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Screening of rice (*Oryza sativa*) germplasm for resistance to brown spot caused by *Cochliobolus miyabeanus*

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ABSTRACT

Brown spot of rice, caused by *Cochliobolus miyabeanus*, remains one of the most destructive diseases affecting rice productivity, particularly under the natural epiphytotic conditions of eastern India. The use of resistant cultivars is the most economical, practical, and environmental safe strategy for managing the disease. The study was carried out during the rainy (*kharif*) seasons of 2021 and 2022 at Bihar Agricultural University, Sabour, Bihar to evaluate 267 rice (*Oryza sativa* L.) genotypes against brown spot under natural disease pressure. Disease severity was assessed following the IRRI Standard Disease Rating Scale (2002). The results revealed considerable variation among genotypes for disease response. Only five entries IET 19512 (US 311), IET 18667 (OR 2089-9), IET 18668 (OR 2060-9), IET 20007 (RPHR 205-14-3-2), and HPR 2529 exhibited high resistance. Additionally, 17 genotypes were categorised as resistant and 20 genotypes as moderately resistant, while the remaining entries were susceptible or highly susceptible. The findings highlight valuable resistant sources that can be utilised in breeding programmes aimed at developing brown spot-resistant rice cultivars suitable for the Indo-Gangetic Plains of eastern India.

Keywords: Brown spot, *Cochliobolus miyabeanus*, Disease rating scale, Reaction group

As the world's most widely consumed cereal, rice (*Oryza sativa* L.) is the primary source of sustenance and livelihood for more than 3.5 billion people, accounting for over one-third of the global population and covering 11% of arable land (Kumar *et al.* 2020, Kumar *et al.* 2021, Kumar *et al.* 2022a). Rice is staple food for 3 billion people and approximately 90% of the world's rice crop is produced and consumed in Asia (Bandumula 2018). India leads globally in rice cultivation area, covering 44.2 million hectares, and ranks second in total rice production, accounting for 116.48 million tonnes annually, after China (Kumar *et al.* 2019). Rice crop suffers from several diseases, but brown spot disease caused by *Cochliobolus miyabeanus* is the most destructive disease (Kumar and Simon 2016). Brown spot disease is a recurring threat in India, occurring every year in varying intensities, ranging from mild to severe, and occasionally reaching epidemic levels. Crop damage heavily due to poor seed germination, leaf spot weakening overall crop, and poor fruit set (Kumar *et al.* 2017). The disease was exposed in India when the Famine Inquiry Committee of 1945 reported that brown spot disease caused by *Drechslera oryzae* was the primary reason of the well-known Bengal Famine of 1942, accounting for 50–90% of yield losses, resulting in deaths of two million people because of hunger (Padmanabhan 1973). During 1979–82, this disease occurred in epidemic form in Bihar as reported by Mishra (1985). Disease was prevalent in north Bihar districts during *kharif* 1991 and decreased rice yield severely in late sown, long duration high yielding traditional varieties like Pankaj, Mahsuri, Jaya, Bakol and Agahani. Although, it can be treated with fungicide and is an inexpensive to control brown spot, but host-resistant is the most economical. Use of resistant varieties is easy, efficient, harmless, and cost-effective means of controlling disease. Resistance is very weak, unstable because of emergence of new or more virulent pathogen species. Therefore, resistance levels should be updated for each individual variety. In this context, competition, identification of the resistant genotypes and cultivars would be an excellent alternative to controlling brown spot disease.

MATERIALS AND METHODS

The study was carried out during the rainy (*kharif*) seasons of 2021 and 2022 at Bihar Agricultural University, Sabour, Bhagalpur (25°23′ N, 87°48′ E; at an elevation of 46 m amsl), Bihar. The site is in the humid subtropical agro-climatic zone of eastern India, characterised by hot and humid summers, a monsoon-dominated rainfall pattern and moderately cool winters. The experimental soil was

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classified as alluvial loam with moderate fertility and good moisture retention capacity, suitable for rice cultivation. Prior to the initiation of the experiment, composite soil samples from the top 0–15 cm layer were collected and analysed for basic physio-chemical properties to ensure baseline uniformity across the field.

