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Morphological characterization and variability analysis for yield and quality traits in rice (*Oryza sativa* L.)

Suraj Gupta and Sonali Kar

Abstract

The present investigation entitled “Morphological characterization and variability analysis for yield and quality traits in rice (*Oryza sativa* L.)” was carried out at the Instructional cum Research Farm of S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, Bastar, Chhattisgarh, India. The experiment was conducted during *Kharif* 2022 in an RBD Design to assess the agro-morphological characterization and genetic variability analysis among the forty genotypes of rice and including six popular standard checks. Out of 10 qualitative characters observed basal leaf sheath colour, auricle, leaf blade colour, panicle length, flag leaf length, and flag leaf width recorded the highest variation among genotypes. The observations for this investigation were recorded for various quantitative and quality traits, viz., days to 50% flowering, plant height, flag leaf length, flag leaf width, panicle length, number of effective tillers, number of filled grain/panicle, test weight, biological yield (Kg/ha), paddy length, paddy breadth, kernel length, kernel breadth, paddy length breadth ratio, kernel length breadth ratio, harvest index (%), grain yield (q/ha) were all observed for this study. A wide range of genetic variability was observed for most of the quantitative traits identified. Grain yield (8.74), harvest index (7.67), and number of filled grain per panicle (7.31), biological yield (7.12), flag leaf width (6.05), paddy length breadth (5.75), panicle length (5.15), paddy length (4.85), test weight (4.68), flag leaf length (4.49), kernel length breadth ratio (3.29), plant height (3.27), paddy width (2.86), kernel length (2.81). The analysis of variance revealed extremely significant variations across genotypes for all of the features tested, showing a sufficient degree of variability among the forty-six genotypes. Plant height, flag leaf length, number of filled grains per panicle, number of effective tillers, biological yield, test weight, kernel length, kernel L/B, harvest index, and grain yield all had moderate genotypic and phenotypic coefficients of variation. This shows that these features could be improved by simple selection. Kernel length had the highest heritability, followed by kernel breadth, kernel L/B ratio, test weight, plant height, paddy breadth, flag leaf length, and quantity of filled grain per panicle. Test weight had the highest genetic advance as a percentage of the mean, followed by the number of full grains per panicle and grain yield (q/ha). High heritability coupled with high genetic advance was reported for character Number of filled grain per panicle, Plant height, Harvest index, Days to 50% flowering. The mean grain yield was 45.09 (q/ha) and it ranged from 28.09 to 61.04. Based on the mean performance of grain yield, genotypes viz., R 2340-267-2-140-1 (61.04 q/ha) Followed by R-BSP-18-3 (60.7 q/ha), R 2220-382-1-243-1 (55.5 q/ha), R 2370-501-1-284-1 (55.2 q/ha) and R 2412-709-1-331-1 (53.5 q/ha). Comparative studies revealed that the genotypes under study showed high grain yield per hectare than the check varieties. High genetic diversity was found between genotypes which may be useful in further breeding programs.

Keywords: Rice (*Oryza sativa* L.), grain yield, variability

Introduction

Rice (*Oryza sativa* L.) is the world's single most important crop, belonging to the family Poaceae. It is one of the most significant cereals and a staple food for more than 2 billion people. In India, rice was grown on about 45 million hectares, with a production of about 127.93 million tones and an average productivity of 2713 Kg/ha (Anonymous, 2022a) [5]. Chhattisgarh is known as the “rice bowl of India” and about 82% of the population of the state is dependent on agriculture for their livelihood. The total rice grown area was 3.6 million hectares, with a production of 6.5 million tones and a productivity of 20.44 Kg/ha (Anonymous, 2021) [5]. Total production of rice during 2021-22 was recorded at 127.93 million tones.

Rice is the most important source of carbohydrate and a primary component of nutrition for the poor. It provides approximately 50-80 percent of the caloric intake each day. 100 grams of edible portion of milled rice comprises. nutrition (345 kcal), carbohydrate (78.2 g), protein (6.8 g) and minerals including phosphorus (160 mg), magnesium (90 mg), calcium (10 mg) and folic acid (8 mg) (Gopalan *et al.* 2007) [14].

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Overall protein density is greater in rice (0.55) compared to other essential cereals such as wheat (0.40) (Bagchi *et al.* 2015)^[6].

Morphological traits have been used to assess the genetic variation and relationships among populations of rice. It is considered as the primary step in the classification and evaluation of germplasm. These qualitative characters are crucial for plant description and influenced by consumer preference, socio-economic scenario and natural selection. Several morphological characters are the major determining factors of rice grain yield including number of panicles per hill, the number of filled grains per panicle, and weight of filled grain per hill.

