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Response of Nepalese Rice Landraces to Brown Spot [*Bipolaris oryzae* (Breda de Haan) Shoemaker] at Rampur, Chitwan, Nepal

Rajan Lamsal*, Surakshya Ghimire, Ritesh Yadav and Hira Kaji Manandhar

Agriculture and Forestry University, Rampur, Chitwan, Nepal
*Corresponding author's email: rajan.plp07@gmail.com

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ABSTRACT

Brown spot disease, caused by the fungus *Bipolaris oryzae*, is a common foliar affliction in rice plants, impacting agricultural yields worldwide. A field experiment was conducted to identify brown spot resistant landraces at Rampur, Chitwan during June to November, 2018. A set of 54 rice genotypes comprising of 52 landraces and two checks (resistant and susceptible) were evaluated for resistance to the disease under field condition in alpha lattice design with three replicates. Area under disease progress curve (AUDPC) values varied significantly among the genotypes. Of the tested 54 genotypes, nine genotypes were found moderately resistant, 38 genotypes susceptible and seven genotypes were found highly susceptible. The maximum incidence (64.9%) of pathogen was found in seed of Hodbachhi followed by Sankharika (64.15%). The minimum average incidence of pathogen was found in check Sabitri (4.05%), which was as par with other 28 genotypes. The yield attributing characters were highly significant among the genotypes. Highest grain yield (1.55 t ha^{-1}) was obtained from Ghusara (1.51 t ha^{-1}) followed by Lalbachhi. Lowest grain yield was obtained from Ghuyeni Saro (0.21 t ha^{-1}) followed by Jaguli Mansuli (0.25 t ha^{-1}). All the yield and yield attributing characters were negatively correlated with AUDPC. Seed-borne infection after harvest was highly significant among the genotypes. The results revealed that among the screened genotypes most of the landraces of rice are susceptible to brown spot.

Keywords: AUDPC, seed-born disease, rice genotypes, resistant genotypes

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INTRODUCTION

Nepal has a wide diversity of rice landraces in all rice-growing areas from low to high altitudes. Despite the availability of various rice landraces in Nepal, there is limited research on identifying and utilizing those with inherent resistance to brown spot disease. By focusing on the discovery and characterization of brown spot-resistant rice landraces, this research aims to contribute to sustainable rice production and food security, particularly in areas prone to poor soil conditions and disease outbreaks. The rice-growing environments are highly diverse, ranging from subtropical in the plains to temperate in the mountain region of the Himalayas, where its cultivation at 2,621 m above sea level in Nepal is the highest recorded (Shahi and Heu 1979). Rice landraces, invaluable genetic resources, play a pivotal role in the development of disease-resistant varieties crucial for global food security. These traditional varieties possess inherent resistance to various pathogens, making them a vital source for breeding programs aimed at enhancing crop resilience.

Breda de Haan in 1900 first described the fungus as *Helminthosposium oryzae*, which was transferred to *Drechslera oryzae* by Subramanian and Jain (1966). Shoemaker (1959) referred it to *Bipolaris oryzae* as most of the conidia germinate from both end cells. Ito and Kuribayashi, (1927) observed teleomorph of the fungus in culture and termed as *Ophiobolus miyabeanus.* Drechsler (1934) considered that the fungus belongs to the genus *Cochliobolus* but Dastur, (1942) formally transferred it to that genus. The loss caused by the disease affects both yield and grain quality (Savary et al 2000). It caused Bengal Famine in 1942, with yield loss of 50- 90%, which resulted in death of 2 million people due to starvation. The pathogen infects the coleoptiles (causing blighting), leaves (forming oval, dark brown to purplish-brown spots) and damages the photosynthetic activities, ultimately killing the leaf. The reduction in yield can be as high as 45% in severe infection and 12% in moderate infection

(IRRI 2012). The disease is also known as poor rice farmer's disease because it occurs mostly in deficient and poor soils (Agrawal 1989, Mia 1998, Zadoks 2002). The disease has been noted to reduce yields from 6 to 90% in Asia (Padmanabhan 1973, Estrada1984, Mew and Gonzales 2002). This research was carried out with the aim of finding brown spot resistant rice landrace.

