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Phenotypic Screening of F_3 Rice (*Oryza sativa* L.) Population Resistance Associated with Sheath Blight Disease

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ABSTRACT

The experiment was conducted during July–December, 2019 in the Agricultural Research Farm Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India. One hundred and twenty-two F_3 rice populations from the cross made between IC277332 (susceptible parent)×IC277275 (moderately resistant parent) were evaluated against sheath blight disease under field conditions. The area under disease progress curve (AUDPC) values categorized rice population into four groups viz., moderately resistant (24), moderately susceptible (38), susceptible (40), and highly susceptible (20). A moderate resistance level to the disease was identified during the study in 24 lines (19.6%) with a mean Percentage Disease Index (PDI) of 12.22%–36.6%. Furthermore, 38 individuals showed moderate susceptibility with AUDPC values (1012–1446 day^{-1}). The maximum PDI and AUDPC value were 76.11 and 2325.56, and the minimum PDI and AUDPC values were 22.78 and 622.22, respectively. The principal component (PCA) biplot analysis showed 71.62% and 12.05% variation, respectively. Unweighted Pair Group Method of Arithmetic Means (UPGMA) cluster analysis grouped the 122 individuals into two major clusters, A and B and sub-clusters. These findings indicated that no rice line resistant to sheath blight had been identified. However, few population lines exhibited moderate resistance, which can be utilized as donor lines to generate sheath blight-resistant rice cultivars. These findings will provide a solid basis for our future breeding and screening activities at the institution.

KEYWORDS: Biplot-analysis, cluster analysis, IC277275, IC277332, sheath blight, UPGMA

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1. INTRODUCTION

Sheath blight (ShB) of rice (*Oryza sativa* L.) is a major rice disease worldwide, including in India. This disease is caused by *Rhizoctonia solani* Kuhn (Teleomorph: *Thanetophorus cucumeris* (Frank) Donk). Rice crops with high attainable yields (Koshariya et al., 2018) are exclusively affected. Yield loss estimate 0–50% in susceptible cultivars has been reported under favorable environmental conditions (Lee and Rush, 1983, Slaton et al., 2003).

R. solani is one of the destructive pathogens of economic significance, second most prevalent to the blast disease (Molla et al., 2020). The disease usually develops during the peak tillering, and it affects all the plant components above the water-line, including leaf sheaths, upper leaves, internodes, and panicles. In general, the presence of one or more comparatively large, oblong, or irregularly elongated lesions on the leaf sheath aids in the disease diagnosis (Uppala and Zhou, 2018). Under favorable conditions, the infection spreads quickly to the upper plant portions and the neighbouring plants through runner hyphae. Finally, the disease is known as sheath blight because it causes the blighting of leaf sheaths. The diseased plants are usually found in a circular pattern, referred to as a 'bird's nest' locally (Hollier et al., 2009). Brown fluffy mycelium and brown to dark brown sclerotia can be seen freely adhering to lesions in wet circumstances and are easily detached from the plants when they reach maturity (Dath, 1990). The disease can also infect panicles, causing empty or partially filled discolored seed-bearing brownish-black blotches or black to ashy grey patches to appear (Acharya et al., 2004).

The disease's control is primarily dependent on chemical fungicides. However, fungicides are neither environmentally friendly nor cost-effective. ShB losses can be managed by developing resistant cultivars. Genetic diversity is a prerequisite of any crop improvement program. Progeny attained from divergent parents shows more significant heterosis and provides a wide range of variability in segregating generation. Till now, only limited resistance has been achieved by transforming rice cultivars with defense genes (Dey et al., 2020). Due to the lack of immune donors in farmed cultivars, breeding for resistance to sheath blight has always been tedious (Bonmann et al., 1992) since the resistance is impacted by agronomic characteristics such as plant height, plant density (Pinson et al., 2005), tillering, and heading date (Pan et al., 1999). Likewise, several studies in rice breeding for sheath blight resistance, and large-scale germplasm screening of wild species for resistant genes, have put a tremendous effort to find resistance lines (Goswami et al., 2019, Pavani et al., 2020). As a result, to date, there is no single report of ShB resistant rice germplasm across the world (Shi et al., 2020). However, a few major resistance genes have been identified from either cultivated rice or wild relatives (Molla et al., 2020) and only a few varieties such as Tetep, ARC 10531, Teqing, Jasmine 85, Tadukan (Yadav et al., 2015, Zarbafi and Ham, 2019) and some of the landraces such as Jarjan, Nepal 555, Nepal 8 (Shiobara et al., 2013) were reported to be moderately resistant. Although extensive attempts have been undertaken worldwide to find disease-resistant germplasm, no resistance cultivars or lines are found against this disease in rice. Plant Breeders utilize genetic diversity knowledge to choose parents for hybridization programs. Knowledge obtained from genetic diversity analysis will also be helpful for developing high-yielding genotypes with sheath blight resistance. Therefore, the study's objective was to estimate the diversity of 122 F_3 rice lines in terms of susceptibility to sheath blight, according to the genetic group and morphological traits under field conditions.

