Appraisal of Genetic Variability for Yield and its Component Characters in Rice (*Oryza Sativa* L.)

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ABSTRACT

Estimation of genetic components of variability was done by taking into consideration twenty nine genotypes of rice collected from diverse locations. Analysis revealed that plant height exhibited high estimates of GCV and PCV preceded by number of tillers and effective tillers per plant, number of spikelets and number of grains per panicle and grain weight per panicle. Heritability was higher for days to 50% flowering followed by days to maturity, plant height and panicle length which suggested that these traits would respond to selection owing to their high genetic variability and transmissibility. High heritability coupled with high genetic advance as per cent of mean was recorded for number of spikelets and number of grains per panicle and grain weight per panicle. These characters indicate the predominance of additive gene effects in their expression and would respond to selection effectively as they are least influenced by environment.

Key words : GCV, genetic advance, heritability, PCV, rice.

INTRODUCTION

Rice is a cereal crop belonging to genus *Oryza* of family *Poaceae*. The genus *Oryza* has twenty two wild and two cultivated species *viz., Oryza sativa* and *Oryza glaberrima*. All these represent ten different genomic types (AA, BB, CC, BBCC, CCDD, EE, FF, GG, HHJJ and HHKK) (Brar and Khus, 1986). All the germplasms found in Asia, America and Europe belong to *Oryza sativa,* while those in West Africa belong to *Oryza glaberrima*. *Oryza sativa* is a cultivated diploid species having 24 chromosomes of AA genome.

Rice provides 21% of global human per capita energy and 15% of per capita protein (FAO, Gender and rice, International Year of Rice, 2004). Asia accounts for over 90% of the world's production of rice, with China, India and Indonesia producing 30.41, 22.12 and 7.97% respectively of total global rice production. It contributes 43% of total food grain production and 46% of the total cereal production of the country.

Breaking of yield barriers in cereal crops including rice has become hard task to breeders. Plateauing of rice yield coupled with shrinking natural resources mainly land and water has caused major challenges to breeders for increasing rice production by at least 3 million tonnes each year to maintain self sufficiency in rice production (Siddiq *et al.* 1994). The challenge of increasing the rice production up to 120 million tonnes by the year 2020 calls for both short and long term planning encompassing genetic as well as crop management options.
The reason for low production in India is due to the non-availability of high yielding varieties

whose development requires the knowledge of existing genetic variability. The large spectrum of genetic variability in segregating population depends on the magnitude of genetic variability encountered among the parents used for hybridization and offer better scope for selection. Therefore, the assessment of variability for yield and its component characters is of utmost importance before planning for an appropriate breeding strategy for genetic improvement. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are helpful tools in detecting the amount of variability present in the germplasm. Heritability and genetic advance are important selection parameters in estimating the resultant effect in selection of best genotypes for yield and its attributing traits. With the above background information the present investigation was undertaken to study the genetic parameters among the twenty nine rice genotypes.

MATERIALS & METHODS

A field experiment was conducted during *Kharif 2011* and 2012 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. To create three different environments, all the genotypes were grown once in *Kharif* 2011 and in two dates with the intervals of 15 days in *Kharif* 2012. The experimental seed material for the present investigation consisted of twenty-nine genotypes of rice; details are furnished in Table 1.

In *Kharif* 2011, all the 29 genotypes were sown in the nursery on 21th June 2011, and 30 days old seedlings were used for transplanting in the field. All entries were grown in a Randomized Block Design with three replications. All the genotypes were grown with a spacing of 20 x 15 cm between row to row and plant to plant respectively, with a row length of 5.0 m. In *Kharif* 2012, all the 29 genotypes were sown in the nursery on two dates *i.e.*, 15th June 2012 and 30th June 2012, and all other factors similar as above.

In all the seasons, field was ploughed and puddled thrice until fine tilth of soil was obtained. The crop was raised under irrigated conditions during *Kharif* 2011 and 2012. Cultural practices like weeding, irrigation and recommended dose of fertilizer were applied to obtain a good crop growth. Five competitive plants were selected randomly from each row of each genotype in each replication. Observations were recorded for the following attributes *viz.,* days to 50% flowering and days to maturity on plot basis, total number of tillers per plant, number of effective tillers per plant, plant height (cm), panicle length (cm), number of spikelets per panicle, number of grains per panicle, spikelets fertility %, grain weight per panicle (g), grain yield per plant (g) and 1000 grain weight (g). Panicle and grain characters were recorded on five panicles of selected plants.

