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GENETIC ANALYSIS IN RICE (*ORZYA SATIVA*) FOR GRAIN YIELD AND ITS COMPONENT CHARACTERS

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Abstract

The choice of plant breeding methodology for upgrading the yield potential largely depends on the availability of reliable information on the nature and magnitude of gene effects present in the population. The present study was undertaken during 2016-2017 with the objective to study the gene action of grain yield and other important traits in rice using the half diallel technique involving six parents namely ADT 36, ADT 45, BPT5204, ASD 16, ADT 37 and ADT 39. Data from the F_1 generation and parents were analyzed using Hayman (1954) method of diallel analysis. Additional statistics needed for the genetic interpretation indicated that all the traits were controlled by the both additive and non-additive genetic variance. Estimates of genetic component variance due to additive (D) and dominant components (H_1 and H_2) were also significant for all the traits studied. The positive F value and K_D/K_R (>1) indicated the distribution of more dominant alleles for number of productive tillers per plant, plant height, 100 grain weight, number grains per panicle, kernel length, kernel breadth and kernel L/B ratio. The negative value of F and K_D/K_R (<1) indicated the distribution of more recessive alleles for the traits days to 50 per cent flowering, panicle length and grain yield per plant. The potence ratio indicated the presence of over dominance in the inheritance of most of the traits including grain yield per plant except 100 grain weight and kernel breadth. Narrow sense heritability indicated the importance of additive genetic variance in the inheritance of most of traits.

Key words : Half diallel, genetic parameters, narrow sense heritability, rice.

Introduction

The choice of plant breeding methodology for upgrading the yield potential largely depends on the availability of reliable information on the nature and magnitude of gene effects present in the population. Hayman's method of diallel analysis, which provides the estimates of the six components such as D-additive genetic variance, H_1 - dominance variance, H_2-positive and negative gene effect, E-environmental component of variance, F-covariance of additive and dominant effect and h_2-doiminant effect help in understanding the performance of parents used in the cross and in determining the characters. Therefore, the present study was undertaken with the objective to study the gene action of grain yield and other important traits in rice using the half diallel technique involving six parents.

Materials and Methods

Six genotypes of rice namely, ADT 36, ADT 45, BPT 5204, ASD 16, ADT 37 and ADT 39 were mated in a half diallel fashion. The resulting fifteen hybrids were evaluated along with their parents for grain yield and its component characters namely, days to first flowering, plant height, number of productive tillers per plant, panicle length, number of grains per panicle, 100 grain weight, grain length, grain breadth, grain L/B ratio and grain yield per plant were laid out in Randomized Block Design with three replications during July-Oct, 2016. Each entry was grown in a 3 m long single row plot with a spacing of 15 × 20 cm. Observations were recorded on five randomly selected plants in each plot on ten grain yield traits. The genetic parameters were estimated as per Hayman's analysis of diallel crosses (Hayman, 1954).

Results and Discussion

The mean sum of square for combining ability revealed that the GCA variance was significant for all

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the characters studied (table 1). This indicated the presence of additive genetic variance for all the ten characters studied. The SCA variances were also significant for all the ten traits studied. This implied the presence of dominance and non-additive genetic variance in the inheritance of these traits. The results amply revealed the importance of both additive and non additive genetic variance for all the ten traits. However, the ratio of GCA/SCA was more than unity for all the traits including grain yield per plant (Narasimman *et al.*, 2007). This indicated the preponderance of additive genetic variance in the improvement of the traits of interest. This was in conformity with the findings of Thirugnana *et al.* (2008), Veeresha *et al.* (2013) and Upadhyay *et al.* (2015).

Estimates of genetic component variance due to additive (D) component and the dominant components ($\$_1$ and $\$_2$) were significant for all the ten traits studied (table 2). Hence, the genetic components of variance *viz.*, D, $\hat{H}_1$ and $\hat{H}_2$ suggested the importance of both additive and dominant genes for all the traits of interest. This was also supported by the significance of both GCA and SCA variances for all the traits studied. The additive and non-additive gene effect may be exploited following inter mating among the progenies within and between promising crosses in early segregating generations. The positive F value and the ratio of K_D/K_R (more than unity) suggested the distribution of more dominant alleles for almost all the traits except days to 50 per cent flowering, panicle length, and grain yield per plant. The negative value of F component and the ratio of K_D/K_R (less than unity) indicated the distribution of more recessive alleles for the traits days to 50 per cent flowering, panicle length, and grain yield per plant.

The environment effect (E) was non-significant for almost all the traits studied. The potence ratio $(\hat{H}_1/D)^{1/2}$ was more than unity, indicating the presence of over dominance in the inheritance of all the traits including grain yield per plant except 100 grain weight and kernel breadth. The ratio of $\hat{H}_2/4\hat{H}_1$ was less than 0.25 for all the ten traits studied. This indicated the unequal allelic frequency or asymmetrical distribution of positive and negative genes in the parents at the loci exhibiting dominance. The ratio of $\hat{h}^2/\hat{H}_2$ was less than one for almost all the traits studied except days to 50 per cent flowering, number of grains per panicle and grain yield per plant. This revealed that seven traits were found to be under the control of at least single group of genes.

