



E-ISSN: 2278-4136  
P-ISSN: 2349-8234  
JPP 2017; 6(3): 832-834  
Received: 08-03-2017  
Accepted: 09-04-2017

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## Genetic variability for yield attributing traits of elite rice Germplasm (*Oryza sativa* L.)

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### Abstract

The present investigation is carried out to study the genetic parameters for yield and yield attributing characters in 100 rice genotypes. Analysis of variance revealed significant differences for all the traits under study, indicating that enough variability is present in the studied material. The characters *viz.*, grain yield/plant and biological yield exhibited high Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV). Days to 50% flowering, plant height, days to maturity, spikelet's fertility and harvest index recorded low estimates of PCV and GCV. Small differences between GCV and PCV were recorded for all the characters studied, indicated less influence of environment on these characters. The characters *viz.*, ear bearing tillers, number of grains per panicle, biological yield, test weight and grain yield/plant exhibited high heritability coupled with high genetic advance, indicating that simple selection could be effective for improving these characters.

**Keywords:** Genetic variability, Genetic advance, Biological yield, Rice

### Introduction

Rice (*Oryza sativa* L.) is the most important staple food crop for more than half of the population in the world. Globally it is cultivated in an area of 161.8 m ha with an annual production of about 748.0 million tones and an average productivity of 4.6 t ha<sup>-1</sup> (FAO, 2016) [4]. Among the rice producing countries. India ranks first in the world in area of rice cultivation with 44.2 million ha and second in production with 104.32 million tons (Directorate of Economics & Statistics (D & ES 2016-17). The slogan 'Rice is life' is the most appropriate for India, as this crop plays a livelihood for millions of rural households. Therefore being the staple food of the population in India, improving its productivity has become a crucial importance. True to the strategy of converting constraints into opportunities, existence of wide yield gaps found across ecologies and zones should be regarded as potential opportunities for raising the yield level and achieving thereby the future targets. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters. Crop improvement in rice depends on the magnitude of genetic variability and the extent to which the desirable genes are heritable. A critical survey of the genetic variability, correct understanding of the gene effects and knowledge on the extent of heritability of these traits would help in planning an effective breeding programme. Keeping in view the above perspectives, the present experiment was carried out to estimate the genetic variability parameters for various yield attributing in rice.

### Materials and methods

The present investigation was conducted at the field experimentation centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, SHUATS, Allahabad. The Experimental material for the present research study comprises 100 rice genotypes and was planted in a Randomised Block Design during *kharif*, 2014. All the standard packages of practices were followed to raise a healthy crop. The observations were recorded for fifteen quantitative characters. The analysis of variance and test of significance was calculated as per the method of Fisher (1963) [5]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated by the formula given by Burton (1952) [2]. Heritability in broad sense was calculated by the formula given by Hanson *et al.* (1956) [7]. From the heritability estimates, the genetic advance was calculated by the following formula given by Johnson *et al.* (1955) [8].

## Results and discussion

Greater variability in the initial breeding material ensures better chances of producing desired forms of a crop plant the analysis of variances indicated the existence of significant differences among the genotypes studied revealing that sufficient variability is present for the different characters and selection would be effective to develop the varieties with desired forms of crop plants, Table 1. The difference between genotypic and phenotypic coefficient of variation was less for all characters studied. The slight difference between GCV and PCV was also reported by Kole *et al.* (2008)<sup>[9]</sup> and Syoum *et al.* (2012). Among the yield characters, a wide range of PCV and GCV was observed for different traits, High PCV and GCV was observed for biological yield (25.64, 22.79) and grain yield/ plant (26.94, 24.44). High PCV with moderate GCV was exhibited by spikelet sterility % (20.66, 18.02). Moderate PCV and GCV was recorded for number of tillers per plant, (15.21, 11.51), ear bearing tillers (18.06, 16.51), number of grains per panicle (16.56, 15.59) and test weight (16.20, 15.87). Moderate PCV with low GCV was observed for panicle length (11.51, 9.83), flag leaf length (10.29, 9.58) and flag leaf width (11.77, 7.67). Low PCV and GCV were observed for days to 50% flowering (9.28, 9.16) plant height (8.38, 8.14), days to maturity (7.20, 7.11), spikelet fertility percentage (7.34, 6.40) and harvest index (4.76, 4.06). High magnitude of phenotypic variation was composed of high genotypic coefficient of variation and less of the environment variations, which indicated high genetic variability for different traits and less influence of environment. Therefore selection on the basis of phenotype alone can be effective for the improvement of these traits.