Table-1. List of 29 genotypes and their sources

S. No.	Name of Genotype	Source
1	HUR-5-1	BHU, Varanasi
2	NDR-3026-3-1 R	NDUA&T, Faizabad
3	PRR-78	IARI, Pusa, New Delhi
4	Pusa Basmati-1	IARI, Pusa, New Delhi
5	IDR-763	BHU, Varanasi
6	HUR-3022	BHU, Varanasi
7	Karahani	Local Collection
8	Sonachur	Local Collection
9	Ketaki joha	CRRI, Cuttack
10	Type-3	IARI, Pusa, New Delhi
11	Anjali	CRRI, Cuttack
12	Pusa-6B	IARI, Pusa, New Delhi
13	IR 58025B	BHU, Varanasi
14	IR 80555B	BHU, Varanasi
15	IR 68897B	BHU, Varanasi
16	IR 79156B	BHU, Varanasi
17	BPT 5204	BHU, Varanasi
18	HUR 105	BHU, Varanasi
19	HUR 2-1	BHU, Varanasi
20	Kala Namak	Local Collection
21	GR-32	Local Collection
22	CR 2496	CRRI, Cuttack
23	Pani Dhan	CRRI, Cuttack
24	Swrna sub-1	BHU, Varanasi
25	Nagina-22	Local Collection
26	GR-32 Improved	BHU, Varanasi
27	Loha chhad	Local Collection
28	Kanak jeer	CRRI, Cuttack
29	Pant Dhan-12	GBPUA&T, Pant Nagar

The experimental data were compiled by taking mean value over randomly selected plants from all the replications in all the seasons and subjected to the following statistical analysis:

1. Analysis of Variance (Panse and Sukhatme, 1961)
2. Genotypic and Phenotypic coefficient of variation (Burton, 1952)
3. Heritability (Lush, 1940).
4. Genetic advance as per cent of mean (Johnson *et al.*,1955)

RESULTS AND DISCUSSION

A wide range of variation was observed among the twenty nine rice (*Oryza sativa* L.) genotypes for twelve quantitative characters. The perusal of data revealed that variance due to treatment was highly significant for all the characters suggesting that there were inherent genetic differences among the genotypes. Significant genetic variation in various component characters exhibited by the genotypes indicated these characters might be effective (Table 2).

The phenotypic co-efficient of variation was in general, higher than the genotypic co-efficient of variation. But the differences between PCV and GCV for many traits was less, suggesting the less influence of environment for the traits days to maturity, days to 50% flowering, plant height, spikelets per panicle, panicle length, number of grains per panicle, spikelets fertility percent, 1000 grain weight and grain weight per panicle (Table 3). Similar findings were earlier reported by Singh and Chakraborty (1996), Devi *et al.* (2006), Prajapati *et al.* (2011).

Among all the traits, plant height exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by number of tillers per plant, number of effective tillers per plant, number of spikelets per panicle, number of grains per panicle, grain weight per panicle, grain yield per plant and 1000 grain weight. This indicates the existence of wide genetic base among the genotypes taken for study and possibility of genetic improvement through selection for these traits. This was in conformity with the findings of Bastia *et al.* (2008) who reported higher PCV and GCV in upland rice for grain yield per plant, number of effective tillers per plant and number of grains per panicle. Chauhan *et al.* (1993) also reported similar findings in upland rice for the trait plant height.

Moderate estimates of PCV and GCV were observed for the traits days to 50% flowering and panicle length. This suggests that the genetic improvement through selection for these traits may not be always effective. Similar results were also obtained by Das *et al.* (2005) in upland rice for panicle length and by Bastia *et al.* (2008) in upland rice for harvest index.

Low estimates of PCV and GCV were observed for the characters days to maturity and spikelets fertility percent suggesting that the direct selection for these traits may not be rewarding. The similar results were also reported by Kaw *et al.* (1999) for days to maturity in cold stress environment.

The coefficient of variation does not give the full estimates of heritable variation. It can be find out with greater degree of accuracy when heritability is combined with genetic advance under study. Hence, heritability and genetic advance were determined to study the scope of improvement in various characters through selection. Heritability and genetic advance are important selection parameters. High heritability estimates along with high genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al.,* 1955). Heritability is a good index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population.

Broad sense heritability was higher for days to 50% flowering, days to maturity, plant height, panicle length, number of spikelets per panicle, number of grains per panicle, grain weight per panicle and 1000 grain weight which suggested that these traits would respond to selection

Table -2. Analysis of variance for twelve characters in 29 rice genotypes over three different environments

S. No.	Characters	Mean sum of squares					
		Replications (df=2)	Environments (df=2)	Interactions (df=4)	Overall sum (df=8)	Treatments (df=28)	Error (df=224)
1	Days to 50% Flowering	15.66	652.39***	1.51	167.77***	1229.76***	16.51
2	Days to Maturity	17.87	862.14***	3.95	221.98***	1164.02***	11.28
3	Plant Height (cm)	54.96	828.92***	6.37	224.15***	7227.44***	63.46
4	Tillersper Plant	1.25	287.16***	4.47	74.34***	86.27***	4.81
5	Effective Tillersper Plant	8.37	212.14***	5.14	57.69***	69.98***	4.59
6	Panicle Length (cm)	0.28	451.24***	2.76	114.26***	71.59***	1.98
7	Spikeletsper Panicle	1238.77*	1070.84**	223.03	688.92*	50574.39***	315.72
8	Grainsper Panicle	1201.20*	18162.50***	193.35	4937.60***	32985.46***	312.96
9	Spikelets Fertility %	8.19	2125.68***	12.10	539.52***	242.48***	20.57
10	Grain Weightper Panicle (g)	0.41	7.56***	0.11	2.05***	13.39***	0.22
11	Grain Yieldper Plant (g)	48.12	4707.93***	54.16	1216.09***	713.90***	57.24
12	1000 grain weight (g)	6.20	299.01***	2.93	77.77***	178.36***	4.57