A total of 267 rice germplasm lines, including landraces, breeding lines and released cultivars, were screened to evaluate their reaction to brown spot disease under natural epiphytotic conditions. Seed material for all test entries was procured from the Department of Plant Breeding and Genetics, Bihar Agricultural University, Sabour, Bihar. The susceptible check variety Pankaj was planted both within the trial as a control and around the perimeter as a spreader row to ensure uniform disease pressure across the field. Seedlings were raised in a well-prepared nursery following standard agronomic procedures, and 25-day-old seedlings were manually transplanted into the main field.

Each entry was planted in two rows of 5 m length, with a uniform spacing of 20 cm × 15 cm, maintaining one vigorous seedling/hill. Gap filling was performed one week after transplanting to maintain plant stand uniformity. Given the large number of entries, the trial was laid out in a non-replicated observational design, commonly adopted for preliminary large-scale screening studies where the primary objective is identification of potentially resistant or susceptible genotypes. To promote spread of uniform disease, all test blocks were surrounded by four rows of the susceptible check Pankaj, planted 30 cm away from the entries.

Recommended fertiliser doses were applied at 120:60:40 kg N: P_2O_5: K_2O/ha. Full doses of P_2O_5 and K_2O, along with 50% of nitrogen and 20 kg $ZnSO_4$/ha, were incorporated during puddling. The remaining nitrogen was applied in two equal splits at the maximum tillering stage (30–35 DAT) and panicle initiation stage (60–65 DAT). Irrigation and weeding operations were carried out uniformly across all plots. No fungicide or plant protection chemical was applied at any stage to allow natural disease development.

For disease assessment, five plants/entry were randomly selected, tagged and monitored starting from the first appearance of brown spot symptoms. Disease scoring was conducted at 15-day intervals using the IRRI Standard Evaluation System (IRRI 2002) 0–9 scale (Table 1). The mean severity score of the tagged plants was used to classify each entry into highly resistant, resistant, moderately resistant, susceptible or highly susceptible categories. Representative symptoms were photographed periodically to assist in confirming field observations.

Meteorological data were collected daily from the Agro-meteorological Observatory of Bihar Agricultural University, Sabour, Bihar. Parameters recorded included maximum and minimum temperatures, relative humidity, total rainfall, and number of rainy days. Monthly averages were compiled to analyse their relationship with disease development and progression. These weather trends, along with seasonal fluctuations associated with the *kharif* period, were considered while interpreting disease severity patterns to highlight the environmental influence on brown spot epidemiology (Fig. 1).

Table 1 Disease rating scale for screening of rice varieties against brown spot (*Cochliobolus miyabeanus*)

Scale	Affected leaf area	Host response
0	No Incidence	Immune (I)
1	<1%	Highly resistant (HR)
2	1–3%	Resistant (R)
3	4–5%	Resistant (R)
4	6–10%	Moderately resistant (MR)
5	11–15%	Moderately resistant (MR)
6	16–25%	Moderately resistant (MR)
7	26–50%	Susceptible (S)
8	51–75%	Highly susceptible (HS)
9	76–100%	Highly susceptible (HS)

RESULTS AND DISCUSSION

Average weather data during 2021 and 2022 experimentation (Fig. 1) shows that August to November was most favourable for brown spot disease development. Number of rainy days, total rainfall, temperature and humidity during this month play pronounce role in the development of brown spot disease. The number of rainy days ranging between 4–10, total rainfall up to 203.6 mm, temperature ranging between 29.8–33.0°C maximum and 16.2–27.4°C minimum accompanied with high humidity (86–89%) aggravated the development of brown spot disease the most. On the other hand, high temperature (36.3°C) accompanied with low humidity had adverse

