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Screening of rice germplasm against multiple diseases under drought condition in middle IGP of Bihar

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Abstract
Rice is one of the most important cereal crop of developing countries and the staple food of about 65% of the world's population. Most traditional rainfed rice varieties are prone to biotic and abiotic stresses. The present study was carried out at the experimental farm of ICAR Research Complex for Eastern Region, Patna, India in *Kharif* season 2017 with an objective to identify brown spot, sheath rot and bacterial leaf blight disease resistant rice genotypes under drought condition. The incidence of brown spot, sheath rot and bacterial leaf blight in paddy ranged from 6.5 to 34.0%, 4.50 to 20.0% and 4.5 to 27.5%, respectively. Among the rice genotypes, the highest severity of brown spot was recorded in Rajendra Sweta (34.0%) whereas the lowest severity was observed in DRR 42 (6.50%) followed by IR83387-B-B-27-4 (6.7%) and Swarna Shreya (6.8%). Minimum severity of sheath rot was recorded in IR83383-B-B-129-4 and DRR42 (4.5%) followed by Swarna Shreya (6.0%). In the case of bacterial leaf blight, lowest severity recorded in Swarna Shreya (4.50%) followed by IR88963-3-7-2-4(5.0%). Among the rice genotype, the minimum severity against all three diseases was observed in DRR 42, Swarna shreya, IR83387-B-B-27-4, IR83383-B-B-129-4 and IR88963-3-7-2-4. These genotypes may be further utilized as the genetic sources in multiple disease resistance rice breeding programmes.

Keywords: rice, drought, biotic stress, disease, brown spot, Sheath rot, bacterial leaf blight

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereals of the world and is staple food of about 65% of the world's population. Rice is cultivated under diverse ecologies, ranging from irrigated to rain-fed and upland to lowland and deep water system (Kumar *et al.* 2014). The production of rice to be achieved by 2020 is 128 million tonnes to feed the growing population of India (Kumar *et al.,* 2010). In India, rice productivity is very low as compared to other developed of the world and this low productivity is due to several biotic and abiotic factors. Rainfed lowland rice is the second most important rice ecosystem, representing about 25% of the total rice production area. Rainfed lowland ecosystem is always prone to drought stress and most traditional as well as high yielding varieties of the present time are susceptible to drought (Kumar *et al.,* 2012). Generally rice crop is affected by more than 20 diseases and certain diseases are more common in rice varieties. Among the different diseases brown spot, sheath blight, blast, stem rot and bacterial leaf blight are considered important in various parts of rice growing areas of the world. Sheath blight is an important soil borne disease caused by *Rhizoctonia solani* that can cause up to 25% yield loss (Kumar *et al.*, 2009). Bacterial leaf blight is caused by *Xanthomonas oryzae* occurs mostly during the wet season and in some areas of Asia, which can reduce crop yield by up to 50% (Latif *et al.*, 2011). Brown spot of rice caused by *Helminthosporium oryzae* can reduce crop yield by up to 40%. However, rice genotypes may vary in their response to disease tolerance. *Sarocladium oryzae* was originally described as *Acrocylindrium oryzae*, the first organism to be associated with rice sheath rot symptoms isolated in Taiwan in 1922 (Mew and Gonzales, 2002). The genus *Sarocladium* was established in 1975 (Gams and Hawksworth, 1975) and currently encompasses 16 species including plant pathogens, saprobes, mycoparasites, endophytes, and potential human pathogens (Giraldo *et al.,* 2015). The genus belongs to the order of the Hypocreales in the Phylum *Ascomycota*. *S. attenuatum* was originally described as a distinct species causing rice sheath rot, but is nowadays considered as a synonym of *S. oryzae* (Bridge *et al.,* 1989). Keeping in view the above facts, the present study was undertaken to identify the rice genotypes against three major rice diseases (brown spot, sheath rot and bacterial leaf blight) under drought stress condition.

