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Shaik Javid
Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Prabharani Chaudhari
Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Pradeep Kumar Sao
Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Mohit Sahu
Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Corresponding Author:
Shaik Javid
Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Genetic assessment of rice (*Oryza sativa* L.) Genotypes for morphological and quality traits

Shaik Javid, Prabharani Chaudhari, Pradeep Kumar Sao and Mohit Sahu

Abstract
The study was conducted during the *Kharif* season of 2023 at the Instructional cum Research Farm, Department of Genetics and Plant Breeding, IGKV, Raipur, India, using sixty four rice genotypes. The Randomized Complete Block Design (RCBD) was employed to assess genetic variability, heritability, and genetic advance. Quantitative traits like harvest index, biological yield, grain yield, and productive tillers exhibited high GCV% and PCV%, with the highest heritability observed in 1000-grain weight. Quality traits like gel consistency, amylose content, and alkali spreading value showed high GCV%, PCV%, and heritability, with most exceeding 90%. High heritability combined with high genetic advance was noted for traits such as grain yield, harvest index, biological yield, and gel consistency, indicating potential for selection.

Keywords: Rice, grain yield, GCV%, PCV%, heritability and genetic advance

Introduction
Rice (*Oryza sativa* L. 2n=24) is a staple food for over one-third of the global population and plays a crucial role in global food security. Belonging to the genus *Oryza* within the Poaceae family, rice is vital for meeting the rising food demand driven by population growth. Asian countries dominate rice production, with China contributing 27.99% and India 23.56% and others. Developing high-yielding varieties is essential to address increasing demand.

Genetic parameters, such as phenotypic and genotypic coefficients of variation, heritability, and genetic advance, are critical for understanding variability within populations and identifying genotypes with desirable traits. Variability arises from genetic differences and environmental influences, with phenotypic variance reflecting both factors. Partitioning phenotypic variance into genotypic and environmental components is essential for effective selection, as genotypic variance indicates true genetic potential.

Heritability and genetic advance are key tools for breeding. Heritability estimates identify traits that can be effectively selected and inherited, while genetic advance quantifies potential improvements. High heritability coupled with substantial genetic advance suggests additive gene action, enabling significant genetic progress through selection. Together, these parameters guide breeders in improving traits critical for crop enhancement (Basavaraj *et al.* 2023) [1].

Materials and Methods
The experiment was conducted on 64 rice genotypes, including the check varieties MTU 1010, IR 64, IR-20, and Swarna, in a Randomized Block Design (RBD) with two replications during the Kharif season of 2023. Manually transplanted with single seedlings per hill, maintaining a spacing of 20 cm between rows and 15 cm between plants.

Observations for yield and quality traits were recorded at the optimal growth stage from five randomly selected plants per line across both replications.

Results and Discussion
The analysis of ten quantitative and sixteen quality traits were conducted using data from five randomly selected plants per genotype in each replication. Analysis of variance revealed highly significant treatment mean sum of squares. Among quantitative traits, high GCV% and PCV% were observed for harvest index (%), biological yield per plant (g), grain yield per plant (g), filled grains per panicle and productive tillers per plant. For quality traits, gel

consistency (mm), amylose content (%) and alkali spreading value exhibited the highest GCV% and PCV% shown in Table 1.

High heritability was noted for both quantitative and quality traits, ranging from kernel length after cooking to productive tillers per plant. The highest heritability among quantitative traits was observed in 1000-grain weight (g), while the lowest was in productive tillers per plant. For quality traits, head kernel length after cooking showed the highest heritability, and alkali spreading value the lowest.

High heritability coupled with high genetic advance as a percentage of the mean was observed for quantitative traits such as harvest index (%), biological yield per plant (g), grain yield per plant (g), filled grains per panicle, effective tillers per plant, 1000-grain weight (g), plant height (cm), days to 50% flowering, and spikelet fertility (%). Similarly, quality traits like gel consistency (mm), amylose content (%), alkali spreading value, head rice recovery (%), paddy L/B ratio, cooked rice L/B ratio, kernel L/B ratio, and elongation ratio also showed high genetic advance. Traits with high heritability and high genetic advance suggest the predominance of additive gene action, facilitating effective selection. Moderate genetic advance was observed for panicle length (mm) among quantitative traits and for kernel length (mm), paddy length (mm), kernel breadth (mm), and milling (%) among quality traits.

