



RESEARCH ARTICLE

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Genetic analysis and correlation studies for grain yield in rice (*Oryza sativa* L.) under the Allahabad agro climatic region

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ABSTRACT : An experiment was conducted to study the variability and association between characters in rice. 36 genotypes of rice were evaluated and obtain information on variability parameters and correlation analysis for 18 characters. Analysis of variance revealed high significant differences for all the 18 characters studied. Phenotypic co-efficient of variation (PCV) was higher than genotype co-efficient of variation (GCV) for all the characters indicating the little influence of environment on the characters. Number of unfilled grains per panicle had maximum GCV followed by grain yield per plant, harvest index, biological yield per plant, number of filled grains per panicle and grain L/B ratio. 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. Grain yield per plant showed positive and significant correlation with number of filled grains per panicle followed by harvest index, biological yield per plant and panicle length at phenotypic and genotypic level. Thus, these characters may serve as effective selection parameters during breeding programme for crop improvement.

KEY WORDS : Variability, Heritability, Genetic advance, Correlation analysis, Rice

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INTRODUCTION

Rice is the most important food crop after wheat and maize. It is the most important staple food among the cereals consumed by more than half the world's population. 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). The population growth in most of the Asian countries, except China, continues to be around 2 per cent 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. Improvement in yield and quality of the cereal is of paramount importance of this nation. An effective rice varietal improvement programme must have sound objectives based on the needs of the farmer and the consumer and for a planned breeding programme to improve yield potential.

Rice breeding strategy involves assembling or generating variable germplasm and selection of superior genotypes from the germplasm for utilizing them in hybridization programme to develop a superior variety. In all these stages, estimation of genetic variability, heritability and genetic advance is necessary. Yield is a complex character being governed by large number of cumulative, duplicative and dominant gene and highly influenced by environment. The success of breeding programme depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable. Variability refers to the presence of differences among the individuals of plant population. Variability results due to difference either in the genetic constitution of the individual of a population or in the environment they have grown. The existence of variability is essential for improvement of genetic material. Selection is also effective when there is significant amount of genetic variability among the individuals in a population (Singh and Narayanam, 2007).

Further yield is the product of many contributing characters, which jointly or singly influence it. It is therefore essential to have knowledge of inter relationships existing among yield components, which is statistically measured through correlation and partitioning the correlation co-efficient into the components of direct and indirect effects. Character association studies provide informations on the nature, extent and direction of correlation between characters. Therefore, there is a need to strengthen the research programme aiming at improving the per hectare yield of rice. For achieving future improvement, there is a great need to develop high yielding cultivars. The plant breeder depends upon variability present in the material for the improvement of quantitative and qualitative characters and their mutual association with seed yield. The present investigation was therefore undertaken to predict an appropriate genotype

for selection so as to improve the seed yield.

EXPERIMENTAL METHODS

The experimental material comprised 34 genotypes and two local checks of hybrid rice grown in Randomized Block Design with three replications at the Research Farm, Department of Genetics and Plant Breeding, Allahabad Agricultural Institute, Allahabad. 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 2m² area. Recommended package of practices were followed to raise a healthy crop (Fig A). Data were recorded on five randomly selected competitive plants of each entries from each replication for eighteen characters *viz.*, days to 50 per cent 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 co-efficients of variation were estimated by following the procedure given by Burton (1952), heritability in broad sense (h^2) by Burton and De Vance (1953) and genetic advance *i.e.* the expected genetic gain by using the procedure given by Johnson *et al.* (1955). The genotypic correlation between yield and its component traits and among themselves were worked out as per the methods suggested by Al-Jibouri *et al.* (1958). The significance was assessed at the 5 and 1 per cent probability level, unless otherwise stated.