The success of any plant breeding programme depends to a large extent on the existence of diversity among genotypes (Beevi and Venkatesan, 2015)^[7]. Since the last few decades, indigenous varieties of rice have been replaced by high yielding varieties resulting in a lack of diversity in rice (Choudhary *et al.* 2013)^[11]. In addition, the yield of grain is affected by the different yield contributing characteristics which are interrelated and strongly influenced by environmental conditions (Prasad *et al.* 2001)^[23]. Yield enhancement is the main breeding goal of the rice breeding programmes, which depends primarily on the degree of interaction between the characteristics and the extent and quality of the variation (Zahid *et al.* 2006 and Prasad *et al.* 2001)^[31, 23]. The degree of association between the component characters and the yield can be determined by correlation coefficients. In this investigation, the study of different genotypes were made with an attempt to generate information on inheritance, relationship of yields and its components and the information thus obtained will be used to define suitable selection criteria for yield improvement.

Materials and Methods

The experimental material consists of 46 genotypes including six zonal checks. The source details of selected genotypes were given in (Table 1) six check varieties Danteshwari, Annada, Narendra 97, Samleshwari, Vandna and Sahbhagi Dhan-1. were used in the conduction of the experimental trial the study on rice was carried out at the Research cum Instructional Farm of S.G. College of Agriculture and Research Station, Jagdalpur, Bastar (C.G.), which was located at 19°5'35" N and 81°57'37" E, at an altitude of 562 meters in Bastar plateau above the main sea level. The experiments were grown in a Randomized Block Design (RBD) with two replications in *Kharif* 2022 (23 June – 09 Dec.) with net plot size of 1.6m × 4.8 m and gross plot size of 2×5 m were used to sow the crop. Recommended agronomic package of practices was followed to raise a good and healthy crop and fertilizer dose of 120:40:40 kg NPK/ha. Five competitive plants of each genotype were randomly selected from each replication for taking the observations. The data were collected from randomly selected plants from the field for eleven quantitative characters *viz.*, Days to 50% flowering, Plant height (cm), Flag leaf length, Flag leaf width, Panicle length, Number of effective tillers, Number of filled grain/panicle, Test weight (g), Biological yield, Harvest index, Grain yield (q/ha). Averages of the data from each replication in respect of different characters were used for various statistical analyses. Statistical analysis of the data was done with opstat. Analysis of variance (ANOVA) estimated according to Panse and Sukhatme (1967)^[32]. Genotypic and

phenotypic coefficients of variation were estimated by the formula suggested by Burton and De Vane (1953) for each character, Heritability percentage was categorized as demonstrated by Robinson *et al.* (1949)^[33], Correlation and Path analysis.

Results and Discussion

Qualitative features have been employed to distinguish rice genotypes. Because they are less impacted by the environment, qualitative features are regarded as morphological characters in the identification of rice genotypes. The current study showed the most variance among genotypes in the basal leaf sheath colour, auricle, leaf blade colour, panicle length, flag leaf length, and flag leaf width. Low variation was seen in different genotypes after the flag leaf angle and awning. In the genotypes, 100% had medium flag leaf width, 72% had medium panicle length, and 76% had no awning. All 46 genotypes had a two-cleft ligule form, with no changes between them. Similar finding were reported by Rao *et al.* (2001)^[24]; Chouhan *et al.* (2014)^[12]; Das and Ghosh (2010)^[13]. Thus characterization of germplasm genotypes establishes distinctiveness among rice genotypes. It is not only important for utilizing the appropriate attribute based donors in breeding programmes, but also essential in the present era for protecting the unique rice.

Most quantitative traits showed a wide range of genetic diversity. Grain yield (8.74), harvest index (7.67), and number of filled grain per panicle (7.31), biological yield (7.12), flag leaf width (6.05), paddy length breadth (5.75), panicle length (5.15), paddy length (4.85), test weight (4.68), flag leaf length (4.49), kernel length breadth ratio (3.29), plant height (3.27), paddy width (2.86), kernel length (2.81), days to 50% flowering (1.88) and kernel width (1.52). Moderate estimate of coefficient of variation were found in number of effective tillers (10.20). Similar results were obtained by Singh *et al.* (2010)^[12] (number of filled grain per panicle, grain yield q/ha, number of effective tillers, panicle length). Coefficient of variation low was considered as good so that character grain kernel width (1.52%) with low coefficient of variation had less variation among the genotypes.

