

## Rice genotypes and the biochemical basis of resistance against brown planthopper, *Nilaparvata lugens* (Stål)

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**ABSTRACT:** Screening of 50 rice genotypes against brown planthopper infestation was conducted in open field conditions over two consecutive years (Kharif 2018-19 and 2019-20). Based on pest population per hill, rice genotypes IR82475-110-2-2-1-2, Akshyadhan, and MTU-1010 had the least brown planthoppers. TN1, Swarna, MTU 7029, Rajendra Kasturi, Baranideep, and Sahbhagidhan had the highest population and were classified as pest-prone. Rice leaf biochemical characteristics examined in selected genotypes, revealed that the pest population was significantly and positively correlated with total sugar ( $r = 0.608$ ), crude protein ( $r = 0.306$ ) and total free amino acid ( $r = 0.358$ ), but significantly negatively correlated with phenol ( $r = -0.429$ ), crude silica ( $r = -0.401$ ), and tannin ( $r = -0.301$ ). Correlation analysis revealed that susceptible entries contained more total sugar, crude protein, and total free amino acids, whereas resistant genotypes contained significantly more phenol, crude silica, and tannins. This study highlighted the significance of antixenotic properties in rice genotypes against brown planthoppers.

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**KEY WORDS:** Screening, host plant resistance, bio-chemicals, antixenosis

### INTRODUCTION

Rice (*Oryza sativa* L.), belonging to the family Poaceae, is an internationally vital cereal and a major food source, providing four-fifths of daily energy to more than half of the world's population (Sharma *et al.*, 2019). Brown planthopper (BPH), *Nilaparvata lugens* (Stål) (Hemiptera, Delphacidae), is an economically important pest (Sharma *et al.*, 2018). This phloem sap feeder transmits rice ragged stunt virus (RRSV) and rice grassy stunt virus (RGSV), and has the potential to

cause more than 60 per cent economic yield loss under favorable environmental conditions throughout Asia (Wei *et al.*, 2019; Kanngan *et al.*, 2023). Several chemical insecticides are registered to control rice BPH, but unscientific and injudicious use of these products breaks the natural pest-defender ratio in the field (Sarao and Mangat, 2014; Roy and Chakraborty, 2022). Host-plant resistance is an important factor in developing an integrated pest management system in low-input farming conditions, especially in India (Pal *et al.*, 2021). Insect resistant varieties/genotypes not only reduce

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the insect pest populations, but are also compatible with other methods of eco-friendly pest management (Rani *et al.*, 2020). In several Indian provinces where *N. lugens* outbreaks occur frequently (Andhra Pradesh, Odisha, Haryana, West Bengal, and Punjab), cultivation of susceptible varieties is the main cause of complete crop loss (Anant *et al.*, 2021). Thus, in order to generate promising cultivars that provide persistent and targeted resistance to BPH field populations, novel resistance mechanisms must be identified. Several biochemical constituents in the plant have been identified as causes of resistance. Direct defenses are mediated by plant characteristics have also been shown to reduce insect growth rates by impairing the digestibility and nutritional quality of tissues (Belete, 2018; Golla *et al.*, 2020). For this purpose, there is a continuous search for new resistant genes from diverse sources such as, landraces, wild relatives, induced mutants, and unrelated species. The present study involved systematic phenotyping of rice genotypes for BPH resistance over a two-year period in open field conditions. These studies will facilitate the use of the accessions for the development of rice varieties with durable resistance against BPH.

## MATERIALS AND METHODS

Fifty rice genotypes were sown in nursery beds, including two susceptible checks (Swarna and TN1), and screened during Kharif 2018-19 and 2019-20 at the Agricultural Research Farm, Banaras Hindu University, Varanasi, to determine the response of tested genotypes to brown planthopper under open field conditions. All genotypes were obtained from the Department of Genetics and Plant Breeding at Banaras Hindu University. After the 21<sup>st</sup> day of sowing, the test genotypes were transplanted in three 2 metre rows with a 15cm distance between hills and a 20cm distance between two rows using a Randomised Block Design with three replications. The susceptible check variety was planted after every 30 rows of test genotypes/varieties. For two years, plants were grown under natural open field conditions with no pest protection measures in place.

