a major danger to rice production. Using these bacteria's hostile activity in the rice sector can assist build effective solutions to safeguard and secure rice harvests against this deadly disease.

Recommendations

Keeping in view the results of present research work it can be recommended thatl.among biocontrol agent IAP-4, IAP-12, IAP-14, IAP-3 and IAP-9 may be used for the control of brown spot of rice in future

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