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Assessment of genetic variability for yield and quality traits in rice (*Oryza sativa* L.) genotypes

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Abstract: Eighty one rice genotypes (*Oryza sativa* L.) 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. Among all the traits number of panicles per hill (26.00) exhibited highest estimates of genotypic coefficient of variation (GCV) and number of tillers per hill (27.37) exhibited highest phenotypic coefficient of variation (PCV) followed by number of spikelets per panicle (24.84), grain yield per hill (19.23), Harvest index (19.33) and Biological yield (17.75). Broad sense heritability was highest for biological yield per hill (99.96), which suggested that this trait would respond to selection owing their high genetic variability and transmissibility. Maximum genetic advance as percent of mean was recorded for number of tillers per hill (96.38) with high value of heritability.

Key words: Rice, GCV, PCV, Heritability, Genetic advance

Introduction

Rice belongs to family gramineae, morphologically, rice is an annual grass and one of the most important cereal crop. Globally, it is grown extensively in tropical and sub tropical regions of the world. Rice is the staple food for the people of these regions, with annual consumption per person in 2007 of 131 kg (FAO 2011). Rice provided 49% of calorie and 39% of the protein in their diet in 2007 (FAOSTAT 2011). In India during the period of 2007-08 rice production was 95.68 million tons and in the period of 2008-09 the production was 84.5 million tons, in 2009-10 it was 89.09 million tons, in 2010-11 it was 95.33 million tons and in 2011-12 it is estimated to be 87.10 million tons (Agriculture Statistics at Glance 2011). 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. Moreover, rice cultivation is considered as one of the most important anthropogenic sources that accounts for the global methane (CH_4) emission to the atmosphere (Singla and Inubushi, 2015; Singla *et al*., 2014). Variation is the basis for plant breeding and it is the occurrence of differences between individuals due to variation in their genetic composition and/or the environment in which they are grown. 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 genetic variability for yield and quality traits has become 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 (Sunil *et al*., 2015). 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 of environment on the expression of the genotypic and reliability of the characters. With above background information the present investigation was undertaken to study the genetic parameters among the eighty one rice genotypes. These grmplasms were showing wide genetic divergence among the constituent in it and may be directly utilized in hybridization programme for improvement of yield related traits (Aparajita *et al*., 2015). The objectives of the present study were to assess genetic variability in rice germplasm for yield. And to identify high yielding rice genotypes for quality traits.

Materials and Methods

The experimental material for the present study comprised of 81 Genotypes of rice laid in randomized block design (RBD) with three replications at the Field Experimentation Centre of Department of Genetics and Plant Breeding, Allahabad School of Agriculture, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad, U.P. during kharif, 2011. Replicates had the spacing of 20 x 15 cm. Day to 50% flowering, plant height, days to maturity, flag leaf length, flag leaf width, number of tillers per hill, number of spikelets per panicle, test weight and yield per plant were analyzed. The genotypes used in the present investigation given below. The recommended doses of fertilizers @ 120:60:40; N: P: K kg/ha were applied in each replicate. The full dose of P_2O_5 and K_2O and the half dose of N were applied as basal dose at the time of transplanting. The rest of the N was applied as top dressing in two split doses: at the time of maximum tillering stage, *i.e.* 30 days after the transplanting, and between panicle initiation and boot leaf stage, *i.e.* 55 days after transplanting. Manual weeding in field was done twice: at 20 days after transplanting and at 50 days after transplanting. Crop was harvested on 1st week of November 2011. The data were analyzed by using analysis of variance (ANOVA) and the genetic parameters such as PCV and GCV were calculated (Burton, 1952), heritability broad sense (h^2) (Burton and De Vane, 1953) and genetic advance in per cent of mean (genetic gain) (Johnson *et.al*., 1955).

List of genotypes used in the present investigation.

S.N.	Designation	S.N.	Designation	S.N.	Designation
1	A2-1	28	A2-28	55	NR1-14
2	A2-2	29	A2-29	56	NR1-15
3	A2-3	30	A2-30	57	NR1-16
4	A2-4	31	A2-31	58	NR1-17
5	A2-5	32	A2-32	59	NR1-18
6	A2-6	33	A2-33	60	NR1-19
7	A2-7	34	A2-34	61	NR1-20
8	A2-8	35	A2-35	62	NR1-21
9	A2-9	36	A2-36	63	NR1-22
10	A2-10	37	A2-37	64	NR1-23
11	A2-11	38	A2-38	65	NR1-24
12	A2-12	39	A2-39	66	NR1-25
13	A2-13	40	A2-40	67	NR1-26
14	A2-14	41	A2-41	68	NR1-27
15	A2-15	42	NR1-1	69	NR1-28
16	A2-16	43	NR1-2	70	NR1-29
17	A2-17	44	NR1-3	71	NR1-30
18	A2-18	45	NR1-4	72	NR1-31
19	A2-19	46	NR1-5	73	NR1-32
20	A2-20	47	NR1-6	74	NR1-33
21	A2-21	48	NR1-7	75	NR1-34
22	A2-22	49	NR1-8	76	NR1-35
23	A2-23	50	NR1-9	77	NR1-36
24	A2-24	51	NR1-10	78	NR1-37
25	A2-25	52	NR1-11	79	NR1-38
26	A2-26	53	NR1-12	80	NDR359 (check)
27	A2-27	54	NR1-13	81	Govind (check)

Results and Discussion

ANOVA revealed highly significant differences among the genotypes for all the characters, indicating presence of high variability among the varieties (Table 1). The estimation of phenotypic coefficient of variation (PCV) was higher than the estimates of genotypic coefficient of variations (GCV) (Table 2). The results are in conformation to the finding of previous study (Deosarkar *et al.,* 1989). A wide range of variation was observed among eighty-one rice (*Oxryza 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 influence of environmental factor on these traits.