2. METHODS AND MATERIALS

2.1. Plant Materials and experimental design

The seeds of one hundred and twenty-two rice population lines of F_3 generation made by the cross of IC277332 (susceptible parent) and IC277275 (moderately resistant parent) was collected from Late Prof. Vineeta Singh, Department of Plant Pathology, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, UP, India. All the experiments were conducted during June–December 2019 in the Agricultural Research Farm Institute of Agricultural Sciences, Banaras Hindu University (25°18´N, 83°03´E, 75.7 MSL, Varanasi, Uttar Pradesh, India.

Healthy seeds were sown alongside susceptible (Pusa Basmati-1) (Shamim et al., 2014) and resistant (Tetep) (Sha and Zhu, 1990) check types in nursery beds prepared by combining soil, sand, and FYM (3:1:1, w/w) Under adequate light and moisture conditions were maintained for the excellent growth of the seedlings. The field experiment was conducted using an alpha lattice design with a plot size of 3×4 m^2. Each treatment was replicated three times. Each population line was grown in a 1m long row with 30 cm between rows and 10 cm between the plants. The appropriate agronomic steps were taken to ensure a good crop.

2.2. Source of the pathogen culture

The highly virulent isolate of *Rhizoctonia solani,* AG-1 IA (MTCC-12227) procured from the Department of Mycology and Plant Pathology, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi was used in this study.

2.3. Artificial inoculation of the pathogen

The field was irrigated just after transplantation. All the

plots were inoculated individually at the tillering stage with immature sclerotia of virulent strain *R. solani*. After inoculation, the spot was covered by cotton and a few drops of sterilized water were added to keep it moist for a longer duration and for uniform disease infection. Inoculation was performed in the evening hours (Singh et al., 2002b).

2.4. Disease evaluation

The disease scoring was scored using a 0–9 scale (SES) (Anonymous, 2014). The disease severity was calculated at weekly intervals up to the 28th day after inoculation (DAI) (Goswami et al., 2019, Pavani et al., 2020) by measuring the relative lesion height (RLH) in each tiller was calculated as described by Sharma et al. (1990).

RLH=(Maximum height at which lesion appear/plant hei ght)×100 …….(1)

The area under disease progress curve (AUPC) (Shaner and Finney, 1997) and Percentage disease index (PDI) (Wheeler, 1969) were calculated as per the formula

$AUDPC=\sum^{n=1}_{i=1}\{[(X_{i+1}+X_i)/2)]\times(t_{i+1}-t_i)\}$ ……(2)

Where, n=the total number of observations,

Xi=disease index expressed as a proportion at the i^{th} observation,

t_i=time at the i^{th} observations.

PDI=(Sum of all ratings ×100)/(Total number of observations × maximum rating scale) ……(3)

2.5. Data recording on agronomic traits

Data from the following parameters were collected according to the guidelines described in standard evaluation systems for rice (Anonymous, 2014).

Plant height (PHT): The average height of 5 plants from the ground level to the tip of the tallest panicle was measured in centimetres (cm) at maturity.

Panicle length (PNL): The Length of the panicle was measured by a centimetre scale starting from the tip of the neck to the tallest spikelet.

