The Pharma Innovation Journal 2025; 14(7): 09-13

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
TPI 2025; 14(7): 09-13

www.thepharmajournal.com
Received: 07-04-2025
Accepted: 09-05-2025

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Phenotypic evaluation of Gene/QTL pyramided samba Mahsuri lines for yield and yield-related traits in rice

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Abstract
Rice (*Oryza sativa* L.) is the world's most significant cereal crop, often referred to as the "Grain of Life" because it is a staple food for over 70% of Indians and sustains 120 to 150 million rural households. Two major diseases affecting rice are rice blast, caused by *Pyricularia oryzae*, and bacterial leaf blight (BLB), caused by *Xanthomonas oryzae pv oryzae*. To combat the damage from these diseases, chemical control methods are often used. However, the continuous use of chemicals increases production costs and negatively impacts the environment. The most effective, cost-efficient, and eco-friendly way to minimize production losses from these diseases is to cultivate rice varieties with inherent resistance. Given this context, the current study was conducted during the rabi season of 2023 at the ICAR-Indian Institute of Rice Research farm in Hyderabad. The objective was to evaluate yield and yield-related traits in rice, assess phenotypic resistance to BLB and blast. The study involved 48 gene/QTL pyramided lines, evaluated in a randomized complete block design with three replications. ANOVA for yield and yield-related traits revealed significant differences among genotypes for all studied characteristics, indicating sufficient variation for selecting superior genotypes for further breeding. Panicle weight, number of tillers per plant, number of productive tillers per plant, and number of filled grains per panicle positively correlated with grain yield per panicle. This suggests that genotypes with heavier panicles, more productive tillers, and a higher count of filled grains per panicle tend to yield more, indicating that these traits should be considered in the selection process.

Keywords: Bacterial leaf blight resistance, blast resistance, grain yield per panicle, superior genotypes

1. Introduction
The most significant cereal crop in the developing world is rice (*Oryza sativa* L.). China, India, Japan, Korea, South-East Asia, and the adjacent Pacific islands produce almost 90% of the world's rice (Singh *et al.*, 2021) [19]. Rice is known as the "Grain of Life" since it is the main staple food consumed by more than 70% of Indians and supports 120 to 150 million rural households (Fiyaz *et al.*, 2011) [4]. India's biggest producer of rice is West Bengal, which accounts for about 15.59 percent of the nation's overall output. Some of the productivity limitations of rice cultivation include a lack of high yielding varieties, pest and disease resistance variations, poor agronomic practices, and a lack of varieties that can endure abiotic stress.

The number of panicles per unit area, the number of spikelets per panicle, the weight of the spikelet, and the spikelet's sterility or filling are the four main factors that affect rice yield. The evaluation of the correlation between the yield and these quantitative traits provide the crucial knowledge for selecting the traits that influence the yield. Through correlation analysis, the quantitative traits and their influence on the yield are demonstrated. (Shivani *et al.*, 2021) [18].

2. Materials and Methods
At the ICAR-Indian Institute of Rice Research in Rajendranagar, Hyderabad, a total of 48 germplasm lines were individually planted in a dry bed nursery. Seedlings that were twenty-five days old from each accession were then transplanted, ensuring a spacing of 20 cm between rows and 15 cm between plants. This was carried out in accordance with a Randomized Block Design, with two replications. All required measures and agricultural practices were implemented to ensure consistent plant population and healthy crop growth.

The agricultural guidelines proposed by ICAR-IIRR in Hyderabad were followed according to the planned timetable throughout the entire growth cycle of the crops. Plant protection measures were applied as required. Fertilizers were administered at a rate of 120 kilograms of

Nitrogen, 60 kilograms of Phosphorus, and 40 kilograms of Potash per hectare. Careful measures were taken to ensure the even distribution of plants for a consistent crop population. In this current study, a total of ten traits were assessed. Data for yield, factors contributing to yield, and quality attributes were noted for three randomly chosen plants within each entry. The average data collected was used for the ultimate statistical analysis.