The current investigation showed that analysis of variance revealed that all of the features showed extremely significant differences across the genotypes under consideration (Table 2). As a result, it suggests that there is enough variation across the genotypes and provides scope for additional improvement. The presence of a high degree of variability could be attributed to the varied sources of breeding materials collected as well as environmental effects on phenotypes. Similar findings were reported by Yashwant *et al.* (2021)^[30] and Gupta *et al.* (2020)^[15].

The variability exploited in breeding programme is desired from the naturally occurring variants and wild relative of main crop species as well as from strains and genetic stocks artificially developed by human efforts. In (Table 3) shows the mean values for all the character studied days to 50% flowering ranged from 99 to 115.00 days with mean of 107.07 days, plant height ranged from 106.50 to 113.50 days with mean value of 113.50 days, plant height ranged from 87.35 to 132.50 (cm) with mean value of 106.12 (cm), flag leaf length ranged from 24.28 to 38.30 with mean value of 29.15, flag leaf width ranged from 1.35 to 1.85 with mean value of 1.60, panicle length ranged from 18.98 to 28.30 (cm) with mean

value of 23.56 (cm), number of filled grain/ panicle ranged from 96.55 to 246.40 with mean value of 153.84, number of effective tillers ranged from 7.00 to 13.70 with mean value of 10.06, biological yield ranged from 6.72 to 11.93 (Kg/ha) with mean value of 9.73 (Kg/ha), test weight ranged from 15.58 to 34.37 with mean value of 24.43, paddy length ranged from 6.90 to 9.50 (mm) with mean value 8.16, paddy breadth ranged from 2.30 to 3.20 with mean value of 2.71, kernel length ranged from 5.40 to 8.40 (mm) with mean value of 6.86, kernel breadth ranged from 2.08 to 2.83 with mean value of 2.32, paddy length breadth ratio ranged from 2.47 to 3.63 with mean value of 3.03, kernel length breadth ratio ranged from 2.23 to 3.86 with mean value of 2.97, harvest index (%) ranged from 32.11 to 60.76 with mean value of 47.10, grain yield showed a wide variation which ranged from 28.9 to 61.4 (q/ha) with mean value of grain yield was 45.9 (q/ha) based on the mean performance of grain yield, genotypes viz., R 2340-267-2-140-1 (61.4 q/ha) followed by R-BSP-18-3 (60.7 q/ha), R 2220-382-1-243-1 (55.5 q/ha), R2370-501-1-284-1 (55.2 q/ha), R 2412-709-1-331-1 (53.5 q/ha). were high yielding genotypes compared to checks. These high yielding genotypes could be utilized in further breeding programme.

The magnitude of the phenotypic coefficient of variation values were found to be slightly larger than GCV values, indicating that environment influences character expression. The number of filled grains per panicle had a moderate GCV with high PCV values. Plant height, flag leaf length, number of filled grains per panicle, number of effective tillers, biological yield, test weight, kernel length, kernel L/B, harvest index, and grain yield all had moderate GCV and PCV values. Days to 50% blooming, flag leaf width, panicle length, paddy length, paddy breadth, and kernel breadth all had low PCV and GCV values. Sathish Kumar *et al.* (2020) [27], Pallavi *et al.* (2022) [22], and Bhargavi *et al.* (2021) [8] reported similar findings.

Heritability determines the resemblance of offspring with their parents. While genetic advance provides information on expected gain for a specific character after selection, high estimates of heritability were observed for kernel length 95.61%, followed by kernel breadth 94.37%, kernel L/B ratio 93.63%, test weight 92.34%, plant height 91.58%, paddy breadth 89.85%, flag leaf length 86.70%, number of filled grain/panicle 82.19%, days to 50% flowering 81.85%, grain yield q/ha 73.23%, biological yield 68.01%, paddy L/B ratio 67.94%, panicle length 66.65%, paddy length 66.39%, harvest index 65.02%, number of effective tillers 64.22%, flag leaf width 58.05%. Flag leaf width had a moderate heritability of 58.05%. None of the characters have low heritability (Table 4). Similar findings were reported by Sudeepthi *et al.* (2020) [29] (grain yield, days to 50% flowering), Konate *et al.* (2016) [17] (test weight, days to 50% flowering), Kumar *et al.* (2020) [18] (length breadth ratio, kernel length, panicle length, kernel breadth, flag leaf length, grain yield, plant height, test weight, harvest index), and Bhor *et al.* (2020) [9] (days to 50% flowering, plant height, panicle length, number of effective tillers, grain yield).