Fig. A : Experimental plot during flowering stage

EXPERIMENTAL RESULTS AND ANALYSIS

Plant breeding along with advances in agronomic and production practices, has played a major role in the advances grain yield per hectare over the past 50 years (Borlaug, 1983). The wider range of variation was

observed for all the quantitative traits (Table 1). It suggested the presence of enough variation for these characters to exploit the variability. Variability exploited in breeding programmes is desired from the naturally occurring variants and wild relative of main crop species as well as from strains and genetic stocks artificially

Table 1: Analysis of variance for different morphological, qualitative and quantitative characters in rice

Sr. No.	Characters	Replications	Genotypes	Error
	d.f	[2]	[35]	[70]
1.	Days to 50% flowering	9.59	168.01**	4.278
2.	Days to maturity	33.23	99.20**	3.041
3.	Plant height	0.17	153.63**	2.572
4.	Panicle length	0.07	8.33**	0.214
5.	Flag leaf length	0.69	34.99**	0.259
6.	Flag leaf width	0.01	0.06**	0.001
7.	Number of tillers/plant	6.00	26.63**	0.610
8.	Number of panicles/plant	9.05	14.40**	0.413
9.	Number of filled grains\panicle	55.97	6029.23**	8.658
10.	Number of unfilled grains\panicle	19.56	439.13**	5.377
11.	Panicle fertility	3.51	99.08**	0.907
12.	Test weight	0.13	13.97**	0.085
13.	Grain L/B ratio	0.01	1.84**	0.046
14.	Hulling	0.003	54.92**	0.080
15.	Head Rice Recovery	3.61	109.93**	0.688
16.	Harvest index	21.18	281.62**	2.545
17.	Biological yield/plant	32.68	1674.48**	11.290
18.	Grain yield/plant	5.37	288.33**	1.148

** indicate significance of value at P=0.01

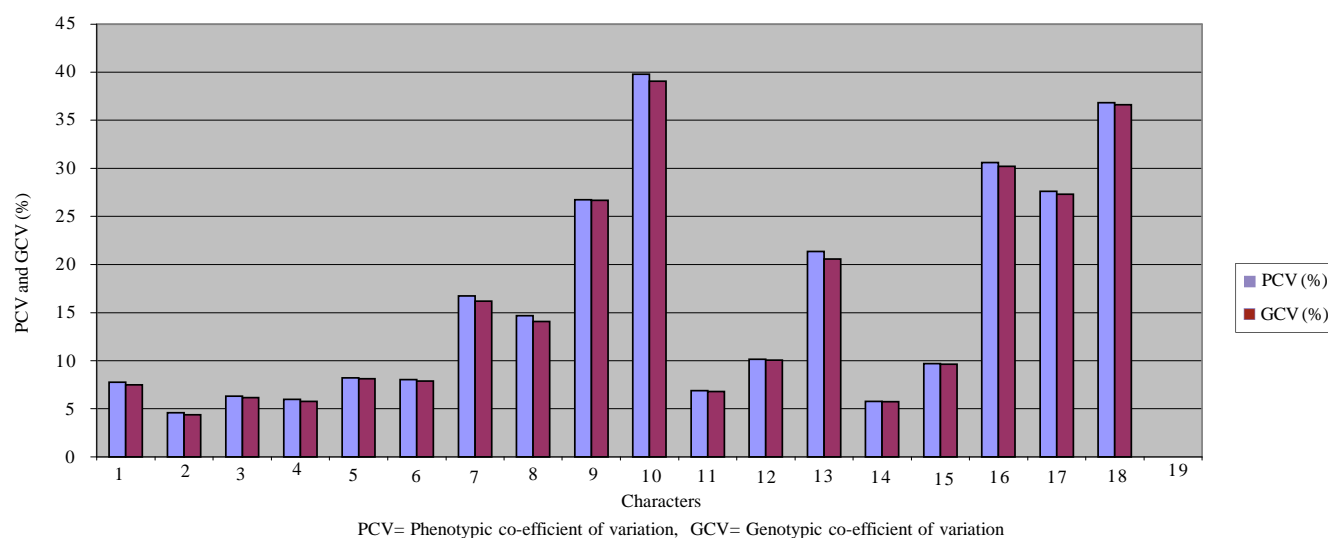


Fig. 1 : Histogram depicting estimates of PCV and GCV for various biometrical characters in rice

developed by human efforts. Variability plays an important role in crop breeding. An insight in to the magnitude of variability present in a crop species is of at most importance, as it provides the basis for selection the total variation present in a population arises due to genotypic and environmental effects. Presence of genetic variability in the breeding material is essential for a successful plant breeding programme. Through this study an attempt was made to assess the mean performance and extent of variability in rice germplasm.

The mean sums of squares for the characters studied are presented in Table 1. The mean sum of squares due to genotypes were 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) and Sharma and Sharma (2007). Estimate of phenotypic variance revealed that number of filled grains per panicle exhibited highest phenotypic variance followed by biological yield per plant. Phenotypic variance as higher than genotypic variance for all the yield and yield contributing characters. This indicates that the influence of environmental factors on these traits. Vivek *et al.* (2004) and Sharma and Sharma (2007) observed the Similar findings in their studies.

