

Gene Action and Combining Ability Analysis Using CMS Based Hybrid Breeding System in Rice (*Oryza sativa* L.)

SHIV KU. MAHTO*, PARMESHWAR KU. SAHU, VIKASH PRAJAPATI, DEEPAK SHARMA AND P.K. CHANDRAKAR

Department of Genetics and Plant Breeding, IGKVV, Raipur-492012, Chhattisgarh
*email: mahtoshivkumar047@gmail.com

ABSTRACT

Combining ability analysis in rice for hybrid rice breeding programme has been carried out in using L x T mating design with three CMS lines and six testers. The general combining ability of parents and specific combining ability of crosses were estimated for grain yield and its attributes. The ANOVA for combining ability of most traits showed that variances due to treatments, parents, hybrids were highly significant. The SCA variance recorded greater than the GCA variance for grain yield and yield components, suggesting the preponderance of dominance and epistatic gene action in expression of these traits. Among the CMS lines, CRMS31A was identified as a good general combiner for grain yield per plant and most attributing traits followed by CRMS32A. Among the testers R-1162-1667-1-1 was found to be good combiner for grain yield/plant followed by PUSABAS-6(P-1460) and INGER 1-114. Five cross combinations viz., IR79156A/ Improved HMT, CRMS31A/BPT4358, CRMS32A/INGER-1-114, CRMS 31A/R-1162-1667-1-1 and CRMS32A/Pusa Bas-6 (P-1460) were found to be outstanding with respect to grain yield per plant.

Key words Rice, Combining ability, gene action, CMS

Rice, most loved cereal of Asia, feeds the majority of the world's population. To cope up with the ever increasing demand for rice it should be met with quantum jump in production in fixed cultivable area. This is a daunting task, in view of plateauing trend observed in yield potential of high yielding varieties and decreasing and declining natural resource base (Gopikannan and Ganesh, 2013). The rising demand and saturation of cultivable field are likely to cause a supply shortage of rice in future. Hybrid rice technology offers an opportunity to boost the yield of rice. Breeding strategies for developing hybrids with high yield potential and better grain quality require the expected level of heterosis and combining ability. The

successful development of rice hybrids by utilizing the cytoplasmic-genetic male sterility system and fertility restoration system mainly depends upon the availability of stable male sterile lines and economically viable hybrid seed production technology. The success further be hastened by choice of suitable outstanding parents with favorable out-crossing would give heterotic hybrids (Ghosh *et al.*, 2013). The combining ability analysis of parents and their crosses provides information on the components of variance viz., additive and dominance variance or their heterotic hybrids. Combining ability offers a powerful tool for estimating the value of a parent to produce superior hybrids and helpful for selection of better parents for effective breeding programme. Its role is important to decide parents, cross and appropriate breeding procedures to be followed to select desirable segregants (Salgotra *et al.*, 2009) keeping this in view the present investigation was carried out to study the combining ability in order to identify good combiners and superior hybrid combinations.

MATERIALS AND METHOD

The material for the present study comprised 18 F₁s of rice generated by using 3 CMS lines, IR-79156A, CRMS-32A and CRMS-31A and 6 testers R-1162-1667-1-1, PUSA.BAS-6-(P-1460), BPT-4358, INGER1-114, INGER1-134 and IMPROVED HMT through line X tester mating design (Kempthorne, 1957) during *Kharif* season 2012. The resultant 18 F₁s and 9 parents are grown in Randomized Completely Block Design with two replications during *Kharif* 2013 in research cum instructional farm, College of Agriculture, I.G.K.V. Raipur (C.G.). Twenty one days old seedlings of parents were transplanted in crossing block in five rows of one meter length keeping 20 X 15 cm spacing and three CMS lines were transplanted in separate blocks to avoid out crossing with other parents. Single seedlings per hill was transplanted, package of practices were followed.