Tiller number per hill (TNH): The number of tillers was counted from the primary and secondary culms of a hill.

2.6. Statistical analysis

Population distribution, analysis of variance (ANOVA) for sheath blight-related parameters, and morphological trait and Pearson's correlations analysis were performed using Window stat 7.5 version. The Euclidean cluster analysis based on UPGMA was conducted in the PAST software 4.0 version. Multivariate principal component analysis was executed using XLSTAT 2018 software.

3. RESULTS AND DISCUSSION

3.1. Distribution and grouping of population

A wide range of diversification among the 122 F_3 rice individuals was examined for various traits (Table 1). Based on the pooled value, simple statistics of all the variables unveiled that plant height of the entries of the plant population ranged from 61.70 cm–134.3 cm with a mean height of 89.88 cm and a standard deviation of 15.27. Skewness and Kurtosis of plant height were analyzed as 0.62 and 0.08, respectively. Panicle length varied from 12.70 cm–23.90 cm with an average of 17.76 cm and a standard deviation of 2.03. Skewness and Kurtosis of panicle length were -0.07 and 0.28, respectively. The number of tillers per plant ranged from 3.9 tillers $plant^{-1}$ to 9.8 tillers $plant^{-1}$. Average tillers per plant were 5.82, and the standard deviation was 1.01, while skewness and kurtosis of the number of tillers were 0.74 and 1.21, respectively.

In addition, the maximum and minimum lesion length after

Table 1: Descriptive statistics of different traits of rice

Traits	Min	Max	Sum	Mean	S. E	σ^2	σ	Median	SK	K	GM	C. V
PHL	61.70	134.30	10965.65	89.88	1.38	233.28	15.27	87.15	0.62	0.08	88.64	16.99
TP	3.90	9.80	709.60	5.82	0.09	1.03	1.01	5.80	0.74	1.21	5.73	17.42
PL	12.70	23.90	2166.54	17.76	0.18	4.13	2.03	17.93	-0.07	0.28	17.64	11.45
7th day	7.78	66.67	3282.52	26.91	1.15	160.72	12.68	25.00	0.68	-0.08	24.00	47.12
14th day	11.11	66.67	4086.00	33.49	1.20	175.61	13.25	32.22	0.40	-0.63	30.81	39.57
21st day	24.44	88.89	6962.22	57.07	1.36	225.67	15.02	56.67	-0.02	-0.79	54.96	26.32
28th day	42.22	100.00	9507.19	77.93	1.18	170.34	13.05	80.00	-0.47	-0.31	76.75	16.75
Mean PDI	22.78	76.11	5959.48	48.85	1.14	158.45	12.59	48.19	0.11	-0.76	47.17	25.77
AUDPC	622.22	2325.56	172259.10	1411.96	36.88	165896.90	407.30	1382.50	0.19	-0.78	1351.46	28.85

SE: Standard error; σ: Standard deviation; σ^2: Variance; SK: Skewness; K: Kurtosis; GM: Geometric mean; CV: coefficient of variation; PHL: Plant height to leaf; PL: Panicle length; TP: Tillers $plant^{-1}$; PDI: Percent disease index; AUDPC: Area under disease progress curve

seven days of inoculation was 66.67 and 7.78, respectively, with an average value of 26.91 and a standard deviation of 12.68. Skewness and Kurtosis at seven days were 0.62 and -0.08, respectively. Similarly, the maximum and minimum lesion length after 14 days of inoculation was 66.67 and 11.11, respectively, while after 21 days of inoculation was 88.89 and 24.44, respectively. The average value at 14 days was 33.49 and for 21 days was 57.07. Standard deviation, skewness, and kurtosis on the 14th day were analysed as 13.25, 0.40 and -0.63, respectively. Also, standard deviation, skewness, and kurtosis of 21st days were 15.02, -0.02, and -0.79, respectively. The maximum and minimum lesion length after 28 days of inoculation was 100 and 42.22, respectively, with an average value of 77.93 and a standard deviation of 13.05. Skewness was analysed as -0.47, while Kurtosis was -0.31 on the 28th day of inoculation.

