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## Studies on genetic variability parameters in rice germplasm (*Oryza sativa* L.)

**Madhuri Singh, Laxmi Singh and Prabharani Chaudhari**

### 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 fifty indigenous rice germplasm were evaluated to estimate the genetic variability parameters in yield and yield contributing characters during *Kharif* 2018. 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 effective tillers per plant, leaf length of blade, thousand grain weight, biological yield per plant and harvest index. High heritability coupled with high genetic advance as per cent of mean was observed for thousand grain weight, leaf length of blade, effective tillers per plant and plant height 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, germplasm and genetic variability

### Introduction

Rice is the staple food of over half of the world's population and 90% of Asians. Rice is known as the grain of life, and is synonymous with food for Asians. In addition to being a staple food and an integral part of social rites, rituals, and festivals in almost all Asian countries, it has a medicinal value too, which was clearly recognized by the medicine systems of the region centuries ago.

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 (Yadav *et al.*, 2013)<sup>[10]</sup>. Traversing diversity in a land race collection is essential for identifying novel genes and hence improvement of the germplasm (Thomson *et al.*, 2007)<sup>[9]</sup>.

A major purpose of varietal characterization is to establish the distinctiveness between the germplasm and also to establish their unique detection profiles on the basis of grouping individuality prescribed by Distinctness Uniformity Stability (DUS) guidelines. Morphological description is the first step for classification and evaluation of the germplasm which is a necessary tool for selecting varieties or lines based on agronomical, morphological, genetic or physiological characters. The adjoining area of Orissa and Chhattisgarh are considered to be the store house of vast genetic variability. The efficiency of selection depends upon the magnitude of genetic variability present in the plant population. Rice is the staple food of over half of the world's population and 90% of Asians. Rice is known as the grain of life, and is synonymous with food for Asians. In addition to being a staple food and an integral part of social rites, rituals, and festivals in almost all Asian countries, it has a medicinal value too, which was clearly recognized by the medicine systems of the region centuries ago. Thus, the surfaces of genetic improvement in any characters depends upon the nature of variability present in the gene pool for that character, to start a judicious plant breeding programme.

## Materials and Methods

The experimental material comprised of fifty indigenous rice germplasm were grown in randomized complete block design with two replications at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during *Kharif* 2018. Crop was raised following recommended package of practices. Observations were recorded on five randomly tagged plants of each genotype per replication. Data were recorded on eleven quantitative characters which includes days to 50% flowering, plant height (cm), effective number of tillers/ plant, leaf length of blade (cm), leaf width of blade (cm), panicle length of main axis (cm), panicle number / plant, thousand grain weight (g), biological yield/ plant (g), harvest index (%) and grain yield/plant(g). Analysis of variance was done based on RBD (Panse and Sukhatme, 1961) for each of the characters separately. The phenotypic and genotypic coefficient of variance, heritability in broad sense (Burton and Devane, 1953) and Genetic advance was estimated (Allard, 1960) [1].

## Results and Discussion

The analysis of variance indicated the existence of highly significant differences among genotypes for all the characters studied (Table 1). This indicated presence of high variability among the genotypes, which provides ample scope for selection for different quantitative characters for rice improvement. A wide range of variation was observed in the rice germplasm for the yield and other quantitative characters (Table 2). Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for days to 50% flowering, plant height, number of tillers/ plant, leaf length of blade, leaf width of blade, 1000 grain weight, biological yield per plant and

harvest index indicating that the characters were less influenced by the environment (Lingaiyah *et al.*, 2015) [3]. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

In this study, the highest PCV and GCV was recorded for effective tillers per plant (32.02 and 30.68), leaf length of blade (25.48 and 23.19), thousand grain weight (21.96 and 21.89), biological yield per plant (30.71 and 27.18) and Harvest index% (29.26 and 28.38). Similar finding also reported by (Limhani *et al.*, 2017). Low PCV and GCV estimates were obtained for days to 50% flowering (9.08 and 9.05). The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value (Ashvani *et al.*, 1997) [7]. Therefore, high heritability helps in effective selection for a particular character. In the present study, high heritability was recorded in thousand grain weight (99.4%), days to 50% flowering (99.3%), leaf length of blade (99.1%), plant height (93.1) and effective tillers per plant (91.8%).

