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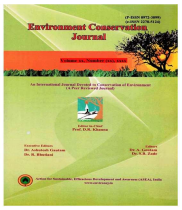

Evaluation of $F_{2:3}$ rice population resistant to *Rhizoctonia solani* Kuhn inciting sheath blight disease

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ABSTRACT

Rice sheath blight caused by the soil-borne fungal pathogen *Rhizoctonia solani* Kuhn is an economically important disease in rice resulting in enormous yield losses worldwide. In the present investigation, a population constituting F_3 lines resulted from the cross made between IC277332 (susceptible parent) and Tetep (resistant parent) were evaluated for sheath blight resistance and other agronomic traits over a season. The rice population lines were categorized into four groups *viz.*, moderately resistant (11), moderately susceptible (63), susceptible (24), and highly susceptible (8), based on area under disease progress curve (AUDPC) values. During the study, nine moderate resistant lines showed, less AUDPC values in comparison to Tetep. Furthermore, 63 individuals (60%) exhibited moderate susceptibility with AUDPC values (677-987 per day). The principal component biplot analysis PC1 and PC2 showed 47.08% and 13.19% variation, respectively. The employment of Unweighted Pair Group Method of Arithmetic Means (UPGMA) cluster analysis led to the grouping of the 106 individuals into 2 major clusters A and B. The results suggested that none of the rice lines was resistant to sheath blight disease. However, few lines showed moderate resistance to the disease which can be exploited for the development of sheath blight-resistant cultivars.

Introduction

Rice production and productivity are affected by certain abiotic and biotic factors which causes yield losses of up to 45% (Margani and widadi, 2018). Among all the biotic stresses, the fungal diseases in rice are most predominant throughout the world. The productivity of rice is affected by several pathogens (Margani and widadi, 2018), of which sheath blight (ShB) disease caused by *Rhizoctonia solani* Kuhn is one of the destructive pathogens of economic significance, second most prevalent to the blast disease (Zheng *et al*., 2013; Molla *et al*., 2020). Rice sheath blight pathogen, *Rhizoctonia solani* [Teleomorph: *Thanatephorus cucumeris* (A.B. Frank) Donk] is a globally ubiquitous and ecologically diverse soil-borne pathogen with a broad host range infecting many important crops worldwide. The pathogen causes severe yield losses to the extent of 5.9 to 69 per cent to rice crops in advanced crop stages (Richa *et al*., 2016; Neha *et al*., 2016). The typical symptoms include oval or ellipsoidal greenish-grey irregular lesions on leaf sheath initially just above the water level later spreading across other plant parts often with grey-white centres surrounded by brown margins which appear maximum at tillering stage (Uppala and Zhou, 2018). As the lesion progress, the centre of the lesion gets bleached with an irregular purple-brown margin and develops new infection

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structures throughout the entire plant, causing significant necrotic damage (Yellareddygari *et al*., 2014; Singh *et al*., 2016). The sclerotia are produced by the pathogen on basal leaf sheaths serves as a primary source of inoculum which appears white when young, later turns brown to dark brown (Uppala and Zhou, 2018), and can remain viable up to 3 years in soil or water (Kumar *et al.,* 2009). The wide host range of the pathotypes and fluctuations in the pathogen within the local population are the crucial factors influencing the management strategies (Mew *et al*., 2004). The control of ShB in the field so far has mainly relied upon the application of chemical fungicides, but their utility is delimited, primarily due to complications related to timing and application cost, weather dependencies, and a potentially damaging environmental impact by increasing pesticide residues (Mew *et al*., 2004). Due to these situations, the advance and use of resistant genotypes may be a highly effective way to manage the disease.