The maximum PDI and AUDPC value were 76.11 and 2325.56, and the minimum PDI and AUDPC values were 22.78 and 622.22, respectively. The average value of PDI was 48.85% and of AUDPC was 1411.96. Standard deviation, skewness, and kurtosis of PDI were 12.59, 0.11, and -0.76, respectively. Also, standard deviation, skewness, and kurtosis of AUDPC were 407.30, 0.19, and -0.78, respectively. Analysis of variance (ANOVA) revealed the variation in the population for different traits were depicted in Table 2.

Table 2: Summary analysis of variance of different traits of rice

Source	df	Mean sum of squares								
		PHL	TN	PL	PDI of 7th day	PDI of 14th day	PDI of 21st day	PDI of 28th day	Mean PDI	AUDPC
T	121	466.57**	2.05*	8.26**	321.44^{ns}	351.21^{ns}	451.35**	340.68**	316.89**	331793.83**
R	1	2558.95**	10.38**	0.76^{ns}	13000.38**	13050.17**	11287.40**	11168.81**	12109.97**	12131695.65**
Error	121	89.49	1.41	5.46	279.63	269.88	291.74	133.69	177.93	206892.07
Total	243									

**: p=0.01; *: p=0.05; ns: Represents non-significance; PHL: plant height to leaf; TN: Tiller number; PL: panicle length; TP: tillers plant^{-1}; PDI: Per cent disease index; AUDPC: Area under disease progress curve; T: Treatments; R: Replication

Among the different traits studied, PDI of 7th and 14th day was non-significant at the genotypic level, whereas in replication, panicle length was non-significant, rest of the traits were significant at (p>0.05%). Principal component biplot analysis was performed to determine the relationship among the traits responsible for sheath blight resistance. The PC1 and PC2 elucidated around 71.62% and 12.05% of the variation, respectively, wherein PC1 and PC2 accounted for 83.67% of the total variability (Figure. 1).

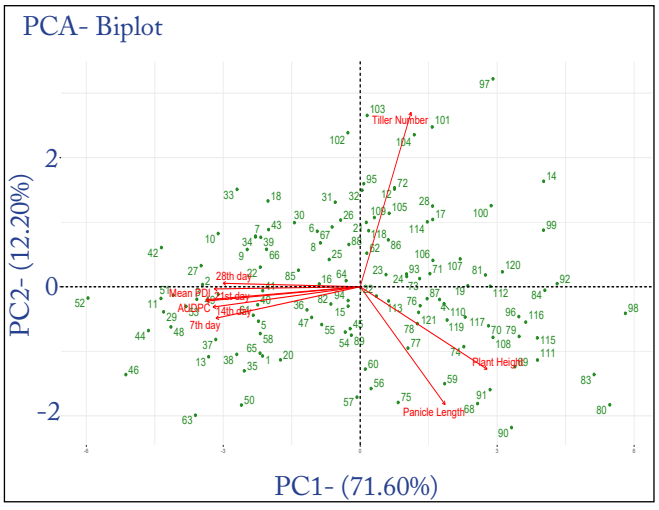

Figure 1: Biplot graph for various traits in the F_3 rice population

The analysis indicated that the traits *viz.*, mean PDI strong positively correlated with PDI at 7th, 14th, 21st, 28th day, and AUDPC. While tiller number plant^{-1} has a less strong correlation to plant height and panicle length.

However, PDI at 7th, 14th, 21st, 28th, mean PDI and AUDPC have formed a separate group (highly correlated). Similarly, panicle length and plant height have formed another group (positively correlated). The position and perpendicular projection of F_3 population positions onto variable vector under field condition identify susceptible lines showed increase in PDI at 7th, 14th, 21st, 28th, mean PDI and AUDPC values. On the contrary, moderate resistant lines moved to quadrant 4 (opposite to quadrant 3), exhibiting increases in plant height and panicle length of plants. However, tiller number had a non-significant correlation with plant height and panicle length.

