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## Assessment of genetic variability, heritability and genetic advance in accessions of rice (*Oryza sativa* L.)

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#### Abstract

Rice gives a great wealth of material for genetical studies because of its wide ecological distribution and enormous discrepancies encountered for multitudinous morphological and physiological characteristic. The rice germplasm provide with ample of genetic diversity and a treasury of valuable genes. It is a rich pool of important genes that plant breeders can exploit for crop improvement. In present investigation, forty six exotic rice germplasm along with four checks were evaluated to estimate the genetic variability parameters in yield and yield contributing characters during *Kharif* 2019. Analysis of variance indicated the existence of significant genotypic differences among the genotypes for the yield, its components for all the characters. High GCV and PCV values were observed for characters *viz.*, biological yield, harvest index, grain yield per plant, effective tillers per plant and 1000 seed weight. High heritability coupled with high genetic advance as per cent of mean was observed for biological yield followed by harvest index, grain yield per plant, effective tillers per plant, days to 50 percent flowering and number of filled grains per panicle which indicated that these traits were controlled by additive type of gene action. It is concluded that variation exists in the germplasm, which provides opportunities for this collection to be useful for genetic improvement.

**Keywords:** Rice, genetic diversity, agromorphological, germplasm, accessions

#### Introduction

Rice (*Oryza sp.*) is the essential cereal food in India belongs to the genus *Oryza* of the tribe Oryzeae of the subfamily Bambusoideae or Ehrhartoideae of the family Poaceae or Graminae. As a staple cereal crop rice feeds more than 50% of the world population (Mather *et al.*, 2007) [8]. Rice is India's main food crop, providing 43% of the caloric demand for more than 70% of the Indian population. Due to rapid growth of the population, rice yield is urgently required to increase to meet the food demand. In order to meet the demand there is a necessity of development of high yielding varieties along with good quality traits. Agro morphological characterization of germplasm is fundamental in order to provide information for plant breeding programs (Das and Ghosh 2011) [4]. Rice genotypes have a greater genetic diversity than elite cultivars (or commercial cultivars) and represent an intermediate stage in domestication between wild rice and elite cultivars (Londoet *et al.*, 2006) [7]. The germplasm of rice provides ample genetic diversity and treasury of useful genes. It is a rich reservoir of essential genes that can be used for crop enhancement by plant breeders (Yadav *et al.*, 2013) [14]. Characterizations of rice germplasm in any breeding programme increases its usefulness. The most predictable agro-morphological method is used to decide the relationship between genotypes (Bajracharya *et al.*, 2006) [2] for germplasm survival and selection of parents with different genetic background, the analysis of actual genetic discovery and its distribution in crop species is important thus making crop improvement more effective (Teklu *et al.*, 2006) [12].

#### Material and methods

The present investigation was carried out during Kharif season 2019 at Research Farm of Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh, India. The experimental material comprises of total 46 rice genotypes i.e. 46 germplasm accessions received from Consortium Research Platform on Agro biodiversity on Germplasm Characterization and Evaluation of rice along with four checks (Samleshwari, Rajeshwari, Maheshwari and Jaldubi). Experimental material i.e. 46 germplasm accessions and four checks were grown in during kharif 2019 under irrigated conditions in Completely randomized block fashion (CRBD) with 2 replications, maintaining the inter and intra row spacing of 20 x 20 cm.

The recommended agronomical practices were followed to raise good crop in the season. Observations were recorded on five randomly chosen plants of each accession for thirty seven agro-morphological traits and thirteen quantitative traits in rice.

### Result and Discussions

The trial materials contained 46 germplasms accessions of rice and 4 checks namely Samleshwari, Rajeshwari, Maheshwari and Jaldubi. The trial was carried out in Randomized Block Design with an objective of agromorphological characterization of rice germplasm accessions based on quantitative and the qualitative characters of germplasm accessions were studied.

### Analysis of variance

The analysis of variance (ANOVA) was performed in Randomized Complete Block Fashion for the genotype accessions are screening highly significant difference among all characters of rice accessions. This indicates that there is high amount of variability present in the genotypes for the

taken observation of all traits. It points sufficient differences found in experimental material of the replication. For quantitative traits, highest mean performance for number of filled grains per panicle (148.23) followed by plant height (118.95).