There was a good correspondence between genotypic and phenotypic co-efficient of variation for all the characters studied. The magnitude of phenotypic co-

efficient of variation was higher than the genotypic co-efficient of variation. GCV is one of the important and useful measurements of range and genetic diversity and provides a mean of compare the genetic diversity for the quantitative traits. In the present investigation, highest phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) was observed in number of unfilled grains per panicle (39.80, 39.08) followed by grain yield per plant (36.83, 36.61) and harvest index (30.62, 30.21) (Fig. A). The lowest PCV and GCV were observed for days to maturity (4.58 and 4.38). Similar results were observed by Sharma and Sharma (2007) for grain yield per plant, flag leaf area and grain L/B ratio and Nayudu *et al.* (2007) for number of panicles per plant and biological yield per plant recorded high PCV and GCV values. Suggested that enough genetic variability is present for these traits. There fore, selection will be more effective in isolating the superior genotypes.

Knowledge of heritability of a character is important as it indicates the possibility and extent to which improvement is possible through selection. It is a measure of genetic relationship between parent and progeny and has been widely used to assess the degree to which a character may be transmitted from parent to offspring. It also indicated that relative importance of heritability and environment in the expression of characters. The estimates of heritability in broad sense ranged from 91.34 to 99.57. The character number of filled grains per panicle exhibited highest estimates of heritability (99.57%) followed by hulling percentage (99.56%), grain yield per plant (98.81%) and test weight (98.19%) (Fig. 2). A

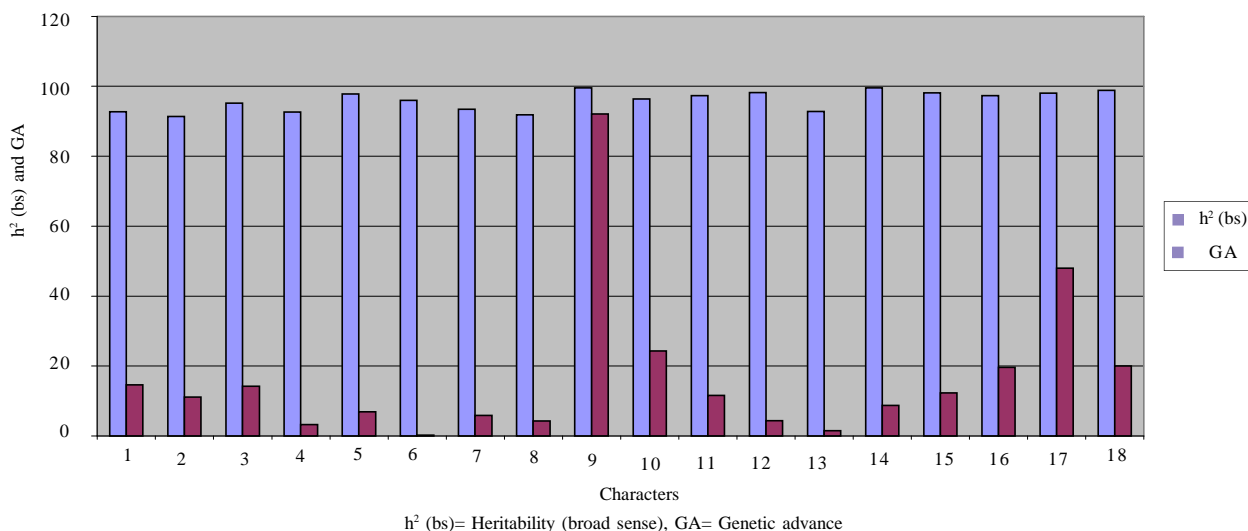


Fig. 2 : Histogram depicting estimates of heritability and genetic advance for various biometrical characters in rice

Table 2(a) : Estimates of phenotype correlation co-efficient (r_p) for yield and component characters in rice

