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Assessment of Genetic Parameters for Yield and Yield Components in Hybrid Rice and Parents

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Abstract

Thirty F_1 rice hybrids along with complete set of 13 parents and checks were evaluated for variability, heritability and genetic advance in different yield and yield contributing traits. The data was recorded on five randomly selected plants for fifteen quantitative characters. The treatment, i.e. mean sum of squares due to genotypes showed significant differences for 14 characters studied, indicating the presence of high genetic variability among the genotypes. The estimates of GCV were lower than the respective PCV, indicating the influence of environmental factors on the expression of the traits studied. Characters like percent pollen fertility (99.9, 33.33), grain yield hill^{-1} (99.2, 31.13), harvest index (98.5, 30.42) and number of filled grains panicle^{-1} (97.8, 30.04) showed high heritability coupled with moderate genetic advance as percent of mean, suggesting that selection for the improvement of these characters may be rewarding. This also indicates greater role of non-additive gene action in their inheritance suggesting heterosis breeding could be used to improve these traits.

Background

In a rice improvement programme, it is the Germplasm, which virtually determine the success and nature of end product. The development of superior rice population involved the intelligent use of available genetic variability both indigenous as well as exotic to cater the need of various farming situations of rice. The grain yield is the primary trait targeted for improvement of rice productivity in both favourable and unfavourable environments from its present level. Knowledge on the genetic architecture of genotypes is necessary to formulate efficient breeding methodology. It is essential to find out the relative magnitude of additive and non additive genetic variances, heritability and genetic gain with regard to the characters of concern to the breeder. The systematic breeding programme involves the steps like creating genetic variability, practicing selection and utilization of selected genotypes to evolve promising varieties. The large spectrum genetic variability in segregating populations depends on the level of genetic diversity among genotypes offer better scope for selection. Heritability and genetic advance are other important selection parameters. The estimates of heritability help the plant breeder in determining the character for which selection would be rewarding. The breeders are interested in selection of superior genotypes based on their phenotypic expression. The major function of heritability estimates is to provide information on transmission of characters from the parents to the progeny. Heritability estimates can anticipate improvement by selection of useful characters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. Therefore, estimates of GCV, PCV, heritability and genetic advance will play an important role in exploiting future research projections of rice improvement.

Methodology

Thirty F1 hybrids along with complete set of thirteen parents (3 CMS and 10 restorers) and three standard checks (one local, one national and one hybrid) were evaluated during Kharif '2012 in RBD with three replications under optimal crop management practices at the field experimentation centre, Department of Genetics and Plant Breeding, SHIATS, Allahabad. The spacing was kept at row-row 20 cm and plant-plant 15 cm. In order to obtain information on the three CMS-lines, their respective maintainer lines were grown, as A-line and B-line are isogenic line except for male sterility. The data was recorded on five randomly selected plants from each replication for fifteen quantitative characters viz. Days to 50% flowering, number of tillers hill-1, number of panicles hill-1, flag leaf length (cm), flag leaf width (cm), plant height (cm), panicle length (cm), number of spikelet's panicle-1, number of filled grains panicle-1, percent pollen fertility, percent spikelet fertility, grain yield hill-1 (g), biological yield hill-1 (g), harvest index (%) and test weight (g) and the averages were used for analysis. The data recorded on the above fifteen characters were subjected to the following statistical analysis: Analysis of variance (ANOVA) [1], Variance and Co-efficient of Variance [2], Heritability (Broad sense) [3], and Genetic Advance [4,5].

Results and Discussions

The mean sum of squares due to genotypes showed significant differences for 14 characters studied among 46 genotypes (Table 1), indicating the presence of high genetic variability among the genotypes. This would prove to be beneficial for improvement of the crop as reported in rice by Reddy and De [6] and Singh et al. [7]. The significant differences among the genotypes studied suggest that variability can be further utilized in crop improvement programme.