Several studies suggested the extensive efforts of workers in rice breeding for sheath blight resistance and large-scale germplasm screening of wild species for resistance genes (Turaidar *et al.,* 2017; Praveen *et al.,* 2019; Goswami *et al*., 2019; Pavani *et al*., 2020). Moreover, assessing the resistance to sheath blight in paddy fields is a very challenging task as the resistance is greatly influenced by agronomic traits such as plant height, the density of plants (Pinson *et al.,* 2005), tillering and heading date (Pan *et al.,* 1999). Studies suggested that resistance to *R. solani* in rice is a complex, quantitative trait that is generally controlled by polygenes (Sha and Zhu, 1989; Pinson *et al*., 2005; Koshariya *et al*., 2018). As a result, to date there is no single report of the sheath bight resistant rice germplasm across the world (Zeng *et al*., 2011; Shi *et al.,* 2020; Bhunkal *et al*., 2015). 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), BPL7-12, BML27-1, BML 21-1 and Kajarahwa (Dubey *et al.,* 2014) were reported to be moderately resistant. Lemont, IR 50, Pusa Basmati-1, BPT-5204 (Yadav *et al.,* 2015) are highly susceptible to the sheath blight disease under field conditions. Therefore, keeping in mind the aforesaid facts, the current research program was planned and designed to discover ShB resistance in the rice population. The present study was undertaken to develop and screen the F_3 population of rice for reaction to sheath blight resistance.

Material and Methods

Plant materials and experimental design

The seeds of 106 rice population lines of F_3 generation resulted from the cross between IC277332 (susceptible parent) and Tetep (resistant parent) were collected from Prof. Vineeta Singh, Department of Mycology and Plant Pathology, Banaras Hindu University, Varanasi, UP, India. All the experiments were conducted during the cropping season 2019-2020 in the Agricultural Research Farm (North Eastern Plain zone, India, 25º18´N, 83º03´E, 75.7 MSL), Banaras Hindu University, Varanasi. The nursery beds were prepared by mixing soil, sand, and FYM (3:1:1, w/w), healthy seeds were sown along with the susceptible (Pusa Basmati-1) (Adhipathi *et al*., 2013) and resistant (Tetep) (Sha and Zhu, 1990) check varieties. Under adequate light and moisture conditions were maintained for the good growth of the seedlings. Alpha lattice design with the plot size of 3×4 m^2 was used to conduct the field experiment. There were three replications for each treatment. Each population line was grown in a 1 m long row with inter and intra row spacing of 30 and 10 cm, respectively. To ensure a good crop, the necessary agronomic measures were followed.

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.

Pathogen inoculation

Single sclerotia based inoculum of a virulent strain of *R. solani* (MTCC-12227) (anastomosis group AG1-1A), was maintained on PDA medium at 28 $\pm$ 2° C. This isolate produces typical ShB symptoms on sheath and leaves and typical mycelial growth and sclerotia production. MTCC-12227 has been used in previous studies (Goswami *et al*., 2018, Goswami *et al*., 2019). Plants at the booting stage were inoculated with the pathogen by placing

immature sclerotia or mycelial bits (approx. 0.25 mg) in leaf sheath (Singh *et al*., 2002a, b). After inoculation, the spots were covered with wet absorbent cotton pre-soaked in sterile water to maintain moist conditions that facilitate the development of infection. Inoculation was carried out in the evening hours so that the inoculated site remains moist for a longer duration.

Scoring of disease severity

The disease scoring was done using a 0-9 scale (SES) (IRRI, 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)

$$RLH = \frac{maximum\ heigh\ \ at\ which\ lesion\ appear}{plant\ heigh} \times 100$$

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

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

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.

$$\text{PDI} = \frac{Sum\ of\ all\ ratings \times 100}{Total\ no.of\ observations \times maximum\ rating\ scale}$$

Data recording on agronomic traits

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

Grain yield (*YLD*): The Weight of the grains per plant was measured by grams (g).

Test weight (*TW*): 100 seed weight per plant was measured by grams (g).

Statistical analysis

The analysis of the obtained data was carried out following the alpha lattice design using Microsoft Office Excel 2019, 32 bit. The values of data were subjected to population distribution, analysis of variance (ANOVA) for sheath-blight related parameters, and morphological traits. Pearson's correlations analysis was performed by Window stat 7.5 version. Euclidean cluster analysis based on UPGMA was performed in the PAST computer software 4.0 version. Multivariate principal component analysis was executed by XLSTAT 2018 software.