3. Results

In the present study, the data was recorded on 10 characters *viz*., days to 50% flowering, plant height, panicle length, panicle weight, number of tillers, number of productive tillers, number of filled grains per panicle, number of unfilled grains per panicle, test weight, single plant yield, along with phenotypic screening for blast and bacterial leaf blight diseases. The data collected from 10 characters is analysed through statistical methods and results were discussed under following heads.

Analysis of variance

The analysis of variance for different characters is presented in Table 1. The treatment *i.e*., mean sum of squares due to genotype showed significant (probability of <0.001) differences for all the characters under study.

Estimation of Genetic Variability, Heritability And Genetic Advance

The estimates of phenotypic and genotypic coefficient of variation for all the characters under study were moderate to high. Slightly PCV is greater than GCV, this indicates that negligible amount of environmental influences on expression of the trait. All the traits under investigation showed high heritability. Traits such as panicle weight, number of filled grains and unfilled grains per panicle manifested high estimates of GCV, PCV, heritability and genetic advance as per cent of mean indicating the prevalence of additive gene action in the inheritance of this trait. Panicle length, number of tillers per plant, test weight and grain yield per plant demonstrated moderate estimates for PCV and GCV, along with high heritability and high genetic advance as a percentage of mean estimates suggesting the presence of a reasonable amount of variation in these traits attributed to both genetic and environmental factors, with the expression of these traits influenced by additive gene effects. Hence, simple selection will be highly rewarding for improving these characters. Three among the ten traits *i.e*., days to 50% flowering, panicle length and plant height exhibited low PCV and GCV which are coupled with high heritability and low to moderate genetic advance as per cent of mean estimates indicating the presence of both additive and non-additive gene actions governing the trait and desirable results may not be obtained by simple selection, Sravani *et. al*. (2022) [20], Shivani *et. al*. (2018) [17].

Genotypic correlation

Correlation studies showed that grain yield per plant exhibited positive and significant associations with plant height (0.254*), panicle weight (0.487**), number of tillers per plant (0.402**), number of productive tillers per plant (0.335**), and number of filled grains (0.369**), indicating a strong link between these traits and yield. On the other hand, there was a negative but non-significant association with the days to 50% flowering (-0.004), number of unfilled grains (-0.049). Panicle length (0.069), test weight (0.17) showed positive but non-significant associations with grain yield. Similar results were validated by Nandeshwar (2010) [10], Rashid *et. al*. (2014) [15], Prasad *et. al*. (2017) [12], Shivani *et. al*. (2018) [17], Nithya *et. al*. (2020) [11], Lingaiah *et. al*. (2020) [9], Lakshmi *et. al*. (2021) [8] and Begum *et. al*. (2021) [2].

Phenotypic correlation

Grain yield per plant exhibited significant positive associations with plant height (0.215**), panicle weight (0.300**), number of tillers per plant (0.332**), number of productive tillers per plant (0.293**), and number of filled grains (0.337**), indicating a robust link between these traits and yield. On the other hand, there was a non-significant negative association with the days to 50% flowering (-0.005), number of unfilled grains (-0.073). Panicle length (0.054), test weight (0.156) positive but non-significant associations with grain yield. These findings are consistent with previous studies by Nandeshwar (2010) [10], Rahman *et. al*. (2014) [13], Ahamed *et. al*. (2021) [1], Begum *et. al*. (2021) [2], Kulsum *et. al*. (2022) [7], Sravani *et. al*. (2022) [20], and Kiran *et. al*. (2023) [6].

Table 1: Analysis of variance for morphological and yield related traits in rice.

