

## RESEARCH ARTICLE

# Combining ability analysis for yield and yield components in rice (*Oryza sativa* L.)

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### SUMMARY

With the aim of increasing interest in exploitation of heterosis in rice, there is an urgent need to make available various CMS lines and good restoration capability lines for combining ability tests. The knowledge of combining ability is useful to assess nicking ability in self-pollinated crops and at the same time elucidate the nature and magnitude of gene actions involved, provides to the breeder about insight of nature and relative magnitude of fixable and non-fixable genetic variances *i.e.* due to dominance or epistatic components. This study provides useful information for the selection of donor parents for effective breeding programme. Such informations are required to design efficient breeding programmes for rapid dynamic and strategic crop improvement for quantitative along with qualitative nature of traits. Variation with in crosses and parents were significant for all the characters and also magnitude of variance among parents vs crosses were also significantly for all characters except day to 50% flowering. The SCA variances were higher than the corresponding GCA variances for all the traits. The significant and positive gca effects for grain yield per plant were exhibited only by 3 males namely, Swarna, NDRK 5026 and NDRK 5032 which were found to be good general combiners. Among 24 hybrids studied, none of the hybrids exhibited high sca effects for all 10 characters.

**Key Words :** Rice, GCA, SCA, Hybrid, Line x tester

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Rice (*Oryza sativa* L.) is the staple food crop of more than half of world's population and the world population particularly that of rice consuming countries increasing at a faster rate. By the year 2025, about 785 million tones of paddy which is 70 per cent more than the current production will be needed to meet the growing demand (Manomani and Fazlullah Khan,

2003). Thus to full-fill the demand of increasing population, developing new high yielding hybrids and improved lines/varieties along with stable performance in different agro climatic is a big challenge. The ultimate aim of the plant breeding is to develop varieties that perform certain functions better than the exiting type. The superiority of the improved type is manifested by certain specific gene combinations and how rapidly these combinations can be obtained in single crop variety depends on the system into which the genes available to the plant breeders are organized. The hybrid rice

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technology now in operation, aims at yield augmentation through higher exploitable heterosis levels. With the aim of increasing interest in exploitation of heterosis in rice, there is an urgent need to make available various CMS lines and good restoration capability lines for combining ability tests. The knowledge of combining ability is useful to assess nicking ability in self-pollinated crops and at the same time elucidate the nature and magnitude of gene actions involved, provides to the breeder about insight of nature and relative magnitude of fixable and non-fixable genetic variances *i.e.* due to dominance or epistatic components. Thus, combining ability analysis is one of the reliable and most prominent tools available to estimate the combining ability effects and foreground selection for desirable parents in hybrid breeding programme. Combining ability helps in the evaluation of inbreds in term of their genetic value, in the selection of suitable parents for hybridization which may be utilized for the commercial cultivation (Lyngdoh *et al.*, 2013). Hence, this study provides useful information for the selection of donor parents for effective breeding programme. Such informations are required to design efficient breeding programmes for rapid dynamic and strategic crop improvement for quantitative along with qualitative nature of traits.

## MATERIAL AND METHODS

The experimental material for the present investigation comprised 24 F<sub>1</sub>s of rice, three CMS lines

(*viz.*, IR 58025A, PMS 8A and PMS 10A) and 8 promising restorer lines (testers) derived by line × tester mating design during *Kharif*, 2014. The resultant 24 F<sub>1</sub>s and 11 parents were evaluated in Randomized Block Design (RBD) with three replications during *Kharif*, 2013 at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology, Kumarganj Faizabad, India. 25 days old seedlings were transplanted with one seedling per hill adopting recommended spacing of 20 x 15 cm and each entry was planted in four rows of 2.5 m length. All the recommended cultural practices and packages were applied for growing healthy and good crop. In each entry, five plants were randomly selected from each replication and following observations were recorded for seedling growth (cm), days to 50% flowering, plant height (cm), total number of tiller per plant, panicle bearing tillers, panicle length (cm), spikelets per panicle, spikelets fertility (%), 1000 grain weight (g) and grain yield per plant (g). The mean data of different traits were subjected to analyze by standard statistical and biometrical method for combining ability by Kempthorne (1957), heterobeltiosis and standard heterosis over (Sarjoo 52) by Fonseca and Patterson (1968).

## RESULTS AND DISCUSSION

The results obtained from the present investigation as well as relevant discussion have been summarized under following heads :

