
RESEARCH ARTICLE

Large scale evaluation, genetic variability and correlation analysis in rice accessions

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Abstract

The present study was focused and conducted to evaluate the genetic variability and relationship among 17 yield and yield-related traits in 104 rice genotypes, including 4 standard check varieties, at S.G. College of Agriculture and Research Station, Jagdalpur, Chhattisgarh. The analysis of genetic variability revealed that grain yield per plant exhibited the highest genotypic and phenotypic coefficients of variation. The traits, test weight and grain yield per plant showed the highest heritability and genetic advance as a percentage of the mean, respectively. Correlation analysis indicated that grain yield per plant had a highly significant positive association with test weight, biological yield per plant, number of filled grains per panicle, number of effective tillers per plant, plant height, kernel breadth, panicle length and grain breadth, while it had a significant negatively associated with days to 50% flowering. These yield-related traits could be targeted for selection to enhance the genetic potential for rice yield improvement.

Keywords: Rice, genetic variability, correlation analysis, GCV, PCV

Introduction

Rice is the world's most crucial grain crop, having become the primary food source for humans due to its global distribution. India is the 2nd biggest producer and consumer of rice globally. In India, rice cultivation spans 47.83 million hectares, achieving a record production of 135.75 million tonnes and an estimated productivity of 2,838 kg per hectare for the 2022-23 period. In various rice-growing regions of India, farmers are cultivating unique landraces that possess special traits like high yield and disease resistance. These landraces hold significant value both commercially and for breeding programs. Many of these germplasms are yet to be fully developed to realize their potential for enhancing rice germplasm and they can be found in many regions of the country. Rice landraces may possess valuable alleles that are rare in modern germplasm (Pervaiz *et al.*, 2010). Genetic variation within plant material is fundamental to crop improvement (Iqbal *et al.*, 2014).

The success of any crop improvement program depends on the availability of this variability and its effective use in breeding efforts. Assessing variability is crucial for identifying traits with higher heritability and potential for genetic improvement. Analyzing character associations is essential to identify positively correlated traits that can contribute to overall grain yield enhancement.

Materials and methods

A total of 100 rice landraces and 4 check varieties - Bastar Dhan 1, Samleshwari, Danteshwari and CG 1919 were utilized in this study. These genotypes were evaluated using an augmented complete block design with 5 blocks at the Research cum Instructional Farm of S.G. College of Agriculture and Research Station, Jagdalpur (C.G.). Each block consisted of 20 test genotypes and 4 check genotypes. The genotypes were planted in 2 rows, each row 3 meters long, with a spacing of 20 cm x 15 cm. Standard cultural practices and management techniques were followed to grow the crop. 6 qualitative and 17 quantitative traits were recorded, including basal leaf sheath color, auricle color, ligule shape, node color, flag leaf attitude, kernel color, days to 50% flowering, plant height (cm), flag leaf length (cm), flag leaf width (cm), number of effective tillers per plant, number of filled grains per panicle, panicle length (cm), grain length (mm), grain breadth (mm), kernel length (mm), kernel breadth (mm), grain L/B ratio, kernel L/B ratio, test weight (g), biological yield per plant (g), grain yield per plant (g) and harvest index (%). Analysis of variance (ANOVA) was performed and genotypic and phenotypic coefficients of variation, heritability (broad sense) and genetic

advance as a percentage of the mean were calculated following the procedures of Burton and Devane (1953). Correlations among the 17 quantitative characters were assessed according to the method of Johnson *et al.*, 1995.

Result and discussion

The variance analysis of 17 quantitative traits revealed significant differences across the 104 genotypes, indicating variation in all the characters examined (Table 1). From the table 2 it is being learnt that the PCV values were slightly higher than GCV values, suggested that environmental factors influence the characters expression. PCV values ranged from 1.34% (flag leaf length) to 12.67% (grain yield per plant). None characters identified high GCV and PCV. Grain yield per plant and the number of filled grains per panicle showed moderate PCV and GCV values ranging from 10 to 20%. Heritability ranged from 11.95% (flag leaf length) to 98.93% (test weight). All characters exhibited high heritability except for flag leaf length, panicle length and kernel L/B ratio. Grain yield per plant and number of filled grains per panicle showed high genetic advance as a percentage of the mean, with values of 24.92% and 20.39%, respectively. Low genetic advance as a percentage of the mean was observed for flag leaf width (8.99%), grain breadth (8.58%), plant height (7.93%), kernel breadth (7.33%), panicle length (3.07%) and flag leaf length (2.55%).