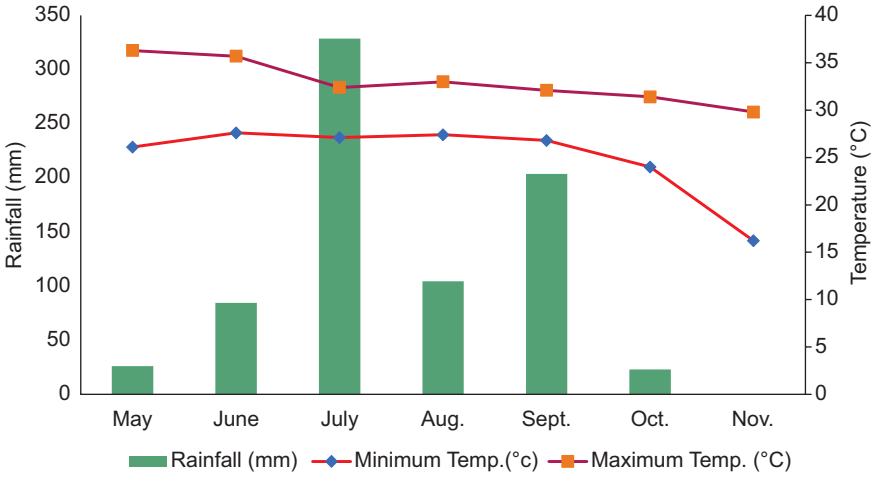

Fig. 1 Average weather data of two seasons during the experimentation.

effect on development of disease resulting in low severity of brown spot of rice. Pal *et al.* (2017) observed correlation between weather parameters and rice sheath blight disease. Dhaliwal *et al.* (2018) also revealed that temperature, rainfall and relative humidity significantly influenced brown spot disease development.

In modern agricultural production system, resistant varieties play vital role in boosting production and simultaneously put down disease pressure. Keeping this fact in mind, altogether 267 germplasm/varieties were screened out for their resistance against *Cochliobolus miyabeanus* during *kharif* 2021 and 2022 (Table 2). Varieties/entries differed among themselves with regard to their resistance/ susceptibility. Out of 267 varieties/entries, only 5 varieties i.e. IET 19512 [US 311(hybrid)], IET18667 (OR 2089-9), IET 18668 (OR 2060-9), IET 20007 (RPHR 205-14-3-2) and HPR-2529 were rated highly resistant having maximum score of 1 against brown spot disease. Seventeen entries, i.e. IET 19726 (IHRT-E-4), IET 19994 (PAU 3110-37-1-1-1), IET 20006 (OR 2166-3), IET 20014 (CN 1403-6-5-1), IET 20015 (CN 1402-11-4-1), IET 19513 [US 312 (hybrid)], IET 18666 (OR 2093-4), IET 19261 (BAU 398-02), IET19264 (OR 2081-5), IET 19566 (BAU-392-02), IET 19561 (AD 02029), IET 19576 (IR 74371-70-1-1-CRR-1), IET 19589 (R 1218-598-1-281-1), IET 19346 (RDR 898), HPR 1068, HPR1156 and IR-78224-22-2-98 were resistant having maximum score of 4, while 20 varieties/ entries were moderately resistant (max. score 6) (Table 3). Rest of varieties/entries showed either susceptible or highly susceptible reaction against brown spot disease. A comprehensive two-year screening assessment of 267 rice varieties/entries revealed that merely five entries (1.87%) showed high resistance to brown spot disease. Seventeen (6.37%), twenty (7.49%), 195 (73.03%) and 30 (11.24%) varieties/entries showed resistant, moderately resistant, susceptible and highly susceptible reaction to disease, respectively (Table 4). Highly resistant and resistant varieties having good agronomic characters may be safely recommended for cultivation in epidemic areas of brown spot as resistant varieties can be simplest, best useful, and cost-effective way to control disease. Using resistant variety not only provides prevention against disease, but also saves time, effort, money in other control methods. Susceptible to highly susceptible varieties/lines/entries may either be recommended to be gradually withdrawn from cultivation in endemic/epidemic areas or be improved by pyramiding brown spot resistance gene to gene pool responsible for the desirable traits. Suitable disease management practices may be adopted in case of compulsions of use of the susceptible varieties.