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Materials and Methods

A field experiment was conducted during *Kharif* seasons of 2017 at ICAR Research Complex for Eastern Region, Patna (Latitude: $25^030`N$, Longitude: $85^015`E$, Elevation: 52 m above mean sea level), Bihar, India. The experiment was conducted with 24 rice genotypes (Table 1) in an alpha lattice design with three replicates. The genotypes were collected from ICAR-IRRI collaboration programme. The climate of the experimental site is humid sub-tropical in nature characterized by the monsoon season from late June to late September and chilly winter nights and foggy or sunny days from November to February. Soil type of the experimental field was clay loam and good texture with neutral pH 7.5. Field was thoroughly prepared and level with laser leveler machine before sowing, so that if rainfall occurred, water should not be stagnant in the field. Experiment was established under direct seeded condition using 2-3 seed per hill in rows 6 m long and spaced 20cm apart. In drought stress trial, N, P_2O_5 and K_2O fertilizer doses of 90-60--50 were applied, respectively. Nitrogen was applied in three splits- (1/3) each at basal, maximum tillering and panicle initiation stages, while the P_2O_5 and K_2O were applied as basal. In experimental field, water was provided only once the next day after sowing so that the seeds can properly germinate. Supplemental irrigation after stress initiation was not provided till harvest even if the stress was very severe.

Assessment of the disease incidence

Each plot was visited on regular basis for recording observations. The disease incidence was recorded at maturity stages of the plant. Data were recorded visually by observing the symptoms. Ten plants were randomly selected from each unit plot and the following parameters were considered for data collection.

Number diseased tillers / plants

Per cent leaf area diseased (LAD)

Disease incidence was calculated by the following formula (Rajput and Bartaria, 1995):

$$\textbf{Disease incidence} = \frac{\text{Number of diseased tillers}}{\text{Total number of inspected tillers} \times 100}$$

Isolation and identification of causal organism

The leaves from the diseased plants were collected from the field and cut into small pieces along with healthy portion. Cut pieces were sterilized by the surface disinfectants e.g. 0.1% mercuric chloride for 30 seconds. After sterilization the cut pieces were washed three times with sterile water. The cut pieces were then placed on sterile blotter paper to remove excess water. The cut pieces were then placed on the Potato Dextrose Agar plate. The plate were labelled and placed in the incubation chamber for 7 days at $25 + 2^o$ C. After 7 days of incubation, the fungi grown on culture media. A portion of culture was taken on slide and observed under microscope and identified the pathogenic fungi *i.e. Helminthosporium oryzae*, *Soracladium oryzae*, with the help of relevant literature (Mew and Gonzales, 2002; Barnet and Hunter, 1972). In bacterial leaf blight causal organism *Xanthomonas oryzae* isolated on nutrient Agar media. A portion of culture was taken by inoculating needle on another Potato Dextrose Agar and nutrient Agar media plates. A small portion from the subculture was inoculated to another Potato Dextrose Agar and nutrient Agar`plate for pure culture. The pathogen, thus purified, was kept in refrigerator for future use. All these operations were done aseptically in the laminar air flow chamber. Diseases severity score was measured on the basis of 0-9 scale (Table 2)

Analysis of data

The data on different characters were subjected to estimates of ANOVA (analysis of variance) by using statistical software OPSTAT.

Results and Discussion

The screening of twenty four genotypes of rice against three diseases revealed that, none of the genotypes was immune towards brown spot, sheath rot and bacterial leaf blight. It was observed that under field conditions, the severity of brown spot disease were fairly significant. The severity of brown spot ranged from 6.50 to 34.00% at maturity stages (Table 3). The highest brown spot disease severity was recorded in Rajendra Sweta whereas the least value was observed in DRR 42 (6.5%) followed by IR 83387-B-B-27-4 (6.7%) and Swarna Shreya (6.8%). Rashed (2001) also reported that the incidence and severity of brown spot were observed 30.75 to 62.75% and 25.25 to 47.50%, respectively at 50 days after transplanting in the hybrids line 321H. The incidence and severity varied from 40.50 to 80% and 45 to 77%, respectively at 70 days after transplanting in rice. Saifulla (1994) also reported that mean brown spot severity ranged from 23.0 to 36.5% in rice genotypes.

