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Research Note

Genetic parameters for grain yield and its component characters in rice

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Abstract:
Thirty eight rice genotypes were evaluated at Field Experimentation Centre, Department of Genetics and Plant Breeding, Allahabad School of Agriculture, SHIATS, Allahabad in Randomized block design with three replications during *kharif-2009*. The experiment was conducted to study the 12 quantitative traits to examine the nature and magnitude of variability, heritability and genetic advance. The mean sum of square for all the 12 characters were significant indicating the presence of substantial amount of variability. High estimates of heritability coupled with high genetic advance as per cent of mean was observed for harvest index (99.66, 78.57) followed by number of spikelets per panicle (99.66, 69.05), number of panicles per hill (99.61, 53.56) and number of tillers per hill (99.81, 51.68). High estimates of heritability coupled with moderate genetic advance as per cent of mean was observed for flag leaf width (65.17, 20.33) followed by days to 50% flowering (99.30, 22.54), panicle length (97.30, 31.32) and biological yield per hill (99.97, 34.59).

Key words:
Rice, GCV, PCV, heritability and genetic advance

A systematic evaluation and characterization of germplasm lines helps in identification of superior genotypes. Characterization of accessions provides the information on morphological and agronomic aspects of the material that is essential for the gene bank management. 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. Heritability coupled with genetic advance would be more useful tool in predicting the resultant effect in selection of the 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 various rice germplasm accessions.

A field experiment was conducted with thirty eight rice genotypes during *kharif* 2009 at the Field Experimentation Centre, Allahabad School of Agriculture, SHIATS, Allahabad in Randomized block design with three replications. Twenty five days old seedlings were transplanted with a spacing of 20 cm and 15 cm between rows and hills, respectively. Five representative hills for each genotype in each replication were randomly selected to record the observations for eleven quantitative traits. In this, the days to 50% flowering was 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), phenotypic and genotypic coefficient of variation, heritability (Broad sense) and genetic advance as per cent of mean were estimated by the formula as suggested by Burton (1952) and Johanson *et al.* (1955).

The analysis of variance indicated the existence of highly significant differences among genotypes for all the characters studied except flag leaf width (Table 1). Less variation for flag leaf width has also been earlier reported by Devi *et al*. (2006) and Yadav *et al*. (2008). A wide range of variability was exhibited by most of the traits under study (Table 2). Phenotypic variance was higher than the genotypic variances for all the characters indicated the influences of environmental factors on these traits. Similar findings were earlier reported by Singh & Chakraborty (1996), Devi *et al.* (2006). High genotypic and phenotypic variances were exhibited by number of spikelets per panicle (5182.62 and

5184.90) followed by biological yield per hill (642.66 and 644.01), plant height (458.41 and 459.85) and days to 50% flowering (117.05 and 117.87). Similar findings were earlier reported by Sawant *et al.* (1994), Deb Choudhari and Das (1998) and Padmaja *et al.* (2008). Coefficient of variation studies indicated that the magnitude of phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters studied, indicating that these characters were less influenced by environment. The PCV and GCV were high for biological yield per hill (65.47 and 65.40) followed by grain yield per hill (48.70 and 48.63), harvest index (38.27 and 38.20) and number of spikelets per panicle (33.53 and 33.52). The lowest PCV and GCV were observed for days to 50% flowering (11.02 and 10.98) followed by flag leaf width (15.14 and 12.22) and panicle length (15.62 and 15.41). Low PCV and GCV values for these traits were also reported by Shivani and Reddy (2000) and Devi *et al.* (2006). 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. Heritability (Broad sense) ranged from 65.17 (flag leaf width) to 99.98 (test weight). The above results were also reported by Shivani and Reddy (2000), Devi *et al.* (2006) and Yadav *et al*. (2008). Maximum and minimum genetic advance (as per cent of mean) was recorded by harvest index (78.57) and flag leaf width (20.33), respectively High estimates of heritability coupled with high genetic advance as per cent of mean was observed for harvest index (99.66, 78.57) followed by number of spikelets per panicle (99.66, 69.05), number of panicles per hill (99.61, 53.56) and number of tillers per hill (99.81, 51.68). High estimates of heritability coupled with moderate genetic advance as per cent of mean was observed for flag leaf width (65.17, 20.33) followed by days to 50 per cent flowering (99.30, 22.54), panicle length (97.30, 31.32) and biological yield per hill (99.97, 34.59). Thus it is interpreted that the characters which showed high heritability with high genetic advance are controlled by additive gene action (Panse and Sukhatme, 1967) 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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Table 1. Analysis of variance for various quantitative characters in rice

Characters	Mean Sum of Square		
	Replications df = 2	Treatments df = 37	Error df = 74
Days to 50% flowering	0.27	351.97**	0.82
Plant height (cm)	0.53	1376.68**	1.44
Tillers per hill	0.00	72.36**	0.04
Panicles per hill	0.03	66.20**	0.08
Flag leaf length (cm)	0.17	190.69**	0.33
Flag leaf width (cm)	0.21	0.12	0.01
Panicle length (cm)	0.78	52.20**	0.47
Spikelets per panicle	0.27	15550.16**	2.28
Biological yield per hill (g)	1.56	1929.34**	1.34
Harvest index	0.74	443.70**	0.49
Test weight (g)	0.00	55.31**	0.00
Grain yield per hill (g)	0.09	86.04**	0.08

**significant at 0.01 level of significance

Table 2. Variability parameters for various quantitative characters in rice germplasm

Characters	VP	VG	PCV (per cent)	GCV (per cent)	Haritability (bs) per cent	Genetic advance as per cent of mean
Days to 50% flowering	117.87	117.05	11.02	10.98	99.30	22.54
Plant height (cm)	459.85	458.41	17.05	17.02	99.69	35.02
Tillers per hill	24.15	24.10	25.13	25.11	99.81	51.68
Panicles per hill	22.12	22.04	26.10	26.05	99.61	53.56
Flag leaf length (cm)	63.78	63.45	21.56	21.50	99.47	44.18
Flag leaf width (cm)	0.05	0.03	15.14	12.22	65.17	20.33
Panicle length (cm)	17.72	17.24	15.62	15.41	97.30	31.32
Spikelets per panicle	5184.90	5182.62	33.53	33.52	99.96	69.05
Biological yield per hill (g)	644.01	642.66	65.47	65.40	99.79	34.59
Harvest index	148.23	147.73	38.27	38.20	99.66	78.57
Test weight (g)	18.44	18.43	20.61	20.61	99.98	42.45
Grain yield per hill (g)	28.73	28.65	48.70	48.63	99.72	40.04