MATERIALS AND METHODS

Research site and experimental materials:

The experiment was conducted at the research field of Agriculture and Forestry University (AFU) Rampur, Chitwan, during June to November 2018. Geographically, it is located at 22° 37' North latitude and 84°25' East longitudes the altitude of this is about 228 masl (Thapa and Dangol 1988). The field was sandy loam soil. The experimental site is located in inner Terai of Nepal. Chitwan is characterized with subtropical climatic condition with cool winter, hot summer, and distinct rainy season with average rainfall of 1919.5 mm. Fifty-two local rice genotypes collected from community seed bank of Bara, Nawalparasi, Jhapa and Dang while 2 (Sabitri, an improved variety, as resistant and Sankharika, a local variety, as susceptible) were included as check for conducting the experiment. The details of the genotypes used in research presented in Table 1.

Table 1. List of 54 rice genotypes included in the study at Rampur, Chitwan, 2018

S.N.	Variety name	District	S.N.	Variety name	District
1	Chhayang	Jhapa	28	Karijker	Bara
2	Gauma	Jhapa	29	Karma	Bara
3	Gauriya	Nawalparasi	30	Kesarbachi	Bara
4	Gheupuri	Jhapa	31	Khedra	Bara
5	Ghusara	Bara	32	Komal dhan	Jhapa
6	Ghuyenisaro	Bara	33	Kusumkali	Bara
7	Godara	Jhapa	34	Laalchand	Dang
8	Golanadi	Jhapa	35	Lalbachhi	Jhapa
9	Gopal	Dang	36	Lalrenjer	Bara
10	Gosulachan	Bara	37	Madhumala	Bara
11	Hadiphor	Jhapa	38	Malathe ate	Bara
12	Hansaraj	Jhapa	39	Malbhog	Bara
13	Hapsa	Jhapa	40	Marshi dhan	Jhapa
14	Hapsa rato	Jhapa	41	Meethai	Nawalparsi
15	Hodbachhi	Jhapa	42	Najir	Jhapa
16	Jagad	Bara	43	Nakhisaro	Bara
17	Jagarnachiya	Bara	44	Pakha	Bara
18	Jaguli mansuli	Jhapa	45	Pakhar	Bara
19	Jhahar dhan	Jhapa	46	Parewapakh	Bara
20	Jhapa basmati	Bara	47	Pulingtar	Jhapa
21	Jharlajhi	Bara	48	Rajala	Bara
22	Jhinuwa	Jhapa	49	Rambela	Jhapa
23	Kaalojeera	Dang	50	Rato anadi	Dang
24	Kajh	Bara	51	Sabitri*	
25	Kalo rato anadi	Jhapa	52	Sankharika**	
26	Kanakirawi	Bara	53	Sikichan	Bara
27	Kanhar	Bara	54	Thapachini	Nawalparasi

*Resistant check, **Susceptible check

Experimental design and field lay-out

The experimental setup employed an Alpha lattice design with 18 blocks, each containing 9 plots, totalling 162 experimental plots. Each plot had dimensions of 2×1 square meters, with a consistent spacing of 20×20 centimeters between rows and plants. Replications were spaced 1 meter apart. The entire field measured 29 meters in length and 14.5 meters in breadth, providing a well-organized and efficiently managed research area for a comprehensive evaluation of the experimental factors.

Disease assessment

Randomly selected ten tillers were tagged from each plot for disease scoring. Disease was recorded from all sample tillers. Starting with the appearance of the first brown leaf spot disease symptoms, tagged tillers within each plot was visually scored for percentage foliar infection (severity) at seven days' interval. A total of six scorings were done. The effect of disease (severity) on rice variety was integrated into area under disease progress curve (AUDPC). The observations were made as per the 0-9 (IRRI 2002).

Estimation of area under disease progress curve

Area under disease progress curve (AUDPC) was calculated by analysing the progress of disease severity (Das et al 1992).

Resistance and susceptibility category of genotypes

The genotypes were categorized into four categories based on the AUDPC values as described by Aryal and Shrestha (2013) as shown in Table 2.