Sr. No.	Character	Days to 50% flowering	Days to maturity	Plant height	Panicle length	Flag leaf length	Flag leaf width	Number of tiller/plant	Number of panicles/plant	Number of filled grains/particle	Number of unfilled grains/particle	Panicle fertility	Test weight	Grain L/E ratio	Hulling	Head Rice Recovery	Harvest index	Biological yield/plant	Grain yield/plant
1.	Days to 50% flowering	1.00	0.85**	0.29	-0.33*	0.28	0.31	0.27	0.21	0.12	-0.02	0.14	-0.05	-0.26	-0.21	-0.22	-0.37*	0.32	-0.02
2.	Days to maturity		1.00	0.38*	-0.22	0.16	0.31	0.28	0.23	0.19	0.03	0.13	0.01	-0.28	-0.27	-0.22	-0.42*	0.45**	0.07
3.	Plant height			1.00	0.37*	0.20	0.36*	0.12	0.19	0.50**	0.10	0.26	0.32	-0.09	-0.19	-0.20	-0.09	0.23	0.17
4.	Panicle length				1.00	-0.02	0.04	-0.16	0.03	0.42*	0.10	0.16	0.18	0.36	0.09	-0.04	0.27	0.25	0.45**
5.	Flag leaf length					1.00	0.44**	-0.07	0.02	-0.00	0.26	-0.20	0.28	0.37	-0.43**	-0.54**	-0.22	0.11	-0.07
6.	Flag leaf width						1.00	-0.17	-0.17	0.35*	0.38*	0.15	0.17	-0.19	-0.44**	-0.38*	0.01	0.27	0.24
7.	Number of tillers/plant							1.00	0.87**	-0.13	-0.16	0.11	0.03	-0.14	-0.00	0.07	-0.42*	0.42*	-0.03
8.	Number of panicles/plant								1.00	-0.07	-0.20	0.17	0.24	-0.07	0.03	-0.01	-0.32	0.46**	0.07
9.	Number of filled grains/particle									1.00	0.18	0.42*	-0.09	-0.10	0.02	0.10	0.29	0.42*	0.60**
10.	Number of unfilled grains/particle										1.00	-0.79**	0.05	0.32	-0.23	-0.19	-0.08	0.19	0.08
11.	Panicle fertility											1.00	-0.11	-0.11	0.20	0.21	0.22	0.05	0.25
12.	Test weight												1.00	0.34	-0.05	-0.25	0.03	0.03	0.03
13.	Grain L/E ratio													1.00	0.11	0.03	0.10	0.01	0.11
14.	Hulling														1.00	0.76**	0.29	-0.05	0.20
15.	Head rice recovery															1.00	0.18	0.05	0.16
16.	Harvest index																1.00	-0.36*	0.55**
17.	Biological yield/plant																	1.00	0.55**
18.	Grain yield/plant																		1.00

* and ** indicate significance of values at P=0.05 and 0.01, respectively

Table 2 (b) : Estimates of genotype correlation coefficient (r_g) for yield and component characters in rice

Sr. No.	Character	Days to 50% flowering	Days to maturity	Plant height	Panicle length	Flag leaf length	Flag leaf width	Number of tillers/plant	Number of panicles/plant	Number of filled grains/panicle	Number of unfilled grains/panicle	Panicle fertility	Test weight	Grain L/B ratio	Hulling	Head Rice Recovery	Harvest index	Biological yield/plant	Grain yield/plant
1.	Days to 50% flowering	1.00	0.92**	0.29	-0.38*	0.30	0.33*	0.31	0.23	0.12	-0.02	0.15	-0.05	-0.26	-0.22	-0.24	-0.39*	0.33*	-0.02
2.	Days to maturity	1.00	1.00	0.40*	-0.24	0.16	0.34*	0.30	0.25	0.20	0.05	0.13	0.02	-0.31	-0.28	-0.23	-0.44**	0.43**	0.08
3.	Plant height	1.00	1.00	1.00	0.40*	0.21	0.38*	0.13	0.21	0.51**	0.10	0.27	0.32	-0.10	-0.19	-0.20	-0.10	0.30	0.17
4.	Panicle length	1.00	1.00	1.00	1.00	-0.01	0.04	-0.17	0.03	0.44**	0.10	0.17	0.18	0.06	0.10	-0.04	0.27	0.27	0.47**
5.	Flag leaf length	1.00	1.00	1.00	1.00	1.00	0.45**	-0.07	0.01	-0.00	0.26	-0.21	0.28	0.08	-0.44**	-0.55**	-0.23	0.12	-0.07
6.	Flag leaf width	1.00	1.00	1.00	1.00	1.00	1.00	-0.15	-0.19	0.36*	0.40*	-0.16	0.18	-0.20	-0.45**	-0.39*	0.01	0.28	0.25
7.	Number of tillers/plant	1.00	1.00	1.00	1.00	1.00	1.00	0.89**	1.00	-0.14	-0.18	0.11	0.02	-0.16	-0.00	0.07	-0.44**	0.43**	-0.04
8.	Number of panicles/plant	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.07	-0.22	0.18	0.25	-0.09	0.03	-0.01	-0.33*	0.47**	0.07
9.	Number of filled grains/panicle	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.18	0.43**	-0.10	-0.10	0.02	0.10	0.30	0.42*	0.62**
10.	Number of unfilled grains/panicle	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.80**	0.05	0.01	-0.23	-0.20	-0.07	0.19	0.09
11.	Panicle fertility	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.12	-0.10	0.20	0.21	0.22	0.05	0.25
12.	Test weight	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.05	-0.04	-0.25	0.03	0.03	0.03
13.	Grain L/B ratio	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.11	0.03	0.11	0.01	0.12
14.	Hulling	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.77**	0.29	-0.05	0.20
15.	Head rice recovery	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.18	0.06	0.16
16.	Harvest index	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.35*	0.56**
17.	Biological yield/plant	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.55**
18.	Grain yield/plant	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

