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Evaluation of hybrid rice for variability and yield contributing characters under Allahabad climatic condition

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ABSTRACT

Rice is the most important food crop after wheat and maize. India, the home of rice, has nearly one third of the world's rice acreage but still suffers from a chronic shortage of the cereal. The knowledge of genetic variability in a given crop species for characters under improvement is important in any plant breeding programme. Heritability with genetic advances is more helpful in predicting the gain under effective selection. Genetic parameters for yield and its correspondent characters in rice were estimated from a trial with 36 rice hybrids evaluated for eighteen characters related to yield. Analysis of variance revealed high significant differences for all the 18 characters studied. Phenotypic coefficient of variation (PCV) was higher than genotype coefficient of variation (GCV) for all the characters indicating the little influence of environment on the characters. All the qualitative characters depicted high estimates of heritability, which indicates preponderance of additive gene action in the inheritance of these characters. High to moderate degree of genetic advance was observed for number of filled grains per panicle followed by biological yield per plant. Therefore, the results suggest that these characters can be used for grain yield selection.

Keywords: Rice, Genetic variability, Heritability, Genetic advance, *Oryza sativa* and Grain yield

Rice is life' was the theme of international year of rice, 2004 denoting is overwhelming importance as an item of food and commerce. Rice (*Oryza sativa*) belongs to family gramineae. Morphologically, rice is an annual grass and one of the most important crops. It is the most important staple food among the cereals consumed by more than half the world's population. Globally it is grown extensively in tropical and sub-tropical regions of the world. India, the home of rice, has nearly one third of the world's rice acreage but still suffers from a chronic shortage of the cereal (Ramiah, 1970). Rice contributes around 45 percent of India's cereal production and is the main staple food for over 60 percent of the population in the country. Despite the age old human concerns about balancing population and food supplies, the world population is expected to continue to grow, possibly reaching 8 billion by 2030 and rice production must be increased by 50% in order to meet the growing demand (Khush and Brar, 2002). Hence, rice breeders are interested in developing cultivars with improved yield and other desirable agronomic characters.

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 90s 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 tones of milled rice is to be produced in India to maintain the present level of self sufficiency. 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.

The systematic breeding programme involves the steps like creating genetic variability, practicing selection and utilization of selected genotypes to evolve promising varieties. In order to obtain higher productivity, genetic improvement of the crop is a prime need. Informations on the nature and magnitude of gene effects for grain yield and its component characters are essential in deciding a sound strategy for the improvement. The large spectrum of genetic variability in segregating population depends on the level of genetic diversity among the genotypes offer better scope for selection. This necessitates a through knowledge of variability owning to genetic factors, actual genetic variation heritable in the progeny and the genetic advance that can be achieved through selection. High heritable estimates were helpful in making selection of superior genotypes on the basis of phenotypic performance of quantitative characters. However, it is very difficult to judge whether observed variability is highly heritable or not. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character into future generations (Sabesan *et al.*, 2009). The large spectrum genetic variability in segregating populations depends on the level of genetic diversity among genotypes offer better scope for selection. Estimates of GCV, PCV, heritability and genetic advance will play an important role in exploiting future research projections of rice improvement. Therefore, an attempt was made in the present studies to estimate the extent of variability, heritability, genetic advance for yield improvement in rice under Allahabad agro climatic condition.

MATERIAL AND METHODS

A field experiment was conducted with an experimental material comprised 34 genotypes and two local checks (Indra sona and Sarju, 52) of hybrid rice grown in randomized block design with three replications at the Research Farm, Department of Genetics and Plant Breeding, Allahabad School of Agricultural, Allahabad during kharif, 2008. The experimental materials for the present study consisted of 34 genotypes of rice hybrids were received from Uttar Pradesh Council of Agricultural Research (UPCAR), Lucknow, Uttar Pradesh. The crop was raised at a spacing of 20 and 15 cm between row to row and plant to plant, respectively. Each entry was sown in a plot of $2m^2$ area. Recommended package of practices were followed to raise a healthy crop. The recommended doses of fertilizers @ 150: 60: 60 N: P: K Kg / ha were applied. The full dose of P_2O_5 and K_2O 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 boot leaf stage i.e. 55 days after transplanting.