Table 2. Resistant and susceptible categories of rice genotypes based on mean AUDPC value

Mean AUDPC	Category	Symbol
> 340	Highly susceptible	HS
260-340	Susceptible	S
180-260	Moderately resistant	MR
<180	Resistant	R

HS= Highly susceptible, S= Susceptible, MR=Moderately resistant, R=Resistant

Harvesting, threshing and total grain yield

The rice crop was harvested depending on their maturity period when the crop turned yellowish to golden colour. Total yield of different genotypes was taken from net plot (whole plot removing the outer two boarder rows). The rice crop was cut, dried for two days and threshed and total grain yield was weighed.

Grain moisture percentage was recorded using moisture meter at the time of weighing. The final grain yield was adjusted at 12% moisture level by using the following formula Paudel (1995).

$$\text{Grain yield} = \frac{(100\text{- MC}) \times \text{Plot yield (kg)} \times 10000\ \text{m}^2 \times 1000}{(100\text{-}12) \times \text{Plot area}}$$

Where, MC= Moisture content of grain in percentage

Seed-borne infection test

Seed samples were taken from each plot and tested in laboratory after harvesting by using standard blotter method (ISTA 1976) for the brown spot pathogen. Two hundred seed of each plot were used for blotter test.

The seeds were plated on Petri dishes having two layered moistened blotting paper in 1:8:16 fashions from the centre to periphery i.e. twenty-five seeds in each plate were plated in two layered moistened blotting paper in 1:8:16 fashions from the centre to periphery i.e. twenty-five seeds in each plate.

The Petri-plates were incubated in an incubator at 25°C. After 7 days, seeds were observed under stereo microscope to find out the seed borne infection by *B. oryzae* and percentage of seed infection was calculated as below:

$$\text{Seed infection (\%)} = \frac{\text{Number of infected seeds} \times 100}{\text{Total number of seeds observed}}$$

Data analysis

The agronomical and disease scoring were tabulated in excel data sheet and the recorded data were subjected to analyse by using the reference of Gomez & Gomez (1984). The data was processed to fit into R-studio and analyses were conducted using R 3.0.3 (R Core Team 2013) and the agricolae v1.1-8 package (de Mendiburu 2014). The data entry was done to develop ANOVA table and different treatments were compared. Using Duncan's multiple range test at 5% level of significance and correlation analysis was done by SPSS. All the figures and graphs were prepared by using Microsoft excel 2013.

RESULTS AND DISCUSSION

Category of rice genotypes on the basis of mean AUDPC values

The AUDPC values increased with time in most of the genotypes. The mean AUDPC value ranged from 226.59 to 401.33 among the genotypes. Of the total 54 rice genotypes screened in the field, based on AUDPC value, none of the genotypes was resistant to the disease. However, nine genotypes viz.Gauriya, Ghusara, Ghuyenisaro, Golanadi, Lalrenger, Malbhog, Marshi Dhan, Najir, and Nakhisaro were found moderately resistant. Similarly, 38 genotypes were susceptible, seven genotypes highly susceptible to brown spot. The mean AUDPC of Brown spot of rice was significant among the treatments. Lowest AUDPC was obtained in Malbhog (226.59) followed by Najir (230.22) which was at par with resistance check Sabitri (307.48) and other 27 genotypes. Highest AUDPC was obtained in Lalbachhi (401.33) followed by Laalchand (387.33) which was at par with suspectible check Sankharika (324.07) and other 12 genotypes. In Chitwan of Nepal, out of 14 rice varieties, none of these varieties were found either resistant or highly resistant to disease. Only 2 varieties were found moderately resistant and rest of them were susceptible to disease (Magar 2015). Similarly, Akwa Ibom State of Nigeria, 12 rice varieties were screened for resistance to brown spot disease under natural infection condition, no one variety was found to be highly resistant, most of the variety were susceptible i.e 50% (Nneke 2012).

