Combining ability analysis for identifying elite parents for heterotic rice hybrids

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ABSTRACT

Seventy six hybrids developed from four CMS lines and nineteen restorers along with parents were evaluated for nine quantitative traits to elucidate the nature of gene action present in the inheritance of important quantitative traits. Preponderance of additive gene action was observed for days to 50 per cent flowering, panicle length, and productive tillers per plant while, predominance of non-additive gene action for plant height, panicle weight, spikelet-fertility percentage, number of filled grains per panicle, 1000 grain weight and grain yield per plant. IR 68897A and IR 79156A among the lines and RPHR 1096, RPHR 1005, RPHR 111-3 and BCW-56 among the testers were found to be good general combiners as they could contribute alleles with positive effect for improving the important quantitative traits. IR 68897A x RPHR 641-1, APMS 6A x RPHR 612-1, IR 79156A x EPLT-104 and IR 68897A x RPHR 111-3 were identified as the most promising.

Key words: rice, combining ability, Line x tester, cytoplasmic genetic male sterile, lines

INTRODUCTION

In the first phase of the hybrid rice breeding programme in India, CMS lines developed by International Rice Research Institute (IRRI) were extensively utilized to develop the hybrids, while continuing to work on development of indigenous parental lines. As a result hybrids were developed utilizing indigenous CMS lines as well as restorer lines, yielding significantly higher than the first generation hybrids and with better grain quality. At Directorate of Rice Research, Hyderabad, a new set of restores in new plant type (NPT) background were developed for use in the hybrid rice breeding programme. In this paper, we report the results of combining ability studies involving nineteen restore lines (in NPT background) and four CMS lines using line x tester analysis.

MATERIALS AND METHODS

The experimental material comprised a set of seventy six crosses (F1's) developed from four stable CMS lines viz., APMS 6A, IR 58025A, IR 68897A and IR 79156A from wild abortive source and nineteen elite, diverse and identified restorer lines. The hybrids were evaluated along with parents and four standard checks viz., PA-6201, KRH-2, DRRH-2 and Jaya in a randomized block design with two replications at three locations viz., Warangal, Kampasagar and Hyderabad of Andhra Pradesh during wet season 2008 under irrigated condition. Each entry raised in three rows of each measuring 1.8 m and plant spacing of 20cm. x 15cm. Standard agronomic practices were followed while raising the crop at all the locations. Observations were recorded on five randomly selected plants for plant height, panicle weight, panicle length, productive tillers plant[-1], spikelet fertility, number of filled grains panicle[-1], 1000 grain weight and grain yield plant[-1] whereas days to 50% flowering was recorded on plot basis. Based on pooled values, combining ability analysis was carried out following the method as suggested by Kempthorne (1957).

RESULTS AND DISCUSSION

Pooled analysis of variance indicated highly significant mean square for all the characters due to parents, crosses, interaction between parents vs. crosses, crosses x environment indicating wide differences among the parental lines and hybrids and differential expression of these genotypes over environments. The interaction due to lines x testers was significant for all the traits indicating the presence of adequate variability

in the experimental material (Table 1). The ratio of general combining ability (gca) to specific combining ability (sca) variances revealed the presence of both additive as well as non-additive gene actions. The variance ratio showed preponderance of additive gene action for days to 50 per cent flowering, panicle length and productive tillers plant^{-1} suggested that these traits

The selection of parents with good general combining ability (gca) effects is a prime requisite for a successful breeding programme, especially hybrid breeding. The characterwise estimation of gca effects of lines and testers revealed that the parents IR 68897A, RPHR 774 and RWC-15 were good general combiners for earliness while, the parents APMS 6A, IR 58025A,