The estimates of genetic parameters including co-efficient of variation, heritability and genetic advance deserve attention in deciding selection criteria for improvement in the concerned characters.

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The estimates of genotypic coefficient of variation (GCV) were lower than the respective phenotypic coefficient of variation (PCV) (Table 2), indicating the influence of environmental factors on the expression of the traits studied which are in agreement with the findings of Chaubey and Singh [8].

PCV was found to be highest in percent pollen fertility (16.20) followed by grain yield hill-1 (15.23), harvest index (14.99) and number of filled grains panicle-1 (14.91). While biological yield hill-1 had the least PCV value (4.30) which was significantly differed by test weight (4.64), panicle length (4.71) and number of spikelets panicle-1 (4.99). Similarly, GCV was found to be highest in percent pollen fertility (16.19) followed by grain yield hill-1 (15.17), harvest index (14.88) and number of filled grains panicle-1

(14.75). But panicle length had the least GCV value (2.63) which was significantly differed by flag leaf width (3.07) and flag leaf length (3.86).

Bidhan et al. [9] also reported high phenotypic and genotypic variances for grain yield, followed by number of filled grains panicle-1. Characters having low values of both GCV and PCV indicated that scope of improvement of these characters by selection was limited.

Genetic co-efficient of variability along with heritability gave an idea of expected genetic gain from selection [2]. Although PCV and GCV is the indicative of the presence of degree of genetic variation, the amount of heritable portion of variation can only be determined with the help of the estimates of heritability and genetic advance. According to Lush [4], heritability (broad sense) is the ratio of genotypic variance to phenotypic variance, expressed in percentage. The estimates of heritability are more advantageous when expressed in terms of genetic advance. Johnson et al. [5] suggested that heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression, without genetic advance the estimates of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability.

A perusal of data on heritability (broad sense) (Table 2) depicted that heritability estimates (%) for 15 quantitative traits under study ranged from 17.9% to 99.9%. Percent pollen fertility (99.9%) showed the highest value of heritability which was statistically at par with percent spikelet fertility (99.4%) and grain yield hill-1 (99.2%), followed by harvest index (98.5%), number of filled grains panicle-1 (97.8%), and plant height (96.4%). Least value was observed in number of panicles hill-1 (17.9%) followed by flag leaf width (22.0%) and panicle length (31.0%). High heritability for grain yield and filled grains panicle-1 was also reported by Panwar [10], Kumar et al. [11], Chaurasia et al. [12] and Kumar et al. [13].

A perusal of data on genetic advance as percent of mean (Table 2) for all the quantitative and qualitative characters under study ranged from

| Sl. no | Characters: | Mean sum of squares | | |
		Replication (d.f.= 2)	Genotypes (d.f.= 45)	Error (d.f.= 90)
1	Days to 50% flowering	5.68	81.69**	1.57
2	Number of tillers hill-1	0.59	6.68*	1.60
3	Number of panicles hill-1	1.27	2.69*	1.62
4	Flag leaf length	0.31	5.17*	1.05
5	Flag leaf width	0.02	0.01	0.01
6	Plant height	1.21	210.71**	2.61
7	Panicle length	0.16	2.46*	1.05
8	Number of spikelet's panicle-1	8.92	131.96**	12.66
9	Number of filled grains panicle-1	6.35	1070.39**	8.12
10	Percent pollen fertility	0.54	565.39**	0.23
11	Percent spikelet fertility	0.53	446.66**	0.88
12	Grain yield hill-1	0.23	65.02**	0.17
13	Biological yield hill-1	1.16	13.40**	0.46
14	Harvest index	1.79	242.90**	1.22
15	Test weight	0.46	2.55*	0.21

Mean sum of squares for 15 characters studied in 46 rice genotypes

Table 1: Mean sum of squares for 15 characters studied in 46 rice genotypes.