Table 3: Mean AUDPC of brown leaf spot on rice genotypes in the field at AFU, Rampur, Chitwan, 2018

Genotypes	Mean AUDPC	Category
Chhayang	280.78^{d-l}	Susceptible
Gauma	286.74^{c-l}	Susceptible
Gauriya	254.07^{g-l}	Moderately resistant
Gheupuri	308.44^{b}	Susceptible
Ghusara	247.33^{h-l}	Moderately resistant
Ghuyenisaro	259.78^{f-l}	Moderately resistant
Godara	301.78^{c-l}	Susceptible
Golanadi	238.52^{i-l}	Moderately resistant
Gopal	322.52^{a-h}	Susceptible
Gosulachan	317.85^{b-i}	Susceptible
Hadiphor	278.44^{d-l}	Susceptible
Hansaraj	307.48^{b-l}	Susceptible
Hapsa	309.04^{b-l}	Susceptible
Hapsa rato	323.56^{a-h}	Susceptible
Hodbachhi	343.26^{a-e}	Highly susceptible
Jagad	365.56^{a-c}	Highly susceptible
Jagarnachiya	294^{c-l}	Susceptible
Jaguli mansuli	275.85^{d-l}	Susceptible
Jhahar dhan	268.07^{e-l}	Susceptible
Jhapa basmati	291.93^{c-l}	Susceptible
Jharlajhi	324.07^{a-h}	Susceptible
Jhinuwa	276.89^{d-l}	Susceptible
Kaalojeera	267.04^{e-l}	Susceptible
Kajh	305.93^{b-l}	Susceptible
Kalo rato anadi	295.04^{c-l}	Susceptible
Kankirawi	332.37^{a-g}	Susceptible
Kanhar	320.96^{a-i}	Susceptible
Karijker	315.26^{b-j}	Susceptible
Karma	311.63^{b-k}	Susceptible
Kesarbachi	331.85^{a-g}	Susceptible
Khedra	317.85^{b-i}	Susceptible
Komal dhan	338.59^{a-f}	Susceptible
Kusumkali	357.26^{a-d}	Highly susceptible
Laalchand	387.33^{ab}	Highly susceptible
Lalbachhi	401.33^{a}	Highly susceptible
Lalrenjer	256.15^{f-l}	Moderately resistant
Madhumala	277.41^{d-l}	Susceptible
Malathe ate	294^{c-l}	Susceptible
Malbhog	226.59^{l}	Moderately resistant

Genotypes	Mean AUDPC	Category
Marshi dhan	234.37^{j-l}	Moderately resistant
Maathai	289.33^{c-l}	Susceptible
Najir	230.22^{kl}	Moderately resistant
Nakhisaro	255.63^{g-l}	Moderately resistant
Pakha	277.93^{d-l}	Susceptible
Pakhar	314.22^{b-j}	Susceptible
Parewapakh	343.26^{a-e}	Highly susceptible
Pulingtar	358.3^{a-d}	Highly susceptible
Rajala	275.85^{d-l}	Susceptible
Rambela	283.11^{c-l}	Susceptible
Rato anadi	280^{d-l}	Susceptible
Sabitri	307.48^{b-l}	Susceptible
Sankharika	324.07^{a-h}	Susceptible
Sikichan	336.52^{a-g}	Susceptible
Thapachini	289.85^{c-l}	Susceptible
Grand mean	300.24	
CV%	18.67	
LSD	2.62	
P value	0.014	
SEM(±)	0.05	

AUDPC: Area under disease progress curve, CV: Coefficient of variation, LSD: Least significant difference, Means followed by the same letter in a column are not significantly different by DMRT at 1% level of significance, SEm (±) indicates standard error of mean

Yield and yield attributing characters

The data on yield and yield attributing charaters such as the average number of panicles per plant, the average panicle length, average number of effective tillers per meter square, and thousand grain weight are presented in Table 4.The average number panicle per plant of rice among the genotypes was highly significantly different. Highest panicle number per plant was obtained from Kanakirawi (19.8) followed by resistant check Sabitri (14.73). The lowest panicle number per plant was obtained from Ghuyeni saro (6.366) followed by Jhapa Basmati (6.366). The average panicle length of rice among the rice genotypes was highly significantly different. Highest panicle length was obtained from Hadiphor (25.92) followed by Jhapa Basmati (25.55). Lowest panicle length was obtained from susceptible check Sankharika (12.09) followed by Thapachini (16.06). The average number effective tiller per meter square was highly significantly different among the rice genotypes. Highest effective tiller number per meter square was obtained from Jagad (195.33) followed by Lalbachhi (185.66) and resistance check sabitri (178.33). Lowest effective tiller number per meter square was obtained from Gauma (81.33) followed by susceptible check Sankharika (101).

