

## Study on Variability, Heritability and Genetic Advance for Agro-Morphological and Grain Quality Parameters in Restorer Lines of Rice (*Oryza sativa* L.)

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### ABSTRACT

Present investigation was carried out with the objectives to estimate variability parameters, heritability and genetic advance for 20 yield and yield contributing characters and quality traits in 50 restorer lines of rice. Analysis of variance revealed the presence of significant variability among the restorer lines of rice under study. The genotypes exhibited the highest magnitude of genotypic and phenotypic variances for harvest index, grain yield per plant and grains per panicle indicating the presence of large variation among the genotypes for these characters. The high heritability with high genetic advance was recorded for harvest index, grain yield per plant, grains per panicle, test weight and productive tillers per m<sup>2</sup>, indicating that most likely the heritability is due to additive gene effects and selection may be effective for these characters.

**Key words:** Genetic advance, Heritability, Restorer lines, Rice Variability.

### INTRODUCTION

Rice (*Oryza sativa* L.) is the main staple food crop of Asia and is being consumed by more than half of the developing countries in the world<sup>6</sup>. It is a nutritious cereal crop, provides 20 per cent of the calories and 15 per cent of protein consumed by world's population. Besides being the chief source of carbohydrate and protein in Asia, it also provides minerals and fibre. Rice straw and bran are important animal feed in many countries. India is the world's second largest producer (157.2 m t) of

rice on an area of 43.85 m. ha and with the productivity of 3.5 t per ha. While, China produces 208.2 m t from an area of 30.5 m. ha with the productivity of 6.8 t per ha (FAOSTAT, 2016). Improvement in crop yield and quality is of prime importance to meet the rising demand owing to constant increase of population. In this context, assessment of variability in the crop for grain yield and yield attributes and quality characters is essential for successful exploitation and improvement of yield and quality through breeding.

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Success in recombination breeding depends on the suitable exploitation of genotypes as parents for obtaining high heterotic crosses and transgressive segregants. For this, the presence of genetic variability in a base population is essential. Choice of parents is not only based on desirable agronomic traits, components of yield and extent of diversity but also on heritability of yield contributing traits. The environment, in which selection is made, is also important because heritability and genetic advance estimates vary with change in environment. The systematic breeding programme involves the steps like creating genetic variability, practicing selection and utilization of selected genotypes to evolve promising varieties. Estimates of GCV, PCV, heritability and genetic advance will play an important role in exploiting future research projections of rice improvement. For the development of high yielding varieties with good quality, there is a need to study the genetic behaviour or genetic parameters of grain yield and quality traits. The present study was conducted to estimate the variability, heritability and genetic advance in 50 selected restorer lines of rice. This study will help in selection of desirable restorer lines for crossing programme to develop high yielding hybrids.

#### MATERIAL AND METHODS

Present investigation was carried out in the fields of Agricultural Research Station, Vadgaon (Maval), Pune during Kharif 2012. The experimental material for the present study consisted of 50 restorer lines of rice of which 30 restorer lines were obtained from Directorate of Rice Research, Hyderabad and 20 lines selected from the germplasm maintained at Agricultural Research Station, Vadgaon (Maval), Pune. The experiment was laid in Randomized Block Design with 50 genotypes in three replications. The recommended dose of fertilizers @ 100:50:50 kg N: P: K/ha was applied. The full dose of P<sub>2</sub>O<sub>5</sub> and K<sub>2</sub>O and half dose of nitrogen were applied as basal dose at the time of

transplanting. The rest of the nitrogen was top dressed in two split doses at the time of maximum tillering stage i.e. 30 days after the transplanting and between panicle initiation and flowering i.e. 60 days after transplanting.

The data on five competitive plants from each genotype in each replication were recorded for days to 50% flowering, days to maturity, total number of productive tillers per plant, productive tillers per m<sup>2</sup>, grains per panicle, panicle length, test weight, harvest index, grain yield per plant and the quality characters like grain length, grain breadth, L/B ratio, colour, alkali spreading value, water uptake, volume expansion ration, kernel length after cooking, kernel linear elongation ratio, amylose and aroma. The treatment means for all the characters were subjected to the statistical analysis. The differences between 50 genotypes for different characters were tested for significance by using analysis of variance technique on the basis of model proposed by Panse and Sukhatme<sup>7</sup>. The genotypic and phenotypic variances were calculated as per the formulae proposed by Burton. Categorization of the range of variation was done as proposed by Sivasubramanian and Madhavamenon<sup>11</sup>.