Results and Discussion

Distribution and grouping of population

The frequency distribution of the studied population suggested the presence of wide variation Table 1. The mean, median and mode values were found to be different, which indicated the asymmetric distribution of data. Among the parameters studied, PHT, PNL, and TNH were negatively skewed, whereas the remaining parameters were positively skewed. Kurtosis values ranged between -1 to +1 for all the traits other than PDI on the 7th day (2.89) and 14th day (2.23), kurtosis values were <3, which showed a frequency of the studied population was platykurtic. The coefficient of variation was found to be reasonable and varied from 7.2 (plant height) to 42.1 (PDI of 7th day), which showed the population had higher variability. The analysis of variance (mean sum of squares) for 9 agronomic traits of 106 population lines is presented in Table 2. Among the treatments, all the traits were found to be significantly different other than PNL and TNH, whereas, in replication, YLD, TW, and PDI of the 28th day showed non-significant results. The results of our study indicate that an appreciable level of variability is present among the population concerning sheath blight resistance and agronomic traits recorded. The estimates of Pearson's correlation coefficients (Table 3) among agronomic traits resulted in a highly significant correlation of mean PDI with AUDPC (0.765). Plant height was negatively associated with PDI of the 28th day (-0.630), the mean PDI (-0.571), and the AUDPC (-0.524). TNH and TW have indicated negligible correlation with all other parameters.

Table 1: Descriptive statistics of different traits of rice population lines during wet season 2019-2020

Trait	Mean	Median	Mode	Kurtosis	Skewness	Range	Min	Max	Sum	C.V(%)
PHT	123.12	124.1	128.8	0.72	-0.67	48.4	92.9	141.3	13049.84	7.2
PNL	19.18	19.105	18.6	-0.27	-0.03	6.82	15.2	22.02	2033.51	7.5
TNH	5.35	5.4	6	-0.57	-0.11	4.8	3.1	7.9	567.75	19.4
YLD	11.04	10.93	#N/A	0.22	0.18	15.17	4.503	19.679	1170.67	25
TW	2.39	2.38	2.1	-0.21	0.27	1.18	1.87	3.055	254.03	10.4
PDI of 7th day	18.65	15.55	15.55	2.89	1.71	36.67	10	46.67	1974.72	42.1
PDI of 14th day	20.05	17.77	17.77	2.23	1.48	36.11	11.11	47.22	2125.83	38.8
PDI of 21st day	37.01	35.56	33.33	0.34	0.56	48.89	13.33	62.22	3923	26.6
PDI of 28th day	58.94	57.78	64.44	0.02	0.21	57.78	31.11	88.89	6248.22	18.6
Mean PDI	33.65	31.67	29.44	1.15	1.07	40.56	18.89	59.44	3567.94	23.9
AUDPC	935.89	863.33	770	1.31	1.17	1191.94	521.11	1713.05	99204.58	26.8

C.V- coefficient of variance; min- minimum value; max- maximum value; sum- total summation; PHT-plant height; PNL- panicle length; TNH-tiller number per hill; YLD- yield of plant; TW- test weight (100 grains); PDI- Percent Disease Index; AUDPC- Area Under Disease Progress Curve; N/A- not available

Table 2: Analysis of variance for various traits of rice during wet season 2019-2020.

Source of Variation	Degrees of freedom	Mean squares										
		PHT	PNL	TNH	YLD	TW	PDI of 7th day	PDI of 14th day	PDI of 21st day	PDI of 28th day	Mean PDI	AUDPC
Treatment	105	161.43**	4.15ns	2.18ns	15.18**	0.13**	124.08**	121.53**	194.34**	240.80**	130.30**	126443.74**
Replication	1	405.83*	534.80**	2.63ns	7.26ns	0.0015ns	407.41*	525.86*	1817.11**	422.02ns	706.05**	812814.48**
Error	105	58.81	6.25	1.47	6.68	0.05	49.78	54.87	101.28	106.36	51.51	51508.09

****significance value at 0.01%, * significance value at 0.001%, ns-non significance; PHT-plant height; PNL- panicle length; TNH-tiller number per hill; YLD- yield of plant; TW-test weight (100 grains); PDI- Percent Disease Index; AUDPC- Area Under Disease Progress Curve**

