



Variability, Heritability and Genetic Advance in Rice (*Oryza sativa* L.)

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ABSTRACT

Forty genotypes were studied for their genotypic and phenotypic coefficient of variation during *Kharif* 2015. Results indicated significant differences among all the characters studied *viz.*, Days to 50% flowering, days to maturity, productive tillers per plant, plant height, panicle length, grains per panicle, test weight, kernel length, kernel breadth, L/B ratio and grain yield per plant. Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation for all the traits but smaller differences between GCV and PCV were recorded for all the characters studied, which indicated less influence of environment on these characters. PCV was higher for Grain yield per plant (26.04%) followed by grains per panicle (23.48%), productive tillers per plant (21.14%), test weight (16.79%), panicle length (12.67%), kernel breadth (11.09%), L/B ratio (9.32%), plant height (8.83%), kernel length (6.45%), days to 50% flowering (4.28%) and days to maturity (2.61%). High heritability coupled with high genetic advance as per cent of mean for the traits Test weight, panicle length and grains per panicle indicating the predominance of additive gene action and hence direct selection is useful with respect to these traits.

Key words: *Genetic advance, Heritability, Rice, Variability.*

Rice (*Oryza sativa* L., $2n = 2x = 24$) is the principal staple cereal food and source of calories for more than half of the world's population. It offers a wealth of material for genetic studies because of its wide ecological distribution and enormous variation encountered for various qualitative and quantitative characters (Kotaiah, 1983). Assessment of variability present in any crop species is an essential prerequisite for formulating an effective breeding programme. As the estimation of genetic variability alone does not give a clear indication of the possible improvement that can be achieved through simple selection it should be used in conjunction with heritability and genetic advance. This necessitates a thorough knowledge of variability owing to genetic factors, actual genetic variation heritable in the progeny and genetic advance that can be achieved through selection. Heritability estimates along with genetic advance was more useful than heritability estimate alone in predicting resultant effect for the selection of the best individual form of segregating population. In the present study an attempt was made to assess genetic variability for different characters in rice.

MATERIAL AND METHODS

The present investigation was conducted at the Agriculture college, Bapatla, during *kharif*,

2015. The experiment was laid out in a randomized complete block design with forty genotypes and three replications. The observations were recorded on ten randomly selected plants from each treatment for days to 50% flowering, days to maturity, productive tillers per plant, plant height, panicle length, grains per panicle, test weight, kernel length, kernel breadth, L/B ratio and grain yield per plant. For days to 50% flowering and days to maturity were recorded on plot basis. The treatment means for all characters were subjected to analysis of variance technique on the basis of model proposed by Panse and Sukhatme (1978). The genotypic (GCV) and phenotypic (PCV) coefficient of variation was calculated by the formulae given by Burton (1952). Heritability in broad sense [$h^2(bs)$] was calculated by the formula as suggested by Johanson *et al.* (1955). From the heritability estimates, the genetic advance (GA) was estimated by the formula given by Johanson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance revealed that the genotypes differed significantly for all the characters indicating presence of considerable variability for all the characters (Table 1). The genotypic coefficient of variation measures the range of variability available in a crop and also enable to compare the amount of variability present in

Table 1. ANOVA for seed yield and yield component characters in rice (*Oryza sativa* L.).

Source of variations	d.f.	Days to 50% flowering	Days to maturity	Productive tillers per plant	Plant height (cm)	Panicle length (cm)	Grains per panicle	Test weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/ B ratio	Grain yield per plant(g)
Mean sum of squares												
Replications	2	10.11	11.41	2.72	25.31	1.03	334.61	0.01	0.06	0.01	0.03	21.31
Treatments	39	43.41**	22.06**	7.69**	229.31**	24.66**	467133**	27.75**	0.35**	0.13**	0.17**	45.83**
Error	78	12.06	10.63	1.43	32.03	1.14	618.01	0.84	0.02	0.01	0.02	9.27

** Significant at 1% level

Table 2. Estimates of variability, heritability and genetic advance as per cent of mean for seed yield and yield components in rice (*Oryza sativa* L.)

Character	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability (%)	Genetic advance as percent of mean (%)
Days to 50% flowering	2.92	4.28	46.43	4.10
Days to maturity	1.34	2.61	26.38	1.42
Productive tillers per plant	16.27	21.14	59.23	25.79
Plant height (cm)	7.24	8.83	67.25	12.24
Panicle length (cm)	11.83	12.67	87.26	22.77
Grains per panicle	19.45	23.48	68.61	33.18
Test weight (g)	16.06	16.79	91.48	31.64
Kernel length (mm)	5.83	6.45	81.77	10.87
Kernel breadth (mm)	9.85	11.09	78.92	18.02
L/ B ratio	7.82	9.32	70.49	13.53
Grain yield per plant (g)	19.63	26.04	56.81	30.47

different characters. All traits under studied have higher phenotypic coefficient of variation than genotypic coefficient of variation. Which may due to higher degree of interaction of genotypes with the environment. It can be seen (Table 2) that PCV was higher for Grain yield per plant followed by grains per panicle, productive tillers per plant, test weight, panicle length, kernel breadth, L/B ratio, plant height, kernel length, days to 50% flowering and days to maturity.

GCV measures the extent of genetic variability percent for a trait but does not assess the amount of genetic variation which is heritable.

The heritability estimates along with genetic advance can be useful to predict effect of selection in selection programmes. Heritability and genetic advance as per cent of mean were high for

the traits Test weight, panicle length and grains per panicle indicating the predominance of additive gene action and hence direct selection is useful with respect to these traits. These results were in confirmation with the Sharma and Sharma (2007) for all these traits.

High heritability combined with moderate genetic advance as per cent of mean for Plant height, kernel length, kernel breadth and L/B ratio indicating the predominance of both additive and non-additive gene action in its inheritance and desired results may not be obtained by simple selection. These results were earlier reported by Tejaswini (2016) for plant height, kernel length and kernel breadth and Krishnaveni and Niveditha (2014) for L/B ratio.

Moderate heritability combined with low genetic advance as per cent of mean was observed for the trait Days to 50% flowering indicating the predominance of non-additive gene action in the inheritance of this trait and the desired results may not be obtained by simple selection. This finding was in accordance with that of Krishna *et al.* (2008). Low heritability accompanied with low genetic advance as per cent of mean was observed for the trait Days to maturity indicating the predominance of non-additive gene action in the inheritance of this trait and desired results may not be obtained by simple selection. Moderate heritability with low genetic advance as per cent of mean for 50% flowering. Similar result was earlier reported by Osman *et al.* (2011).

Heritability and genetic advance as per cent of mean were low for days to maturity. This finding was reported by Verma *et al.* (2011) indicating non-additive gene action in the inheritance of these traits and the desired results may not be obtained by simple selection.

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