| Sl. no. | Characters | Variance | | | GCV | PCV | h²(b.s.) (%) | GA as % of mean (5%) |
		$\sigma^2 g$	$\sigma^2 p$	$\sigma^2 e$				
1	Days to 50% flowering	26.71	28.28	1.57	5.80	5.97	94.4	11.61
2	Number of tillers hill-1	1.70	3.29	1.60	8.03	11.20	51.4	11.85
3	Number of panicles hill-1	0.35	1.98	1.62	4.27	10.09	17.9	3.72
4	Flag leaf length	1.37	2.42	1.05	3.86	5.13	56.7	5.99
5	Flag leaf width	0.002	0.007	0.005	3.07	6.55	22.0	2.97
6	Plant height	69.37	71.98	2.61	7.39	7.53	96.4	14.94
7	Panicle length	0.47	1.52	1.05	2.63	4.71	31.0	3.01
8	Number of spikelets panicle-1	39.77	52.43	12.66	4.34	4.99	75.9	7.79
9	Number of filled grains panicle-1	354.09	362.21	8.12	14.75	14.91	97.8	30.04
10	Percent pollen fertility	188.39	188.61	0.23	16.19	16.20	99.9	33.33
11	Percent spikelet fertility	148.60	149.47	0.88	13.88	13.92	99.4	28.51
12	Grain yield hill-1	21.62	21.79	0.17	15.17	15.23	99.2	31.13
13	Biological yield hill-1	4.31	4.78	0.46	4.09	4.30	90.3	8.00
14	Harvest index	80.56	81.78	1.22	14.88	14.99	98.5	30.42
15	Test weight	0.78	0.99	0.21	4.13	4.64	79.2	7.56

* $\sigma^2 g$ = Genotypic variance; GCV = Genotypic coefficient of variation;
GA = Genetic advance
$\sigma^2 p$ = Phenotypic variance; PCV = Phenotypic coefficient of variation;
$\sigma^2 e$ = Environmental variance; h² (b.s.) = Heritability broad sense;

Table 2: Estimates of genetic parameters for 15 characters in 46 rice genotypes.

2.97% (flag leaf width) to 33.33% (percent pollen fertility) Moderate genetic advance was shown by percent pollen fertility (33.33%), grain yield hill-1 (31.13%), harvest index (30.42%) and number of filled grains panicle-1 (30.04%). Low genetic advance was observed in panicle length (3.01%) and number of panicles hill-1 (3.72%).

Characters like percent pollen fertility (99.9%, 33.33%), grain yield hill-1 (99.2%, 31.13%), harvest index (98.5%, 30.42%) and number of filled grains panicle-1 (97.8%, 30.04%) showed high heritability coupled with moderate genetic advance. Number of panicles hill-1 (17.9%, 3.72%) and flag leaf width (22.0%, 2.97%) showed comparatively low heritability and low genetic advance. High heritability coupled with moderate genetic advance for number of filled grains panicle-1 was also reported by Bidhan et al. [9] and Verma et al. [14]. Elayaraja et al. [15] also reported high heritability associated with moderate genetic advance for number of grains panicle-1 and grain yield plant-1. Vivek et al. [16] also reported high heritability coupled with comparatively high genetic advance for grain yield, followed by harvest index.

Although characters like days to 50% flowering, plant height and biological yield hill-1 had high heritability values, they exhibited less genetic advance as percent of mean, suggesting preponderance of non-additive gene action in the inheritance of these traits. Mehetre et al. [17] also reported high heritability with low genetic advance for days to 50% flowering.

The characters having high heritability coupled with high genetic advance as percent of mean indicated the broad sense of additive gene effects in its inheritance and such characters could be improved by selection [18]. Whereas low heritability and low genetic advance shows non-additive gene action. However, characters showing high values of heritability coupled with moderate genetic advance viz. percent pollen fertility, grain yield hill-1, harvest index and number of filled grains panicle-1 suggest that selection for the improvement of these characters may be rewarding. It also indicates greater role of non-additive gene action in their inheritance suggesting heterosis breeding could be useful for improving these traits.

Acknowledgement

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