The thousand grain weight was significantly different among the rice genotypes. Highest thousand grain weight was obtained from resistance check Sabitri (25.366) followed by Pakhar (24.36). Lowest thousand grain weight was obtained from Jaguli Mansuli (11.56) followed by Marshi Dhan (15.33). The average grain yield was significantly different among the rice genotypes. Highest grain yield was obtained from Ghusara (1.55) followed by Lalbachhi (1.51) which was at par with other 3 genotypes. Lowest grain yield was obtained from Ghuyeni saro (0.210) followed by Jaguli Mansuli (0.250) which was at par with 8 others rice genotypes. Panicle traits, as important determinants of sink capacity, have been studied by many genetic researchers (Cui et al 2002, Hong and Leng 2004, Xu et al 2004, Mei et al 2006, Xing et al 2008). Many of these studies focused on panicle size (number of spikelets per panicle), which shows a large range of variation and is the major objective of improvement in rice breeding (Tian et al 2006).

Table 4. Yield and yield attributing traits of rice genotypes at Rampur Chitwan, 2018

Genotypes	No. of panicles/plant	Panicle length (cm)	Number of effective tiller/m^2	Thousand grain weight (g)	Grain yield (t ha^{-1})
Chhayang	8.94^{n-s}	24.37^{a-e}	129.67^{q}	22.13^{k}	0.61^{k-p}
Gauma	11.2^{d-g}	24.93^{a-c}	81.33^{F}	23.23^{f}	0.48^{p-u}
Gauriya	7.87^{s-x}	22.49^{d-m}	122.33^{t-v}	20.87^{m}	0.35^{r-x}
Gheupuri	6.97^{x-A}	19.13^{s-v}	158.33^{g}	16.23^{y}	0.29^{v-x}
Ghusara	9.53^{k-q}	24.23^{a-f}	161.67^{f}	21.63^{l}	1.56^{a}
GhuyeniSaro	6.37^{A}	20.93^{j-s}	165.67^{e}	17.43^{wx}	0.21^{x}
Godara	6.67^{y-A}	24.24^{a-e}	174.67^{d}	22.83^{g}	0.73^{h-l}

