

## Studies on genetic variability for yield components in rice (*Oryza sativa* L.)

<sup>1</sup>Dinesh K. Tiwari, <sup>2</sup>Praveen Pandey, <sup>2</sup>Sachchidanand Tripathi, <sup>1</sup>S. Prasad Giri, and <sup>1</sup>Jawahar L. Dwivedi

<sup>1</sup>Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad-224229(U.P.), India; <sup>2</sup>Department of Genetics and Plant Breeding, Allahabad Agricultural Institute-Deemed University, Allahabad-211007 (U.P.), India.  
Corresponding author: P. Pandey, pandeypraveen1986@yahoo.com

**Abstract.** The present experiment comprised with 3 CMS lines (viz IR58025A, NMS4A and PMS10A) and 20 diverse genotypes were crossed in a line x tester mating design to identify suitable parents for heterosis breeding. The analysis of variance revealed that for treatments, parents, crosses and parents vs. crosses are highly significant for various characters under studied i.e. days to 50% flowering, effective tillers per plant, panicle length, number of spikelets per panicle, number of fertile spikelets, spikelet fertility percent, grain yield per plant, 100 grain weight, biological yield, harvest index except due to crosses for 100 grain weight. The higher magnitude of PCV and GCV was recorded for 100 grain weight, grain yield per plant, number of fertile spikelets, pollen fertility percent, effective tillers per plant, panicle length, number of spikelets per panicle and harvest index. All the characters showed high broad sense heritability, while in narrow sense estimates were higher for biological yield, spikelet fertility percent and number of fertile spikelets and moderate for most of traits except effective tillers per plant and panicle length. High heritability coupled with high genetic advance was recorded for number of fertile spikelets, spikelet fertility percent and pollen fertility percent indicated the major role of additive gene action in the inheritance of these characters. Thus, these characters may serve as an effective selection parameter during breeding programme.

**Key words:** rice, variability, heritability, genetic advance, yield components.

**Introduction.** Grain yield is the primary trait targeted for improvement of rice productivity in both favourable and unfavourable environments from its present level. Most of the Asian countries have been able to keep pace between rice production growth rate and that of population during the last four decades. This has been mainly possible due to the contributions made by the green revolution technologies. However, it is of great concern to note that the rate of growth in rice production has started declining during 90's and there has been a plateauing effect. The population growth in most of the Asian countries, except China, continues to be around 2% per year. Hence it is very pertinent to critically consider whether the rice production can be further increased to keep pace with population growth. With the current green revolution technologies it is estimated that by 2020 at least 115-120 million tons of milled rice is to be produced in India to maintain the present level of self sufficiency. Is there a need for a paradigm shift in rice research to meet the challenges of the future decades for ensuring food security? After a brief review of rice research in India and considering the gains obtained through green revolution technologies, the possibilities and prospects of utilizing the gene revolution technologies are considered for further enhancing the production and productivity of rice for not only ensuring food security but also nutritional security. Rigorous efforts are needed to improve the production of rice in the country by diversifying its uses and by developing rice hybrids for specific traits of economic importance.

The study of genetic variability is the pre-requisite for any crop improvement programme. Knowledge on the genetic architecture of genotypes is necessary to formulate efficient breeding methodology. Breeding strategies is chiefly influenced by the choice of germplasm. Any wrong choice of germplasm to initiate the selection process results in the wastage of resources. The systematic breeding programme involves the steps like creating variability practicing selection and utilization of selected genotypes to evolve promising varieties. Efficient and economic crop improvement scheme refers to the collection of superior alleles into a single population. Over the past century selection of desirable parents for hybridization programme has been found as an effective operating implement in developing high yielding crop varieties upon which, the modern agriculture can rely. Grain yield is a complex character, which depends on its main components (viz number of spikes per plant, spike length, number of grains per spike and 1000 grain weight). These components are further dependent for their expression on several morphological traits, which are interrelated with each other and therefore, the parents selected for the breeding programmes aimed at increased seed yield should possess wide range of genetic variation for the above said characters. Besides, it could be of interest to know the magnitude of variation due to heritable component, which in turn would be a guide for selection for the improvement of a population. In other words, for the improvement in any crop species, the knowledge of genetic variability for characters of economic importance and their heritability and genetic advance is of utmost importance in planning future breeding programme.