The identification and deployment of resistant varieties remain the most effective, economical, and environmental

Table 2 Reaction of various germplasm/varieties of rice against brown spot

Entry no.	Germplasm/varieties	Reaction	Entry no.	Germplasm/varieties	Reaction
1.	RDR918	S	2.	RR433-2	S
3.	MTU1088	S	4.	DDR105	S
5.	RPHR1053-6-4	S	6.	UPR2654-17-1-1	S
7.	RP4334-TSH-41-8-1-1	S	8.	RPHR288-6	MR
9.	RP4407-TSH-42-12-13	S	10.	AD02029	R
11.	RP4060-105-6-8-2-5-1	S	12.	NDR1036-4-3	MR
13.	US311 (Hybrid)	HR	14.	NDR1091-3-2	MR
15.	US312 (Hybrid)	R	16.	BAU392-02	R
17.	MTUHR-2091 (Hybrid)	S	18.	BAU175-90	S
19.	PAU3042-3-3-4	MR	20.	BidhanDhan-2	S
21.	CB21012	S	22.	IR74371-70-1-1-CRR-1	R
23.	UPR2554-9-1	S	24.	OR1752-3	S
25.	UPR2654-20-1	S	26.	R1218-598-1-281-1	R
27.	UPR2545-11-2-3	MR	28.	KJTRH-4 (Hybrid)	S
29.	MGD-102	S	30.	JRH-4 (Hybrid)	S
31.	HKR2002-52	S	32.	JRH-5 (Hybrid)	S
33.	HKR2002-69	S	34.	CB97042	S
35.	HKR2002-69	S	36.	UPRTGH-332 (Hybrid)	S
37.	PAU3116-25-5-1	MR	38.	RP-Bio197	HS
39.	MTU1082	S	40.	RP-Bio189	HS
41.	CRK26.1	MR	42.	RP-Bio226	HS
43.	R979-67-2-44-1	S	44.	RP-Bio170	HS

Contd.

Table 2 (*Continued*)

Entry no.	Germplasm/varieties	Reaction	Entry no.	Germplasm/varieties	Reaction
45.	R1248-1489-2-822-1	S	46.	CB01-001	S
47.	HRI-157 (Hybrid)	S	48.	UPR3199-464-1-2	S
49.	NK3376 (Hybrid)	S	50.	HKR2002-85	S
51.	GK5003	S	52.	HKR2002-87	S
53.	RR270-56	S	54.	R1124-69-1-45-1	S
55.	RRU-9630	S	56.	NDR-9930076	S
57.	OR2093-4	R	58.	NDR3112-1	S
59.	OR2089-9	HR	60.	HKR2002-86	MR
61.	OR2060-9	HR	62.	JGL7046	S
63.	RR433-2-1	MR	64.	RDR898	R
65.	CRR383-22	S	66.	CRAC2224-1048	S
67.	DDR-97	S	68.	CRK22-1-2	HS
69.	BAU398-02	R	70.	CRK26-1-2-1	S
71.	OR2081-5	R	72.	OR1912-25	S
73.	RPHR635-1-9-4	S	74.	AD01252	S
75.	UPR3193-99-471-1-1	S	76.	RP4669-4-IR73933-8	S
77.	RNR754	MR	78.	Pusa1277-04-80S	
79.	RNR755	S	80.	RAU1-16-48S	
81.	R1243-1220-1-1	S	82.	RP4667-15-2-1-5-6-B	S
83.	R1473-521-249-1-1	S	84.	HKR03-24	HS
85.	R1249-1440-3-1	S	86.	UPR2642-11-1-2	HS
87.	R1130-80-1-52-1	S	88.	UPRI2004-17	S
89.	JR 411	S	90.	UPRI2004-18	S
91.	NP3113	S	92.	OR1912-22	S
93.	PAU3110-37-1-1-1	R	94.	CB20001	S
95.	PAU3105-45-3-1-3	S	96.	MGD-101	S
97.	KJT4-4-36-12-13-2	S	98.	HKR2002-81	S
99.	CRAC2224-910	MR	100.	R979-78-2-62-1	S
101.	CRAC2223-312	S	102.	R1124-258-3-86-1	S
103.	CRAC2222-533	S	104.	PAU2520-3-2-3-2-1-2	S
105.	RP4331-5-1-2-1-4-5-B	S	106.	KJT6-6-16-28-9	S
107.	CR 2462	MR	108.	CN1229-APA-3-2	S
109.	CR2463-16	S	110.	SJR7 (OM1706)	S
111.	RP4668-2-IR-74293	MR	112.	SJR19 (WAB337-B-B)	S
113.	CRK15-1-1	S	114.	NDR9432 (IR68828)	S
115.	OR2166-3	R	116.	NDR9430 (IR68850)	S
117.	RPHR205-14-3-2	HR	118.	NDR2075	S
119.	RPHR711-1-2-3	MR	120.	NDR2083	S
121.	RPHR17-13-4-1	S	122.	RP4075-159-109-38	HS
123.	RPHR25-104-1-2	S	124.	RR272-21	HS
125.	JGL8764	S	126.	JGL11689	HS
127.	CN1265-7-16	MR	128.	HKR03-27	HS
129.	CN1403-8-9-3	S	130.	HKR03-41	HS
131.	CN1403-6-5-1	R	132.	HKR03-57	HS
133.	CN1402-11-4-1	R	134.	RAU735-17-2	S