The data were recorded on five randomly selected competitive plants of each entries from each replication for eighteen characters viz., days to 50% flowering, days to maturity, plant height, panicle length, flag leaf length, flag leaf width, number of tillers per plant, number of panicles per plant, number of filled grains per panicle, number of unfilled grains per panicle, spikelet fertility, test weight, grain L/B ratio, hulling percentage, head rice recovery, harvest index, biological yield per plant and grain yield per plant. Phenotypic and genotypic coefficients of variation were estimated by following the procedure given by Burton (1952), heritability in broad sense (h2) by Burton and Devane (1953) and genetic advance i.e. the expected genetic gain by using the procedure given by Johnson *et al.* (1955).

RESULT AND DISCUSSION

In this study the range and analysis of variance indicated potential genetic variability in the material under consideration. These results indicated better scope for genetic improvement through conventional breeding. The analysis of variance revealed significant variations among the genotypes for all the character examined (Table 1). The phenotypic variance was partitioned into genotypic variances for a clear understanding of the pattern of variation. Number of filled grains per panicle exhibited the highest genotypic variance (2006.86) and also the highest phenotypic variance (2015.52). However, flag leaf weight had the lowest magnitude of genotypic and phenotypic variance of 0.02 and 0.02 respectively. Genotypic coefficient of variation measures the variability of any character. The extent of the environmental influence on any character is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation.

Phenotypic coefficients of variation were slightly higher than the genotypic coefficients of variation for all the traits studied. This indicates the presence of environmental influence to some degree in the phenotypic expression of the characters. Iftekharuddeula *et al.* (2001) and Akinwale *et al.* (2011) observed similar result.

The mean sums of squares for the characters studied are presented (Table 1). The mean sum of squares due to genotypes was significant for all the characters. This suggested that the genotype selected were genetically variable and considerable amount of variability existed among them. Thus indicates ample scope for selection for different qualitative and quantitative characters for rice improvement. Similar results in rice were also reported by Mall *et al.* (2005), Singh *et al.* (2006), Sharma and Sharma (2007) and Akinwale *et al.* (2011).

A wide range of phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) was observed for different traits. PCV ranged from 4.58 to 39.80 and GCV ranged from 4.38 to 39.08. The highest PCV and GCV was observed for number of unfilled grains per panicle followed by grain yield per plant, harvest index, biological yield per plant, number of filled grains per panicle and grain L/B ratio (Fig 1.).

Table 1. Genetic parameters of variation for different morphological, qualitative and quantitative characters in rice