Table 3: Pearson's correlation analysis for various traits of rice during wet season 2019-2020

Variables	PHT	PNL	TNH	YLD	TW	PDI of 7th DAY	PDI of 14th DAY	PDI of 21st DAY	PDI of 28th DAY	Mean PDI	AUDPC
PHT	1	0.287	0.001	0.166	0.185	-0.482	-0.487	-0.398	-0.630	-0.571	-0.524
PNL	0.287	1	-0.265	-0.066	0.016	-0.201	-0.157	-0.102	-0.185	-0.181	-0.165
TNH	0.001	-0.265	1	0.249	-0.130	0.129	0.106	0.195	0.147	0.167	0.166
YLD	0.166	-0.066	0.249	1	0.112	0.099	0.037	0.070	-0.018	0.048	0.060
TW	0.185	0.016	-0.130	0.112	1	0.006	-0.041	-0.095	-0.204	-0.107	-0.082
PDI of 7th DAY	-0.482	-0.201	0.129	0.099	0.006	1	0.966	0.718	0.630	0.911	0.926
PDI of 14th DAY	-0.487	-0.157	0.106	0.037	-0.041	0.966	1	0.741	0.637	0.920	0.940
PDI of 21st DAY	-0.398	-0.102	0.195	0.070	-0.095	0.718	0.741	1	0.648	0.880	0.909
PDI of 28th DAY	-0.630	-0.185	0.147	-0.018	-0.204	0.630	0.637	0.648	1	0.845	0.765
Mean PDI	-0.571	-0.181	0.167	0.048	-0.107	0.911	0.920	0.880	0.845	1	0.990
AUDPC	-0.524	-0.165	0.166	0.060	-0.082	0.926	0.940	0.909	0.765	0.990	1

PHT-plant height; PNL- panicle length; TNH-tiller number per hill; YLD- yield of the plant; TW- test weight (100 grains); PDI- Percent Disease Index; AUDPC- Area under disease progress curve, curve and *PDI* per cent disease index; the range is based on the minimum value of the group plus CD value.

