

Short Communication

Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.)

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Eighty one rice (*Oryza sativa* L.) genotypes were evaluated during *kharif* 2010 for thirteen quantitative traits to examine the nature and magnitude of variability, heritability (broad sense) and genetic advance. Analysis of variance revealed that the differences among eighty one genotypes were significant for all the characters except flag leaf width. Among the all traits number of spikelets per panicle exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by harvest index, grain yield per hill and number of panicles per hill. Broad sense heritability was highest for biological yield per hill, which suggested that this trait would respond to selection owing their high genetic variability and transmissibility. Maximum genetic advance as per cent of mean was recorded for number of spikelets per panicle with high value of heritability.

Keywords: Variability, heritability, genetic advance , rice

Rice (*Oryza sativa* L.) is the most important cereal crop of the world and about 90 per cent of the people of south-East Asia consume rice as staple food. According to FAO, the productivity level of rice in India is very low (3.21 t/ha) as compared to the average productivity of the china (6.35 t/ha) and world (4.15 t/ha). The Agricultural statistics of 2009 reveals the rice productivity of various states – Punjab (4.022 t/ha), Andhra Pradesh (3.247 t/ha), Haryana (2.726 t/ha), whereas Uttar Pradesh showed 2.17 t/ha. The production is very low in India due to non-availability of high yielding varieties. Development of high yielding varieties requires the knowledge of existing genetic variability. The large spectrum of genetic variability in segregating population depends on the amount of the genetic variability among genotypes and offer better scope for selection. The magnitude of heritable variation in the traits studied has immense

value in understanding the potential of the genotype for further breeding programme. Assessment of variability for yield and its component characters becomes absolutely essential 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 useful in detecting the amount of variability present in the germplasm. Heritability coupled with high genetic advance would be more useful tool in predicting the resultant effect in selection of the best genotypes for yield and its attributing traits. It helps in determining the influence environment on the expression the genotypic and reliability of characters. With the above background information the present investigation was undertaken to study the genetic parameters among the eighty one rice genotypes.

Materials and Methods

A field experiment was conducted with eighty-one rice genotypes during *khari* 2010 at the Field Experimentation Centre, Department of Genetics and Plant Breeding, Allahabad School of Agriculture, SHIATS, Allahabad in Randomized Block Design (RBD) with three replications. Twenty seven days old seedlings were transplanted with a spacing of 20 cm and 15 cm between rows and hills, respectively. Five representative hills for each genotypes in each replications were randomly selected to record the observations for eleven quantitative traits *viz.*, plant height, number of tillers per hill, number of panicles per hill, flag leaf length, flag leaf width, number of spikelets per panicle, panicle length, biological yield per hill, harvest index, test weight and grain yield per hill. Two characters *viz.*, days to 50 per cent flowering and days to maturity were computed on plot basis. The mean data after computing for each character was subjected to standard method of analysis of variance following Panse and Sukhatme (1967), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability in broad sense (h^2) and genetic advance as per cent of mean were estimated by the formula as suggested by Burton (1952) and Johanson *et al.* (1955).

Results and Discussion

A wide range of variation was observed among eighty one rice (*Oryza sativa* L.) genotypes for thirteen quantitative characters. The perusal of data revealed that variance due to treatment was highly significant for all the characters. This suggested 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. Phenotypic variance was higher than the genotypic variances for all the characters thus indicated the influences of environmental factor on these traits.