Sao *et al.* (2024) [2, 3] evaluated fifty three rice genotypes for genetic variability in yield and related traits. PCV exceeded GCV for all traits. High heritability with significant genetic advance was observed in test weight, plant height, filled and unfilled grains per panicle, total grains per panicle, panicles per plant, total tillers, biological yield, grain yield, and harvest index, indicating strong selection potential.

Sahu *et al.* (2024) [3] evaluated fifty three rice genotypes during *Kharif* 2023, noting higher PCV than GCV for all traits. Yield traits, including grain count per panicle, grain yield, panicle and tiller numbers, harvest index, test weight, plant height, biological yield, and panicle length, exhibited high heritability with substantial genetic advance, indicating additive gene action and strong selection potential for genetic improvement.

Table 1: Estimation of variability parameters for yield & quality traits

S. No	Character	Mean	Range		GCV %	PCV %	$h_{(bs)}^2$	GA as % of mean
			Min.	Max.				
1.	Days to 50% flowering	99.00	74.00	133.00	12.70	13.83	84.30	24.02
2.	Plant height (cm)	118.32	80.00	151.00	13.28	14.23	87.00	25.52
3.	No. of productive tillers per plant	6.00	3.00	10.00	23.38	27.97	69.86	40.26
4.	Panicle length (cm)	23.46	18.00	29.00	8.09	9.34	75.05	14.44
5.	No. of filled grains per panicle	90.00	34.00	166.00	27.17	28.09	93.52	54.13
6.	Spikelet fertility (%)	82.53	53.00	96.10	10.25	12.09	84.78	23.04
7.	1000 grain weight (g)	25.13	13.00	37.00	18.15	18.40	97.29	36.88
8.	Biological yield per plant (g)	43.85	18.00	88.00	37.10	39.86	93.07	77.25
9.	Grain yield per plant (g)	12.10	4.00	24.00	31.38	34.00	85.20	59.67
10.	Harvest Index (%)	30.73	7.70	60.00	41.14	43.16	90.86	80.79
11	Hulling %	83.51	71.00	91.60	4.16	4.31	93.35	8.29
12.	Milling %	75.57	44.90	86.80	7.69	7.84	96.26	15.56
13.	Head rice recovery %	62.61	27.20	82.60	18.02	19.89	90.59	40.05
14.	Paddy length (mm)	8.42	6.90	10.50	8.82	9.08	94.39	17.66
15.	Paddy breadth (mm)	2.72	1.80	3.50	13.98	14.29	95.76	28.20
16.	Paddy L/B ratio	3.15	2.30	4.70	16.84	17.35	94.17	33.67
17.	Kernal length (mm)	6.06	5.10	8.10	9.21	9.27	98.72	18.86
18.	Kernal breadth (mm)	2.29	1.80	2.90	8.82	9.54	85.40	16.80
19.	Kernal L/B ratio	2.67	1.90	4.10	14.64	15.25	92.22	28.98
20.	Kernal length after cooking (mm)	8.10	5.70	11.30	14.32	14.41	98.74	29.32
21.	Kernal breadth after cooking (mm)	3.06	2.00	5.10	16.45	16.66	97.47	33.45
22.	Cooked rice L/B ratio	2.69	1.40	4.20	16.55	16.93	95.58	33.34
23.	Elongation ratio	1.33	1.00	1.70	11.44	11.60	97.17	23.23
24.	Gel consistency (mm)	56.14	25.00	100.00	57.91	58.33	98.55	93.12
25.	Alkali spreading value	3.69	3.00	7.00	27.91	30.37	84.46	52.85
26.	Amylose content %	15.55	3.20	29.70	35.33	35.83	97.23	71.76

GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, $h_{(bs)}^2$ = Heritability in broad sense, GA as % of mean = Genetic advance as % of mean.

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