The total number of brown planthoppers (both

nymphs and adults) was counted on five randomly chosen hills from each genotype and variety. To count the number of BPH individuals, each hill was tilted and tapped twice or three times at the base, and the hoppers that fell into the water were counted. The obtained data were transformed appropriately and statistically analysed for interpretation. AICRIP provided a population-based rating for entries (2005). Standard protocols were used to evaluate biochemical constituents in rice leaves of all genotypes. During the crop's booting stage, leaf samples (Leaf blade of leaf sheath) were collected and brought to the laboratory to estimate total sugars, phenols, tannins, and total free amino acids using the methods of Bray and Thorpe (1954) and Moore and Stein (1948). Piper (1945) proposed methods for analysing crude protein, while Yoshida *et al.* (1959) estimated crude silica.

The data from the study of rice germplasm for resistance to brown planthoppers were statistically analysed using analysis of variance (ANOVA). At  $p < 0.05$ , the least significant difference test was used to distinguish between the various treatment means. The mean values, ranges, and standard deviations of the previous data were also calculated. The data collected from several tests on biochemical parameters were examined using analysis of variance (ANOVA). Data were square root transformed prior to statistical analysis as needed. Tukey's HSD test ( $p < 0.05$ ) was used with SPSS software (version 27.0: Inc., Chicago, IL, USA) to determine the statistical significance of biochemical parameters among tested rice landraces. The relationship between several BPH resistance traits in the tested rice genotypes and varieties was established using SPSS software, pairwise correlation, and Pearson's correlation method.

## RESULTS AND DISCUSSION

During 2018-19, all 50 rice genotypes showed significant variation in the mean number of brown planthopper population (nymph and adult) during the crop's vegetative and reproductive stages (Table 1). Among the 50 rice genotypes, none of the genotypes was free of brown planthopper infestation, and the lowest population of planthoppers was recorded on IR82475-110-2-2-

1-2 (1.07 insects/ hill), which was statistically at par with Akshyadhan (1.67), MTU-1010 (2.12.), and IR-96248-16-3-3-2B (2.28.), followed by Pantdhan-12 (3.52), HUR-917 (3.81), BRRIDhan-62 (4.05), IR\_92978-192-1-2(CR-306) (4.14) and DDR-42 (4.50) which were classified as brown planthopper resistant genotypes. The highest population of brown planthoppers was found on the variety Swarna (35.14) which did not differ statistically from MTU 7029 (26.59), followed by Rajendra Kasturi (24.76) which together were classified as susceptible genotypes/varieties. The susceptible check variety, TN1, had the highest population of planthoppers (41.68) and was classified as a highly susceptible variety against the brown planthopper.

Similarly, in Kharif 2019-20, the mean number of brown planthoppers at the vegetative and reproductive stages differed significantly between the different genotypes (Table 1). The lowest population of planthoppers was recorded in IR82475-110-2-2-1-2 (1.55.), which was statistically comparable to Akshyadhan (1.80.), MTU-1010 (1.98 nos.), and IR-96248-16-3-3-2B (2.58), BRRIDhan-62 (3.37), IR\_92978-192-1-2(CR-306) (3.72), HUR-917 (4.12), DDR-42 (4.54) and classified as resistant genotypes against brown planthopper. On the other hands, the variety Swarna had the highest number of brown planthoppers (32.85), followed by MTU 7029 (27.25), Baranideep (25.34), Sahbhagidhan (25.24.), Sahbhagidhan (25.24) and Rajendra Kasturi (25.20) all of which were classified as susceptible genotypes/varieties, whereas susceptible check variety TN1 had the highest number of planthoppers (42.29 nos.) and was classified as a highly susceptible variety against brown planthopper. Slight variation in the insect infestation was observed during the Kharif 2019–20, which might be due to environmental factors.