Table 1. Analysis of Variance (ANOVA) for Line x Tester and combining ability

S V	Df	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Replication	1	82.29	3.49	1.29	0.03	0.31	3.18	11.69	19.03*	33.11**	137.19**	5.56**	12.13*	0.17	0.81	3.61	1.22
Treatment	26	0.79*	14.1**	2.27**	0.01	0.24	0.8*	2.85**	4.22**	3.24*	11.1**	0.4	2.41**	1.82*	0.99	7.16**	1.58*
Parent	8	21.75**	399.9**	14.03**	0.02	83.39**	21.33**	11.59**	3425.81**	3471.01**	4377.8**	610.53**	1784.21**	4.16**	170.3**	116.05**	547.68**
Hybrid	17	10.59**	343.92**	16.13**	0.05**	195.25**	2.68**	12.23**	2324.43**	2186.09**	4638.13**	299.03**	128.92**	41.87**	50.04**	194.54**	94.75**
Parents Hybrid	1	0.34	598.78**	0.37	0.003	55.94**	21.32**	16.32*	872.1**	726.42**	0.43	232.7**	456.12**	57.87**	280.65**	8.5	969.41**
Line	2	24.08**	521.05**	20.73**	0.04	33.08**	3.42*	32.15**	3046.12**	2311.54**	3666.88**	423.23**	15.45*	0.33	13.45**	81.25**	68.56**
Tester	5	6.13**	109.33**	16.24**	0.08**	386.27**	1.88	6.39	4512.42**	2175.19**	6129.78**	517.55**	319.89**	32.13**	99.22**	363.42**	83.76**
Line Tester	10	10.11**	425.79**	15.15**	0.03*	132.19**	2.94**	11.17**	1086.1**	2166.45**	4086.56**	164.92**	56.11**	55.04**	32.77**	132.75**	105.48**
Error	26	0.79	14.08	2.27	0.01	0.24	0.8	2.85	4.22	3.24	11.1	0.4	2.41	1.82	0.99	7.16	1.58
Variance of GCA		0.56	-12.29	0.37	0.003	8.6	-0.032	0.9	299.24	8.54	-54.24	33.94	12.39	-4.31	2.61	9.95	9.95
Variance of SCA		4.66	205.86	6.44	0.01	65.96	1.07	4.16	540.94	1081.6	2037.73	82.26	26.85	26.61	15.89	62.79	62.79
Variance of GCA/Variance of SCA		0.12	-0.06	0.057	0.3	0.13	-0.29	0.216	0.553	0.008	-0.027	0.412	0.461	-0.161	0.164	0.158	0.158

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|--------------------------|-----------------------------------|------------------------------------|--------------------------------|
| 1. Days to 50% flowering | 5. Flag leaf angle (in degree) | 9. No. of sterile spikelet/panicle | 13.1000 grain weight (g) |
| 2. Plant height (cm) | 6. Productive tiller per plant | 10. Total No. of spikelet/panicle | 14. Grain yield per plant (g) |
| 3. Flag leaf length (cm) | 7. Panicle length (cm) | 11. Spikelet fertility (%) | 15. Biological yield/plant (g) |
| 4. Flag leaf width (cm) | 8.No. of fertile spikelet/panicle | 12.pollen fertility (%) | 16. Harvesting index |

Observations were recorded on 5 randomly selected plants in both the replications for eleven character viz. Days to 50% flowering, Plant height, flag leaf length, flag leaf width, flag leaf angle, Productive tiller per plant, panicle length, No. of spikelet per panicle, no of fertile spikelet per panicle, no of sterile spikelet per panicle, spikelet fertility percentage, Pollen fertility percentage, 1000 grain weight, Grain yield per plant, biological yield per plant and harvesting index. The mean data was analyzed for combining ability following the standard method of Kempthorne, 1957.