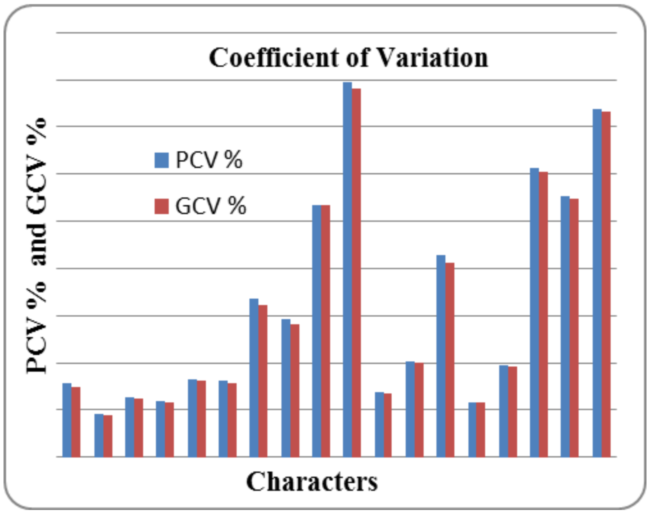
S.No	Characters	Mean square	$\sigma^2 g$	$\sigma^2 p$	GCV	PCV	h^2(bs)	GA
1	Days to 50% flowering	168.0156**	54.58	58.86	7.48	7.77	92.73	14.66
2	Days to maturity	99.2093**	32.06	35.10	4.38	4.58	91.34	11.15
3	Plant height	153.6355**	50.35	52.93	6.16	6.32	95.14	14.26
4	Panicle length	8.3370**	2.71	2.92	5.76	5.98	92.65	3.26
5	Flag leaf length	34.9900**	11.58	11.84	8.13	8.23	97.81	6.93
6	Flag leaf width	0.0600**	0.02	0.02	7.88	8.04	95.97	0.28
7	Number of tillers\plant	26.6312**	8.67	9.28	16.18	16.74	93.42	5.86
8	Number of panicles/plant	14.4031**	4.66	5.08	14.07	14.68	91.86	4.26
9	Number of filled grains\panicle	6029.2308**	2006.86	2015.52	26.68	26.74	99.57	92.09
10	Number of unfilled grains \panicle	439.1348**	144.59	149.96	39.08	39.80	96.41	24.32
11	Panicle fertility	99.0867**	32.73	33.63	6.79	6.88	97.30	11.62
12	Test weight	13.9760**	4.63	4.72	10.07	10.16	98.19	4.39
13	Grain L/B ratio	1.8459**	0.60	0.65	20.57	21.36	92.81	1.54
14	Hulling	54.9269**	18.28	18.36	5.75	5.76	99.56	8.79
15	Head Rice Recovery	109.9323**	36.41	37.10	9.62	9.71	98.14	12.32
16	Harvest index	281.6217**	93.03	95.57	30.21	30.62	97.34	19.60
17	Biological yield/plant	1674.4894**	554.40	565.69	27.32	27.60	98.00	48.02
18	Grain yield/plant	288.3321**	95.73	96.88	36.61	36.83	98.81	20.04

Genetic variance ($\sigma^2 g$), Phenotypic variance ($\sigma^2 p$), Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), broad sense heritability (h^2(bs)) and Genetic advance (GA) , ** significant P= 0.05

Whereas, moderate estimates of PCV and GCV were observed for characters like number of tillers per plant, number of panicles per plant and test weight and low estimates of PCV and GCV were observed for characters like head rice recovery, flag leaf length, flag leaf width, days to 50% flowering, panicle fertility, plant height, panicle length, hulling percentage and days to maturity. There was a good correspondence between genotypic and phenotypic coefficient of variation for all the characters studied. The magnitude of phenotypic coefficient of variation was higher than the genotypic coefficient of variation. Therefore, selection will be more effective in isolating the superior genotypes. Similar results were observed by Sharma and Sharma (2007) for grain yield per plant, flag leaf area and grain L/B ratio, Akinwale et al. (2011) for number of filled grains per panicle, number of tillers per plant and grain yield per plant and Nayudu *et al.* (2007) for number of panicles per plant and biological yield per plant recorded high PCV and GCV values.

The high heritability (broad sense) estimates ranged from 91.34 (days to maturity) to 99.57 (number of grains per panicle) (Table 1). High heritability was recorded for number of filled grains per panicle(99.57 percent) followed by hulling percentage (99.56 per cent), grain yield per plant(98.81 percent), test weight (98.19 per cent) and head rice recovery (98.14 per cent), indicating the relative importance of heritable variation in the expression of characters. Same results revealed by Suman *et al.* (2005) for number of tillers per plant, number of filled grains per panicle and harvest index and Sharma and Sharma (2007) for grain yield per plant, flag leaf area and grain L/B ratio. The genetic advance as per cent of mean was high for number of filled grains per panicle (92.09) followed by biological yield per plant (48.02), number of unfilled grains per panicle (24.32), grain yield per plant (20.04) whereas it was the lowest for flag leaf width (0.28) (Table 1). High heritability coupled with high genetic advance was observed for number of filled grains per panicle and biological yield per plant, indicating that these characters were least influenced by environment and selection for these characters would be quite effective in enhancing grain yield per plant. Suman *et al.* (2005) and Akinwale *et al.* (2011) reported earlier that high heritability coupled with high genetic advance observed for number of filled grains per panicle and Vivek *et al.* (2005) observed for biological yield per plant.