The estimates of Pearson's correlation coefficients among plant height, tillers per plant, PDI at 7th, 14th, 21st, and 28th day, mean PDI and AUDPC along with significance based on the p-value. The trait PDI on the 7th day was found to be positively correlated with PDI on the 14th day (0.971), mean PDI (0.939), and AUDPC (0.950). PDI on the 14th day is positively correlated with mean PDI (0.955) and AUDPC (0.966). At the same time, PDI on the 21st day was positively correlated with mean PDI (0.946) and AUDPC (0.950). At the same time, plant height is negatively correlated

with mean PDI (-0.758) and PDI on the 14th day (-0.751). However, tiller number showed no correlation with plant height and panicle length (Table 3).

The Unweighted Pair Group Method of Arithmetic Means (UPGMA) cluster analysis led to the grouping of the 122 individuals into 2 main clusters and sub-clusters. The mapping panel is divided into 2 main clusters I and II (Figure 2). Clusters I can again be divided into IA consisting of 15 highly susceptible populations and IB consisting of 23 population lines belonging to 19 susceptible and 4 highly susceptible. Cluster II is further sub-divided into IIA and IIB. Subcluster IIA is again sub-divided into IIA1 and IIA2, consisting of 23 and 33 population lines designated as susceptible and moderately susceptible, respectively. Similarly, subcluster IIB is again sub-divided into IIB1 and IIB2, with 12 and 16 lines depicted as moderately resistant and moderately susceptible, respectively.

3.2. Screening of rice F_3 population against sheath blight disease resistance under field conditions

Crop variety/cultivar assessment against various crop diseases is critical (Mew et al., 2004), and a continuous process is necessary not only for identifying the source of resistance genes or QTLs but also for detecting the occurrence of virulence pathotypes in comparison to particular crop diseases (Singh et al., 2016). However, despite screening hundreds of rice germplasms, including improved accessions, wild types, landraces, and mapping populations, no source of ShB resistance has been identified (Shiobara et al., 2013, Shamim et al., 2014, Goswami et al., 2019, Bal et al., 2020). In the present investigation, a total of 122 F_3 rice population lines derived from the cross between IC 277332 (susceptible) and IC 277275 (moderately resistant) were screened under field conditions for rice sheath blight resistance. Meanwhile, similar results were obtained when 108 germplasms were screened under both natural and artificially inoculated conditions by Chandra et al. (2016). Dong et al. (2012) investigated the F_2 population of rice consisting of 286 individuals and found a deep-water rice variety with good resistance to sheath blight which was produced by crossing between 'HH1B' and 'RSB03'. Based on the area under the disease progress curve (AUDPC), all the rice individuals were categorized into four categories viz., moderately resistant (MR: AUDPC=622.2–1011.1), moderately susceptible (MS: AUDPC=1012–1446), susceptible (S: AUDPC=1447–1866) and highly susceptible (HS: AUDPC=1867–2326) (Table 4).

Table 3: Pearson's correlation analysis of various traits of rice

Variables	PHT	TN	PL	7th day*	14th day*	21st day*	28th day*	Mean*	AUDPC
PHT	1	0.062	0.612	-0.629	-0.689	-0.751	-0.749	-0.758	-0.747
TN	0.062	1	0.029	-0.344	-0.305	-0.264	-0.271	-0.316	-0.312
PL	0.612	0.029	1	-0.425	-0.429	-0.427	-0.418	-0.456	-0.451
7th day	-0.629	-0.344	-0.425	1	0.971	0.826	0.716	0.939	0.950
14th day	-0.689	-0.305	-0.429	0.971	1	0.847	0.751	0.955	0.966
21st day	-0.751	-0.264	-0.427	0.826	0.847	1	0.836	0.946	0.950
28th day	-0.749	-0.271	-0.418	0.716	0.751	0.836	1	0.887	0.849
Mean PDI	-0.758	-0.316	-0.456	0.939	0.955	0.946	0.887	1	0.997
AUDPC	-0.747	-0.312	-0.451	0.950	0.966	0.950	0.849	0.997	1

*: Percent disease index; PHL: Plant height to leaf; TN: Tiller number; PL: panicle length; TP: Tillers plant^{-1}; PDI: Percent disease index; AUDPC: Area under disease progress curve