RESULT AND DISCUSSION

Analysis of variance for yield and different yield contributing characters (Table 1) revealed significant variations for all the characters viz., days to 50% flowering, plant height(cm), productive tiller per plant, panicle length(cm), no. of spikelet per panicle, spikelet fertility percentage, pollen fertility percentage, 1000 grain weight (gm), grain yield per plant(gm), biological yield per plant(gm) and harvesting index (%).The analysis further revealed highly significant differences for most of all the characters among the lines, testers and their hybrids these indicates that they are suitable for combining ability studies. The parents, parent X hybrid are significant for all traits except five traits that revealed good scope for manifestation of heterosis in all the studied traits. These results coincide with the findings of (Jayasudha and Sharma, 2009; Rahimi *et al.*, 2010). Line X Tester analysis is also found significant for all the character, indicated that specific combining ability attributed heavily in the expression of these traits and provide the importance of dominance or non additive variances for all the traits. Several researchers have reported the predominance of dominant gene action for a majority of the yield traits in rice (Faiz *et al.*, 2006).

The GCA variance was found highest for no. of fertile spikelet/panicle (299.24) followed by spikelet fertility percentage (33.94), pollen fertility (%) (12.39) and Biological yield per plant (g) (9.95). The SCA variance was found highest for total number of spikelet/panicle (2037.73) followed by number of sterile spikelet/panicle (1081.6), number of fertile spikelet/panicle (540.94), plant height (205.86), spikelet fertility (82.26), flag leaf angle (65.96), biological yield per plant (gm) (62.79), harvesting index (%) (62.79). Similar

results were also observed by Satyanarayana *et al.*, 2000 and Bisne and Motiramani, 2005. The present results indicate the preponderance of non-additive gene action in the expression of all the traits studied and a very good prospect for the exploitation of non- additive genetic variation for traits through hybrid breeding.

Estimation of GCA effects (Table-2) of lines revealed that CRMS31A (0.63) was identified as a good general combiner for grain yield per plant followed by CRMS32A (0.59). CRMS 31A is also good general combiner for pollen fertility, spikelet fertility, no. of fertile spikelet/panicle, panicle length, plant height and days to 50% flowering. Among the testers R-1162-1667-1-1 (6.04) was found to be good combiner for grain yield per plant and followed by PUSA.BAS-6-(P-1460) (2.3) and INGER-1-114(1.97). Tester R-1162-1667-1-1 was also highly significant for biological yield, harvest index, seed index, spikelet fertility%, no. of fertile spikelet/panicle, total spikelets/ panicle and plant height. The present findings had also been reported earlier by Venkatesan *et al.*, 2007, Dalvi and Patel, 2009, Bagheri and Jelodar, 2010, Saidaiah *et al.*, 2010 and Ghosh *et al.*, 2013.

Specific combining ability (SCA) of a cross is the estimation and the understanding of the effect of non additive gene action for a trait. Non-additive gene action of a trait is an indicator for the selection of a hybrid combination. Therefore, a highly significant SCA effect is desirable for a successful hybrid breeding program. Among the 18 hybrids, 12 hybrids have shown significant SCA effects (Table-3) in which five hybrids have shown the positive significant SCA effects and seven hybrids have shown the negative significant SCA effects for grain yield per plant. The highest positive significant SCA effects have shown by cross IR 79156A /IMPROVED HMT (6.39) followed by CRMS31A/BPT4358 (4.51), CRMS32A/INGER-1-114 (4.02), CRMS 31A/R-1162-1667-1-1 (3.67) and CRMS32A/Pusa Bas-6 (P-1460) (3.09) were found to be outstanding with respect to grain yield per plant. Cross IR 79156A /IMPROVED HMT was also highly significant for pollen fertility, spikelet fertility, no. of fertile spikelet/panicle, plant height and days to 50% flowering. Similar findings were also supported by Bisne and Motiramani, 2005, Sao and Motiramani, 2006, Dalvi and Patel, 2009, Bagheri and Jelodar, 2010, Saidaiah *et al.*, 2010, Mirarab *et al.*, 2011 and Ghosh *et al.*, 2013.