Heritability in broad sense ( $h^2_b$ ) was calculated by the formula given by Lush and categorized as suggested by Johnson *et al*<sup>3</sup>. The genetic advance as per cent of mean was estimated and classified as suggested by Johnson *et al*<sup>3</sup>.

Ten paddy seeds selected randomly from each genotype of each replication were dehusked by hand and the grain length and breadth was measured by using grain vernier in mm. The kernel length and breadth ratio was calculated using the formula given by Murthy and Govindaswamy<sup>5</sup>. Colour was identified through visible observation. Alkali spreading value, water uptake, volume expansion ration, kernel length after cooking, kernel linear elongation ratio, amylose and aroma were estimated using standard procedures.

## RESULTS AND DISCUSSION

Analysis of variance revealed the existence of significant differences among all the genotypes for all the characters included in the study. Significant differences (ANOVA) were revealed among all the 50 genotypes for all the yield and quality characters are presented in the Table 1 and 2. The estimates of genetic parameters viz., phenotypic and genotypic coefficient of variation (PCV and GCV), heritability in broad sense, genetic advance and genetic advance as per cent of mean were computed for 9 yield contributing characters were presented in Table 3. The highest estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for harvest index (36.99%; 37.79%) followed by grain yield per plant (20.07%; 21.05%). The characters, number of grains per panicle (14.72%; 14.98%), test weight (14.14%; 14.27%) and number of productive tillers per sq.m (11.76%; 13.39%) had recorded moderate estimates of variability in the decreasing order of their magnitude. However, low estimates of coefficients of variation were observed for the characters number of productive tillers per plant (9.94;10.80), days to maturity (4.25;4.35), panicle length (3.97;4.54) and days to 50% flowering (2.96%; 3.04 in the decreasing order of their magnitude.

Highest heritability was recorded in test weight (98%), days to maturity (96%), grains per panicle (96%), harvest index (96%), days to 50% flowering (95%), grain yield per plant (91%), number of productive tillers per plant (85%), number of productive tillers per sq.m (77%) and panicle length (77%) in the decreasing order of their magnitude.

The characters viz., number of productive tillers per sq. m (115.21%), grains per panicle (34.71%) and harvest index (33.52%) exhibited high genetic advance. On the contrary, the characters viz., days to maturity (13.15%) and grain yield per plant (11.98%) showed moderate genetic advance and the characters viz., days to 50% flowering (7.21%), test weight (6.90%), productive tillers per plant (3.26%), and panicle length (1.60%) showed low genetic advance.

The characters viz., harvest index (74.59%) grain yield per plant (39.43%), grains per panicle (29.78%), test weight (28.87%) and productive tillers per sq. m. (21.27%) exhibited high genetic advance as percent of mean. Productive tillers per plant (18.84%) showed moderate genetic advance and the characters viz., days to maturity (8.57%), panicle length (7.15%) and days to 50% flowering (5.95%) showed low genetic advance as per cent of mean.

The genotypes exhibited the highest magnitude of genotypic and phenotypic variances for harvest index, grain yield per plant and grains per panicle indicating the presence of large variation among the genotypes for these characters. Similar results were reported by Rema Bai *et al*<sup>8</sup>. and Sharma and Dubey<sup>9</sup>. The characters test weight and number of productive tillers per m<sup>2</sup> has recorded moderate range of phenotypic and genotypic coefficient variation in the genotypes studied. Similarly, Shivani and Sree Rama Reddy<sup>10</sup> observed moderate to high genotypic and phenotypic coefficient of variation for test weight, grain yield per plant. The characters panicle length, days to maturity and days to 50% flowering registered low estimates of genotypic coefficient of variation and phenotypic coefficient of variation indicating the low range of variation found in these characters in the present experimental material, thus offers little scope for further improvement of these characters. Similar results were also observed by Ghosh and Deepak Sharma<sup>2</sup>. They found that phenotypic and genotypic coefficient of variation was relatively low for days to 50% flowering, panicle length.

