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## Analysis of genetic variability (PCV, GCV, heritability and genetic advancement) among thirteen different rice genotypes in north India

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### Abstract

The analysis of genetic variability was done for 13 rice genotypes in the student instructional farm during *Kharif* 2014-15 at Narendra Dev University of Agriculture and Technology, Kumarganj, Faizabad. The experiment was conducted in a randomized block design (RBD) with 3 replications. In general, phenotypic coefficients of variation (PCV) estimates were higher than genotypic coefficients of variation (GCV) estimates for all the studied characters in all genotypes displaying the influence of environment effect on the studied characters. The higher estimates of PCV and GCV were observed for grains per panicle, spikelet's per panicle and flag leaf area. High heritability coupled with high genetic advance was observed for spikelet's per panicle, grains per panicle, flag leaf area, test weight and plant height, indicate the lesser influence of environment in expression of these traits and prevalence of additive gene action in their inheritance hence, amenable of simple selection.

**Keywords:** PCV, GCV, heritability

### Introduction

Rice is a major source of food for more than 2.7 billion people on a daily basis and is planted on about one-tenth of the earth's arable land. It is the single largest source of food energy for more than half of the world's population. A 100 g of rice provides 345.0 kcal, 78.2 g of carbohydrates and 6.8 g of protein (Gopalan *et al.* 2007) [4] inclusive of considerable amount of recommended Zinc and Niacin. Rice protein is biologically richest as its digestibility is very high (88%). Rice provides almost 50-80% of daily calorie intake amongst the poor class of the society. Besides its important significance, it is rich in genetic diversity in the form of thousands of land races and progenitor species (Nagaraju *et al.* 2002) [6].

Globally, India stands first in rice area and second in rice production, after China. It contributes about 40 to 43% of total food grain production and is playing a vital role in the food and livelihood security system. Rice is cultivated world-wide over an area about 483.10 million metric tonnes. In Indian agriculture; rice is the main source of livelihood for more than 150 million rural households. The total area of rice crop in India is 43.90 million hectare, which produces 108 million metric tonnes with an average productivity is 2490 kg/ha.

The development of new genotypes requires some knowledge about the genetic variability presents in the germplasm of the crop to build efficient breeding program. The knowledge about genetic variability can help to know if these variations are heritable or non-heritable. The magnitude of variation due to heritable component is very important because, it would be a guide for selection of parents for crop improvement (Dutta *et al.* 2013) [3]. Therefore, selection for high yield requires knowledge about genetic variability and good understanding of correlation between yield and yield components regarding to the genetic material that is on hand. Genetic variability for agronomic traits is the key component of breeding program for broadening the gene pool of rice (Dutta *et al.* 2013) [3].

The success of breeding program depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable (Tiwari *et al.* 2011) [9]. Variability refers to the presence of differences among the individuals of plant population. Variation results due to difference either in genetic constitution of the individual of a plant population or in 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 breeding materials.

## Materials and Methods

The experiment was conducted in the Student instructional farm of NDU&T in *Kharif* 2014-15. The site is located between latitude of 24° 47' north to 26° 56" north and longitudes of 81° 12' east and 83° 98' east, on an altitude of 113 meters above the mean sea level. The seeds of rice genotype were sown in nursery bed. After 21 days, single seedling per hill was transplanted with 20 cm row to row and 15 cm plant to plant spacing in randomized complete block design (RBD) with three replications. Observations were recorded on days to 50% flowering, days to maturity, plant height, panicle bearing tillers per plant, spikelet's per panicle, grains per panicle, spikelet's fertility (%), test weight (g), biological yield (g), harvest index (%) and grain yield (g). Estimation of genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) were done according to the formula given by Burton and De Vane (1953) [13].

$$GCV = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100 \text{ or } \frac{\sigma_g}{\bar{x}} \times 100$$

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Heritability in broad sense ( $h^2_b$ ) was calculated according to the formula suggested by Hanson *et al.* (1956).

$$h^2_b = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

$\sigma_g^2$  = Genotypic variance

$\sigma_p^2$  = Phenotypic variance

Genetic advance (GA) was estimated by using the formula given by Johnson *et al.* (1955) [11].