In general, the character that shows high heritability with high genetic advance are controlled by additive gene action (Patil *et al.*, 2003) [8] and can be improved through simple or progeny selection methods. Selection for the traits having high heritability coupled with high genetic advance is likely to accumulate more additive genes leading to further improvement of their performance (Johnson *et al.*, 1955) [4]. In this study high heritability coupled with high genetic advance as percent of mean was observed for thousand grain weight, leaf length of blade, effective tillers per plant and plant height. The characters showing high heritability along with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding. similar findings were reported by (Limhani *et al.*, (2017).

**Table 1:** analysis of variance for different quantitative characters

S. No.	Sources of variation	Mean sum of square		
		Replication	Treatment	Error
	Degree of freedom	1	49	49
1	Days to 50% flowering	2.56	139.12**	0.457
2	Plant height (cm)	1.37	993.42**	35.76
3	Effective tillers per plant	0.22	11.48**	0.49
4	Leaf length of blade (cm)	0.25	63.03**	0.29
5	Leaf width of blade (cm)	0.019	0.079**	0.0074
6	Panicle length of main axis (cm)	7.74	14.37**	3.17
7	Panicle no. per plant	2.78	2.51**	1.78
8	Thousand grain weight (g)	0.15	57.51**	0.18
9	Biological yield per plant (g)	3.83	140.97**	17.16
10	Harvest index (%)	24.73	314.64**	38.02
11	Grain yield per plant (g)	3.38	31.95**	5.87

(Note- \*\* Significant at 1% level of probability, \* Significant at 5% level of probability)

**Table 2:** Estimates of variability parameters for quantitative characters

S. No.	Characters	Grand mean	Minimum	Maximum	CV (%)	PCV (%)	GCV (%)	h <sup>2</sup> (bs)%	GA	GA (as% of mean)
1	Days to 50% flowering	92.02	79.5	104.5	0.737	9.08	9.05	99.3	17.1	18.58
2	Plant height (cm)	118.59	65	163.7	5.042	19.13	18.45	93.1	43.48	36.66
3	Effective tillers per plant (No.)	7.64	4.6	16.1	9.194	32.02	30.68	91.8	4.63	60.60
4	Leaf length of blade (cm)	37.79	26.85	44.6	1.43	14.89	14.82	99.1	11.48	30.38
5	Leaf width of blade (cm)	0.817	0.24	1.24	10.564	25.48	23.19	82.8	0.36	44.06
6	Panicle length of main axis (cm)	23.89	16.65	30.3	7.461	12.4	9.9	63.8	3.89	16.28
7	Panicle no. per plant	6.731	5.4	9.4	19.87	21.79	8.95	16.9	0.51	7.58
8	Thousand grain weight (g)	24.46	10.04	31.40	1.761	21.96	21.89	99.4	10.99	44.93
9	Biological yield per plant (g)	28.95	13.9	45.05	14.3	30.71	27.18	78.3	14.34	49.53
10	Harvest index (%)	45.38	22.28	58.31	13.58	29.26	25.91	78.4	21.46	47.29
11	Grain yield per plant (g)	12.7	5.8	22.8	19.04	34.18	28.38	68.9	6.18	48.66

Note- CV% = coefficient of variance in percent, PCV% = Phenotypic coefficient of variation, GCV% = Genotypic coefficient of variation, h<sup>2</sup>% = Heritability in broad sense, GA% = Genetic advance in percent value

## Conclusion

In conclusion, High GCV and PCV values were observed for effective tillers per plant, leaf length of blade, thousand grain weight, biological yield per plant, and harvest index. Which indicated that selection on the basis of phenotype alone can be effective for the improvement of these traits. High heritability coupled with high genetic advance as percent of mean was observed for thousand grain weight, leaf length of blade, effective tillers per plant and plant height. Which indicated that these traits were controlled by additive type of gene action in the inheritance of these characters, these characters can be further improved by following simple selection procedure. These traits can be improved by intermating superior genotypes of segregating population developed from combination breeding.

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