Contd.

Table 2 (*Continued*)

Entry no.	Germplasm/varieties	Reaction	Entry no.	Germplasm/varieties	Reaction
135.	NWGR99074	S	136.	UPR2643-23-1-1	S
137.	NLR3010	S	138.	UPR2642-34-1-1	S
139.	MTU1099	S	140.	UPR2659-2-1-1	S
141.	MTU1100	S	142.	UPR2643-15-1-2	S
143.	CB03-008	HS	144.	R1207-306-2-168-1	S
145.	CB03-039	S	146.	CB 04-110	S
147.	CB03-064	S	148.	CB 01-288	S
149.	CB 03-334	S	150.	HPR 2130	S
151.	CB 02-586	S	152.	HPR 2317	S
153.	CB 21006	S	154.	HPR 2337	S
155.	CB 01-001	S	156.	HPR 2529	HR
157.	CB 97042	S	158.	HPR 2530	S
159.	CB 02-012	S	160.	HPR 2308	S
161.	CB 03-039	S	162.	HPR 2322	S
163.	TNRH 113R	S	164.	HPR 2413	HS
165.	TNRH 142R	S	166.	HPR 2505	S
167.	TNRH 142R	S	168.	ARC 10365	HS
169.	CORH 3	S	170.	ARC 10515	HS
171.	TNRH 142R	S	172.	ARC 10535	S
173.	TNRH 142R	S	174.	ARC 10555	S
175.	TNRH 142R	S	176.	ARC 10560	S
177.	IR 78221-19-6-23	S	178.	ARC 10573	S
179.	IR 78221-19-6-82	S	180.	ARC 10662	S
181.	IR 78221-19-6-99	S	182.	IR 64	S
183.	IR 78224-22-2-4	S	184.	Rasi	MR
185.	IR 78224-22-2-98	R	186.	HR 12	MR
187.	SK 20	HR	188.	Ajaya	S
189.	VOPH 3102	MR	190.	TN 1	S
191.	VHC 1329	S	192.	Vikramarya	S
193.	VL 4040	S	194.	IR 50	S
195.	VL 4569	S	196.	Nidhi	S
197.	VL 4930	S	198.	Swarnadhan	S
199.	VL 7174	S	200.	IHRT-E-1	S
201.	VL 7504	HS	202.	IHRT-E-2	S
203.	VL 10036	S	204.	IHRT-E-3	S
205.	VL 30018	S	206.	IHRT-E-4	R
207.	VL 30019	S	208.	IHRT-E-5	S
209.	VL 30029	S	210.	IHRT-E-6	S
211.	VL 30118	S	212.	IHRT-E-7	S
213.	VL 30246	S	214.	IHRT-E-8	S
215.	VL 30336	S	216.	IHRT-E-9	S
217.	HPR 2143	HS	218.	IHRT-E-10	S
219.	HPR 1068	R	220.	IHRT-ME-1	HS
221.	HPR 1156	R	222.	IHRT-ME-2	HS
223.	Bhrigodan	S	224.	IHRT-ME-3	S