Table 1.   Pooled analysis of variance for combining ability (LXT) for yield and yield components in rice

	d.f	Mean sum of squares								
		Days to 50% Flowering	Plant Height	Panicle length	Panicle Weight	Productive tillers plant^{-1}	Spikelet Fertility %	Filled Grain Panicle^{-1}	1000 Grain Weight	Grain Yield Plant^{-1}
Locations	2	53.97**	13818.24**	30.47**	24.86**	171.83**	704.63**	14526.95**	82.87**	176.66**
Replications x locations	2	3.81	4.44	1.88	0.75*	0.15	11.31	361.54	4.60	4.12
Treatments	98	109.53**	528.53**	19.62**	3.16**	5.20**	127.58**	7096.55**	27.18**	220.37**
Parents	22	110.83**	890.10**	19.35**	2.42**	3.57**	128.82**	6313.57**	49.09**	40.21**
Parent vs. Hybrids	1	2788.78**	2966.76**	888.67**	114.39**	58.41**	167.17**	149022.35**	277.76**	11392.83**
Hybrids	75	73.42**	389.96**	8.12**	1.90**	4.97**	126.69**	5433.88**	17.41**	124.26**
Lines	3	592.56**	1288.23**	45.00**	3.04	57.34**	4.44	27506.04**	91.84**	96.15
Testers	18	126.91**	1063.81**	15.60**	3.67**	3.61	188.81	9239.46**	26.05**	180.50
Line x Tester	54	26.75**	115.44**	3.57**	1.24**	2.52**	112.78**	2939.12**	10.40**	107.07**
Parents x Locations	44	6.92**	60.46**	0.61	0.35**	1.98**	29.12**	326.38**	3.13*	4.92
(Parent vs. Cross) X Locations	2	137.27**	22.73	3.17*	1.45**	12.57**	11.57	253.00	2.94	152.37**
Crosses x Locations	150	8.91**	50.61**	2.67**	0.71**	3.97**	55.46**	1381.70**	6.42**	64.46**
Lines x Locations	6	16.52*	36.75	6.30*	3.24**	26.70**	126.25*	4369.16**	17.06**	197.18**
Testers x Locations	36	16.67**	74.61*	3.22	0.71	3.16	62.27	1722.56*	6.99	73.17
LinesxTesters x Locations	108	5.90**	43.38**	2.29**	0.57**	2.97**	49.26**	1102.11**	5.65**	54.18**
Error	294	1.72	12.21	1.00	0.19	0.75	6.70	132.01	2.18	6.82
σ²gca		5.18	16.84	0.42	0.04	0.43	1.28	263.96	0.81	1.88
σ²sca		4.13	16.96	0.39	0.17	0.28	17.46	463.31	1.27	16.43
σ²gca/ σ²sca		1.25	0.99	1.06	0.26	1.50	0.07	0.56	0.63	0.11

*and **- Significant at 5 and 1 per cent probability levels, respectively

can be improved by transgressive breeding. Sanjeevkumar *et al.* (2007) for days to fifty per cent flowering Sarma *et al.* (2007) and Swain *et al.* (2003) for plant height and Gnanasekharan *et al.* (2007) for productive tillers plant^{-1} reported similar results was observed. The predominance of non-additive gene action for plant height, panicle weight, spikelet-fertility percentage, number of filled grains panicle^{-1}, 1000 grain weight and grain yield plant^{-1}. This is in agreement with earlier reports (Banumathy *et al.,* 2003, Bisine and Motiramani, 2005). The heterosis breeding could be a better option for improving these traits.

RPHR 1096, RPHR 111-3 and BCW-56 were better general combiners for late flowering. The parental lines IR58025A, IR 68897A, RPHR 1124, SG-22-289-3, IR 63879, IR 65515 and RPHR 774 appeared to be good general combiners for dwarfness.

The parental lines IR 79156A and RPHR 111-3 had the highest gca effects for panicle length while, APMS 6A and RPHR 111-3 for panicle weight. In respect of number of productive tillers plant^{-1} IR 68897A, IR 79156A and RPHR 612-1 exhibited significant positive gca effects. The parents such as

RPHR 1009, IR 63879, IR 65515, BCW-56 and 3699-R for spikelet fertility percentage, APMS 6A, RPHR 1005, RPHR 111-3, RPHR 1009 and 3699-R for number of filled grains panicle^{-1}, IR 68897A, RPHR 641-1, IR 65515, BCW-56 and RPHR 774 for 1000 grain weight recorded significant positive gca effect. Based on gca effects the male parents RPHR 619-2,

111-3 (5.14), IR 58025A x RPHR 1009 (4.65), IR 79156A x RPHR 1005 (4.21), IR 79156A x RPHR 1009 (3.79), IR68897A x RPHR 619-2 (3.62), IR 79156A x IR 65515 (3.60), IR 58025A x RWC-15 (3.56), IR 68897A x RPHR 1096 (3.30), IR 58025A x RPHR 111-3 (2.08) and IR 68897A x IR 63879 (1.94).