Genetic advance (GA) =  $h_b^2 \cdot K \cdot \sigma_p$

Genetic advance in per cent of mean =  $\frac{GA}{\bar{X}} \times 100$

Where,

K = Selection differential at 5 per cent selection intensity. (K = 2.06)

$h^2_b$  = Heritability coefficient (Broad sense)

$\sigma_p$  = Phenotypic standard deviation

$\bar{X}$  = Mean of the character

## Results and Discussion

Analysis of variance revealed highly significant and exploitable variability among all the genotypes for twelve characters (Table 1). Greater variability in the initial breeding materials ensures better chances of producing desired recombinants for improvement of the crop. This suggests the presence of variation among the genotypes for all these traits. The phenotypic (PCV) and genotypic (GCV) coefficient of variation for the twelve characters during *kharif* 2014-15 have been presented in Table 2. In general, the magnitude of phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits. The high estimates of phenotypic coefficient of variation (>20%) were recorded for spikelet's per panicle (21.47) and grains per panicle (20.30). The moderately estimates (10-20%) of PCV were recorded for flag leaf area (19.68), test weight (15.40), grain yield per plant (14.50), panicle bearing tillers per plant (14.07), plant height (11.40), biological yield per plant (10.42), while spikelet fertility (7.14), harvest index (6.65), days to 50% flowering (3.79) and days to maturity (3.48) showed low estimate (<10%) of PCV. The high estimates of genotypic coefficient

**Table 1:** Analysis of variance for 12 characters in rice genotypes in *Kharif* 2014-15

S. No.	Characters	Mean Sum of Squares		
		Replications	Treatments	Errors
	Degree of freedom	2	12	24
1.	Days to 50% flowering	1.87	43.80**	1.89
2.	Days to maturity	0.92	62.77**	1.86
3.	Plant height	6.26	345.15**	4.07
4.	Panicle bearing tillers/plant	0.14	3.80*	1.67
5.	Flag leaf area (cm <sup>2</sup> )	0.00	76.23**	0.34
6.	Spikelets/panicle	1.94	2626.63**	3.91
7.	Grains/panicle	0.83	1834.29**	3.53
8.	Spikelet fertility (%)	2.93	115.50**	2.57
9.	Test weight (g)	0.16	33.66**	0.43
10.	Biological yield (g)	5.78	17.64**	2.37
11.	Harvest index	5.86	11.62*	4.10
12.	Grain yield /plant (g)	0.002	5.39**	0.55

\*, \*\* significant at 5 and 1% probability levels, respectively

**Table 2:** Estimates of grand mean, range, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense ( $h^2_b$ ) and genetic advance in percent of mean (GA %) for 12 characters in rice genotypes under *Kharif* 2014-15.

S. No.	Characters	Grand mean	Range		PCV (%)	GCV (%)	$h^2_b$	GA in % of mean
			Max.	Min.				
1.	Days to 50% flowering	105.02	111.00	97.66	3.79	3.55	88.03	6.87
2.	Days to maturity	135.00	142.66	127.66	3.48	3.33	91.54	6.58
3.	Plant height(cm)	95.14	115.16	77.90	11.40	11.20	96.54	22.68
4.	Panicle bearing tillers/plant	10.96	12.90	9.46	14.07	7.68	29.84	8.64
5.	Flag leaf area (cm <sup>2</sup> )	25.71	30.67	13.71	19.68	19.55	98.66	40.01
6.	Spikelet's/panicle	137.98	189.98	67.06	21.47	21.42	99.55	44.04
7.	Grains/panicle	122.00	143.11	60.16	20.30	20.24	99.42	41.58
8.	Spikelet fertility (%)	88.74	94.98	75.12	7.14	6.91	93.60	13.77
9.	Test weight (g)	22.02	28.34	16.89	15.40	15.10	96.21	30.52
10.	Biological yield (g)	26.22	31.40	22.74	10.42	8.60	68.14	14.63
11.	Harvest index	38.65	41.99	35.78	6.65	4.09	37.96	5.20
12.	Grain yield /plant (g)	10.15	12.91	8.47	14.50	12.50	74.30	22.20

of variation (>20%) were recorded for spikelet's per panicle (21.42) and grains per panicle (20.24). The moderately estimates (10-20%) of GCV were recorded for flag leaf area