High heritability combined with high genetic advance was observed for traits such as grain yield per plant and number of filled grains per panicle, similar findings of Akshay *et al.*, (2022).

Table 1: mean sum of square

	Source of variation						
	Block	Treatment	Checks	Test entries	Check Vs Test	Error	Total
DF	4	103	3	99	1	12	119
Days to 50% flowering	2505.56**	105.37**	610.18**	191.81**	9965.75**	0.89	175.52
Plant height (cm)	595.11**	92.29**	414.70**	99.05**	-1543.79**	1.75	100.07
Flag leaf length (cm)	48.64**	12.62**	16.80**	13.90**	-126.92**	7.52	13.31
Flag leaf width (cm)	0.043**	0.028**	0.057**	0.027**	0.070**	0.001	0.026
No. of effective tillers/ plant	4.91**	1.55**	1.78**	1.69**	-12.84**	0.13	1.52
Panicle length (cm)	26.04**	3.27**	8.00**	3.97**	-80.32**	1.19	3.82
Number of filled grains per panicle	2718.35**	531.33**	919.16**	479.58**	4491.21**	3.30	551.59
Grain length (mm)	0.338**	0.781**	4.217**	0.690**	-0.543**	0.003	0.687
Grain breadth(mm)	0.163**	0.076**	0.009**	0.080**	-0.170**	0.002	0.071
Kernel length (mm)	0.432**	0.499**	3.271**	0.434**	-1.393**	0.001	0.447
Kernel breadth (mm)	0.172**	0.055**	0.159**	0.059**	-0.651**	0.005	0.054
Grain L/B ratio	0.234**	0.215**	0.734**	0.210**	0.210**	-0.831**	0.004
Kernel L/B ratio	0.249**	0.219**	1.400**	0.195**	-0.873**	0.030	0.201
Test weight (g)	14.238**	13.692**	3.625**	14.466**	-32.773**	0.030	12.333
Biological yield/ plant	231.039**	48.969**	49.434**	49.799**	-34.610**	2.567	50.410
Harvest index (%)	104.58**	34.34**	10.22**	29.57**	579.35**	1.29	33.37
Grain yield/ plant (g)	116.69**	27.76**	15.62**	24.91**	345.87**	0.26	27.97

Table 3: Genetic variability parameters of rice genotypes

Character	Heritability (%)	GA	GA % of mean	GCV (%)	PCV (%)
Days to 50% flowering	95.91	9.22	10.54	5.23	5.34
Plant height (cm)	91.17	8.37	7.93	4.03	4.22
Flag leaf length (cm)	11.95	0.72	2.55	3.58	1.34
Flag leaf width (cm)	82.71	0.14	8.99	4.80	5.28
Number of effective tillers /plant	68.07	0.91	11.37	6.69	8.11
Panicle length (cm)	25.79	0.67	3.07	2.94	5.79
Number of filled grains / panicle	96.97	20.85	20.39	10.05	10.21
Grain length (mm)	98.26	0.81	10.20	5.0	5.04
Grain breadth (mm)	86.69	0.23	8.58	4.47	4.81
Kernel length (mm)	98.68	0.65	10.81	5.28	5.32
Kernel breadth (mm)	64.89	0.17	7.33	4.42	5.49
Grain L/B ratio	90.49	0.40	13.64	6.96	7.32
Kernel L/B ratio	55.58	0.30	11.18	7.28	9.76
Test weight (g)	98.93	3.39	15.47	7.55	7.59
Biological yield/ plant (g)	78.33	5.55	10.24	5.61	6.34
Harvest index	83.72	4.85	14.07	7.47	8.16
Grain yield / plant (g)	95.47	4.72	24.92	12.38	12.67