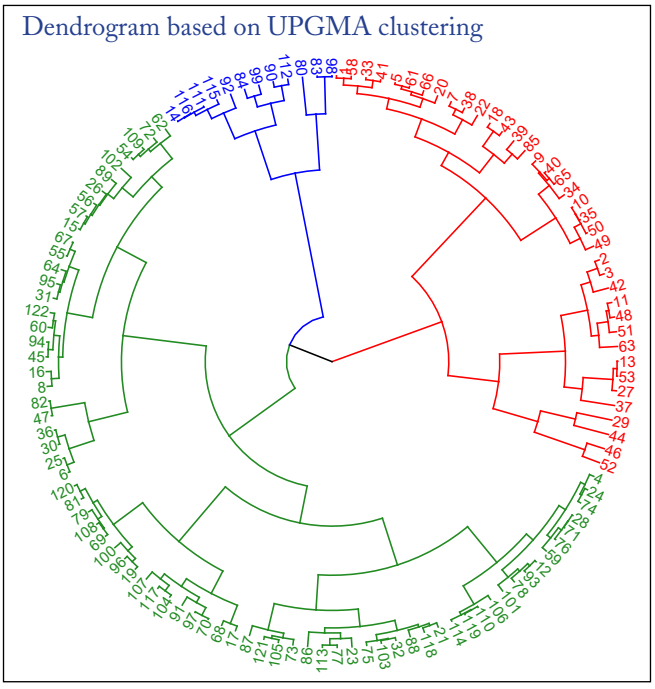

Figure 2: Dendrogram based on UPGMA clustering of rice population based on various morphological traits

Table 4: Host reaction of F_3 population lines of rice-based on AUDPC and mean PDI values

Host response	AUDPC	Mean PDI (%)	Rice Population	No. of lines
Moderately resistant	622.2–1011.1	<36.1	RST1-14, RST1-19, RST1-69, RST1-70, RST1-79, RST1-80, RST1-81, RST1-83, RST1-84, RST1-90, RST1-92, RST1-96, RST1-97, RST1-98, RST1-99, RST1-100, RST1-108, RST1-111, RST1-112, RST1-115, RST1-116, RST1-117, RST1-120, Tetep.	24
Moderately susceptible	1012–1446	36.2–49.44	RST1-4, RST1-12, RST1-17, RST1-21, RST1-23, RST1-24, RST1-28, RST1-32, RST1-54, RST1-59, RST1-62, RST1-68, RST1-71, RST1-72, RST1-73, RST1-74, RST1-75, RST1-76, RST1-77, RST1-78, RST1-86, RST1-87, RST1-88, RST1-89, RST1-91, RST1-93, RST1-94, RST1-101, RST1-104, RST1-105, RST1-106, RST1-107, RST1-109, RST1-110, RST1-113, RST1-114, RST1-118, RST1-119	38
Susceptible	1447–1866	49.5–62.5	RST1-1, RST1-5, RST1-6, RST1-7, RST1-8, RST1-9, RST1-15, RST1-16, RST1-18, RST1-20, RST1-22, RST1-25, RST1-26, RST1-30, RST1-31, RST1-33, RST1-34, RST1-36, RST1-38, RST1-39, RST1-40, RST1-41, RST1-43, RST1-45, RST1-47, RST1-55, RST1-56, RST1-57, RST1-58, RST1-61, RST1-60, RST1-64, RST1-65, RST1-66, RST1-67, RST1-82, RST1-85, RST1-95, RST1-102, RST1-103	40
Highly susceptible	1867–2326	>62.5	RST1-2, RST1-3, RST1-10, RST1-11, RST1-13, RST1-27, RST1-29, RST1-35, RST1-37, RST1-42, RST1-44, RST1-46, RST1-48, RST1-49, RST1-50, RST1-51, RST1-52, RST1-53, RST1-63, PB-1	20