* and ** indicate significance of values at P=0.05 and 0.01, respectively

perusal of genetic advance for different traits revealed that it varied from 0.28 to 92.09. The number of filled grains per panicle exhibited highest estimates of genetic advance (92.09) and biological yield per plant (48.02).

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) 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 nature and the extent of association that existed between the grain yield and its components and the association between the yield component characters were studied. Grain yield per plant positive and significant correlation with number of filled grains per panicle (r_p 0.60**, r_g 0.62**) followed by harvest index (r_p 0.55**, r_g 0.56**), biological yield per plant (r_p 0.53**, r_g 0.55**) and panicle length (r_p 0.45**, r_g 0.47**) (Table 2a) and non-significant positive with panicle fertility (r_p 0.25, r_g 0.25) followed by flag leaf width (r_p 0.24, r_g 0.25), hulling percentage (r_p 0.20, r_g 0.20), plant height (r_p 0.17, r_g 0.17), head rice recovery (r_p 0.16, r_g 0.16), grain L/B ratio (r_p 0.11, r_g 0.11), number of unfilled grains per panicle (r_p 0.08, r_g 0.09), days to maturity (r_p 0.07, r_g 0.08), number of panicles per plant (r_p 0.07, r_g 0.07) and test weight (r_p 0.03, r_g 0.03) at phenotypic and genotypic level (Table 2b). Whereas, grain yield per plant didn't exhibit negative significant and non-significant negative correlation with days to 50 per cent flowering (r_p -0.02, r_g -0.02), number of tillers per plant (r_p -0.03, r_g -0.04) and flag leaf length (r_p -0.07, r_g -0.07) at phenotypic and genotypic level.

Grain yield per plant was positive and significantly correlated with number of filled grains per panicle followed by harvest index, biological yield per plant and panicle length. These results are in agreement with Jadhav and Dudhare (2007) for harvest index and number of filled grains per panicle and Markar and Siddiqui (1996) for panicle length.

Number of filled grains per panicle exhibited positive and significant correlation with grain yield per plant, panicle fertility and biological yield per plant. Panicle length exhibited positive and significant correlation with grain yield and number of filled grains per panicle. Panicle

fertility exhibited positive but non-significant correlation with grain yield per plant followed by harvest index, head rice recovery, hulling percentage and biological yield per plant at phenotypic and genotypic level. Harvest index exhibited positive and significant correlation with grain yield per plant (r_p 0.56**, r_g 0.56**) at phenotypic and genotypic level. Similarly Gauraha *et al.* (2011) worked on the genetic analysis of yield and yield attributing characters in linseed, Iraddi *et al.* (2014) on Genetic analysis of sugar content in segregating populations derived from cross between grain sorghum x sweet sorghum and Gami and Chauhan (2014) on Indian mustard.

Conclusion :

From the present investigation it is evident that the wide range of variability for different traits coupled with high heritability and high genetic advance for important yield traits. 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, genetic advance, positive and significant correlation on grain yield.

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