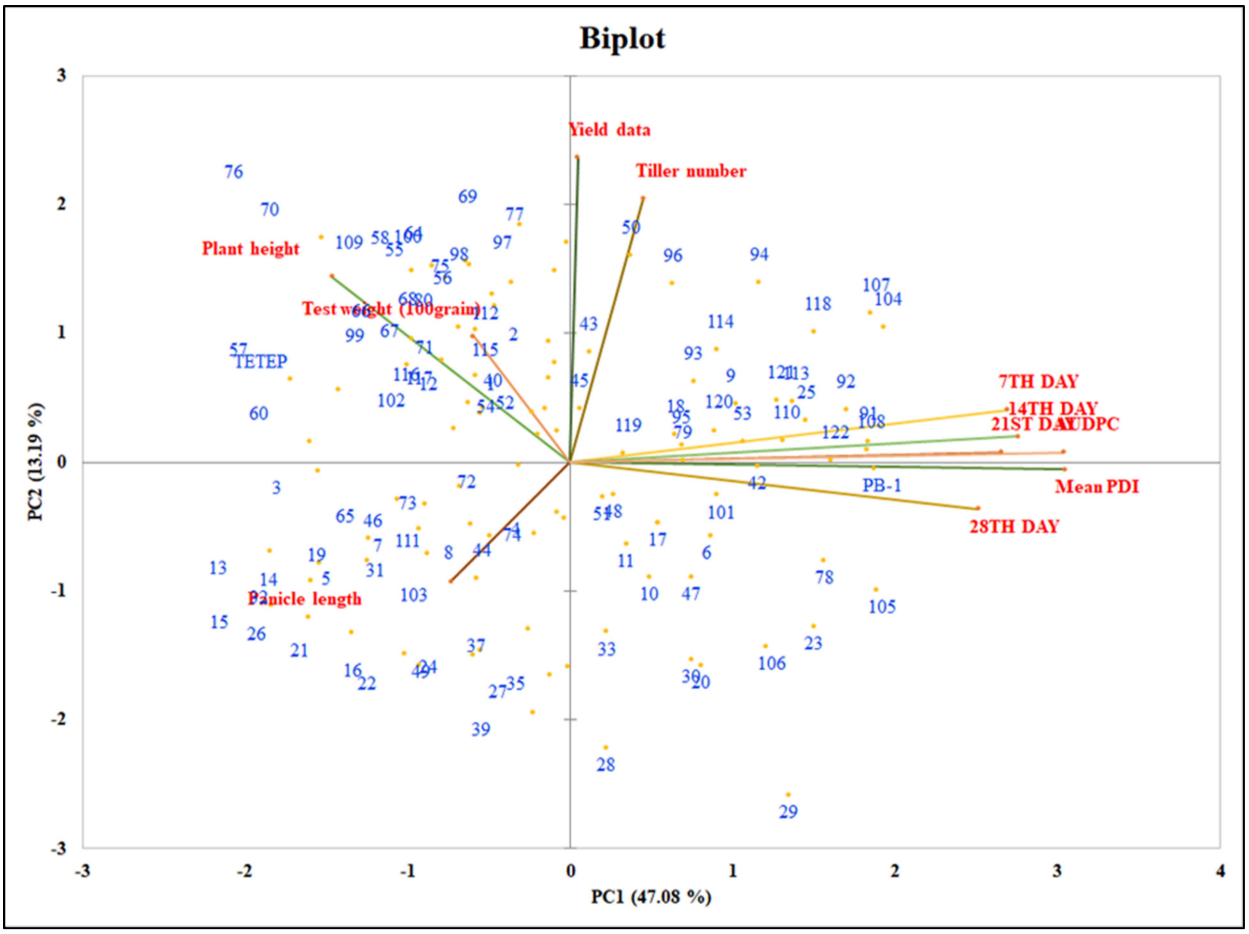

Figure 1: Biplot graph for various traits in the F_3 rice population. PCA biplot graph conceded connection between variables by vector angle. The analysis indicated that the traits *viz.*, mean PDI strong positively correlated with PDI at 7th, 14th, 21st, 28th day, and AUDPC. While plant height has a less strong correlation to tiller number per plant and panicle length. Similarly, yield data is strongly correlated with tiller number per plant.

The PCA biplot analysis for the F_3 population was carried out to find the grouping pattern of various agronomic traits under field conditions. The population by trait biplot analysis accounted for 60.24% of the variation among the F_3 population by the first two components. The PC1 captured 47.08% of variation and PC2 explained 13.19% variation of the total variability (Figure 1). The longest vector load such as mean PDI and AUDPC were observed to be the main distinguishing factors for grouping the population. PCA biplot figure conceded connection between variables by vector angle. The analysis indicated that the traits *viz.,* mean PDI, and AUDPC depicted a negative correlation with PHT and TW but they had no correlation with YLD and TNH. PCA biplot diagram displayed a good separation of the population lines which was high in agreement with the UPGMA clustering. The biplot diagram (Figure 1) indicated significant discrimination of the population lines into quadrangles. The Unweighted Pair Group Method of Arithmetic Means (UPGMA) cluster analysis led to the grouping of the 106 individuals into 2 major clusters, A and B. The dendrogram of the 106 individuals was constructed using correlation coefficient (CP) = 0.62. The largest cluster, A constituted 85 F_3 population lines which were further subdivided into 2 sub-clusters namely, A1 and A2. The sub-group A1 had a total of 11 individuals which were moderately resistant, including Tetep. Subcluster

A2 was further subdivided into A2-1 and A2-2. The dendrogram designated that the sub-group A2-1 contained 20 individuals with varying degrees of SB resistance including 8 susceptible and 12 moderately susceptible individuals. The largest sub-group, A2-2 consisted of 54 moderately susceptible individuals which represent 50% of the total population.

Cluster B, consisting of 21 individuals, was further sub-divided into two groups B1 and B2 with a similarity coefficient of 0.59. Out of these, 14 individuals which were found susceptible were assigned into sub-group B1 and the remaining 7 individuals along with PB-1 were reassigned into sub-group B2 which are highly susceptible (Figure. 2).