Source of variation	d.f.	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle weight (g)	Number of tillers per plant	Number of Productive tillers per plant
		Mean sum of squares					
Replications	2	1.67	133.08	1.02	0.28	4.42	7.34
Genotypes	47	158.70**	499.68**	8.11**	0.94**	37.01**	37.11**
Error	94	0.67	47.50	2.66	0.39	2.10	2.73

Source of variation	d. f.	Number of filled grains	Number of Unfilled grains	Test weight (g)	Grain yield per plant (g)
		Mean sum of squares			
Replications	2	148.36	1.71	0.34	8.48
Genotypes	47	1506.89**	351.26**	20.11**	254.87**
Error	94	187.58	15.38	0.05	20.67

** Significant at 1 per cent level

Table 2: Mean performance of the rice genotypes studied for morphological and yield-related traits

	DFF	PH (cm)	PL (cm)	PW(g)	NT	NPT	NFG	NUFG	TW(g)	GYP(g)
Mean	111.01	108.46	23.71	2.96	17	15	129	21	18.44	28.05
Range -Min.	90	80.2	19.4	1.2	9	7	75	2	10.4	9.5
-Max.	121	137.4	29.8	5	27	24	201	55	24.2	58.1
S.Em	0.47	3.97	0.94	0.36	0.83	0.95	7.90	2.26	0.13	2.62
CD	1.333	11.191	2.649	1.019	2.585	2.687	22.240	6.370	0.374	7.374
CV	0.739	6.355	6.833	6.939	9.353	10.949	10.559	10.466	1.250	16.191

S.Em= Standard Error from Mean, DFF= Days to 50 per cent flowering, PH= Plant height, PL= Panicle length, PW= Panicle weight, NT = No. of tillers per plant, NPT = No. of productive tillers per plant, NFG = No. of filled grains per panicle, NUFG=No. of unfilled grains per panicle, TW= Test weight, GYP= Grain yield per plant.

Table 3: Variability, heritability and genetic advance as per cent of mean for morphological and yield-related traits in rice genotypes

S. No.	Character	Coefficient of variation		Broad sense Heritability (%)	Genetic advance asper cent of mean
		PCV (%)	GCV (%)		
1	Days to 50% flowering	6.57	6.53	98.73	13.38
2	Plant height (cm)	12.98	11.31	76.03	20.33
3	Number of tillers per plant	21.49	19.78	40.56	7.45
4	Number of productive tillers per plant	24.9	22.40	31.81	16.77
5	Panicle length	8.92	5.68	84.68	37.50
6	Panicle Weight	25.58	14.42	80.71	41.45
7	Number of Unfilled grains per panicle	52.81	49.51	70.09	27.88
8	Number of filled grains per panicle	19.30	16.16	87.91	95.64
9	Test weight (g)	14.08	14.02	99.20	28.78
10	Grain yield per plant(g)	35.42	31.50	79.05	57.69

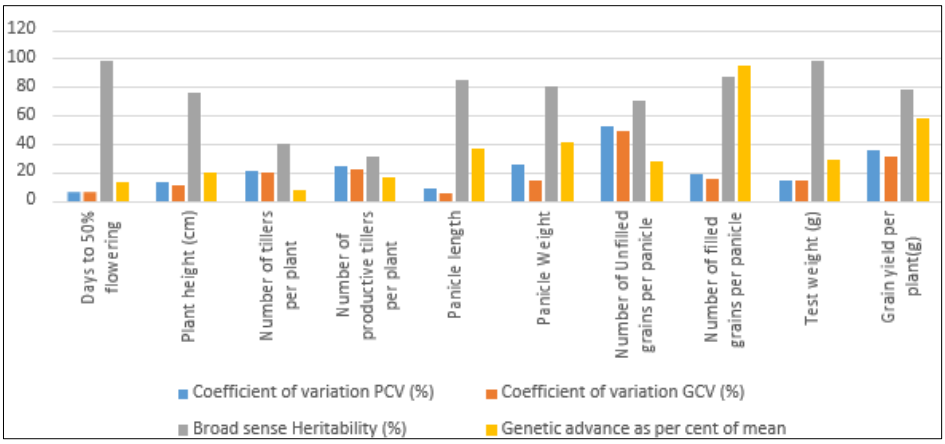

Fig. 1: Frequency distribution of PCV (%), GCV (%), broad sense heritability (%), GAM for 10 characters recorded