High heritability coupled with high genetic advance was reported for Characteristics such as the test weight, number of filled grains per panicle, grain yield q/ha, kernel L/B ratio,

kernel length, number of effective tillers, flag leaf length, plant height. High heritability coupled with moderate genetic advance was reported for character like biological yield, harvest index, paddy width, paddy L/B ratio, kernel width, panicle length, paddy length, days to % flowering. Moderate heritability coupled with moderate genetic advance reported for character like flag leaf width. Similar finding were reported by Lakshmi *et al.* (2020) [19] (days to 50% flowering), Ningomban *et al.* (2022) [21] (grain yield, plant height, number of filled grain per panicle, harvest index, biological yield, panicle length). Bhargavi *et al.* 2021 [8] (grain yield), Yashwant *et al.* (2021) [30] (grain yield, harvest index, biological yield, plant height, days to 50% flowering).

Table 1: List of 46 genotypes used in experiment during *Kharif* 2022 including checks

S. No.	Entry	Genotype Name
1.	SPVT 1-1	R2321-172-1-103-1
2.	SPVT 1-2	R 2311-129-1-85-1
3.	SPVT 1-3	C3-3-3
4.	SPVT 1-4	Danteshwari (ch)
5.	SPVT 1-5	R 2307-68-1-35-1
6.	SPVT 1-6	R 2307-63-2-45-1
7.	SPVT 1-7	R 2320-91-1-51-1
8.	SPVT 1-8	R 2404-607-1-353-1
9.	SPVT 1-9	R2297-21-1-5-1
10.	SPVT 1-10	R2302-34-1-14-1
11.	SPVT 1-11	R 2302-27-1-13-1
12.	SPVT 1-12	R2370-501-1-284-1
13.	SPVT 1-13	R2370-500-2-283-1
14.	SPVT 1-14	Annada (ch)
15.	SPVT 1-15	R 2412-709-1-331-1
16.	SPVT 1-16	R2328-214-1-119-1
17.	SPVT 1-17	R 2297-64-2-23-1
18.	SPVT 1-18	R 2370-487-1-267-1
19.	SPVT 1-19	R 2419-1246-1-608-1
20.	SPVT 1-20	R 2340-270-1-142-1
21.	SPVT 1-21	R 2460-RP5537-DRR-SPS-38-1
22.	SPVT 1-22	R 2340-267-2-140-1
23.	SPVT 1-23	R-BSP-18-3
24.	SPVT 1-24	R 2406-399-1-204-1
25.	SPVT 1-25	Narendra 97 (ch)
26.	SPVT 1-26	R 2485-PHD-SPS-28-1
27.	SPVT 1-27	C 6-11-1
28.	SPVT 1-28	R 2307-91-1-61-1
29.	SPVT 1-29	R 2340-243-1-275-1
30.	SPVT 1-30	RPRE-21-4
31.	SPVT 1-31	DH-18-SXR-49
32.	SPVT 1-32	Samleshwari (ch)
33.	SPVT 1-33	R 2485-PHD-SPS-16-1
34.	SPVT 1-34	C 7-1-3
35.	SPVT 1-35	RPRE-21-2
36.	SPVT 1-36	R 2303-32-1-15-1
37.	SPVT 1-37	R 2294-58-1-17-1
38.	SPVT 1-38	R 1882-306-4-243-1
39.	SPVT 1-39	R 2311-142-1-122-1
40.	SPVT 1-40	R 2322-178-2-167-1
41.	SPVT 1-41	R 2220-382-1-243-1
42.	SPVT 1-42	JDP-0321
43.	SPVT 1-43	JDP-1021
44.	SPVT 1-44	Bastar Dhan-1
45.	SPVT 1-45	Vandna (ch)
46.	SPVT 1-46	Sabhagi Dhan-1 (ch)