The results further revealed that most of the characters exhibited wide range of Variability (Table 2). Days to 50% flowering shows significant differences among genotypes at ($p < 0.05$) with genotype R-18 taking the shortest time (82 days) to attained 50% flowering while genotype Sarju-52 took the longest period (114 days). Days to maturity follows the same trend with days to 50% flowering which ranges between 117 and 143 days with genotype R-18 taking the shortest shortest period (117 days) to mature while genotype Sarju-52 takes the longest period (143 days) to mature.



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

Fig 1. Histogram depicting estimates of PCV and GCV for various morphological, qualitative and quantitative characters in rice

Plant height shows significant difference ($p<0.05$) among the genotypes at maturity. Genotype R-25 is significantly taller with a height of 129.2 cm while genotype R-16 is the shortest (104.6 cm). Number of tillers per plant varied significantly among the genotypes. The number of tillers per plant ranges between 14.13 and 25.00. The maximum number of tillers per plant was depicted by genotype R-12 (25.00) followed by R-14 (24.07) and R-16(24.00). The minimum number of tillers per plant was depicted by genotype R-27 (14.13). The panicle length ranged from 25.87 to 32.33 cm. Maximum panicle length was exhibited by genotype R-24 (32.33 cm) followed by R-34(31.33 cm), and R-05(30.80 cm). Minimum length of panicle was depicted by genotype Sarju- 52 (25.87 cm).

The number of panicles per m^2 is significantly affected by genotypes. It varies from 12.47 in R-27 to 21.60 in genotype R-12. Number of filled grains per panicle is one of the most important components of yield and probably this character will be helpful in breaking the yield plateau. Number of filled grains per panicle differs significantly among the tested genotypes. The highest filled grain number (251.93) is recorded in genotype R-24 followed by R-06 (246.20) and R-33(242.60). Test weight ranged from 14.77 to 25.60 (g). Maximum test weight was depicted by genotype R-10(25.60 g) followed by Indra sona (25.32 g) and R-13(24.57 g). Minimum test weight was depicted by genotype R-01(14.77 g). The highest grain yield (58.87g) is observed in R-34 ($p<0.05$) while the lowest grain yield (14.33g) is observed in genotype Sarju-52. The high grain yield performance of genotype R-34 could be attributed to the high number of grains per panicle, high panicle weight and large number of panicles per plant. Many research workers reported similar findings in rice by Mall *et al.* (2005), Singh *et al.* (2006) and Sharma and Sharma (2007).

The qualitative characters also ply important role in rice improvement programme. The results further revealed that hulling percentage ranged from 61.37 to 80.05 percent. Highest hulling percentage was depicted by genotype R-03 (80.05 percent) followed by R-07 (79.13 percent) and R-02 (78.80 percent). Whereas, genotype R-09(61.37 percent) was observed to be having lowest hulling percentage as the overall ranking. Head rice recovery was ranged 53.32 to 73.38 percent. Highest head rice recovery was exhibited by genotype R-07 (73.38 percent) followed by R-06 (72.37 percent) and R-26 (71.63 percent). Lowest head rice recovery was exhibited by genotype R-08 (53.32 percent). This indicates that R-07 and R-06 had highest in head rice recovery, which is at par with each other. Rice in international market 78% head rice and there is consistent demand for good head rice (Juliano, 1965). Hence, greater emphasis should be given to head rice recovery in the rice breeding programmers of the state and country.

CONCLUSION

The overall results indicated that there is adequate genetic variability present in the material studied. Hence, Selection on the basis of characters like panicle length, number of filled grains per panicle, panicle fertility, hulling percentage and harvest index to be the most improved selection criteria for seed yield in rice. Therefore, due emphasis is to be paid on above mentioned characters for improving the productivity during selection. Moreover, these traits are also having high heritability and genetic advance on grain yield.

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