Table 10: Correlation for morphological and yield-related traits in 48 rice genotypes

Character		DFF	PH	PL	PW	NT	NPT	NFG	NUFG	TW
DFF	rg	1.000	0.1359	0.1221	0.1285	0.0702	-0.0765	0.0381	-0.0689	-0.0041
	rp	1.000	0.1002	0.0766	0.122	0.0614	-0.0653	0.0396	-0.0691	-0.0053
PH	rg		0.3772**	-0.2772	0.0799	0.0013	-0.1198	-0.0038	0.3096*	0.2548
	rp		0.2495**	-0.1549	0.0854	0.0211	-0.0828	0.0272	0.2735**	0.2158**
PL	rg			0.1005	0.1652	0.2467	0.1303	0.2796	0.3568*	0.0696
	rp			0.1057	0.151	0.1338	0.119	0.1642*	0.2298**	0.0546
PW	rg				0.1898	0.1749	0.502**	0.3238*	0.3221*	0.487**
	rp				0.0686	0.0708	0.5157**	0.1264	0.1847*	0.3009**
NT	rg					0.9905	-0.0479	0.1043	-0.0142	0.4022**
	rp					0.8972**	-0.0459	0.0829	-0.0114	0.332**
NPT	rg						0.0683	0.0709	-0.035	0.3358**
	rp						-0.0568	0.0662	-0.0248	0.293**
NFG	rg							0.1298	-0.035	0.3693**
	rp							0.0886	-0.155	0.3376**
NUFG	rg								-0.1872	-0.0499
	rp								0.0542	-0.0736
TW	rg									0.176
	rp									0.1569

** Significant at 1 per cent level of probability, * Significant at 5 per cent level of probability DFF= Days to 50 per cent flowering, PH= Plant height, PL= Panicle
length, PW= Panicle weight, NT = No. of tillers per plant, NPT = No. of productive tillers per plant, NFG = No. of filled grains per panicle, NUFG=No. of unfilled grains per panicle, TW= Test weight, GYP= Grain yield per plant

4. Conclusion

The analysis of variance (ANOVA) for yield and yield-related traits in rice genotypes showed significant differences among the genotypes for all the studied characters, indicating sufficient variation among the genotypes and suggesting the potential for selecting superior genotypes with improved traits for further breeding programs. The mean performance of 48 genotypes was evaluated for various morphological and yield-related traits.

The study provides valuable insights into the phenotypic and genotypic coefficient of variation coupled with heritability and genetic advance as per cent of the mean of various agro-morphological traits in rice genotypes. For traits such as panicle weight, grain yield per panicle and number of unfilled grains per panicle shown high PCV, GCV coupled with high heritability and genetic advance as per cent of mean and other traits such as days to 50 percent flowering, panicle length, panicle height, number of tillers per plant, test weight and number of filled grains per panicle exhibited low to moderate GCV,PCV along with high heritability and low to moderate genetic advance as per cent of mean suggesting that presence of the reasonable amount of variation and prevalence of additive gene action. Hence, simple selection can effectively lead to improvement. However, number of filled grains per panicle exhibited high genetic variation with low heritability and low to moderate genetic advance as per cent of mean suggesting that simple selection may not be sufficient to achieve desired results due to the influence of both additive and non-additive gene action.

The study provides insights into the relationships between various agronomic traits in rice genotypes. Panicle weight, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle were positively associated with grain yield per panicle, implying that genotypes that are characterized by heavier panicle weight, high number of productive tillers per plant, a greater count of filled grains per panicles tend to produce higher grain yield. Indicating that the above traits can be considered in the selection process. Other trait such as number of unfilled grains per panicle manifested negatively correlated with the grain yield, indicating that simultaneous improvement may not be preferable with these traits in breeding programs, but they still provide valuable information. Further breeding programmes should be refined in such a way to break undesirable linkages between traits for simultaneous improvement of both yield and yield component traits.

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