Contd.

Table 2 (*Concluded*)

Entry no.	Germplasm/varieties	Reaction	Entry no.	Germplasm/varieties	Reaction
225.	IHRT-ME-4	HS	226.	IHRT-M-15	S
227.	IHRT-ME-5	HS	228.	IHRT-M-16	S
229.	IHRT-ME-6	S	230.	IHRT-M-17	S
231.	IHRT-ME-7	S	232.	IHRT-M-18	HS
233.	IHRT-ME-8	HS	234.	IHRT-M-19	HS
235.	IHRT-ME-9	HS	236.	IHRT-S-1	S
237.	IHRT-ME-10	S	238.	IHRT-S-2	S
239.	IHRT-ME-11	S	240.	IHRT-S-3	S
241.	IHRT-M-1	S	242.	IHRT-S-4	S
243.	IHRT-M-2	S	244.	IHRT-S-5	S
245.	IHRT-M-3	S	246.	IHRT-S-6	S
247.	IHRT-M-4	S	248.	IHRT-S-7	MR
249.	IHRT-M-5	S	250.	IHRT-S-8	S
251.	IHRT-M-6	S	252.	HPR-12	S
253.	IHRT-M-7	HS	254.	TN 1	S
255.	IHRT-M-8	S	256.	Vikramarya	S
257.	IHRT-M-9	S	258.	Swarnadhan	S
259.	IHRT-M-10	HS	260.	Rasi	S
261.	IHRT-M-11	S	262.	IR-64	S
263.	IHRT-M-12	S	264.	IR-50	S
265.	IHRT-M-13	S	266.	Ajaya	S
267.	IHRT-M-14	S			

Table 3 Germplasm/varieties graded as highly resistant, resistant and moderately resistant against brown spot disease of rice (mean of three observations at 15-day intervals in each season)

Sl. no.	Reaction group	Germplasm/Varieties
1.	Highly resistant (0–1%)	IET 19512 [US 311 (hybrid)], IET 18667 [OR 2089-9], IET 18668 [OR 2060-9], IET 20007 [RPHR 205-14-3-2], HPR-2529 Total = 5
2.	Resistant (1–5%)	IET 19726 [IHRT-E-4], IET 19994 [PAU 3110-37-1-1-1], IET 20006 [OR 2166-3], IET 20014 [CN 1403-6-5-1], IET 20015 [CN 1402-11-4-1], IET 19513 [US 312 (hybrid)], IET 18666 [OR 2093-4], IET 19261 [BAU 398-02], IET 19264 [OR 2081-5], IET 19566 [BAU-392-02], IET 19561 [AD 02029], IET 19576 [IR 74371-70-1-1-CRR-1], IET 19589 [R 1218-598-1-281-1], IET 19346 [RDR 898], HPR 1068, HPR 1156, IR-78224-22-2-98 Total = 17
3.	Moderately resistant (6–25%)	IET 19555 [RPHR 288-6], IET 19562 [NDR 1036-4-3], IET 19563 [NDR 1091-3-2], IET 19370 [HKR 2002-86], IET 18747 [PAU 3042-3-3-4], IET 19272 [UPR 2545-11-2-3], IET 19287 [PAU 3116-25-5-1], IET 19295 [CRK 261], IET 19252 [RR 433-2-1], IET 19986 [RNR 754], IET 19997 [CRAC 2224-910], IET 20001 [CR 2462], IET 20003 [RP 4668-2-IR 74293-95-1-1-2-2-B], IET 20012[CN 1265-7-16], CB 04-110, VOPH-3102, Rasi, HR 12, IET 19767 [IHRT-S-7], IET 20008 [RPHR 711-1-2-3] Total = 20

