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Short Communication

Recombination Breeding in Rice (*Oryza sativa* L.)

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Key words**:** Rice, Combining ability, Heterosis, Recombination breeding

Rice (*Oryza sativa* L.) is the staple food for most of the Asians. Rice is cultivated in almost all the continents except Antarctica. Rice is produced in 44 million hectares in India, with the production 117.47 million tones. In Tamil Nadu it is cultivated in 17.21 lakh hectares, with the production of 61.32 lakh million toners [1]. The rural peoples are struggling for one square of food and urban peoples are two squares of food. This may be due to the low absorption and may be due to low purchasing power. Hence, it becomes imperative to augment the rice production to meet out the need in a sustainable manner at low cost. Studies on combining ability and heterosis in rice is important to identify to potential parents, to achieve efficient recombinants. In the present investigation, an attempt was made to identify superior parents of effect hybridization and excavate the better recombinants through the estimation of specific combining ability coupled with high heterosis for yield and yield component traits.

Six rice genotypes viz., ADT 37, ADT 43, ADT 45, ASD 16, CO 51 and CO 47 were matted in 6×6 full diallel fashion at the Plant Breeding Farm, Annamalai University, Annamalainagar during, January 2019. Twenty-five days old seedlings of the six parents and their 30 F_1 hybrids were transplanted in two row plots of 3 M length during July, 2019, with a spacing of 20 × 15 cm, in RBD, with three replications. Observations were recorded on five randomly selected plants for the traits viz. X_1: Days to 50 per cent flowering, X_2: Plant height at maturity, X_3: Number of productive tillers per plant, X_4: Panicle length, X_5: Number of filled seeds per panicle, X_6: Seed length, X_7: Seed breadth, X_8: Seed L/B ratio, X_9: Hundred Seed weight and X_{10}: Seed yield per plant. Diallel analysis was performed as per the method outline by [2], method I and model 1. A scoring procedure was adopted, in which, +1 was given to positive significant *gca* and *sca* effects separately and –1 was given to negative significant *gca* and *sca* effects. Negative score was considered as favourable for the traits viz. days to 50 per cent flowering, plant height at maturity and breadth of seeds, as per the method suggested by [3]. Heterosis was estimated using the standard formulae.

The ANOVA indicated significant differences among the genotypes selected for the present inquiry, for all the traits of interest. Hence, further analysis is appropriate (Table 1). Similar results were earlier reported by [4-6].

Table 1 Analysis of variance for ten traits in rice

Source	df	Mean sum of square									
		Days to 50% flowering	Plant height at maturity	No. of productive tillers plant^{-1}	Panicle length	No. of filled seeds panicle^{-1}	Seed length	Seed breadth	Seed L/B ratio	Hundred seed weight	Seed yield plant^{-1}
Replication	2	8.25	0.9611	0.2593	0.5091	2.2089	0.0096	0.0192	0.0240	0.0081	0.3687
Genotype	35	57.9903**	9.7400**	11.4251**	2.0739**	186.0000**	0.8245**	0.0679**	0.1740**	0.0963**	51.7654**
Error	70	9.5545	0.8861	0.6783	0.5075	1.6183	0.0219	0.0188	0.0193	0.0108	0.3611

**Significant at 1 per cent level

The ANOVA for combining ability variance indicated the importance of both GCA and SCA. It may indicate that the traits of interest were controlled by additive dominance and epistatic gene interaction (Table 2). Similar results were also reported by [7-8]. However, the ratio of GCA and SCA indicated the importance of dominance and non-additive epistasis for days to 50 per cent flowering, plant height at maturity and seed breadth. For all other traits the importance of additive, additive × additive gene action was evidenced.

Scoring based on *gca* effects of the parents indicated that P_5 was the best general combiner followed by P_3 (Table 3). Similar results was reported by [9-10]. Similarly, scoring based on *sca* effects revealed that the hybrids viz. $P_1 \times P_5$, $P_5 \times P_3$ as well as $P_5 \times P_4$ could be adjudged as best specific combiners (Table 4). These results are in conformity with the earlier findings of [11-15].

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Table 2 Analysis of variances for combining ability effects for ten traits in rice

Source	df	Mean sum of square									
		Days to 50% flowering	Plant height at maturity	No. of productive tillers plant^{-1}	Panicle length	No. of filled seeds panicle^{-1}	Seed length	Seed breadth	Seed L/B ratio	Hundred seed weight	Seed yield plant^{-1}
GCA	5	21.1353^{**}	5.9156^{**}	7.7758^{**}	0.4280^{*}	163.9027^{**}	0.6661^{**}	0.0081	0.0990^{**}	0.0610^{**}	59.4794^{**}
SCA	15	31.0118^{**}	3.3818^{**}	3.4163^{**}	0.7908^{**}	26.9801^{**}	0.3867^{**}	0.0227^{**}	0.0823^{**}	0.0275^{**}	6.2060^{**}
RCA	15	7.0444^{*}	2.2173^{**}	2.8778^{**}	0.6792^{**}	63.0630^{**}	0.0325^{**}	0.0274^{**}	0.0200^{**}	0.0270^{**}	14.2295^{**}
Error	70	3.1848	0.2954	0.2261	0.1692	0.5394	0.0073	0.0063	0.0064	0.0036	0.1204
GCA/SCA	0.33	0.6815	1.7492	2.2760	0.5412	6.0749	1.7225	0.3568	1.2029	2.2181	9.5841
GCA/RCA	0.33	3.0002	2.6679	2.7019	0.6301	2.5990	20.4953	0.2956	4.9500	2.2592	4.1800

