Evaluation of F2:3 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 F3 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 (Taraiard 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 blight 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, Teging, 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 Kajarahrwa (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, 25°18’N, 83°03´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 ± 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

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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)

\[ RLH = \frac{\text{maximum height at which lesion appear}}{\text{plant height}} \times 100 \]

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

\[ \text{AUDPC} = \sum_{i=1}^{n-1} \left\{ \frac{(X_{i+1} + X_i) / 2 \times (t_{i+1} - t_i)}{\text{time at the } i^{th} \text{ observations}} \right\} \]

Where, \( n \) = the total number of observations,
\( X_i \) = disease index expressed as a proportion at the \( i^{th} \) observation,
\( t_i \) = time at the \( i^{th} \) observations.

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

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   | 35.65  | 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 | 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 | 4.15 | 4.15 | 15.18 | 0.13 | 124.08         | 121.53          | 194.34         | 240.80         | 130.30   | 126443.7 |
| Replication         | 1                  | 405.83 | 534.80 | 2.63 | 7.26 | 0.00  | 407.41         | 525.86          | 1817.1         | 422.02         | 706.05   | 812814.4 |
| Error               | 105                | 58.81  | 6.25 | 4.17 | 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 F₃ 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 F₃ 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 F₃ 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 F₃ 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.
Evaluation of F₂,₃ rice population resistant to *Rhizoctonia solani*

Screening of F₃ 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 F₃ 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 susceptible (Table 4).

### Table 4: Grouping the rice F₃ 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 |

*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 F₃ 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 F₃ 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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