sustainable strategy for managing rice diseases, including brown spot (Leung *et al.* 2003). Resistant cultivars can be reliably cultivated in both endemic and epidemic zones because they reduce disease pressure, improve yield stability, and minimise dependence on chemical fungicides. Variation in disease response among rice varieties is primarily attributed to their inherent genetic differences, and such diversity in genetic makeup forms the basis for selecting and breeding resistant lines. Numerous studies conducted over the years have confirmed extensive variability in the susceptibility of rice genotypes to brown spot disease.

Several researchers have evaluated rice germplasm for brown spot resistance. Channakeshava and Pankaja (2018) screened 50 rice varieties and observed a wide

Table 4 Percentage of germplasm/varieties showing different reaction to brown spot

Sl. no.	Reaction group	No. of germplasm/ varieties	Percentage (%)
1.	Immune (I)	0	0
2.	Highly resistant (HR)	5	1.87
3.	Resistant (R)	17	6.37
4.	Moderately resistant (MR)	20	7.49
5.	Susceptible (S)	195	73.03
6.	Highly susceptible (HS)	30	11.24

range of reactions. Out of these, 11 genotypes i.e. Sagbatta, Kavekantak, JGL-1798, Honnekattu, Raksha, BI-33, KMP-201, BR-2655, Klame, Rasi, and Togarshi were categorised as resistant, while 31 showed moderately resistant reactions. These findings highlight the availability of valuable resistance sources within traditional and locally adapted germplasm. Similarly, Alam *et al.* (2016) evaluated 25 rice germplasm lines against brown leaf spot caused by *Helminthosporium oryzae*. Among these, NDR-359, CR-1, N-18, and CR-2 expressed a highly resistant reaction, whereas seven varieties including IR36, Prasd, PR-103, Narendra-2, IR-597, Cross-116, and OC-1339 were classified as resistant. Six more genotypes such as Narendra Dhan-97, Pusa NR-381, Narendra-80, IET-849, Jallahari, and Jal Nidhi exhibited moderate resistance, while the remaining entries were rated as susceptible to highly susceptible.

Chauhan *et al.* (2000) evaluated 59 germplasm lines and reported that several entries exhibited resistant or moderately resistant reactions. Notably, Kalamkata, Rangi, and Lohana-1 were identified as highly resistant sources, whereas Aditya, Dular, Pallavi, and Areba showed moderate resistance. Interestingly, accessions such as Lohana-1, Rangi, and Jhillidhan not only demonstrated strong resistance to brown spot but also possessed desirable grain quality traits such as high linear elongation, making them promising donors for future breeding programmes aimed at improving both grain quality and disease resistance (Kumar *et al.* 2022b).

Further evidence of genetic variability in resistance has been reported in Bihar, where Jha *et al.* (2004) screened 101 cultivars during the 1999 and 2000 *kharif* seasons. Among these, two entries IET 13818 (OR-165-97-15) and IET 13830 (Rewa 14-174) were highly resistant. Additionally, 12 genotypes displayed resistant reactions, five showed moderate resistance, and the remaining cultivars ranged from moderately susceptible to highly susceptible. Under drought or low-water conditions, Yaqoob *et al.* (2011) assessed 31 rice genotypes and found that late-maturing lines such as HHZB, IR80416-B-32-3, IR84677-34-1-B, and HHZ11-Y6-Y1-Y1 were highly resistant; in contrast, most medium- and early-maturing genotypes expressed susceptibility, indicating the influence of plant maturity and physiology on disease response.