(19.55), test weight (15.10), grain yield per plant (12.50) and plant height (11.20), while Biological yield per plant (8.60), panicle bearing tillers per plant (7.68), spikelet fertility (6.91),

harvest index (4.09), days to 50% flowering (3.55) and days to maturity (3.33), showed low estimate (<10%) of GCV. The results were in conformity with Chaudary *et al.* (2013) [2]. High estimates of broad sense heritability ( $h^2b$ ) (>75%) under field condition in *Kharif* 2014-15, was recorded for the spikelet's per panicle (99.55), grains per panicle (99.42), flag leaf area (98.66), plant height (96.54), test weight (96.21), spikelet's fertility (93.60), days to maturity (91.58) and days to 50% flowering (88.03). The moderate (50-75%) estimation of broad sense heritability ( $h^2b$ ) was recorded for grain yield per plant (74.30) and biological yield per plant (68.14). The low (<50%) broad sense heritability ( $h^2b$ ) was recorded in harvest index (37.96) and panicle bearing tillers per plant (29.84).

The genetic advance in per cent of mean under field condition in *Kharif* 2014-15, was found high (>20%) for spikelet's per panicle (44.04), grains per panicle (41.58), flag leaf area (40.01), test weight (30.52), plant height (22.68), grain yield per plant (22.20), and moderately for (>10%) harvest-index (17.37) and spikelet's fertility (13.77) and low (<10%) panicle bearing tillers per plant (8.64), days to 50% flowering (6.87) and harvest index (5.20). High heritability coupled with high genetic advance in per cent of mean was observed for the all the characters except panicle bearing tillers per plant, days to 50% flowering and harvest index.

The estimate of heritability alone is not very much useful on predicting resultant effect for selecting the best individual because it includes the effect of both additive gene as well as non-additive gene. High genetic advance only occurs due to additive gene action (Panse and Shukhatme 1967) [7]. So heritability coupled with genetic advance would be more useful than heritability alone.

High heritability along with high genetic advance was observed for spikelets per panicle, grains per panicle, flag leaf area, test weight and plant height, indicating that these characters are largely controlled by additive gene action, which indicates that improvement in these characters is possible through mass selection and progeny selection. Similar study was done by Chandramohan *et al.* (2016) [1].

High heritability coupled with moderate genetic advance values was recorded for spikelet's fertility suggested the role of both additive and non-additive gene effects in their inheritance, therefore, adoption of breeding procedures which could exploit both the gene actions would be a prospective approach (Krishna *et al.* 2008 and Patil and Sarawgi, 2005) [5, 8].

Days to 50% flowering and days to maturity exhibited high level of heritability along with low estimates of genetic advance, whereas, low values of both the parameters were observed for panicle bearing tillers per plant and harvest index. These results indicated the role of non-additive genes in inheritance of these characters hence improvement of these traits through heterosis breeding rather than selection could be adopted. Vanisree *et al.* (2013) [10] also reported non additive gene action for plant height and days to 50 % flowering.

## Conclusion

From the present study, it can conclude that, there is adequate genetic variability present in the material studied. Highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for spikelet's per panicle and grains per panicle, indicating that these characters could be used as selection for crop improvement. High heritability along with high genetic advance was observed for spikelets per panicle, grains per panicle, flag leaf area, test

weight and plant height, indicating that these characters are largely controlled by additive gene action and these characters can be improved by the mass selection and progeny selection. Therefore, the results suggest that the number of panicles per plant, panicle weight and the number of grains per panicle are important yield contributing traits and selection based on these traits would be most effective.

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