This combination of high heritability and high genetic advance as a percentage of the mean suggested the influence of additive gene effects, indicated that simple selection procedures could effectively enhance these traits (Akshay *et al.*, 2022). Similarly, high heritability along with moderate genetic advance was reported for traits like test weight, harvest index, grain L/B ratio, number of effective tillers per plant, kernel length, days to 50% flowering and biological yield per plant. Saha *et al.*, (2019) for days to

50% flowering; Panwar and Mathur, (2007) for test weight and days to 50% flowering. On the other hand, high heritability coupled with low genetic advance was recorded for traits such as flag leaf width, grain breadth, plant height and kernel breadth. While test weight exhibited high heritability, panicle length showed low genetic advance, indicating the involvement of both additive and non-additive gene actions, which makes simple selection less effective for these traits.

Table 3: Correlation analysis of rice genotypes for yield and yield attributing traits

Characters	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Number of effective tillers/plant	Panicle length (cm)	Number of filled grains/panicle	Grain length (mm)	Grain breadth (mm)	Kernel length (mm)	Kernel Breadth (mm)	Grain L/B ratio	Kernel length (mm)	Test weight (g)	Biological yield /plant (g)	Harvest index (%)	Grain yield / plant (g)
Days to 50% flowering	1.00	-0.220* 0.521**	0.232*	-0.086	-0.200*	0.399**	-0.249*	-0.123	-	0.330**	0.241*	0.163	0.066	-0.446** 0.297**	-	0.316**	0.404**
Plant height (cm)		1.000	0.217*	-0.086	0.224*	0.489**	0.246*	0.206	0.334**	0.208*	0.318**	-0.123	-0.071	0.461**	0.549**	0.376**	0.493**
Flag leaf length (cm)			1.000	0.069	0.006	0.179	0.009	0.063	0.150	0.142	0.060	-0.076	0.025	0.105	0.127	0.031	0.077
Flag leaf width (cm)				1.000	-0.160	-0.213*	-	-0.058	0.215*	-0.090	0.214*	-0.189	-0.192	0.181	-0.092	-0.109	-0.104
Number of effective tillers / plant					1.000	0.157	0.098	-0.127	0.099	-0.032	0.079	-0.177	-0.129	0.046	0.470**	0.557**	0.564**
Panicle length (cm)						1.000	0.432**	0.107	0.053	0.139	-0.002	0.043	0.106	0.093	0.351**	0.297**	0.352**
Number of filled grains / panicle							1.000	-0.117	-0.095	-0.043	0.040	-0.027	-0.038	-0.056	0.449**	0.614**	0.601**
Grain length (mm)								1.000	-0.011	0.881**	-0.123	0.690**	0.700**	0.515**	0.193*	0.143	0.177
Grain Breadth (mm)									1.000	0.046	0.839**	-	0.512**	0.606**	0.415**	0.183	0.308**
Kernel length (mm)										1.000	-0.071	0.557**	0.731**	0.490**	0.230*	0.194*	0.224*
Kernel Breadth (mm)											1.000	-	0.676**	0.595**	0.435**	0.298**	0.389**
Grain L/B ratio												1.000	0.851**	-0.091	-0.173	-0.038	-0.118
Kernel length (mm)													1.000	-0.011	-0.129	-0.041	-0.089
Test weight (g)														1.000	0.598**	0.441**	0.552**
Biological yield / plant (g)															1.000	0.648**	0.885**
Harvest index (%)																1.000	0.924**
Grain yield / plant (g)																	1.000

*, ** significant at 5% and 1% level, respectively

These findings are consistent with previous studies by Khaire *et al.*, (2017), Kunkerkar *et al.*, (2017), Ketan and Sarkar (2014) and Jamal *et al.*, (2009). High heritability paired with low genetic advance suggests non-additive gene action in the inheritance of these traits, as noted by Nirmaladevi *et al.*, (2015). Panicle length and flag leaf length exhibited low heritability and low genetic advance, which is consistent with results reported by Ali *et al.*, 2018 and Pradeep *et al.*, 2018 for the number of filled grains per panicle.