Similar findings were earlier reported by 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 tillers per hill exhibited highest (27.36 and 27.87%) genotypic coefficient of variation and phenotypic coefficient of variation followed by number of panicles per hill (26.00 and 27.30%), number of spikelets per panicle (24.48 and 24.84%), flag leaf length (23.23 and 23.27%).

The highest values of genotypic coefficient of variance (GCV) and phenotypic coefficient of variation (PCV) for these traits suggested the possibility of yield improvement through selection of these traits. Flag leaf width (22.29 and 22.38%), plant height (20.35 and 20.36%), grain yield per hill (19.03 and 19.23%), harvest index (19.12% & 19.33%), biological yield per hill (17.73 and 17.75%) showed moderate value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Panicle length (10.87 and 11.01%) and test weight (8.51 and 8.65%), days to 50% flowering (5.40 and 5.59%), days to maturity (4.95 and 5.09%) exhibited low genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values for these traits was also reported by Shivani and Reddy (2000), Prajapati *et al.* (2011) and Anandrao *et al.*(2011). Low PCV and GCV estimates for days to 50% flowering have also been reported by Sinha *et al.* (2004) and Patil *et al.* (2003), respectively.

The coefficient of variation doesn't offer full scope of heritable variation. It can be found 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 useful 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 (99.96%), plant height (99.91%), flag leaf length (99.72%) , flag leaf width (99.14%) grain yield per hill (97.92%) harvest index percent (97.88%), panicle length (97.47%), number of spikelets per panicle (97.15%), test weight (96.81%), days to maturity (94.82%), days to 50% flowering (93.46%), and number of panicles per hill (90.74%). which suggested that these traits would respond to selection owing to the high genetic variability and transmissibility. Similar finding was earlier reported by Verma (2010) and Anandrao *et al.* (2011). Maximum and minimum genetic advance as percent of mean was recorded for number of tillers per

Table-1: Estimation of variability parameters for various quantitative characters in 81 Rice genotypes

Sl. No.	Characters	GCV (%)	PCV (%)	h^2 (%)	GA (%)
1	Days to 50% flowering	5.40	5.59	93.46	10.94
2	Plant height	20.35	20.36	99.91	39.84
3	Flag leaf length	23.23	23.27	99.72	45.54
4	Flag leaf width	22.29	22.38	99.14	43.81
5	No. of tillers per hill	27.36	27.87	96.38	54.54
6	No. of panicles per hill	26.00	27.30	90.74	53.42
7	Panicles length	10.87	11.01	97.47	21.56
8	Days to maturity	4.95	5.09	94.82	9.95
9	Biological yield per hill	17.73	17.75	99.96	34.73
10	Harvest index	19.12	19.33	97.88	37.82
11	No. of spikelets per panicle	24.48	24.84	97.15	48.61
12	Test weight	8.51	8.65	96.81	16.92
13	Grain yield per hill	19.03	19.23	97.92	37.64

Table-2: ANOVA for 13 characters in 81 rice genotypes

		Mean sum of squares		
S.N.	**Characters**	**Replication (d. f.=2)**	**Genotypes (d. f. =80)**	**Error (d. f.=160)**
1	Days to 50% flowering	3.44	107.25**	2.44
2	Plant height	2.35	1671.61**	0.51
3	Flag leaf length	0.34	188.48**	0.18
4	Flag leaf width	0.00030*	0.32303*	0.00093*
5	Tillers per hill	3.67	91.50**	1.13
6	Spikelet per panicle	24.98	4383.83**	42.41
7	Panicles per hill	1.22	55.90**	1.84
8	Panicle length	0.11	22.17**	0.19
9	Days to maturity	1.37	141.33**	2.53
10	Biological yield	3.27	942.97**	0.11
11	Harvest index	1.34	118.71**	0.85
12	Test weight	0.20	11.29**	0.12
13	Grain yield per hill	0.17	113.71**	0.80

*Significant at 5% level of significance.

**Significant at 1% level of significance.

hill (54.54%) and days of maturity (9.95%) respectively. number of tillers per hill (54.54%), Number of panicles per hill (53.42%), Number of spikelets per panicle (48.61%), Grain yield per hill (37.64%)showed high genetic advance as percent of mean. High genetic advance as percent of mean for the number of number of panicles per hill was earlier observed by Prajapati *et al.*(2011), biological yield (34.73%), harvest index(37.82%) panicle length (21.56%), plant height (39.84%), showed moderate genetic advance as percent of mean. days to 50% flowering (10.94%), days of maturity (9.95%) showed low genetic advance as percent of mean. low genetic advance as percent of mean for days of maturity 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 number of spikelets per panicle(97.15% & 48.61%), harvest index (97.88% & 37.82%) grain yield per hill (97.92% & 37.64%), plant height (99.91% & 39.84%).

Thus it is interpreted that the characters *viz.* number of spikelets, grain yield per hill, harvest index and plant height 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 and can be improved by inter-mating of superior genotypes of segregating population from recombination breeding programme.

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