Table 2. General Combining Ability (GCA) effect of different parents for characters under study

Parent	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Line																
IR79156A	-1.42**	4.78**	-1.22**	0.06**	-0.23*	0.36*	1.89**	-10.41**	-9.63**	-20.04**	0.34*	-1.03**	-0.17	-1.22**	0.26	-1.85**
CRMS31A	1.42**	2.73**	-0.17	-0.06**	1.7**	-0.61**	0.94**	18.34**	-6.27**	12.1**	5.76**	1.22**	0.16	0.63*	-2.72**	2.7**
CRMS32A	0	-7.52**	1.39**	0	-1.53**	0.25	-0.95**	-7.93**	15.91**	7.94**	-6.1**	0.19	0.01	0.59*	2.46**	-0.85
SE	0	0.73	0.32	0.02	0.09	0.14	0.32	0.37	0.27	0.35	0.14	0.3	0.25	0.22	0.54	0.26
Testers																
R-11162-1667-1-1	-0.5*	4.4**	0.52	-52	-0.12**	-0.6*	0.86	23.26**	25.46**	48.68**	1.07**	-0.28	4.54**	6.04**	11**	2.77**
PUSA BAS-6-(P-1460)	-0.83**	1.53	-2.01**	-0.02	-6.57**	0.12	1.35*	-18.07**	-14.14**	-32.19**	-0.93**	-1.14*	-1.96**	2.3**	-1.05	5.33**
BPT438	-0.67**	0.59	-1.17*	0.02	-8.18**	-0.01	0.46	18**	-11.12**	7.32**	8.1**	7.61**	-0.87*	-3**	-1.35	-5.1**
INGER 1-114	0.83**	5.19**	-0.89	0.18**	13.69**	0.62*	-0.88	-22.96**	22.71**	-0.39	-15.1**	-5.69**	-0.45	1.97**	6.08**	-0.07
INGER 1-134	1.67**	-3.08*	2.4**	-0.12**	4.23**	0.57*	0.9	31.54**	-17.06**	14.51**	10.87**	9.1**	-0.08	-4.48**	-11.46**	-0.21
IMPROVED HMT	-0.5**	-5.66**	1.15*	0.07*	-0.73**	-0.7**	-0.98	-32.14**	-5.84**	-37.93**	-4.06**	-9.6**	-1.18**	-2.83**	-3.23**	-2.65**
SE	0.19	1.16	0.5	0.04	0.14	0.23	0.5	0.59	0.43	0.56	0.22	0.47	0.39	0.34	0.85	0.4

* = Significance $p > 0.05$, ** = Significance $p > 0.01$

1. Days to 50% flowering 5. Flag leaf angle (in degree) 9. No. of sterile spikelet/panicle 13. 1000 grain weight (g)
2. Plant height (cm) 6. Productive tiller per plant 10. Total No. of spikelet/panicle 14. Grain yield per plant (g)
3. Flag leaf length (cm) 7. Panicle length (cm) 11. Spikelet fertility (%) 15. Biological yield/plant (g)
4. Flag leaf width (cm) 8. No. of fertile spikelet/panicle 12. pollen fertility (%) 16. Harvesting index (%).

Table 3. Specific combining Ability (SCA) effect of hybrids for various characters