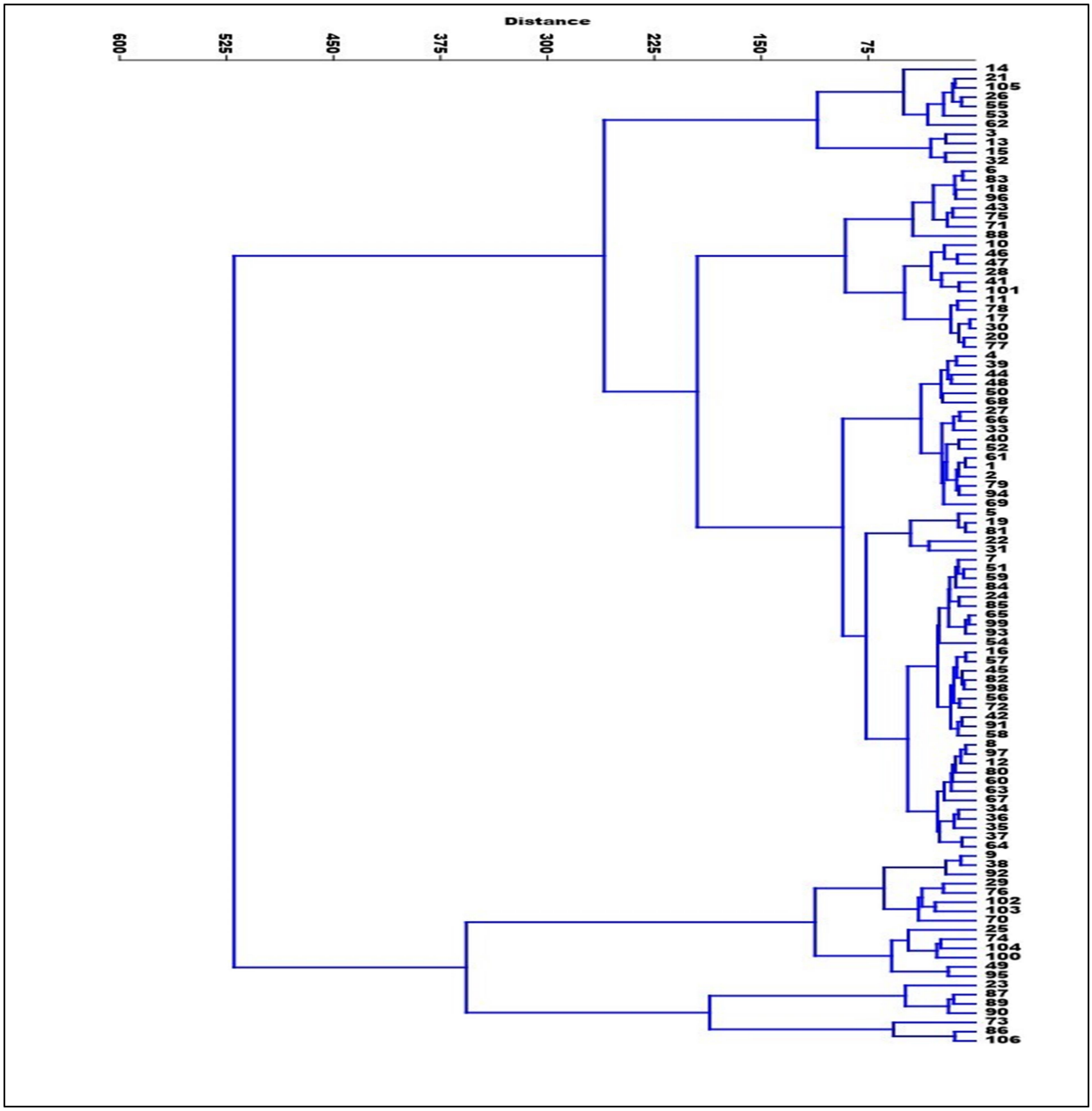

Figure 2: Dendrogram based on UPGMA clustering of rice population based on various traits during the wet season of 2019.