Table 1 : Analysis of variance for combining ability for ten different characters.

Source of variation	Degrees of freedom (df)	Mean Sum of Squares									
		Days to 50 per cent flowering	Number of productive tillers per plant	Plant height	Panicle length	Number of grains per panicle	100 grain weight	Grain yield per plant	Kernel length	Kernel breadth	Kernel L/B ratio
GCA	5	47.68**	46.15**	350.16**	46.19**	690.92**	0.31**	34.74**	0.20**	0.15**	0.22**
SCA	15	13.24**	7.20**	102.75**	6.03**	166.29**	0.02**	12.2**	0.05**	0.02**	0.05**
Error	40	0.22	0.03	0.74	0.10	1.33	0.001	0.12	0.001	0.001	0.001
GCA/SCA	-	3.60	6.40	3.40	7.66	4.15	15.5	2.84	4.00	7.5	4.4

* Significant at 5 percent level. ** Significant at 1 percent level.

Table 2 : Estimates of genetic components and their ratios for ten characters studied.

Traits Genetic components	Days to 50 per cent flowering	Number of productive tillers per plant	Plant height	Panicle length	Number of grains per panicle
D	12.88 ± 4.92**	22.72 ± 3.98**	141.86 ± 66.89*	15.74 ± 2.18**	410.08 ± 53.26**
F	-5.20 ± 12.02	6.16 ± 9.71	2.36 ± 163.40	-4.26 ± 5.32	197.4 ± 130.12
H_1	50.9 ± 12.49**	30.06 ± 10.09**	438.35 ± 169.80**	24.90 ± 5.52**	641.33 ± 135.21**
H_2	38.61 ± 11.16**	21.25 ± 9.02*	376.65 ± 151.68*	17.60 ± 4.93**	493.95 ± 120.79**
h^2	43.70 ± 7.51**	17.64 ± 6.07**	9.97 ± 102.09	14.93 ± 3.32**	549.89 ± 81.30**
E	0.2 7± 1.86	0.06 ± 1.50	0.74 ± 25.28	0.13 ± 0.82	1.35 ± 20.13
(H_1/D) ½	1.99	1.15	1.76	1.26	1.25
$H_2/4H_1$	0.19	0.18	0.21	0.18	0.19
K_D/K_R	0.82	1.27	1.01	0.81	1.48
h^2/H2	1.13	0.83	0.03	0.85	1.11
h(ns)%	60.54	70.25	51.46	75.09	59.05

Table 2 contd…

Traits Genetic components	100 grain weight	Grain yield per plant	Kernel length	Kernel breadth	Kernel L/B ratio
D	0.17 ± 0.01**	6.64 ± 5.69	0.17 ± 0.02**	0.10 ± 0.02**	0.14 ± 0.03**
F	0.04 ± 0.02**	-4.05 ± 13.91	0.12 ± 0.04**	0.06 ± 0.04	0.07 ± 0.09
H_1	0.08 ± 0.02**	46.31 ± 14.46**	0.21 ± 0.04**	0.10 ± 0.04*	0.23 ± 0.09**
H_2	0.06 ± 0.01**	32.73 ± 12.91**	0.18 ± 0.04**	0.07 ± 0.04*	0.19 ± 0.08*
h^2	0.05 ± 0.01	53.69 ± 8.69**	0.09 ± 0.02	0.01 ± 0.02	0.06 ± 0.05
E	0.001 ± 0.002	0.14 ± 2.15*	0.001 ± 0.01	0.001 ± 0.01	0.00 ± 0.07
$(H_1/D)^{½}$	0.69	2.64	1.10	0.99	1.26
$H_2/4H_1$	0.19	0.18	0.21	0.18	0.21
K_D/K_R	1.42	0.79	1.95	1.75	1.49
h^2/H_2	0.77	1.64	0.48	0.13	0.30
h(ns) %	81.72	59.33	46.38	65.47	53.26

Days to 50 per cent flowering, number of grains per panicle, and grain yield per plant were found to be under the control more than one group of genes. The narrow sense heritability was always higher for almost all the traits including grain yield per plant. This indicated the importance of additive genetic variance in the inheritance of all these traits. This suggested that the individual genotype can be evaluated readily from their phenotypic expression. Simple selection would be more effective in the sets of materials exhibiting greater additive genetic variability and desirable mean performance. Present study revealed the importance of both additive and non-additive gene action in the improvement of grain yield traits. In such case, simple pure line selection or modified pedigree selection may not be possible. Hence, improvement can be expected by delaying the selection to later segregeating generations, when the dominance and epistatic interactions disappear and resorting to intermating of superior segregants followed by recurrent selection (Frey, 1984; Hallaure, 1986; Delogu *et al*., 1988). Diallel selective mating system can also be adopted (Jenson, 1970). In the presence of over dominance, the best scheme to develop hybrids would be reciprocal recurrent selection.

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