Table 2. General combining ability (gca) effects of parents for grain yield associated traits in rice

LINES	Days to 50% flowering	Plant height	Panicle length	Panicle weight	Productive tillers	Spikelet fertility %	Filled grains	1000 grain weight	Grain yield plant^{-1}
APMS6A	1.62**	2.75**	-0.61**	0.19**	-1.04**	-0.01	19.28**	-1.01**	-1.16**
IR-58025A	1.39**	-3.35**	-0.44**	0.06	0.17*	0.24	4.42**	-0.34*	-0.14
IR-68897A	-3.30**	-2.44**	0.33**	-0.19**	0.51**	-0.24	-16.93**	1.10**	1.05**
IR-79156A	0.28*	3.03**	0.71**	-0.06	0.36**	0.02	-6.77**	0.25	0.26
SE(Lines)	0.13	0.34	0.10	0.04	0.08	0.26	1.18	0.15	0.27
TESTERS									
RPHR 619-2	0.49	4.42**	0.71**	0.40**	0.51*	-1.1	4.24	0.6	4.28**
EPLT-104	-0.47	3.50**	0.32	0.49**	-0.16	-2.19**	11.47**	0.3	1.10
RPHR 1124	-1.43**	-8.59**	-1.67**	-0.13	-0.25	-1.42*	3.14	-0.77*	-2.05**
SG-22-289-3	-2.76**	-4.57**	-0.90**	-0.75**	0.01	0.94	-14.07**	-1.12**	-1.45*
RPHR 1096	2.99**	5.02**	0.13	0.17	-0.74*	-0.12	11.35**	-0.68*	1.31*
RPHR 1005	0.82**	-1.65*	-0.67**	0.23*	0.13	-0.25	35.09**	-2.14**	0.94
RPHR 641-1	1.32**	3.89**	0.68**	0.17	0.50**	0.93	-3.34	1.66**	0.32
RPHR 1190-2	0.78**	-3.54**	-0.52*	-0.50**	0.14	-6.91**	-31.52**	0.32	-2.48*
IR 63879	1.12**	-6.47**	-0.32	-0.37**	0.13	3.28**	-17.49**	0.42	0.32
RPHR 111-3	3.82**	12.41**	1.63**	0.67**	-0.13	0.31	31.37**	0.05	5.84**
IR 65515	0.91**	-8.46**	0.22	0.02	0.43*	2.99**	-7.80**	1.26**	-0.51
RPHR 1009	-1.72**	8.88**	0.02	0.36**	0.05	4.94**	29.99**	0.55	0.57
BCW-56	2.20**	9.11**	1.05**	0.45**	-0.14	2.57**	0.21	1.69**	3.50**
RPHR 774	-5.26**	-13.02**	-0.43	-0.53**	-0.71**	-2.19**	-36.25**	1.09**	-6.45**
RWC-15	-2.88**	-3.36**	-1.13**	0.05	-0.58**	0.21	2.58	-0.5	-0.94
PNR-3158	-0.34	1.16	-0.21	-0.23*	0.28	0.12	-10.00**	-1.27**	-1.78**
IR 28142	-1.80**	-0.49	0.03	0.06	0.03	2.92**	12.74**	-1.11**	0.38
RPHR 612-1	2.95**	2.06**	0.16	-0.37**	0.60**	-4.41**	-19.17**	0.05	-0.10
IR 63877	-0.76**	-0.31	0.92**	-0.19	-0.09	-0.62	-2.54	-0.39	-2.80**
SE (Testers)	0.28	0.75	0.22	0.09	0.18	0.57	2.57	0.33	0.59

*and **- Significant at 5 and 1 per cent probability levels, respectively.