Screening of F_3 population of rice for sheath blight (*Rhizoctonia solani* AG-1 IA) resistance under field condition

Assessment of crop varieties/cultivars against diverse crop diseases is essential (Mew *et al*., 2004), and a continual process required not only for finding the source of resistance genes or QTLs but also for recognizing the incidence of virulence pathotypes in contrast to specific crop diseases (Singh *et al*., 2016). However, various researchers have attempted to screen thousands of rice germplasms including improved accessions, wild types, landraces, and mapping populations but they couldn't come up with any source of resistance to ShB (Zuo *et al.,* 2009; Williocquet *et al.,* 2012; Dubey *et al.,* 2014). In present study, a total of 106 F_3 individuals of rice were screened for sheath blight resistance using highly virulent strain of *Rhizoctonia solani* AG-1 IA (MTCC-12227) under field conditions. Depending on the area under disease progress curve (AUDPC) values, the rice population was classified into four categories viz., (I) moderately resistant (MR: AUDPC = 521-676), (II) moderately susceptible (MS: AUDPC = 677-987), (III) susceptible (S: AUDPC = 988-1314), and (IV) highly susceptible (HS: AUDPC = 1315-1713) (**Table 4**). Eleven lines (9.8%) (SB-T-3, SB-T-13, SB-T-14, SB-T-15, SB-T-21, SB-T-26, SB-T-32, SB-T-53, SB-T-55, SB-T-62, and TETEP) were found moderately resistant with mean percent disease index (PDI) between 12.22 to 23.33. Furthermore, our present experiment, revealed that a relatively higher set of 63 individuals (60%) (SB-T-1, SB-T-2, SB-T-4, SB-T-5, SB-T-7, SB-T-8, SB-T-10,SB-T-11, SB-T-12, SB-T-16, SB-T-17, SB-T-19, SB-T-22, SB-T-24, SB-T-27, SB-T-28, SB-T-30, SB-T-31, SB-T-33, SB-T-34, SB-T-35, SB-T-36, SB-T-37, SB-T-39, SB-T-40, SB-T-41, SB-T-42, SB-T-44, SB-T-45, SB-T-46, SB-T-47, SB-T-48, SB-T-50, SB-T-51, SB-T-52, SB-T-54, SB-T-56, SB-T-57, SB-T-58, SB-T-59, SB-T-60, SB-T-61, SB-T-63, SB-T-64, SB-T-65, SB-T-66, SB-T-67, SB-T-68, SB-T-69, SB-T-72, SB-T-79, SB-T-80, SB-T-81, SB-T-82, SB-T-84, SB-T-85, SB-T-91, SB-T-93, SB-T-94, SB-T-97, SB-T-98, SB-T-99, SB-T-101) exhibited moderately susceptible reaction with mean percent disease index (PDI) between 24.44 to 35.55 when compared to the susceptible control check (Pusa Basmati-1).

Of the remaining population, twenty-four isolates (22.6%) (SB-T-6, SB-T-9, SB-T-18, SB-T-20, SB-T-29, SB-T-38, SB-T-43, SB-T-49, SB-T-70, SB-T-71, SB-T-74, SB-T-75, SB-T-76, SB-T-77, SB-T-78, SB-T-83, SB-T-88, SB-T-92, SB-T-95, SB-T-96, SB-T-100, SB-T-102, SB-T-103, SB-T-104) exhibited susceptible reaction with mean percent disease index 36 to 46.9. Eight (7.5%) population lines (SB-T-23, SB-T-25, SB-T-73, SB-T-86, SB-T-87, SB-T-89, SB-T-90, PB-1) were found to be