Similar results are recorded by Ravi kumar (2015)<sup>[11]</sup> for biological yield and Umesh *et al.* (2015)<sup>[14]</sup> for grain yield per plant (26.94, 24.44). Similar results for low to moderate values of GCV and PCV were also found by Ananadarao *et al.* (2011)<sup>[1]</sup>.

## Heritability

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. Heritability is classified as low (below 30%), medium (30-60%) and high (above 60%). The reliability of the phenotypic value depends on the estimates of heritability for a particular character. Therefore, high heritability helps in the effective selection for a particular character. High estimate of heritability were exhibited for all the character under study except flag leaf width (Table 2). High heritability values indicate that the characters under study are less influenced by environment in their expression. The plant breeder, therefore adopt simple selection method on the basis of the phenotype of the characters which ultimately improves the genetic

background of these traits Similar results have been reported by Sarawgi *et al.* (2000)<sup>[13]</sup>, Gannamani (2001)<sup>[6]</sup> and Sao (2002)<sup>[12]</sup>.

## Genetic advance

The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.*, 1955)<sup>[8]</sup>. The estimates of genetic advance as per cent of mean provide more reliable information regarding the effectiveness of selection in improving the traits. Genetic advance denotes the improvement in the genotypic value of the new population over the original population.

Among the studied characters, high, moderate and low estimates of genetic advance as percent of mean was recorded and it varied from 7.13 (Harvest index) to 45.68 (Grain yield / plant). (Table 2). grain yield/ plant (45.68), biological yield (41.71), spikelet Sterility % (32.37), test weight (32.05), ear bearing tillers (31.09) and number of grains per panicle (30.23) recorded high estimates of genetic advance, whereas moderate estimate of genetic advance were recorded for characters like number of tillers per plant (18.98), days to 50% flowering (18.63), flag leaf length (18.37), panicle length (17.29), plant height (16.29), days to maturity (14.46), spikelet fertility % (11.50) and flag leaf width (10.31). Low estimate of genetic advance was recorded for harvest index (7.13). In the present study, High heritability coupled with high genetic advance as per cent of mean was observed for ear bearing tillers, number of grains per panicle, biological yield, test weight and grain yield/plant, indicating the predominance of additive gene action (Panse and Suhatme, 1957) and their amenability for further improvement through simple selection. High heritability estimates coupled with moderate genetic advance was recorded days to 50% flowering, plant height, number of tillers per plant, panicle length, flag leaf length, days to maturity and spikelet fertility%. Moderate heritability coupled with moderate genetic advance as per cent of mean was observed for flag leaf width. High heritability estimates coupled with low genetic advance as per cent of mean was exhibited by harvest index. Characters which showed high heritability coupled with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding (Samadhia, 2005). Similar findings were also reported for biological yield and grain yield/plant by Ravi Kumar *et al.* (2015)<sup>[11]</sup>, and Umesh *et al.* (2015)<sup>[14]</sup>. Therefore, it is concluded that the characters which showed high genotypic value coupled with high heritability and genetic advance should be considered for direct selection. Grain yield / plant and biological yield per plant showed high GCV, PCV, heritability and genetic advance.

**Table 1:** Analysis of variance for fifteen quantitative characters in 100 rice Genotypes.

,, Degree of freedom		Replication	Treatment	Error
		1	99	99
S. No.	Source	Mean squares		
1	Days to 50 % flowering	3.1250	171.4555**	2.1856
2	Plant Height (cm)	10.2152	183.8499**	5.4042
3	Number of tillers per plant	0.1741	6.8982**	1.6950
4	Ear bearing tillers	1.9110	7.5695**	0.6773
5	Panicle length (cm)	0.0772	13.5290**	2.1206
6	Flag leaf length (cm)	0.0136	19.4166**	1.3857
7	Flag leaf width (cm)	0.0005	0.0387**	0.0156
8	Number of grains /panicle	13.3335	1340.6851**	80.8774
9	Days to maturity	0.0315	175.9741**	2.2423

10	Spikelet Fertility %	0.0040	51.6491**	7.0258
11	Spikelet Sterility %	0.0040	51.6491**	7.0258
12	Biological yield (g)	87.8077	362.1344**	42.5433
13	Harvest index (%)	0.0123	7.1565**	1.1339
14	Test weight (g)	0.0150	24.1454**	0.4877
15	Grain yield /plant (g)	14.3434	74.6448**	7.2370

\*, \*\* significant at 5 and 1 percent level of probability respectively.