Genotypes	No. of panicles/plant	Panicle length (cm)	Number of effective tiller/m^2	Thousand grain weight (g)	Grain yield (t ha^{-1})
Golanadi	7.47^{v-z}	23.12^{c-i}	121.67^{u-w}	20.23^{op}	0.49^{o-t}
Gopal	7.27^{x-A}	20.63^{l-s}	117^{z}	23.47^{e}	0.71^{i-m}
Gosulachan	10.57^{g-k}	23.37^{c-h}	137.67^{lm}	16.27^{y}	1.46^{ab}
Hadiphor	12.2^{cd}	25.93^{a}	153.33^{h}	21.47^{l}	0.45^{p-v}
Hansaraj	9.07^{m-r}	23.13^{c-i}	125.33^{rs}	17.5^{wx}	0.74^{h-l}
Hapsa	11.2^{d-g}	21.35^{h-r}	154.67^{h}	19.87^{q}	0.46^{p-v}
Hapsa rato	6.73^{y-A}	23.24^{c-h}	146^{k}	19.17^{s}	1.41^{ab}
Hodbachhi	10.13^{g-m}	22.96^{c-k}	136^{mn}	17.6^{w}	0.45^{p-v}
Jagad	7.33^{w-A}	21.76^{g-p}	195.33^{a}	24.13^{c}	1.45^{ab}
Jagarnachiya	7.33^{w-A}	24.58^{a-d}	136.33^{mn}	22.4^{ij}	1.19^{cd}
Jaguli mansuli	8.73^{o-t}	19.57^{q-v}	120.67^{v-x}	11.57^{A}	0.25^{wx}
Jhahar dhan	10.33^{g-l}	18.36^{uv}	120.33^{wx}	23.33^{ef}	0.98^{e-g}
Jhapa basmati	6.6^{zA}	25.55^{ab}	137.33^{lm}	19.53^{r}	0.66^{j-o}
Jharlajhi	8.8^{o-t}	19.21^{s-v}	145.33^{k}	23.27^{f}	0.28^{v-x}
Jhinuwa	9.77^{i-o}	25.05^{a-c}	105.67^{BC}	20.43^{n}	0.68^{j-n}
Kaalojeera	12.34^{c}	23.05^{c-j}	125.33^{rs}	22.43^{ij}	0.45^{p-v}
Kajh	9.6^{j-p}	22^{g-p}	138.33^{l}	23.77^{d}	1.04^{d-f}
Kalo/rato anadi	12.53^{c}	18^{vw}	136^{mn}	19.17^{s}	0.55^{m-q}
Kankirawi	19.8^{a}	21.36^{h-r}	137.67^{lm}	18.27^{uv}	1.28^{bc}
Kanhar	7.53^{u-z}	22.12^{f-p}	106.67^{B}	18.13^{v}	0.88^{f-i}
Karijker	9.67^{i-p}	21.08^{i-s}	119.33^{x}	17.37^{x}	0.89^{f-h}
Karma	8.87^{n-s}	20.87^{k-s}	123.33^{tu}	17.43^{wx}	0.57^{l-q}
Kesarbachi	8.6^{p-u}	22.59^{d-m}	110.67^{A}	22.17^{k}	0.3^{u-x}
Khedra	12.13^{cd}	20.58^{m-t}	123.67st	17.47^{wx}	0.46^{p-v}
Komal dhan	11.8^{c-f}	20.16^{o-u}	103.67^{D}	21.47^{l}	0.56^{l-q}
Kusumkali	10.73^{f-i}	23.54^{b-g}	151^{i}	20.23^{op}	0.76^{h-k}
Laalchand	8.4^{r-w}	19.46^{r-v}	124^{r-t}	22.27^{jk}	0.34^{s-x}
Lalbachhi	8.93^{n-s}	22.27^{e-o}	185.67^{b}	19.5^{r}	1.52^{a}
Lalrenjer	8.4^{r-w}	20.48^{m-t}	104.33^{CD}	21.57^{l}	0.3^{u-x}
Madhumala	9.07^{m-r}	22.73^{d-l}	135.33^{no}	19.53^{r}	0.5^{n-t}
Malathe ate	10.87^{e-h}	23.64^{b-g}	135.33^{no}	21.47^{l}	0.82^{g-j}
Malbhog	12.53^{c}	21.09^{i-s}	149^{j}	19.87^{q}	0.57^{l-q}
Marshi dhan	10.47^{g-k}	21.69^{g-q}	150.33^{ij}	15.33^{z}	1.1^{c-e}
Meethai	11^{e-h}	19.17^{s-v}	133.67^{op}	20.13^{p}	0.49^{o-t}
Najir	11.87^{c-e}	20.62^{l-s}	125.67^{r}	21.57^{l}	0.42^{q-w}
Nakhisaro	7.73^{t-y}	20.34^{n-u}	117.33^{yz}	20.33^{no}	0.51^{n-s}
Pakha	10.33^{g-l}	20.54^{m-t}	125.33^{rs}	22.63^{h}	0.46^{p-v}
Pakhar	9.93^{h-n}	20.63^{l-s}	133.33^{p}	24.37^{b}	0.76^{h-k}
Parewapakh	10.6^{g-k}	22.26^{e-o}	166^{e}	20.27^{n-p}	0.8^{g-j}
Pulingtar	9.07^{m-r}	18.48^{t-v}	119^{xy}	18.87^{t}	1.08^{de}
Rajala	8.6^{p-u}	21.53^{g-r}	173.33^{d}	22.47^{hi}	1.13^{c-e}
Rambela	10.67^{g-j}	20.07^{p-v}	123^{tu}	23.37^{ef}	0.8^{g-j}
Rato anadi	9.33^{l-r}	20.53^{m-t}	153.67^{h}	24.27^{bc}	0.84^{g-j}
Sabitri	14.73^{b}	22.33^{e-n}	178.33^{c}	25.37^{a}	1.18^{cd}
Sankharika	9.93^{h-n}	12.1^{x}	101^{E}	18.43^{u}	0.53^{m-r}
Sikichan	7.47^{v-z}	22.02^{g-p}	103.67^{D}	17.43^{wx}	0.33^{t-x}
Thapachini	8.47^{q-v}	16.07^{w}	103.33^{D}	15.47^{z}	0.45^{p-v}
Grand mean	9.66	21.51	131.28	20.31	0.78
CV%	24.31	12.26	17.39	13.6	19.27
LSD	1.09	2.12	1.99	0.17	0.18
P value	<2e-16	<2e-16	<2e-16	<2e-16	<2e-16
SEM(±)	0.31	0.35	3.17	0.37	7.6