PDI: Percent disease index; AUDPC: Area under disease progress curve

The majority of the F_3 rice population was conferred as susceptible when compared with susceptible control cultivar (Pusa Basmati-1). Moreover, Praveen et al. (2018) in their investigation, performed screening on 57 germplasms of rice through artificial inoculation under field conditions and found most of the germplasms were highly susceptible, except Orgoja, which was resistant and Gopal Ghosh that was moderately resistant. Our present investigation revealed 24 lines (19.6%) (RST1-14, RST1-19, RST1-69, RST1-70, RST1-79, RST1-80, RST1-81, RST1-83, RST1-84, RST1-90, RST1-92, RST1-96, RST1-97, RST1-98, RST1-99, RST1-100, RST1-108, RST1-111, RST1-112, RST1-115, RST1-116, RST1-117, RST1-120 and Tetep) were moderately resistant with a mean percent disease index (PDI) between 22.7–36.00. A set of 38 lines (RST1-4, RST1-12, RST1-17, RST1-21, RST1-23, RST1-24, RST1-28, RST1-32, RST1-54, RST1-59, RST1-62, RST1-68, RST1-71, RST1-72, RST1-73, RST1-74, RST1-75, RST1-76, RST1-77, RST1-78, RST1-86, RST1-87, RST1-88, RST1-89, RST1-91, RST1-93, RST1-94, RST1-101, RST1-104, RST1-105, RST1-106, RST1-107, RST1-109, RST1-110, RST1-113, RST1-114, RST1-118, RST1-119) exhibited moderate susceptibility with a mean per cent disease index (PDI=36.30–49.50). Moreover, our present experiment, revealed that a relatively higher set of 40 (32.7%) individuals (RST1-1, RST1-5, RST1-6, RST1-7, RST1-8, RST1-9, RST1-15, RST1-16, RST1-18, RST1-20, RST1-22, RST1-25, RST1-26, RST1-30, RST1-31, RST1-33, RST1-34, RST1-36, RST1-38, RST1-39, RST1-40, RST1-41, RST1-43, RST1-45, RST1-47, RST1-55, RST1-56, RST1-57, RST1-58, RST1-61, RST1-60, RST1-64, RST1-65, RST1-66, RST1-67, RST1-82, RST1-85, RST1-95, RST1-102, RST1-103) showed susceptible reaction with a mean % disease index (PDI=49.7–62.5). Of the remaining population, 20 (16.5%) lines (RST1-2, RST1-3, RST1-10, RST1-11, RST1-13, RST1-27, RST1-29, RST1-35, RST1-37, RST1-42, RST1-44, RST1-46, RST1-48, RST1-49, RST1-50, RST1-51, RST1-52, RST1-53, RST1-63, PB-1) were conferred as highly susceptible when compared to the control (Tetep). Our results agreed with Pavani and Singh et al. (2018) who screened 196 genotypes in open field conditions over the seasons and reported that the majority of genotypes were found to be moderately susceptible compared to resistant check Tetep.

Despite screening thousands of rice germplasms, only a few rice cultivars offer resistance to ShB that have been reported, viz., Teqing (Pinson et al., 2005), Jasmine 85 (Liu et al., 2009), Tetep (Channamallikarjuna et al., 2010), Pecos (Sharma et al., 2009), Sabitri (Chaudhary, 2016). Moreover, a high level of resistance has been reported in rice lines viz., YSBR 1 in China (Zuo et al., 2009), BPL 7–12 and BML 27–1 in India (Dubey et al., 2014a, b) and Pecos

in Malaysia and USA (Sharma et al., 2009, Willocquet et al., 2011). Moderate to a good level of resistance has been reported from different wild rice accessions like *O. nivara, O. barthi, O. meridionalis, O. officinalis, O. rufipogon,* and *O. latifolia* (Ram et al., 2008, Prasad and Eizanga, 2008). Moreover, our results agree with the previous reports of several studies (Nadarajah et al., 2014, Hossain et al., 2014, Tejaswini et al., 2017, Pavani et al., 2020).

4. CONCLUSION

Rice germplasms lacked the complete resistance against sheath blight. The goal of our research was to look for resistance in an F_3 population line resulting from a cross between IC277332 and IC277275. The plants were in turn recorded with certain agronomic traits to study their correlation with PDI. Out of 122 rice population lines, twenty-four moderate resistant lines were showed fewer AUDPC values than Tetep (R-check). None of the rice lines was completely resistant to sheath blight disease.

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