The severity of bacterial leaf blight (0-9 scale) ranged from 5.00 to 27.50, respectively at maturity stage (Table 3). The highest severity was recorded on rice cultivation 'IR84899-B-182-3-1-1-2' whereas the lowest severity of bacterial leaf blight was recorded on 'Swarna Shreya' followed by IR88963-3-7-2-4. These finding were supported by Akhtar *et al.*, (2003) who found that BLB disease of rice prompted by *Xanthomonas oryzae* pv. *oryzae* has created a serious situation in all provinces of Pakistan *viz.*, Punjab, Khyber Pakhtukhwa, Sindh, Baluchistan including Pakistan occupied Kashmir. Kumar *et al.* (2013) also reported variability in rice genotypes in response to bacterial leaf blight and brown spot. They reported 4.7% to 52.6% infestation of bacterial leaf blight in 87 rice genotypes grown under aerobic condition. The severity of sheath rot in grade (0-9 scale) ranged from 4.50 to 20.0%, at maturity stages (Table 3). The highest severity was recorded on Rajendra Bhagwati (20.0%) whereas the lowest severity was observed on DRR 42 and IR83383-B-B-129-4 (4.50%).

It was also observed that some genotypes were showing low severity to more than one disease. IR83387-B-B-27-4, Swarna Shreya, IR 83383-B-B-129-4, DRR 42 and IR 83383-B-B-129-4 were showing low severity against all the three diseases. Low severity for both Brown spot and Bacterial leaf blight were found in IR87759-5-2-1-3 and IR 84899-B-179-13-1-1-1. IR83929-B-B-291-3-1-1 and IR84898-B-168-24-1-1-1 were showing low severity against Brown spot and sheath rot while two rice genotypes *viz.*, IR87759-5-2-1-3 and IR88963-3-7-2-4 were showing low severity against sheath rot and Bacterial leaf blight together. Previous studies have also shown that some rice genotypes carry combined resistance to more than one disease. Dubey *et al.*,(2014) studied a set of 100 rice genotypes and found that two rice genotypes *viz.,* BPL 7-12 with rice blast resistance gene *Pi54* and *Pi1* and BML 27-1 with *Pi54* also possess sheath blight QTL, *qSBR11-1* and provided resistance to both the diseases.

Table 1: Detailed information of the rice varieties in the experiment

Sl. No	Name of genotypes	Maturity Duration (days)	Breeding line/ released variety
1	IR 88964-24-2-1-4	120-125	Advanced breeding line
2	IR 88964-11-2-2-3	115-120	Advanced breeding line
3	RP 5212-56-12-9-3-2-1-1	120-125	Advanced breeding line
4	IR 88867-9-1-1-4	115-120	Advanced breeding line
5	IR 83387-B-B-27-4	120-125	Advanced breeding line
6	IR84899-B-183-CRA-19-1	120-125	Advanced breeding line
7	IR84894-143-CRA-17-1	115-120	Advanced breeding line
8	Swarna Shreya	120-125	Released variety
9	IR83929-B-B-291-2-1-1-2	120-125	Advanced breeding line
10	IR88964-11-2-2-4	120-125	Advanced breeding line
11	IR87759-5-2-1-3	120-125	Advanced breeding line
12	IR88963-3-7-2-4	115-120	Advanced breeding line
13	IR87746-26-2-1-1	120-125	Advanced breeding line
14	IR83929-B-B-291-3-1-1	120-125	Advanced breeding line
15	IR 83383-B-B-129-4	130-135	Advanced breeding line
16	IR84898-B-168-24-1-1-1	115-120	Advanced breeding line
17	IR84899-B-182-3-1-1-2	120-125	Advanced breeding line
18	IR 84899-B-179-13-1-1-1	120-125	Advanced breeding line
19	DRR 42	120-125	Released variety
20	Sahbhagi Dhan	115-120	Released variety
21	IR64	120-125	Released variety
22	Rajendra Sweta	135-140	Released variety
23	Rajendra Bhagwati	120-125	Released variety
24	MTU 1010	120-125	Released variety