Figure in column with same letter are not significantly different ($p=0.05$) according to DMRT, LSD = Least significance difference, SEM = Standard error of mean difference, ** highly significant at $p<0.001$

Correlation between grain yield and AUDPC

Based on correlation coefficient value, grain yield showed negatively correlated with area under disease progress curve.

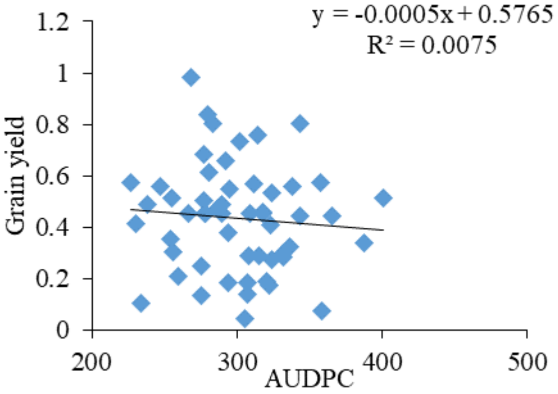

Figure 1. Correlation of Area under disease progress curve with Grain yield

Seed-borne infection count

Seed-borne inoculum after harvest was highly significant among the genotypes. The maximum average incidence of pathogen was found in seed of Hodbachhi (64.9%) followed by Sankharika (64.15%), which was as par with Pulingtar.The minimum average incidence of pathogen was found in resistance check Sabitri (4.05%), which was as par with Rambela, Rajala, Parewapakh, Pakhar, Pakha, Meethai, Marsidhan, Malbhog, Malathe ate, Laalchand, Kusumkali, Komal dhan, Keserbachi, Karijker, Karma, Kanhar, Kankirawi, Jhinuwa, Jagad, Hapsarato, Hansaraj, Chhayang, Gauriya, Ghusara, Golanadi, Gopal, Gosulachan and Hadiphor. Also, in the present study, moderately resistant genotypes like Gauriya, Ghusara and Golanadi observed in the field had less seed infection by *B. oryzae*. Similar results were also found by other researchers in Nepal (Lamsal 2006, Aryal 2013, Devkota 2014). Lamsal (2006) and Devkota (2014) reported lowest seed infection in Sabitri (12.5%). These results proved that these genotypes are still maintaining the same reaction of resistance *B. oryzae* in our conditions.

Table 5. Incidence of *B. oryzae* in rice seed of various genotypes after harvest

Treatments	Incidence (%)
Chhayang	4.05^{q}
Gauma	25.82^{k}
Gauriya	4.05^{q}
Gheupuri	32.56^{g}
Ghusara	4.05^{q}
Ghuyenisaro	23.16^{n}
Godara	26.54^{k}
Golanadi	4.05^{q}
Gopal	4.05^{q}
Gosulachan	4.05^{q}
Hadiphor	4.05^{q}
Hansaraj	4.05^{q}
Hapsa	22.76^{no}
Hapsa rato	4.05^{q}
Hodbachhi	64.9^{a}
Jagad	4.05^{q}
Jagarnachiya	29.65^{i}
Jaguli mansuli	24.71^{l}
Jhahar dhan	35.95^{f}
Jhapa basmati	48.71^{d}
Jharlajhi	28.63^{j}
Jhinuwa	4.05^{q}
Kaalojeera	26.18^{k}
Kajh	62.36^{b}
Kalorato anadi	57.08^{c}
Kanakirawi	4.05^{q}