RPHR 1096, RPHR 111-3 and BCW-56 were good general combiners for grain yield and exhibited superior gca effects (Table 2).

The top 15 crosses with significant sca effects along with their gca effects of their parents were given (Table 4). The cross combination IR 68897A x RPHR 641-1 showed highest sca value (9.94) for grain yield per plant followed by APMS 6A x RPHR 612-1 (8.46), IR 79156A x EPLT-104 (8.00), IR 68897A x RPHR

These crosses were derived from parents having high, average and low gca effects. The crosses IR 68897A x RPHR 111-3 and IR 68897A x RPHR 619-2 involved parents with high x high gca effects suggesting additive x additive type of gene action. Manuel and Palaniswamy (1989) also reported interaction between positive and positive alleles in crosses involving high x high combiners which can be fixed in subsequent generations if no repulsion phase

Table 3.   Specific combining ability effects of hybrids for nine traits

Cross combination	DFF	Plant height	Panicle length	Panicle weight	Productive tillers	Spikelet fertility %	No.of filled grains panicle^{-1}	1000 grain weight	Grain yield plant^{-1}
IR 68897A x RPHR 641-1	0.16	3.30*	0.85	0.96**	0.42	1.25	46.32**	2.59**	9.94**
APMS 6A x RPHR 612-1	0.04	-2.56	1.20**	0.52**	0.39	6.79**	34.91**	0.92	8.46**
IR 79156A x EPLT-104	1.13*	2.59	0.32	0.43*	0.03	1.00	4.93	-1.07	8.00**
IR 68897A x RPHR 111-3	2.76**	6.91**	0.99**	1.03**	1.25**	0.50	42.60**	-1.08	5.14**
IR 58025A x RPHR 1009	0.60	0.38	0.12	0.02	-0.86*	1.55	16.67**	0.82	4.65**
IR 79156A x RPHR 1005	0.51	3.80*	-0.44	-0.15	-0.09	2.30*	-21.52**	2.82**	4.21**
IR 79156A x BCW-56	-2.70**	-4.35**	-0.21	0.18	0.13	-0.55	3.19	0.24	4.07**
IR 68897A x RPHR1190-2	3.47**	-1.58	0.12	-0.29	-0.30	-6.16**	5.49	-0.60	3.95**
APMS 6A x RPHR 1009	0.21	8.74**	0.49	0.91**	0.16	4.90**	24.23**	-0.85	3.79**
IR 68897A x RPHR 619-2	-0.74	-0.37	0.03	0.45*	0.38	5.60**	35.73**	-1.04	3.62**
IR 79156A x IR65515	5.26**	-3.05*	0.70	0.43*	0.00	0.80	9.51	0.37	3.60**
IR 58025A x RWC-15	0.44	1.62	-1.20*	-0.47*	0.27	-3.26**	-9.24	0.35	3.56**
IR 68897A x RPHR 1096	-1.90**	5.20**	0.42	0.02	0.26	1.09	6.26	-0.85	3.30**
IR 58025A x RPHR 111-3	-0.61	0.09	-0.24	0.02	-0.85*	-0.94	-16.02**	0.92	2.08
IR 68897A x IR 63879	0.14	-0.78	-0.06	0.15	-0.34	-2.47*	-3.41	-0.54	1.94
SE (crosses)	0.57	1.50	0.44	0.18	0.36	1.15	5.15	0.67	1.18

*and **- Significant at 5 and 1 per cent probability levels, respectively

linkages are involved. On the other hand crosses IR 68897A x RPHR 641-1, IR 79156A x BCW-56, IR 68897A x RPHR 1190-2, IR 68897A x RPHR 1096, IR 58025A x RPHR 111-3 and IR 68897A x IR 63879 involved parents with high x low gca effects indicating the involvement of additive x dominance genetic interaction. Peng and Virmani (1990) and Maurya and Singh (1997) also reported about the possibility of interaction between positive alleles from good combiner and negative alleles from poor combiners in high x low crosses and suggested for the exploitation of heterosis in F1 generation as their high yield potential would be unfixable in succeeding generations. In this case with high x low, the expression of high positive sca effects may be due to the dominant and recessive interaction expected to produce desirable segregants in subsequent generations (Lingham, 1961).