The studies on rice resistance to BPH, have been carrying out since long. Various traditional and wild rice varieties were identified as one of the major sources of resistant donors against BPH through mass screening technique (Roy *et al.*, 2022). Subudhi *et al.* (2020), who tested 94 popular elite rice varieties for diverse ecologies in various states against BPH and discovered that eleven of these

varieties were moderately resistant. Resistant varieties reported in this study included Balum-2, Megharice-3, Imp sabaramati, GR-7, Karjat-3, MTU 1061, MTU 1075, RTN-3, R-Suwasini, Pravat, and Santepal. Kakde and Patel (2018) tested 18 rice cultivars and reported that GR-104, GR-103, GR-102, and GR-101 were resistant to brown planthopper, Mashuri, IR-28, and GR-11 were classified as susceptible, and Jaya and Gurjari were found to be highly susceptible to brown planthopper infestation. Bhogadhi *et al.* (2015) tested 27 entries, including landraces and improved lines, for resistance to BPH biotype 4. In both field and seedbox screening, entries BM71, ACC5098, ACC2398, MTU1001, and Rathu Heenathi demonstrated resistance to BPH biotype 4. Roy *et al.* (2022) also screened 218 rice landraces in greenhouse and open-field conditions for three years in a row, identifying five landraces, RL4, RL27, RL35, RL42 and RL5 as resistant to BPH. Previous findings were not comparable to the current findings because the current study's screening used different rice genotypes that were not included in the previous research. The geographical variable has an effect on the population, particularly that of the brown planthoppers.

Plant biochemical traits such as total sugars, phenol, crude silica, crude protein, total free amino acid, and tannin content are also useful indicators of resistance/susceptibility of the test lines from germplasm pools (Panda and Khush, 1995). The total sugar content of leaf sheath of different genotypes at the maximum tillering stage of the crop was observed to range from 12.72 to 31.36 mg/g, with significant variability among the genotypes. Akshyadhan had the lowest total sugar content (12.72) and susceptible check TN1 had the highest total sugar content. The total phenol content in the selected rice genotypes at the maximum tillering stage was found to be in the range of 4.17-9.33 mg/100g, with significant variability between genotypes. The amount of total phenol was found to be highest in IR82475-110-2-2-1-2 (9.33), and lowest total phenol content was found in susceptible Sambha SUB-1 (4.17) and TN1 (4.27). Crude silica content in the selected rice genotypes ranged from

Table1 Field evaluation of rice genotypes against brown planthoppers infestation (Mean number per five hills) during Kharif 2018-19 and 2019-20 (Mean of values at vegetative and reproductive stages of the crop)

Genotypes	Kharif 2018-19	Kharif 2018-19	Resistance
IR82475-110-2-2-1-2	1.07 (1.42)	1.55 (1.58)	R
Sahbhagidhan	23.22 (4.88)	25.24 (5.08)	S
PUSA Basmati-1	5.85 (2.60)	6.24 (2.67)	R
UGR-1	21.30 (4.64)	22.13 (4.75)	S
Bansphul	5.37 (2.51)	5.36 (2.52)	R
CGZR-1	22.62 (4.80)	22.22 (4.79)	S
IR 96248-16-3-3-2B	2.28 (1.80)	2.58 (1.89)	R
MTU-1010	2.12 (1.76)	1.98 (1.72)	R
Sathi	5.32 (2.51)	5.34 (2.51)	R
Pantdhan-12	3.52 (2.11)	4.55 (2.35)	R
Akshyadhan	1.67 (1.63)	1.80 (1.67)	R
NDR-359	5.30 (2.50)	6.09 (2.66)	R
Rajendra Kasturi	24.76 (5.02)	25.20 (5.06)	S
Baranideep	23.56 (4.93)	25.34 (5.09)	S
IR-92960-75-1-3	23.92 (4.90)	22.27 (4.73)	S
IR-92978-192-1-2 (CR-306)	4.14 (2.26)	3.72 (2.17)	R
BRR1 Dhan-62	4.05 (2.25)	3.37 (2.09)	R
Sambha sub-1	21.50 (4.72)	22.32 (4.82)	S
MTU 7029	26.59 (5.20)	27.75 (5.30)	S
HUR-917	3.81 (2.19)	4.12 (2.26)	R
DDR-42	4.50 (2.34)	4.54 (2.35)	R
Swarna	35.14 (5.95)	32.85 (5.77)	S
TN1	41.68 (6.49)	42.29 (6.57)	HS
S.E. (m)±	0.14	0.12	-
C.D. at 5%	0.42	0.35	-
C.V. %	5.43	6.04	-

\*Mean of three replications; \*\*Figures in the parentheses are square root transformed values; Resistance – R- resistant; S - susceptible; HS – highly susceptible