**Material and Methods.** The parental material comprised with 3 CMS lines (viz IR58025A, NMS4A and PMS10A) used as females (lines) were crossed with 20 diverse genotypes used as male (testers) in a line x tester mating design. Thus, the resultant sixty hybrids along with their 23 parents and one standard check variety (Sarjoo-52) were evaluated in a randomized block design with three replications at Crop Research Station-Masodha, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad. The experimental site is located at 26.47 °N latitude, 82.12 °E longitudes and an altitude of 113 m above mean sea level. This site is in the eastern Gangetic plains of India and has sandy loam soil texture. Each genotype was raised in 2.5 m long single row plot keeping 20 x 15 cm spacing. The recommended agronomic practices followed to raise good crop stand. The data were recorded on 10 randomly selected plants from each replication for various quantitative traits studied were viz: days to 50% flowering, plant height (cm), pollen fertility (%), effective tillers per plant, panicle length (cm), number of spikelets per panicle, number of fertile spikelets, spikelet fertility (%), 100 grain weight (g), grain yield per plant (g), biological yield (g), and harvest index (%). Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse & Sukhatme (1967). PCV and GCV were calculated by the formula given by Burton (1952), heritability by Burton & De Vane (1953) and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Johnson et al (1955) in order to estimate the genetic variation among parents and hybrids.

**Results and Discussion.** The analysis of variance (Table1) revealed that for treatments, parents, crosses and parents vs. crosses are highly significant for various characters under studied i.e. days to 50% flowering, effective tillers per plant, panicle length, number of spikelets per panicle, number of fertile spikelets, spikelet fertility%, 100 grain weight, grain yield per plant, biological yield and harvest index except due to crosses for 100 grain weight, indicating the existence of sufficient amount of variability. These results were in conformity with the earlier findings of Janardhanam et al (2000), Satyanarayana et al (2000), Panwar (2005), Saravanan et al (2006), Kumar et al (2006), Kumar et al (2007) and Salgotra et al (2009).

The perusal of coefficient of variability indicated that wide range of variability was present at both phenotypic and genotypic levels for all the characters under studied. The magnitude of phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits which may be due to higher degree of interaction of genotypes with the environment (Kavitha & Reddy 2002). The differences in the magnitude of PCV and GCV for 100 grain weight, grain yield per plant, number of fertile spikelets, pollen fertility percent, effective tillers per plant, panicle length, number of spikelets per panicle and harvest index were of high order. Phenotypic and genotypic coefficient of variation were moderate for 100-grain weight followed by grain yield per plant harvest index, number of fertile spikelets per panicle, spikelet fertility percent and pollen fertility percent and it was low for days to 50% flowering, plant height and biological yield; indicating little opportunity of selection for these characters. High coefficients of variability for various characters observed in the present study were in agreement with the findings of Rao & Srivastava (1994). Ganesan et al (1995) reported moderate amount of variability (10-20%) for days to panicle emergence, plant height and days to 50% flowering while low GCV was observed for days to 50% flowering and plant height further confirming the findings in the present investigation. High coefficient of variability indicated that there is a scope of selection and improvement of these traits. Low values indicated the need for creation of variability either by hybridization or mutation followed by selection. Similar findings were also reported by Chaubey & Singh (1994), Sharma & Richharia (1995), Singh et al (2006) and Pandey et al (2010).

The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability (Lush 1949). Robinson et al (1949) viewed that the knowledge of heritability of a character is important to the breeder, as it indicates the possibility and extent to which improvement is possible through selection. It is a measure of genetic relationship between parents and their progeny and has been widely used in determining the degree to which a character may be transmitted from parents to offspring. High heritability is not enough to make efficient selection in the advanced generations unless it is accompanied by substantial amount of genetic advance. Burton (1952) pointed out that the heritability in combination with intensity of selection and amount of variability present in the population influences gains to be obtained from selection. Thus, genetic advance is yet another important selection parameter which although independent, represents the expected genetic advance under selection. It measures the differences between the mean genotypic values of the selected lines and the mean genotypic values of original population from which these were selected.

According to Panse (1957) if a character is governed by non-additive gene action, it may give high heritability but low genetic advance, whereas, if it is governed by additive gene action, high heritability along with high genetic advance provided good scope for further improvement. In the present study, high broad sense heritability estimates were obtained for all of the characters, indicating the major role of additive gene action in inheritance of these traits, while in narrow sense, estimates were higher for biological yield, spikelet fertility percent and number of fertile spikelets and moderate for most of traits except effective tillers per plant and panicle length which exhibited low heritability in narrow sense. A high estimates of narrow sense heritability would mean that selection can be effectively made on phenotypic basis by mass selection, whereas progeny testing would be required if heritability is low and environmental influence is high. The broad sense heritability of these characters are in accordance with those of Maurya (1976) for days to heading, grains per panicle and test weight; Bhattacharya (1978) for grain yield per plant; Haung (1984) for 1000 grain weight, number of panicles per unit area, number of spikelets per panicle and fertility percent; Maurya et al (1986) for test weight and panicle length; Singh et al (1990) for spikelets per panicle, biological yield, and harvest index and Ganesan et al (1995) for days to panicle emergence, plant height, panicle length, harvest index and 100-grain weight; Vivek et al (2005), Pandey & Anurag (2010) for test weight and grain yield.