The cross combinations IR 79156A x EPLT-104, IR 79156A x IR 65515, APMS 6A x RPHR 612-1, IR 58025A x RPHR 1009, IR 79156A x RPHR 1005, APMS 6A x RPHR 1009 and IR 58025A x RWC-15 involved low x low combining parents indicating over dominance and epistatic interactions. The results clearly indicated that the high performance of hybrid need not be the ones with high sca effect and vice versa. Similar results were also obtained by Peng and Virmani (1990), Anand Kumar et al. (2006). In spite of the involvement

of both poor general combiners in some crosses or one of the parents as poor general combiner, these cross combinations expressed significant sca effects in desirable direction which might be due to interaction between favourable genes contributed by the parents having diverse indica and tropical japonica background. Yield is a cumulative function of various components; the contribution of components for yield is through component compensation mechanism. It was proved in some of the crosses which were characterized by significant positive sca effect for seed yield also exhibit significant positive sca effects for some of the major yield components. For example, the cross combination APMS 6A x RPHR 612-1 showed significant positive sca effects for grain yield per plant along with panicle length, panicle weight, spikelet fertility percentage and filled grains per panicle.

This indicates that the crosses, which are best for yield contributing traits like productive tillers per plant, panicle length, panicle weight, spikelet fertility percentage and 1000 grain weight would also perform well for yield. The per se performance, sca effects of crosses, gca effects of parents and standard heterosis in superior hybrid combinations are presented in (Table 4). The cross combinations which recorded significant heterosis over the best yielding hybrids checks i.e., PA-6201 and KRH-2 also exhibited

Table 4. Per se performance, sca effects and standard heterosis of F₁ hybrids and gca estimates of the parents in rice

Cross combination	Mean performance	STANDARD HETEROSIS		Sca effect	gca female	gca male
		OVER PA-6201	OVER KRH-2			
IR 68897A x RPHR 641-1	37.14	47.78	44.69	9.94**	1.05*	0.32
APMS 6A x RPHR 612-1	33.03	31.44	28.69	8.46**	-1.16*	-0.10
IR 79156A x EPLT-104	35.19	40.05	37.12	8.00**	0.26	1.10
IR 68897A x RPHR 111-3	37.85	50.61	47.46	5.14**	1.05*	5.84**
IR 58025A x RPHR 1009	30.91	22.99	20.42	4.65**	-0.14	0.57
IR 79156A x RPHR 1005	31.24	24.33	21.73	4.21**	0.26	0.94
IR 79156A x BCW-56	33.66	33.95	31.15	4.07**	0.48	3.50*
IR 68897A x RPHR 1190-2	28.35	12.81	10.45	3.95**	1.05*	-2.48*
APMS 6A x RPHR 1009	29.03	15.51	13.09	3.79**	-1.16	0.57
IR 68897A x RPHR 619-2	34.78	38.41	35.51	3.62**	1.05*	4.28*
IR 79156A x IR 65515	29.18	16.10	13.68	3.60**	0.26	-0.51
IR 58025A x RWC-15	28.30	12.62	10.27	3.56**	-0.14	-0.94
IR 68897A x RPHR 1096	31.50	25.33	22.71	3.30**	1.05*	1.31
IR 58025A x RPHR 111-3	33.60	33.72	30.92	2.08	-0.14	5.84**
IR 68897A x IR 63879	29.14	15.94	13.51	1.94	1.05*	0.32

*and **- Significant at 5 and 1 per cent probability levels, respectively.

significant sca effects, as confirmed earlier by Sreeramachandra *et al.* (2000).

Most of these hybrids possessed morphological characters of new plant type (NPT) rice inherited from their male parents thereby offering good scope for developing super rice hybrids with increased yield potential. The present study has helped in identifying and understanding the gene action in inter-subspecific hybrids throwing light on the extent of heterosis and combining ability effects.

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