7.06 to 13.87 percent, with significant variability between genotypes. The lowest percentage of silica was found in susceptible check TN-1 (7.06%). However, Akshyadhan (13.87%) was observed with the highest percent of crude silica content. The crude protein content was found to be between 2.16-7.67 mg/g and was significantly lower in the resistant genotype IR82475-110-2-2-1-2 (2.16 mg/g) and higher in the susceptible genotype IR-92960-75-1-3 (7.67 mg/g). Total free amino acids were found to be in the range of 13.02-26.95 mg/g, with the resistant genotype IR82475-110-2-2-1-2 having the lowest content (13.02), while the susceptible genotype Swarna had the highest amount (26.95). Similarly, the tannin content ranged from 0.41 to 5.21 mg/g and was significantly lower in the highly susceptible genotypes IR-92960-75-1-3 (0.41) than in the resistant genotypes Akshyadhan (5.21).

The planthopper population was significantly and positively correlated with total sugar ( $r = 0.608$   $P < 0.001$ ), crude protein ( $r = 0.306$   $P < 0.001$ ), and total free amino acid ( $r = 0.358$   $P < 0.001$ ) (Table 2). The phenol, crude silica, and tannin content had a significant negative correlation with the brown planthopper population ( $r = -0.429$ ,  $r = -0.401$ ,  $r = -0.301$ , respectively,  $p < 0.001$ ). As a result, total sugar, crude protein, and total free amino acids were found to be related to susceptibility to brown planthopper population because they favoured brown planthopper development and growth, whereas phenols, crude silica, and tannins content in leaves lowered brown planthopper infestation and were likely associated with resistance to brown planthopper in the test genotypes.

Many biochemical variables, such as total sugars, reducing sugars, total phenols, and silica, have been linked to insect resistance (War *et al.* 2012). Padhi (2004) and Chandramani *et al.* (2009) found that the susceptible check TN 1 had more total sugars than the resistant entries. Johnson (2009) reported that various entries with a higher concentration of phenolic compounds make the plant resistant. Rani *et al.* (2020) reported that the higher the sugar content, the higher the occurrence of insect pests, despite the fact that the silica content of vulnerable susceptible varieties such as TN1 and BPT5204, as well as the resistant genotypes C-1247 and C-8

Table 2 Correlation coefficient of brown planthopper population with biochemical constituents of rice genotypes

	BPH	TS	P	CS	CP	TFAA	T
BPH	1.000	0.608**	-0.429**	-0.401**	0.306**	0.358**	-0.301**
TS		1.000	-0.728**	-0.732**	0.413**	0.394**	-0.470**
P			1.000	0.767**	-0.602**	-0.583**	0.655**
CS				1.000	-0.745**	-0.685**	0.761**
CP					1.000	0.951**	-0.935**
TFAA						1.000	-0.944**
T							1.000

BPH - brown planthopper, TS - total sugar, P - phenol, CS - crude silica, CP - crude protein, TFAA - total free amino acid, T - tannins content.

\*\*Significant at 0.01 level

588, were the highest. Similarly, Basanth *et al.* (2017) discovered that the resistant genotypes contained more phenol than the susceptible control variety TN 1. The susceptible genotypes had higher sugar content than the highly resistant genotypes. Likewise, Kumar *et al.* (2021) found that total and reducing sugars, free amino acids were higher in susceptible entries, while total phenols and tannins were significantly higher in resistant genotypes. The phenolic compounds and crude silica content are reported to be the feeding deterrents to BPH in rice and generally have a positive correlation with host plant resistance (Pati *et al.*, 2023). Enhanced silica content in plant defence against rice insect pests has been observed (Han *et al.*, 2015). Rizwan *et al.* (2022) also examined the role of silicon in rice insect pest resistance. These findings were consistent with the results of the current investigation. The resistant genotypes identified against insect pests indicate a reduction in protection costs while maintaining environmental sustainability. Furthermore, such genotypes should be used as donors in a hybridization programme to improve resistance to insect pests.

## ACKNOWLEDGMENTS

The authors would like to express their gratitude to the University Grant Commission (UGC) of New Delhi for its fellowship and financial support in carrying out the experiments. The authors also thank the anonymous arbitrators, particularly one who assisted in the refinement of this manuscript over several iterations.

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