Table 4: Grouping the rice F_3 population lines against sheath blight pathogen

Host response	PDI %	AUDPC	Rice Population
MR (11)	≤23.3	521-676	SB-T-3, SB-T-13, SB-T-14, SB-T-15, SB-T-21, SB-T-26, SB-T-32, SB-T-53, SB-T-55, SB-T-62, Tetep
MS (63)	24.4 - 35.5	677-987	SB-T-1, SB-T-2, SB-T-4, SB-T-5, SB-T-7, SB-T-8, SB-T-10,SB-T-11, SB-T-12, SB-T-16, SB-T-17, SB-T-19, SB-T-22, SB-T-24, SB-T-27, SB-T-28, SB-T-30, SB-T-31, SB-T-33, SB-T-34, SB-T-35, SB-T-36, SB-T-37, SB-T-39, SB-T-40, SB-T-41, SB-T-42, SB-T-44, SB-T-45, SB-T-46, SB-T-47, SB-T-48, SB-T-50, SB-T-51, SB-T-52, SB-T-54, SB-T-56, SB-T-57, SB-T-58, SB-T-59, SB-T-60, SB-T-61, SB-T-63, SB-T-64, SB-T-65, SB-T-66, SB-T-67, SB-T-68, SB-T-69, SB-T-72, SB-T-79, SB-T-80, SB-T-81, SB-T-82, SB-T-84, SB-T-85, SB-T-91, SB-T-93, SB-T-94, SB-T-97, SB-T-98, SB-T-99, SB-T-101
S (24)	36 - 45.9	988-1314	SB-T-6, SB-T-9, SB-T-18, SB-T-20, SB-T-29, SB-T-38, SB-T-43, SB-T-49, SB-T-70, SB-T-71, SB-T-74, SB-T-75, SB-T-76, SB-T-77, SB-T-78, SB-T-83, SB-T-88, SB-T-92, SB-T-95, SB-T-96, SB-T-100, SB-T-102, SB-T-103, SB-T-104
HS (8)	> 46.0	1315-1713	SB-T-23, SB-T-25, SB-T-73, SB-T-86, SB-T-87, SB-T-89, SB-T-90, PB-1

***MR* moderately resistant, *MS* moderately susceptible, *S* susceptible, *HS* highly susceptible, *AUDPC* area under disease progressive curve and *PDI* percent disease index; range is based on minimum value of the group plus CD value**

highly susceptible when compared to resistant control (Tetep). According to Chaudhary (2016), disease severity was found to be one of the significant variables for assessing ShB resistance in rice and he evaluated twelve rice genotypes and determined three resistant genotypes of rice *viz.,* Sabitri, Jasmine-85, and Betichikon was affected by low disease severity. Similarly, Yadav *et al*., (2014) also found a landrace, ARC 10351, and a variety Tetep that depicted moderate resistant reaction against sheath blight. Moreover, Shiobara *et al.,* (2013) reported three landraces *i.e*., Nepal 555, Jarjan, and Nepal 8 as resistant against ShB after screening for three years continuously under field conditions. Despite screening thousands of rice germplasms, only a few rice cultivars and lines 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). Moreover, our results are in agreement with the previous reports of several studies (Dey *et al*., 2016; Tejaswini *et al*., 2017; Goswami *et al*., 2019; Pavani *et al*., 2020 and Bal *et al*., 2020). However, few lines showed moderate resistance to the disease which can be exploited for the development of sheath blight-resistant cultivars.

Conclusion

The complete resistance against sheath blight is lacking in rice germplasm. Our study was an effort to screen for resistance in an F_3 population resulted from a cross between IC277332 (susceptible parent) and Tetep (resistant parent). The plants were in turn recorded with certain agronomic traits to study their correlation with PDI. Out of 106 rice population lines, 9.8% of lines depicted moderate resistance (MR), 60% lines were moderately susceptible (MS), 22.5% lines were susceptible (S), and 7.5% lines were highly susceptible (HS). We found nine moderate resistant lines (SB-T-3, SB-T-13, SB-T-14, SB-T-15, SB-T-21, SB-T-26, SB-T-32, SB-T-53, SB-T-55) which showed less AUDPC values than Tetep (R - check). None of the rice lines was resistant to sheath blight disease. The majority of the F_3 population were moderately susceptible (63) in comparison to Pusa Basmati-1 (S-check). Identified resistant lines can be used as donors/pre-breeding lines for the development of sheath blight-resistant rice cultivars. The data gathered in this study will be valuable in developing a breeding program and managing the sheath blight disease in rice. Furthermore, in the coming future, it is necessary to perform breeding experiments and evaluation of a large number of rice population against *R. solani* to determine resistance lines.

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Conflict of interest

The authors declare that they have no conflict of interest.

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