High heritability coupled with high genetic advance as per cent of mean was recorded for harvest index, grain yield per plant, number of grains per panicle, test weight and number of productive tillers per m<sup>2</sup> indicating that most likely the heritability is due to additive gene effects and selection may be effective for these characters. Similar results were observed by Chauhan<sup>1</sup>, who reported high expected genetic advance as well

as high heritability for harvest index. The character high productive tillers per plant exhibited high heritability and moderate genetic advance indicating that both additive and non-additive gene effects were involved in the genetic control of this character. Days to 50% flowering, days to maturity and panicle length exhibited high heritability and low genetic advance as percent of mean. These results were in consonance with the earlier findings of Kundu *et al*<sup>4</sup>. and Rema Bai *et al*<sup>8</sup>. for panicle length in rice.

The overall results indicated the presence adequate genetic variability in the material studied. The high heritability with high genetic advance was recorded for harvest index, grain yield per plant, grains per panicle, test weight and productive tillers per m<sup>2</sup>. Highest estimates of genotypic coefficient of variation and phenotypic coefficient of variation were recorded for harvest index followed by grain yield per plant. Therefore selection for these traits is very effective and can be utilised in the breeding programmes.

**Table 1: Analysis of variance (ANOVA) for yield and its components in rice**

S.No.	Characters	Source of Variation		
		Replications (df=2)	Genotypes (df=49)	Error (df=98)
1.	Days to 50% flowering (No.)	1.34	39.3**	0.668
2.	Days to maturity (No.)	1.32	129.68**	1.92
3.	No. of productive tillers per m <sup>2</sup>	2531.5	13369.51**	1202.64
4.	Productive tillers per plant (No.)	0.764	9.437**	0.538
5.	Panicle length (cm)	0.43	2.60**	0.24
6.	Grains per panicle (No.)	18.06	893.65**	10.75
7.	Test weight (g)	0.235	34.47**	0.204
8.	Harvest index (%)	27.51	840.97**	12.045
9.	Grain yield per plant (g)	0.46	115.350**	3.71

\*, \*\* Significant at 5% and 1% levels, respectively

**Table 2: Analysis of variance (ANOVA) for quality characters in rice**

S.No.	Character	Source of Variation		
		Replications (df=2)	Genotypes (df=49)	Error (df=98)
1.	Kernel length (mm)	0.270	0.898**	0.166
2.	Kernel breadth (mm)	0.002	0.070**	0.0008
3.	Kernel L/B ratio	0.001	0.500**	0.002
4.	Alkali spreading value	0.380	3.835**	0.339
5.	Water uptake (ml/10g)	163.5	6563.9**	51.28
6.	Volume expansion ratio	0.028	0.487**	0.054
7.	Kernel length after cooking (mm)	0.765	3.317**	0.680
8.	Kernel elongation ratio	0.009	0.080**	0.002
9.	Amylose content (%)	0.078	50.40**	0.011

\*, \*\* Significant at 5% and 1% levels, respectively

Table 3: Estimates of variability and genetic parameters for yield and its components in rice

S. No.	Character	Mean	Range			Coefficient of variation (%)		Heritability in broad sense ( $h^2_b$ )	Genetic advance (GA) (%)	Genetic advance as per cent of mean (GAM)
						Genotypic (GCV)	Phenotypic (PCV)			
1.	Days to 50% flowering (No.)	121.20	115..33	-	126.67	2.96	3.04	0.95	7.21	5.95
2.	Days to maturity (No.)	153.37	138.33	-	174.6	4.25	4.35	0.96	13.15	8.57
3.	No. of productive tillers per m <sup>2</sup>	541.59	419.33	-	734.67	11.76	13.39	0.77	115.21	21.27
4.	Productive tillers per plant (No.)	17.33	14.00	-	22.60	9.94	10.80	0.85	3.26	18.84
5.	Panicle length (cm)	22.36	19.60	-	24.67	3.97	4.54	0.77	1.60	7.15
6.	Grains per panicle (No.)	116.56	83.33	-	156.67	14.72	14.98	0.96	34.71	29.78
7.	Test weight (g)	23.90	14.93	-	34.61	14.14	14.27	0.98	6.90	28.87
8.	Harvest index (%)	44.94	23.74	-	104.22	36.99	37.79	0.96	33.52	74.59
9.	Grain yield per plant (g)	30.39	19.93	-	47.33	20.07	21.05	0.91	11.98	39.43

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