**Genotypic and Phenotypic coefficient of variance:** The RCBD analysis offers details on variance, i.e. genotypic variance (GCV) and phenotypic variance (PCV). In all features, PCV is greater than GCV, suggesting that the setting is more influential over all characters. The genotypic variation was lower than the phenotypic variance, suggesting that the climate has a masking effect on the expression of genetic variability. The characters viz., biological yield (37.90), harvest index (36.94), grain yield per plant (26.95%), effective tillers per plant and 1000 seed weight have high genotypic and phenotypic coefficient of variation that showed the presence of considerable amount of variability for these characters for all genotypes. Similar findings were reported by Tuhina-Khatun *et al.*, (2015) <sup>[13]</sup>, Limbani *et al.*, (2017), and Singh *et al.*, (2018).

**Table 1:** Analysis of variance for grain yield and its contributing traits in rice germplasm accessions

S.N	Source of variance	DF	1	2	3	4	5	6	7	8	9	10	11	12	13
1.	Replication	1	0.04	0.350	0.290	0.013	0.049	0.01	0.001	179.510	87.870	0.076	0.11	0.35	60.050
2.	Genotype	49	443.26**	285.35**	7.31**	3.58**	2.38**	92.91**	0.03**	799.09**	146.91**	15.53**	404.94**	109.74**	1854.49**
3.	Error	49	0.958	2.884	0.426	0.034	0.296	0.588	0.003	334.499	25.259	0.199	1.967	3.000	46.973

\* Significant at 5% level,

\*\* Significant at 1% level

1	Days to 50% flowering	8	Number of filled grains per panicle
2	Plant height (cm)	9	Number of unfilled grains per panicle
3	Panicle length (cm)	10	1000 Grain weight (g)
4	Total tillers per plant	11	Biological yield per plant (g)
5	Effective tillers per plant	12	Grain yield per Plant(g)
6	Leaf length (cm)	13	Harvest Index
7	Leaf width (cm)		

**Table 2:** Genetic Parameter of variation for grain yield and its contributing traits in rice germplasm accessions

S.no.	Characters	Mean	Range		Critical difference -5%	CV%	Coefficient of variation		h <sup>2</sup> %	GA	GA % mean
			Max	Min			PCV	GCV			
1	Days to 50% flowering	81.88	106.00	59.00	1.97	1.19	18.20	18.16	99.56	30.56	37.33
2	Leaf length (cm)	55.48	69.42	41.10	1.54	1.38	12.33	12.25	98.79	13.89	25.06
3	Leaf width (cm)	1.37	1.70	1.20	0.10	3.85	8.75	7.85	81.76	0.20	14.66
4	Plant height (cm)	118.95	148.37	98.20	3.41	1.42	10.09	9.99	98.82	24.43	20.52
5	Panicle length (cm)	25.79	29.90	21.40	1.31	2.53	7.62	7.19	89.00	3.60	13.97
6	Total number of tiller per plant	8.51	11.50	5.70	0.37	2.17	15.78	15.63	40.99	20.10	13.56
7	Effective tiller per plant	7.86	10.30	5.30	1.09	6.91	14.70	12.98	60.21	11.53	42.34
8	Number of filled grains per panicle	148.23	196.66	98.83	36.75	12.33	16.06	10.28	98.10	2.71	31.90
9	Number of unfilled grains per panicle	27.51	44.80	11.60	10.10	18.27	33.72	28.35	77.88	1.85	23.59
10	1000 grain weight (g)	22.24	28.80	13.50	0.89	2.00	12.61	12.45	97.47	5.63	25.32
11	Biological yield (g)	37.63	67.63	17.35	2.81	3.72	37.90	37.72	99.03	29.09	77.32
12	Grain yield per plant (g)	27.10	54.55	17.68	3.48	6.39	27.70	26.95	94.67	14.64	54.03
13	Harvest Index	81.37	137.28	32.62	13.77	8.42	37.89	36.94	95.05	60.38	74.20

**Heritability and Genetic Advance:** In heritability ( $h^2$ ) analysis and genetic advancement, high heritability with high genetic advancement is proof of heritability due to additive gene actions and choices for that unique desirable phenotype would be advantageous and successful. Maximal heritability paired with maximal genetic advance as percent of the population mean is reported. High heritability along with high genetic advance was observed for biological yield followed

by harvest index, grain yield per plant, effective tillers per plant, days to 50 percent flowering and number of filled grains per panicle. Babu *et al.*, (2012) <sup>[1]</sup>, Chakrovorty *et al.*, (2013) <sup>[3]</sup>, and Srujana G *et al.*, (2017) <sup>[11]</sup>.

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