Table 2: Analysis of variance for yield and yield attributing traits

S. No.	Source of variation	Mean sum of square		
		Replication (df=1)	Treatment (df=31)	Error (df=62)
1.	Days to 50% flowering	4.250	40.66**	4.06
2.	Plant height (cm)	0.490	273.60**	12.02
3.	Flag leaf length (cm)	0.080	24.08**	1.70
4.	Flag leaf width (cm)	0.020	0.04**	0.009
5.	Panicle length (cm)	3.160	7.35**	1.47
6.	Number of filled grains per panicle	394.9	1293.00**	126.40
7.	Number of effective tillers	43.140	4.83**	1.05
8.	Biological yield (Kg)	0.260	2.52**	0.48
9.	Test weight (g)	3.290	32.80**	1.31
10.	Grain Length (mm)	0.003	0.78**	0.16
11.	Grain Width (mm)	0.024	0.11**	0.01
12.	Kernel Length (mm)	0.143	1.33**	0.03
13.	Kernel Width (mm)	0.438	0.04**	0.00
14.	Paddy L/B ratio	0.029	0.16**	0.03
15.	Kernel L/B ratio	0.125	0.29**	0.01
16.	Harvest index (%)	6.08	61.53**	13.04
17.	Grain yield (q/ha)	0.31	1.04**	0.161

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

Table 3: Mean, Standard error and Coefficient of Variation of 17 characters under study

Characters	Minimum X_{min}	Maximum X_{max}	Mean (\bar{X})	Std. Error (SE)	Coefficient of variation (CV %)
Days to 50% flowering	99.00	115.50	107.07	2.15	1.88
Plant height (cm)	87.35	132.50	106.12	1.77	3.27
Flag leaf length (cm)	24.28	38.23	29.15	0.58	4.49
Flag leaf width (cm)	1.35	1.85	24.91	0.62	6.05
Panicle length (cm)	18.98	28.30	23.56	0.68	5.15
Number of filled grains per panicle	96.55	246.40	153.84	0.09	7.31
Number of effective tillers	7.00	13.70	10.06	12.19	10.20
Biological yield (Kg)	6.72	11.93	9.73	0.74	7.12
Test weight (g)	15.58	34.37	24.43	1.99	4.68
Paddy Length (mm)	6.90	9.50	8.16	5.65	4.85
Paddy breadth (mm)	2.30	3.20	2.71	0.23	2.86
Kernel Length (mm)	5.40	8.40	6.86	0.11	2.51
Kernel Width (mm)	2.08	2.83	2.32	0.12	1.52
Paddy L/B ratio	2.47	3.63	3.03	0.07	5.75
Kernel L/B ratio	2.23	3.86	2.35	0.10	3.29
Harvest index (%)	32.11	60.76	47.10	0.11	7.67
Grain yield (q/ha)	28.09	61.04	45.09	5.08	8.74

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

Table 4: Genetic parameters of variation for yield and yield attributing characters

Characters	Heritability	(%) GA	GA%M	GCV	PCV
Days to 50% flowering	81.85	7.97	7.45	4.00	4.42
Plant height (cm)	91.58	22.55	21.24	10.78	11.23
Flag leaf length (cm)	86.70	6.41	22.00	11.47	12.32
Flag leaf width (cm)	58.05	0.18	11.18	7.12	9.35
Panicle length (cm)	66.65	2.88	12.24	7.28	8.92
Number of filled grain per panicle	82.19	45.10	29.32	15.70	17.32
Number of effective tillers	64.22	2.27	22.56	13.67	17.06
Biological yield (Kg)	68.01	1.72	17.64	10.38	12.59
Test weight (g)	92.34	7.86	32.15	16.24	16.90
Paddy length (mm)	66.39	0.93	11.44	6.82	8.37
Paddy breadth (mm)	89.85	0.45	16.65	8.53	9.00
Kernel length (mm)	95.61	1.62	23.63	11.73	12.00
Kernel width (mm)	94.37	0.29	12.47	6.23	6.42
Paddy L/B ratio	67.94	0.43	14.20	8.36	10.15
Kernel L/B ratio	93.63	0.75	25.15	12.62	13.04
Harvest index (%)	65.02	8.18	17.37	10.45	12.96
Grain yield (q/ha)	73.23	1.17	25.49	14.46	16.90

Conclusion

The present study found highly significant differences across

genotypes for all of the traits evaluated, which can be used to design high-yielding cultivars. The presence of genetic

variability in the examined genotypes for quantitative character showed the possibility of developing hybrid varieties by direct selection of parental genotypes. R 2340-267-2-140-1 (61.04 q/ha) was the best seed yield genotype, followed by R-BSP-18-3 (60.7 q/ha), R 2220-382-1-243-1 (55.5 q/ha), R 2370-501-1-284-1 (55.2 q/ha), and R 2412-709-1-331-1 (53.5 q/ha). Comparative investigations revealed that the genotypes under consideration produced more grain per hectare than the check varieties. A high level of genetic variation was discovered between genotypes, which may be valuable in future breeding programmes.

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