Correlation coefficient analysis is crucial for determining the degree and strength of the association between two variables (Table 3). Grain yield per plant showed a strong positive correlation with characteristics like harvest index, biological yield per plant, number of filled grains per panicle and number of effective tillers per plant. As reported by Panigrahi *et al.*, 2018 for number of effective tillers per plant and panicle length, test weight, plant height, kernel breadth, panicle length and grain breadth. Positive significant correlation was also recorded by kernel length, as finding by Aristya *et al.*, (2021), Manasa *et al.*, (2022), Aishwarya *et al.*, (2023) and Singh *et al.*, (2018). Conversely, a highly negative significant correlation was found with days to 50% flowering, while a negative nonsignificant correlation was observed with grain L/B ratio, flag leaf width and kernel L/B ratio.

Days to 50% flowering exhibited a positive significant correlation with flag leaf width, while showing a strong negative significant correlation with plant height, biological yield per plant, harvest index, test weight, kernel breadth, panicle length and grain yield per plant. Number of effective tillers per plant demonstrated a

highly positive significant correlation with grain yield per plant, harvest index and biological yield per plant, while showing a negative significant correlation with days to 50% flowering. These findings are consistent with the results reported by Abhilash *et al.*, 2018 and Segeena *et al.*, 2019 for grain yield per plant. Number of filled grains per panicle exhibited a highly positive significant correlation with the harvest index, followed by grain yield per plant, biological yield per plant and panicle length. Flag leaf width was strongly negatively associated with grain yield per plant and there was a negative correlation between grain yield and days to 50% flowering. These findings are in accordance with Panigrahi *et al.*, 2018, who reported similar correlations for panicle length, grain yield per plant and a negative correlation with test weight.

Grain breadth showed a highly significant positive correlation with kernel breadth, test weight, biological yield per plant, plant height and grain yield per plant. It also exhibited a highly significant negative correlation with grain L/B ratio, kernel L/B ratio and days to 50% flowering, consistent with the findings of Jebakani *et al.*, (2023). Kernel breadth was strongly positively correlated with several plant characteristics, including grain breadth, test weight, biological yield, grain yield, plant height and harvest index. However, it was strongly negatively correlated with grain and kernel L/B ratios, as well as the days to 50% flowering. The kernels L/B ratio was strongly positively correlated with the L/B ratio of grains, as well as with kernel length and grain length. However, it was strongly negatively correlated with kernel breadth and grain breadth. According to Parte *et al.*, 2022, these findings were specifically observed for grain L/B ratio.

Test weight was analyzed strongly positively correlated with several characters, including grain breadth, biological yield per plant, kernel breadth, grain yield per plant, grain length, kernel length, plant height and harvest index. But it was negatively associated with days to 50% flowering.

Hence, it is being suggested that selection for traits like harvest index, biological yield per plant, number of filled grains per panicle, plant height, number of effective tillers per plant, test weight, panicle length, grain breadth and kernel breadth could positively impact rice yield. These traits are interconnected and when improved together, can enhance overall grain yield production. This study revealed that rice landraces exhibit significant genetic diversity. All 104 rice germplasms displayed a wide range of variation in both quantitative and qualitative traits. Selection of grain yield per plant and number of filled grains per panicle which had high heritability combined with high genetic

advance as percentage of mean might be beneficial. Correlation analysis identified harvest index, biological yield per plant, number of filled grains per panicle, test weight, plant height, grain breadth and kernel breadth as the key contributors to yield. These traits can be used to select desirable genotypes for future breeding programs and as parents in rice hybridization programs. High-yielding rice genotypes included Bayakhuta (31.27g), Mutiya Dhan (31.02g), SGCARS 1025 (29.87g), Tikee Chudi (28.87g) and Kukda Mor (28.49g). These genotype have the potential for use in upcoming breeding programs.

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