Screening efforts outside India have also revealed significant diversity. Mosharraf *et al.* (2004) evaluated 29 genotypes across two seasons (*aman* and *boro*) in Bangladesh. During the *aman* season, 25 genotypes were moderately resistant and one was resistant; during the *boro* season, 26 genotypes were moderately resistant. Anita *et al.* (2005), in their study conducted over three *kharif* seasons (2001–2003), inoculated 124 genotypes with a conidial suspension of *Bipolaris oryzae* and categorised 16 genotypes as moderately susceptible, while the remaining entries exhibited susceptible reactions.

Studies using molecular and quantitative genetic approaches have also contributed to understanding brown spot resistance. Sato *et al.* (2008) identified three QTLs associated with brown spot resistance and reported that among 14 cultivars examined, HJ-G1 and HJ-G2 were moderately resistant, whereas the others were susceptible. Magar (2015) screened 14 rice varieties in Nepal and reported that none exhibited resistance based on the IRRI disease rating scale. Most were classified as susceptible or highly susceptible, with AUDPC values ranging from 88.5–260.65, indicating high disease pressure under local conditions. Likewise, Devkota (2014) and Pantha *et al.* (2017) identified Sabitri as a resistant variety and Sawa Mansuli as a highly susceptible variety in separate evaluations.

Recent investigations reinforce the importance of identifying robust resistance sources, as many germplasm collections still tend to show susceptible reactions. For instance, Timalsina (2023) screened ten rice genotypes in Nepal and reported that none were highly resistant, mirroring results from earlier studies such as Magar (2015). Similarly, Bhandari *et al.* (2024**)** evaluated sixty genotypes at Banke, Nepal and observed that only a very small proportion displayed moderate resistance, with most genotypes falling into susceptible or highly susceptible categories. These observations are consistent with the present study, where resistant entries were limited, highlighting the persistent challenge of locating strong, durable resistance within diverse germplasm pools.

Physiological and biochemical defense traits have increasingly been recognized as important components of resistance. Ashfaq *et al.* (2021) demonstrated that resistant and moderately resistant genotypes exhibited higher levels of phenolic compounds, peroxidase activity and related biochemical markers when challenged with *Bipolaris oryzae*. Such findings help explain the differential disease reactions observed across entries in our trial and offer additional criteria for selecting superior donors in breeding programmes. The presence of resistant and moderately resistant genotypes in our study suggests that these accessions may carry similar biochemical defense mechanisms, which warrant further physiological or molecular investigation.

In addition to phenotypic screening, recent work has emphasised the relationship between brown spot resistance and agronomic traits. Kumar *et al.* (2022**)** reported significant correlations between disease severity, AUDPC values and

yield-related traits in a large panel of genotypes evaluated in eastern India. Their results supported the concept that brown spot resistance can contribute indirectly to improved productivity, particularly under endemic conditions. The resistant and moderately resistant entries identified in our study, therefore, have potential not only as donors of disease resistance but also as contributors to yield stability.

The development of hybrid and mutant lines with improved resistance has been another notable advancement. Shamshad *et al.* (2024**)** identified several resistant mutants and hybrid derivatives based on biochemical indices such as lignin content and antioxidant activity. These findings demonstrate that induced genetic variation and modern breeding approaches can effectively enhance resistance levels. While our study focused on traditional germplasm and adapted materials, integrating such improved sources into breeding pipelines may accelerate the development of high-yielding, disease-resistant cultivars suitable for regions prone to brown spot epidemics.

Overall, the extensive variation in disease reactions documented across studies underscores the importance of continuous screening and identification of resistant donors. Adoption of resistant varieties not only enables farmers to protect their crops and stabilise yields but also reduces the cost and labour associated with fungicide applications and other supplementary control measures. In contrast, susceptible and highly susceptible varieties should gradually be phased out from cultivation in endemic or epidemic zones unless they possess critical agronomic or market-preferred traits. Such varieties can be improved through the pyramiding of brown spot resistance genes into their genetic background. In situations where farmers must grow susceptible varieties, integrated disease management practices should be strongly encouraged to minimise yield losses.

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