*Significant at 5 per cent level; **Significant at 1 per cent level

Table 3 Scoring based on *gca* effects of parents

Parents	Traits										
	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	Total
P_1	0	1	0	0	1	-1	0	-1	1	1	2
P_2	-1	-1	-1	-1	-1	1	0	1	-1	-1	-5
P_3	0	-1	1	1	1	1	0	0	-1	1	3
P_4	-1	0	-1	0	-1	1	0	0	0	-1	-3
P_5	1	-1	1	0	1	1	0	1	1	1	6
P_6	0	0	-1	0	-1	0	0	1	-1	-1	-3

Table 4 Scoring based on *sca* effects of hybrids

S. No.	Hybrids	Traits										
		X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	Total
1	$P_1 \times P_2$	0	1	-1	0	-1	1	1	1	0	0	2
2	$P_2 \times P_1$	-1	0	-1	-1	0	0	0	0	0	1	-2
3	$P_1 \times P_3$	0	0	0	-1	1	1	0	1	0	-1	1
4	$P_3 \times P_1$	0	1	-1	0	-1	0	0	0	0	0	-1
5	$P_1 \times P_4$	-1	0	0	0	0	1	1	1	-1	-1	0
6	$P_4 \times P_1$	-1	1	-1	0	0	1	0	0	-1	-1	-2
7	$P_1 \times P_5$	0	0	1	1	1	1	-1	0	1	1	5
8	$P_5 \times P_1$	0	1	-1	0	1	1	0	0	1	1	4
9	$P_1 \times P_6$	0	-1	0	1	-1	1	0	1	1	0	2
10	$P_6 \times P_1$	0	-1	-1	1	1	1	-1	0	1	1	2
11	$P_2 \times P_3$	1	0	0	0	-1	-1	0	0	1	0	0
12	$P_3 \times P_2$	0	0	-1	0	1	0	0	0	0	-1	-1
13	$P_2 \times P_4$	1	0	0	0	1	0	0	0	0	1	3
14	$P_4 \times P_2$	0	-1	0	0	0	-1	1	0	0	1	0
15	$P_2 \times P_5$	0	0	0	0	1	-1	0	-1	0	-1	-2
16	$P_5 \times P_2$	1	0	0	0	1	0	0	-1	0	0	1
17	$P_2 \times P_6$	0	-1	0	0	1	0	-1	-1	0	1	-1
18	$P_6 \times P_2$	0	-1	0	0	1	0	-1	1	0	0	0
19	$P_3 \times P_4$	0	1	0	0	0	-1	0	-1	0	0	-1
20	$P_4 \times P_3$	0	-1	0	1	0	0	0	0	0	1	1
21	$P_3 \times P_5$	1	0	1	0	0	-1	0	0	1	1	3
22	$P_5 \times P_3$	0	-1	1	1	1	0	1	0	1	1	5
23	$P_3 \times P_6$	0	0	1	1	-1	-1	0	0	0	1	1
24	$P_6 \times P_3$	0	-1	0	1	0	0	0	-1	0	-1	-2
25	$P_4 \times P_5$	0	-1	0	0	-1	-1	1	0	-1	-1	-4
26	$P_5 \times P_4$	0	0	1	1	1	1	0	0	1	0	5
27	$P_4 \times P_6$	0	0	0	0	1	0	0	0	0	1	2
28	$P_6 \times P_4$	0	-1	0	0	0	0	0	0	0	0	-1
29	$P_5 \times P_6$	0	0	0	-1	-1	-1	0	0	0	-1	-4
30	$P_6 \times P_5$	0	0	-1	0	-1	0	0	0	0	-1	-3

Table 5 Performance of the parents and hybrids based on mean, *gca*, *sca* effects and standard heterosis

Best parents based on mean	*gca* effects	Best hybrid based on mean	*sca* effects	*gca* effects of the parents	d_{iii}	Common cross
P_5	NS	$P_1 \times P_5$	+S	H × H	$P_1 \times P_5$	$P_1 \times P_5$
P_1	+S	$P_3 \times P_5$	+S	H × H	$P_3 \times P_5$	$P_3 \times P_5$
P_3	+S	$P_5 \times P_3$	+S	H × H	$P_5 \times P_3$	$P_5 \times P_3$

The performance of parents as well as hybrids based on mean, combining ability effects and standard heterosis is furnished in (Table 5). Similar observations have been reported earlier by [16-19]. It indicated that superior hybrids based on mean also best specific combiners their parents were best general combiners. The standard heterosis was also high with these hybrids. The result amply indicated the importance of non-additive gene action in the expression of the traits in interest. Selection may be postponed to later segregating generations.

SUMMARY

Combining ability and heterosis were estimated involving six parents and their 30 F_1 hybrids (evolved through full diallel matting). Based on the score made on *gca* effects, the parents viz., P_5 and P_3 were adjudged as potential parents. The hybrid viz., $P_1 \times P_5$, $P_5 \times P_3$ and $P_5 \times P_4$ were culled out as potential filials. Both dominance and epistasis were found to control the expression of all the traits of interest. Selection may be made on the later segregating generations.

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