Table 1

Analysis of variance for parents and crosses for different characters in rice

Source of Variation	d.f	Days to 50% flowering	Plant height (cm)	Pollen fertility (%)	Effective tillers per plant	Panicle length	No. of spikelets per panicle	No. of fertile spikelets	Spikelet fertility	100 grain weight	Grain yield per plant	Biological yield	Harvest index
Replications	2	4.148	2.664	8.663	28.509	0.896	4.771	31	8.173	0.263	31.286	4.427	53.447
Treatments	82	58.77**	149.523**	800.797**	19.779*	45.394**	743.789**	2903.65**	827.503**	1.057**	191.073**	279.939**	293.609**
Parents	22	78.993**	98.753**	2789.196**	22.534**	31.963**	441.573**	7502.783**	2262.308**	1.922**	238.647**	332.089**	660.198**
Crosses	59	34.572**	88.768**	21.551*8	18.156**	50.575**	832.031**	462.647**	25.074**	0.674	97.657**	196.847**	113.934**
Parents vs crosses	1	1041.531**	4855.013**	3031.476**	54.916**	34.995**	2192.517**	45742.06**	16604.69**	4.595**	4655.558**	4036.336**	2829.241*
Error	164	2.689	4.742	7.106	1.599	2.723	4.596	6.407	2.327	0.052	2.57	4.927	5.173

Table 2

Mean, coefficient of variation, heritability and genetic advance for different characters in rice

S. No.	Characters	GM+SE	Coefficient of variation		Heritability		Genetic advance	Genetic as advance % of mean
			GCV	PCV	Broad sence	Narrow sence		
1	Days to 50% flowering	101.23 ± 1.33	4.27	4.56	87.82	19.34	8.32	8.22
2	Plant height	105.11±1.77	6.61	6.92	91.13	16.38	13.66	13.00
3	Pollen fertility percent	82.21±2.17	19.78	20.05	97.61	28.31	33.06	40.22
4	Effective tillers per plant	14.64±1.03	16.81	18.90	79.15	7.50	4.51	30.80
5	Panicle length	22.05±1.34	17.09	18.66	83.92	2.91	7.11	32.26
6	No. of spikelets per panicle	175.52±1.74	8.94	9.02	98.23	29.54	32.04	18.25
7	No. of fertile spikelets	141.70±2.06	21.93	22.00	99.31	44.72	63.80	45.02
8	Spikelet fertility percent	80.12±1.24	20.69	20.78	99.23	53.53	34.02	42.45
9	100 grain weight	2.04±0.186	28.28	30.38	86.60	23.34	1.11	54.22
10	Grain yield per plant	28.37±1.31	27.93	28.50	96.10	20.34	16.00	56.40
11	Biological yield	72.41±1.81	13.22	13.57	94.27	74.32	19.21	26.53
12	Harvest index	39.39±1.85	24.89	25.55	94.92	24.3	19.67	49.95

\*Significant at 5% level and \*\* significant at 1% level , GM= Grand mean, SE= Standard error

High heritability alone does not guarantee large gain from selection unless sufficient genetic advance (GA) attributed to additive gene action is present. High heritability coupled with high genetic advance was recorded for number of fertile spikelets, spikelet fertility percent and pollen fertility percent. These findings are in close agreement with the findings of Sivasubramanian & Madhavamenon (1973), Bhattacharya (1978), Wilfred & Prasad (1993), Ganesan et al (1995), Singh et al (2002), Mohammad et al (2002) and Vaithiyalingan & Nadarajan (2006). Singh (1992) recorded high heritability coupled with low genetic advance for panicle length and 1000 grain weight which is in conformity with present experiment. High heritability and low genetic advance suggesting greater role of non-additive gene action in their inheritance of these characters. Therefore heterosis breeding could be used to improve these traits.

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Authors:

Dinesh Kumar Tiwari, Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad-224229 (U.P), India; e-mail: dktiwari252003@yahoo.co.in

Praveen Pandey, Department of Genetics and Plant Breeding, Allahabad Agricultural Institute – Deemed University, Allahabad- 211007(U.P.), India; e-mail: pandeypraveen1986@yahoo.com

Sachchidanand Tripathi, Department of Genetics and Plant Breeding, Allahabad Agricultural Institute - Deemed University, Allahabad-211007 (U.P.), India; e-mail: sntmscag@yahoo.co.in

Shiv Prasad Giri, Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad-224229, (U.P.), India; e-mail: girisp06@rediffmail.com

Jawahar Lal Dwivedi, Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad- 224229, U.P.(India); e-mail: dwivedi\_jl@rediffmail.com

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