* Significant at 5% level, ** significant at 1% level and *** significant at 0.1% level of significance against pooled error

owing to their high genetic variability and transmissibility. Thus, selection based on phenotypic values would be effective for these traits. These findings are in agreement with those of Venuprasad *et al.* (2003) under managed moisture stress condition in rice for days to maturity and number of effective tillers per plant; Kundu *et al.* (2008) for number of grains per panicle and 1000 grain weight in tall *indica* aman rice and Kole and Hasib (2008) for plant height, days to 50% flowering, panicle length, kernel length and kernel L/B ratio in scented rice. Moderate heritability was accorded for number of tillers per plant, number of effective tillers per plant, spikelets fertility % and grain yield per plant. None of the characters exhibited low heritability.

Maximum and minimum genetic advance as per cent of mean was recorded for plant height, number of tillers per plant, number of effective tillers per plant, number of spikelets per panicle, number of grains per panicle, grain weight per panicle, grain yield per plant and 1000 grain weight followed by days to 50% flowering, days to maturity, panicle length and spikelets fertility %.

High heritability coupled with high genetic advance as per cent of mean was recorded for the characters *viz.,* number of spikelets per panicle, number of grains per panicle and grain weight per panicle. These results are in collaboration with the results obtained by Gyanendrapal *et al.* (2011) for grain yield per plant, spikelets per panicle, effective tillers per plant and days to 50% flowering, Krishna *et al.* (2010) for number of total spikelets per panicle and number of filled spikelets per panicle, Kundu *et al.* (2008) for grain yield per plant and 1000 grain weight in tall *indica* aman rice and Singh *et al.* (2007) for days to 50% flowering, grains per panicle and plant height. These characters indicate the predominance of additive gene effects in their expression and would respond to selection effectively as they are least influenced by environment.

Table-3. Mean, Range, PCV, GCV, Heritability (broad sense) and Genetic advance as per cent of mean for 12 characters in rice over three different environments

S. No.	Character	Mean	Range	PCV	GCV	h^2b	GA as % of mean
1.	Days to 50% Flowering	99.15	77.89 - 118.78	12.41	11.71	89	22.77
2.	Days to Maturity	133.80	108.78 - 150.78	8.82	8.46	92	16.70
3.	Plant Height(cm)	116.11	81.94 - 172.71	25.25	24.30	93	48.17
4.	No. of Tillers/ Plant	14.30	8.62 - 20.91	26.04	21.04	65	35.01
5.	No. of Effective Tillers/ Plant	11.31	6.87 - 17.84	30.44	23.83	61	38.43
6.	Panicle Length(cm)	25.10	20.42 - 31.28	12.42	11.08	80	20.37
7.	No. of Spikelets/ Panicle	208.61	105.07 - 346.76	36.82	35.82	95	71.79
8.	No. of Grains/ Panicle	169.02	87.02 - 297.37	37.15	35.65	92	70.46
9.	Spikelets Fertility %	81.06	66.29 - 87.66	8.30	6.13	55	9.32
10.	Grain Weight/ Panicle(g)	2.92	1.78 - 8.13	44.43	41.44	87	79.63
11.	Grain Yield/ Plant(g)	31.51	12.57 - 56.07	36.21	27.11	56	41.80
12.	1000 Grain Weight(g)	17.52	8.07 - 24.39	27.90	25.09	81	46.47

Classes of Heritability (%)		Classes of Genetic advance as percentage of mean	
High	>70 %	High > 35%	
Medium	50-70%	Medium 25-35%	
Low	< 50 %	Low < 25%	

High heritability associated with moderate genetic advance as per cent of mean was observed with plant height, 1000 grains weight, number of tillers per plant and number of effective tillers per plant. Thus, these traits are influenced by both additive and non additive gene effects. Similar results were also recorded by Venuprasad *et al.* (2003) for days to maturity under managed moisture stress environment, Verma *et al.* (2000) for plant height, days to flowering and 100 grain weight and Ganesan *et al.* (1995) for kernel length in early varieties of rice.

CONCLUSION

It can be concluded that selection of traits *viz.,* plant height, panicle length, number of tillers and number of effective tillers per plant, number of spikelet's and number of grains per panicle and grain weight per panicle were controlled by additive gene action, which could be improved through simple selection methods.

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