Similar findings were earlier reported by Singh & Chakraborty (1996), Devi *et al.* (2006), Prajapati *et al.* (2011). Coefficient of variation studied indicated that estimates of phenotypic coefficient of variation (PCV) were slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters (Table 1). Among the all traits number of spikelets per panicle (23.34% and 23.52%) exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by harvest index (22.68% and 23.34%), grain yield per hill (20.64% and 21.24%) and number of panicles per hill (20.21% and 26.34%). The high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for these traits suggested the possibility of yield improvement through selection of these traits. Biological yield per hill (19.88% and 19.94%), number of tillers per hill (19.26% and 22.79%), test weight (18.12% and 18.39%), flag leaf length (14.40% and 17.56%), plant height (13.37% and 14.13%) and flag leaf width (12.10 and 12.83%) showed moderate value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Days to maturity (5.65% and 5.86%), days to 50% flowering (7.49% and 7.97%) and panicle length (7.79% and 9.91%) exhibited low genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Low genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values for these traits was also reported by Shivani and Reddy (2000), Devi *et al.* (2006), Prajapati *et al.* (2011) and Anandrao *et al.* (2011). Low PCV & GCV estimates for days to 50% flowering and panicle length have also been reported by Shinha *et al.* (2004) and Patil *et al.* (2003), respectively.

The coefficient of variation doesn't offers the full scope of heritable variation. It can be find out with greater degree of accuracy when heritability is conjunction with genetic advance 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 (Johanson *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 biological yield per hill (99.33%), number of spikelets per panicle (98.47%), test weight (97.11%), harvest index (94.39%), grain yield per hill (94.33%), days to maturity (92.97%), plant height (89.60%), flag leaf width (88.85%), days to 50 per cent flowering (88.36%), number of tillers per hill (71.41%), flag leaf length (66.99%) and panicle length (61.76%), which suggested that these traits would respond to selection owing to their high genetic variability and transmissibility. Similar finding was earlier reported by Verma (2010) and Anandrao *et al.* (2011).

Number of panicles per hill (58.85%) showed moderate heritability in broad sense. Maximum and minimum genetic advance as per cent of mean was recorded for number of spikelets per panicle (75.39%) and flag leaf width (0.31%), respectively. Number of spikelets per panicle (75.39%), biological yield per hill (36.09%) and plant height (27.51%) showed high genetic advance. High genetic advance as per cent of mean for number of spikelets per panicle was earlier observed by Prajapati *et al.* (2011). Days to 50 per cent flowering (16.12%), days to maturity (15.84%) and grain yield per hill (13.16%) showed moderate genetic advance as per cent of mean, while, flag leaf length (7.91%), number of tillers per hill (6.38%), number of panicles per plant (5.11%), panicle length (2.94%) and flag leaf width (0.31%) showed low genetic advance as per cent of mean. Low genetic advance as per cent of mean for number of panicles per plant was earlier observed by Babu *et al.* (2011) and Prajapati *et al.* (2011). High heritability coupled with high genetic advance was recorded for number of spikelets per panicle (98.47% and 75.39%), biological yield per hill (99.36% and 36.09%), plant height (89.60% and 27.51%) and harvest index (94.39% and 16.75%).

Table 1. Genetic parameters for grain yield and its component characters in rice

S.N	Characters	GCV (%)	PCV (%)	h ² bs (%)	GA (%)
1	Days to 50 % flowering	7.49	7.97	88.36	16.12
2	Plant height (cm)	13.37	14.13	89.60	27.51
3	Number of tillers per hill	19.26	22.79	71.41	6.38
4	Number of panicles per hill	20.21	26.34	58.85	5.11
5	Flag leaf length (cm)	14.40	17.56	66.99	7.91
6	Flag leaf width (cm)	12.10	12.83	88.85	0.31
7	Panicle length (cm)	7.79	9.91	61.76	2.94
8	Number of spikelets per panicle	23.34	23.52	98.47	75.39
9	Days to maturity	5.65	5.86	92.97	15.84
10	Biological yield per hill (g)	19.88	19.94	99.33	36.09
11	Harvest index	22.68	23.34	94.39	16.75
12	Test weight (g)	18.12	18.39	97.11	9.92
13	Grain yield per hill (g)	20.64	21.24	94.33	13.16

Thus it is interpreted that the characters *viz.*, number of spikelets per panicle, biological yield per hill, plant height and harvest index were controlled by additive gene action, which could be improved through simple selection methods. The characters showing high heritability with low genetic advance indicated the presence of non-additive gene action. Hence selection could be postponed for these characters or these characters could be improved by intermating of superior genotypes of segregation population from recombination breeding.

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