Table 2: Disease severity scale of brown leaf spot, sheath blight and bacterial leaf blight

Name of diseases	Scale
Brown Spot	1 = No incidence
	2 = Less than 1%
	3 = 1-3%
	4 = 4-5%
	5 = 11-15%
	6 = 16-25%
	7 = 26-50%
	8 = 51-75%
	9 = 76-100%
Sheath rot	0 =No infection observed
	1 = Less than 1%
	3 = 1-5%
	5 = 6-25%
	7 = 26-50%
	9 = 51-100%
Bacterial leaf blight	0 = no lesion
	1 = 1-5% lesion area
	3 = 6-12% lesion area
	5 = 13-25% lesion area
	7 = 26-50% lesion area
	9 = 51-100% lesion area

Table 3: Disease incidence of different rice germplasm against multiple diseases

Sl. No	Name of genotypes	Brown spot	Bacterial leaf blight	sheath rot
1	IR 88964-24-2-1-4	10.00	6.50	13.00
2	IR 88964-11-2-2-3	17.50	11.00	14.00
3	RP 5212-56-12-9-3-2-1-1	12.00	16.50	12.00
4	IR 88867-9-1-1-4	11.00	13.50	12.50
5	IR 83387-B-B-27-4	6.70	5.20	5.50
6	IR84899-B-183-CRA-19-1	32.50	16.50	18.00
7	IR84894-143-CRA-17-1	7.00	12.00	11.00
8	Swarna Shreya	6.80	4.50	6.00
9	IR83929-B-B-291-2-1-1-2	9.00	12.50	14.00
10	IR88964-11-2-2-4	10.00	8.00	6.50
11	IR87759-5-2-1-3	12.00	6.50	6.00
12	IR88963-3-7-2-4	9.00	5.00	6.50
13	IR87746-26-2-1-1	24.50	24.00	12.00
14	IR83929-B-B-291-3-1-1	7.50	13.00	6.50
15	IR 83383-B-B-129-4	7.00	6.60	4.50
16	IR84898-B-168-24-1-1-1	6.90	13.50	5.50
17	IR84899-B-182-3-1-1-2	11.00	27.50	18.50
18	IR 84899-B-179-13-1-1-1	7.50	6.00	14.00
19	DRR 42	6.50	6.80	4.50
20	Sahbhagi Dhan	11.00	13.00	19.50
21	IR64	22.00	18.00	14.50
22	Rajendra Sweta	34.00	23.50	17.00
23	Rajendra Bhagwati	30.00	21.50	20.00
24	MTU 1010	16.00	19.50	19.50
	SE(m)	1.67	1.35	1.91
	LSD (0.05)	4.91	3.96	5.62
	C.V.	17.33	14.92	23.08

Conclusions

Based on above findings it was observed that none of the genotypes was immune towards brown spot, sheath rot and bacterial leaf blight. Among the rice genotype, the minimum severity against all three diseases was observed in DRR 42, Swarna shreya, IR83387-B-B-27-4, IR83383-B-B-129-4 and IR88963-3-7-2-4. Molecular validation and identification of resistance gene showing low severity reaction against all the three disease need to be done. Identification of rice line with gene (s) conferring broad spectrum resistance may be further utilized as the genetic sources in multiple diseases resistance rice breeding programme.

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