Treatments	Incidence (%)
Kanhar	4.05^{q}
Karam	4.05^{q}
Karijker	4.05^{q}
Kesarbachi	4.05^{q}
Khedra	29.32^{ij}
Komal dhan	4.05^{q}
Kusumkali	4.05^{q}
Laalchand	4.05^{q}
Lalbachhi	23.56^{mn}
Lalrenger	4.053^{q}
Madhumala	30.64^{h}
Malathe ate	4.05^{q}
Malbhog	4.05^{q}
Marshi dhan	4.05^{q}
Meethai	4.05^{q}
Najir	40.08^{e}
Nakhisaro	21.96^{o}
Pakha	4.05^{q}
Pakhar	4.05^{q}
Parewapakh	4.05^{q}
Pulingtar	64.13^{a}
Rajala	4.05^{q}
Rambela	4.05^{q}
Ratoanadi	24.33^{lm}
Sabitri	4.05^{q}
Sankharika	64.15^{a}
Sikichan	26.18^{k}
Thapachini	17.92^{p}
Grand mean	18.014
CV %	3.37567
LSD	0.84931
F value	***

CV: Coefficient of variation, LSD: Least significant difference, Means followed by the same letter in a column are not significantly different by DMRT.

Correlation between mean AUDPC and Seed Infection (%)

Based on the correlation coefficient value, seed infection (%) was positively correlated with mean area under disease progress curve of disease in different genotypes during field screening. It was found that as the value of AUDPC increased, seed infection (%) was also increased. Thus the value of seed infection (%) (r=0.09) was positively correlated with area under disease progress curve (AUDPC).

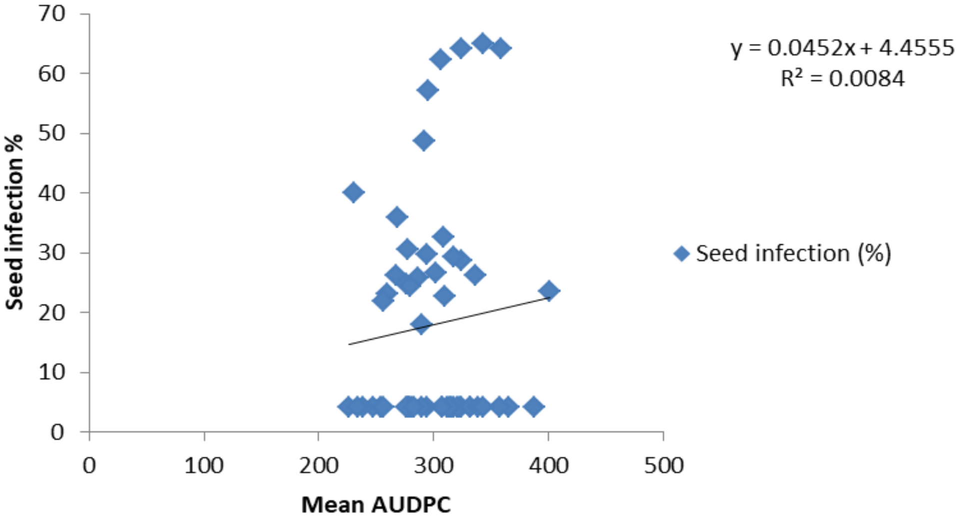

Figure 2. Correlation between mean AUDPC and seed infection (%)

CONCLUSIONS

From the present experimental studies, it can be concluded that the genotypes varied highly in brown spot incidence, AUDPC and seed infection. Among 54 rice genotypes, Malbhog and Najir were found to be the most resistant with mean AUDPC values of 226.59 and 230.22, respectively and slow disease progress rates. The genotype Lalbachhi was found highly susceptible with mean AUDPC of 401.33 and fast disease progress rate. Sabitri still had the lowest percentage of seed infection (4.05%). Lalbachhi was found to be tolerant to the disease as it gave higher yield inspite of their higher AUDPC and maximum seed infection. Many genotypes recorded more susceptible to brown leaf spots than the susceptible check Sankharika.

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AUTHORS' CONTRIBUTION

Rajan Lamsal: Data collection, organization of experimental dataset, data visualization, literature review, data analysis and report writing

Surakshya Ghimire: Data analysis and report writing.

Ritesh Yadav and Hira Kaji Manandhar: Regular constructive comments and support during this research work; guidance during the preparation of the manuscript.

CONFLICT OF INTEREST

The authors have no conflict of interest to declare.

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