**Table 2:** Estimates of variability, heritability and genetic advance as per cent of mean for yield component characters in rice (*Oryza sativa* L.).

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean (5% level)
			Minimum	Maximum	PCV %	GCV %		
1	Days to 50% Flowering	100.46	76.50	134.50	9.28	9.16	97	18.63
2	Plant Height (cm)	116.02	92.70	139.60	8.38	8.14	94	16.29
3	Number of Tillers/ Plant	13.60	9.00	17.90	15.21	11.84	61	18.98
4	Ear Bearing Tillers	11.25	8.15	16.22	18.06	16.51	84	31.09
5	Panicle Length (cm)	24.30	19.00	30.05	11.51	9.83	73	17.29
6	Flag Leaf Length (cm)	31.35	25.13	42.18	10.29	9.58	87	18.37
7	Flag Leaf Width (cm)	1.40	1.02	1.75	11.77	7.67	43	10.31
8	Number of grains / panicle	161.02	80.45	241.10	16.56	15.59	89	30.23
9	Days to Maturity	130.84	105.50	160	7.20	7.11	97	14.46
10	Spikelet Fertility (%)	73.79	59.01	52.57	7.34	6.40	76	11.50
11	Spikelet Sterility (%)	26.21	17.42	40.99	20.66	18.02	76	32.37
12	Biological Yield (g)	55.48	29.21	92.90	25.64	22.79	79	41.71
13	Harvest Index (%)	42.76	36.30	47.97	4.76	4.06	73	7.13
14	Test Weight(g)	21.67	15.18	32.72	16.20	15.87	96	32.05
15	Grain Yield/ Plant (g)	23.76	12.96	42.71	26.94	24.44	82	45.68

GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation

## References

- Ananadrao SD, Singh CM, Suresh BG, Lavanya GR. Evaluation of rice hybrids for yield and yield component characters under North East Plain Zone. The Allahabad farmer. 2011; 67(1):63-68.
- Burton GW. Quantitative inheritance in grasses. Proc. 6th Int. Grassland Cong. 1952; 1:127-83
- Directorate of Economics & Statistics (D&ES), 2nd advance estimates, 2016-2017.
- FAO. Food and Agricultural organization. Online Interactive Database on Agriculture. Faostat, 2016. www.fao.org.
- Fisher RA, Yates F. Statistical tables for biological, agricultural and medical research. Oliver and Boyd, London, 1963.
- Gannamani N. Study of heterosis and combining ability by utilizing cytoplasmic genetic male sterility and fertility restoration system in rice (*Oryza sativa* L.), M. Sc. (Ag.) Thesis, GAU, Raipur. 2001.
- Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedza. Agronomy Journal. 1956; 48(6):268-272.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955; 47(7):314- 318.
- Kole PC, Chakraborty NR, Bhat JS. Analysis of variability, correlation and path coefficients in induced mutants of aromatic non-basmati rice. Tropical Agricultural Research & Extension, 2008; 11:105-108.
- Panse VG, Sukhatme PV. Statistical Methods for Agricultural workers. Indian Council of Agricultural Research, New Delhi. 1967, 103-108.
- Ravi Kumar, Suresh Babu G, Satish Kumar Rai, Sandhya. Genetic variability and divergence studies in elite rice genotypes for biometrical traits. The Ecoscan. 2015; 9(1-2):209-212.
- Sao A. Studies on combining ability and heterosis in F1rice hybrids using cytoplasmic male sterile lines, M. Sc. (Ag.) Thesis, IGAU, Raipur, 2002.
- Sarawgi AK, Rastogi NK, Soni DK. Studies on some quality parameters of indigenous rice in Madhya Pradesh. Annuals of Agricultural Research, 2000; 21(2):258-261.
- Umesh Jaiswal HK, Sravan T, Showkata Waza, Rahul Bhardwaj. Estimation of genetic variability, heritability and genetic advance for yield and quality traits in some indigenous Basmati rice (*Oryza sativa*. L) Genotypes. International Journal of Farm Sciences. 2015; 5(4):32.