/	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
IRMS78156A/																
R-1162-1667-1-1	-1.92**	-13.7**	-0.66	-0.06	3.56**	-0.03	-0.02	-14.24**	-19.37**	-33.54**	-0.18	0.52	1.45*	-3.38**	-5.43**	-2.24**
PUSA.BAS-6- 1460)	0.42	6.5**	3.79**	-0.08	-1.03**	1.81**	0.76	9.49**	17.83**	27.33**	-3.02**	-1.4	2.55**	-0.59	6.12**	-6.13**
BPT-4358	-1.25**	7.98**	1.22	0.07	-12.53**	-0.26	0.01	-4.26**	10.72**	6.51**	-4.17**	-1.16	5.07**	-1.74**	1.87	-5.03**
INGER 1-114	3.25**	-7.77**	-1.86*	0.23**	6.93**	0.01	-0.01	14.47**	13.48**	27.88**	4.43**	-3.78**	2.14**	-0.41	7.64**	-5.33**
INGER 1-134	-1.08	-6.6**	-1.09*	-0.1	9.48**	-0.29	0.21	-9.23**	8.95**	-0.28	-2.69**	-1.84*	-8.33**	-0.26	-9.61**	7.09**
IMPROVED HMT	0.58**	13.58**	-1.4	-0.05	-6.4**	-1.23	-0.95	3.76**	-31.62**	-27.89**	5.62**	7.66**	-2.88**	6.39**	-0.59	11.64**
CRMS31A/																
R-1162-1667-1-1	2.25*	1.1	0.73	0.03	0.73**	0.35	-2.35	-6.04**	9.57**	3.57**	-3.91**	0.02	2.57**	3.67**	6.56**	1.53*
PUSA.BAS-6-(P- 1460)	-0.92	5.4**	-3.74**	0.08	-3.68**	-2.17**	-0.71	-16.71**	13.77**	-2.97**	-7.41**	-2.33**	0.13	-2.49**	-3.79**	-1.23*
BPT-4358	-0.08**	8.23**	-0.63	-0.15**	5.13**	0.16	-0.31	-8.11**	15.46**	7.32**	-5.85**	-1.73*	-3.05**	4.51**	5.41**	5.25**
INGER 1-114	-3.08**	6.83**	-0.67	-0.21**	1.93**	0.13	-2.38	-5.97**	-25.43**	-31.27**	9.24**	3.36**	-3.09**	-3.61**	-11.38**	1.42*
INGER 1-134	-0.42	-15.7**	4.3**	-0.13*	-3.71**	1.43**	3.24**	46.62**	16.79**	63.38**	3.34**	8.06**	6.99**	0.49	8.92**	-5.63**
IMPROVED HMT	2.25**	-5.87**	0.01	0.12*	-0.4	0.1	2.52**	-9.79**	-30.18**	-40.03**	4.59**	-7.38**	-3.56**	-2.56**	-5.71**	-1.35*
CRMS32A/																
R-1162-1667-1-1	-0.33	12.6**	-0.07	0.02	-4.29**	-0.32	2.37**	20.28**	9.79**	29.98**	4.09**	-0.55	-4.03**	-0.29	-1.13	0.71
PUSA.BAS-6-(P- 1460)	0.5	-11.9**	-0.05	0.01	4.71**	0.36	-0.05	7.22**	-31.61**	-24.36**	10.43**	3.73**	-2.68**	3.09**	-2.33	7.36**
BPT-4358	1.33**	-16.22**	-0.59	0.09	7.4**	0.1	0.3	12.37**	-26.18**	-13.82**	10.02**	2.89**	-2.02**	-2.76**	-7.28**	-0.22
INGER 1-114	-0.17	0.9	-0.59**	-0.02	-8.86**	-0.14	2.39**	-8.5**	11.94**	3.39**	-13.68**	0.42	0.95	4.02**	3.74**	3.91**
INGER 1-134	1.5**	22.3**	-3.21**	-0.02	-5.77**	-1.14**	-3.45**	-37.4**	-25.74**	-63.11**	-0.66	-6.22**	1.34*	-0.23	0.69	-1.46*
IMPROVED HMT	-2.83**	-7.72**	1.39	-0.07	6.8**	1.13**	-1.57*	6.03**	61.79**	67.92**	-10.21**	-0.27	6.44**	-3.83**	6.31**	-10.29**
SE																

These promising lines, testers and crosses revealed wide scope for enhancing the grain yield in the CMS line or three line breeding system based rice improvement programme to develop rice hybrids.

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