**Table 1 : Analysis of variance for combining ability in rice**

Source of variance	d.f.	Seedling growth	Days to 50% flowering	Plant height (cm)	No. of total tillers/ plant	Panicle bearing tillers/ plant	Panicle length (cm)	Total spikelets / panicle	Spikelet fertility %	Test weight(g)	Grain yield / plant (g)
Replication	2	3.48	0.26	2.565	0.15	1.02	0.37	23.48	1.154	1.04	3.20
Females	2	85.09**	20.59**	595.93**	60.32**	25.11**	3.92	11793.92**	121.40**	2.22	128.10**
Males	7	97.53**	214.92**	366.67**	24.54**	23.86**	9.56**	6015.72**	145.19**	16.69**	211.33**
Females x males	14	35.92**	48.53**	249.26**	32.68**	36.20**	15.67**	1853.42**	0.18	6.26**	789.28**
Error	68	1.24	1.64	4.11	0.99	0.55	1.37	15.97	2.82	0.94	1.67
<b>Components of variance</b>											
<sup>2</sup> g F		2.05	-1.16	14.44	1.18	-0.46	-0.49	414.19	-2.60	-0.17	-38.43
<sup>2</sup> gM		6.85	18.49	13.05	-0.84	-1.37	-0.68	462.48	-4.29	1.16	-226.36
<sup>2</sup> g pooled		3.35	4.19	14.06	0.62	0.70	0.54	427.35	3.06	0.19	89.68
<sup>2</sup> s		11.56	15.66	82.07	10.42	11.86	4.91	615.55	61.01	1.71	846.71
( <sup>2</sup> g/ <sup>2</sup> g) <sup>1/2</sup>		1.85	2.04	3.74	0.78	0.8	0.73	20.67	1.74	0.43	9.46
<sup>2</sup> A		6.71	8.39	28.13	1.26	-1.42 (0)	-1.08 (0)	854.72	-6.12 (0)	-0.39 (0)	179.37
<sup>2</sup> D		11.56	15.66	82.07	10.42	11.86	4.91	615.55	61.01	1.71	846.71
h <sup>2</sup> n		33.83	32.63	26.60	9.80	10.13	14.67	57.50	8.74	15.58	17.45

where, \* and \*\* indicate significance of values at P=0.05 and 0.01, respectively.

(<sup>2</sup>s/<sup>2</sup>g)<sup>1/2</sup>- Degree of dominance ((0)- ratio no calculated due to negative <sup>2</sup>g)

<sup>2</sup>g- Variance due to GCA

<sup>2</sup>s- Variance due to SCA

**Analysis of variance :**

ANOVA for combining ability (Table 1) revealed that crosses and parents as whole were found to differ significantly. Variation with in crosses and parents were significant for all the characters and also magnitude of variance among parents vs crosses were also significantly for all characters except day to 50% flowering. The variations among testrs were observed to be significant for all the characters, whereas in male sterile lines variations were found to be significant for all characters except number of total tillers per plant, spikelets fertility, test weight and grain yield per plant. The interaction between males and females were significant for all the characters except panicle length. The aforesaid findings suggested the importance of both additive and non-additive gene effects represented by general and specific

combining ability variances, respectively, for majority of the traits. Combining ability analysis revealed that both GCA and SCA variances were important for inheritance of various studied traits. with additive and non-additive nature of gene action. The SCA variances were higher than the corresponding GCA variances for all the traits (Saidaiah *et al.*, 2010), indicated preponderance of non-additive gene effects. The maximum gca variance (427.35) and sca variance (846.71) variance was recorded for total spikelets per panicle and grain yield per plant, respectively. The importance of additive as well as non-additive gene effects with predominance of non-additive gene effects in inheritance of grain yield and yield components of rice were agreement with earlier findings of Saleem *et al.* (2010), Saidaiah *et al.* (2010), Rashid *et al.* (2007), Saravanan *et al.* (2006), Singh *et*

**Table 2 : Contribution of males, females and males x females**

Sr. No.	Characters	Per cent contribution of		
		Males	Females	Males x females
1.	Seedling growth	50.35	12.55	37.09
2.	Days to 50% flowering	67.61	18.50	30.53
3.	Plant height (cm)	35.41	16.44	48.13
4.	No. of total tillers/ plant	23.16	16.26	60.56
5.	Panicle bearing tillers/ plant	23.06	6.93	69.99
6.	Panicle length (cm)	22.75	2.66	74.58
7.	Total spikelets/ panicle	45.94	25.99	28.32
8.	Spikelet fertility%	26.53	6.23	67.14
9.	Test weight(g)	55.90	2.12	41.95
10.	Grain yield / plant (g)	21.57	20.00	86.42

**Table 3 : Estimates of general combining ability (GCA) effects of parents for 10 characters in rice**

Parents	Seedling growth	Days to 50% flowering	Plant height (cm)	No. of total tillers/ plant	Panicle bearing tillers/ plant	Panicle length (cm)	Total spikelets / panicle	Spikelet fertility %	Test weight (g)	Grain yield / plant (g)
<b>Males</b>										
NDRK 5026	3.20**	-6.22**	0.62	0.38	0.68**	0.04	-35.88**	0.06	1.63**	2.17**
NDRK 5023	1.07**	1.89**	13.24**	0.13	0.33	-1.17**	1.46	-1.24*	-1.12**	0.25
NDRK 5031	-4.77**	4.22*8	0.82	1.80**	2.37**	1.14**	49.78**	-7.80**	0.40	-6.97**
NDRK 5032	3.98**	-0.11	2.26**	2.64**	0.47*	1.17**	14.30**	-1.04**	1.14**	1.19**
Swarna	-2.69**	6.89**	-7.07**	0.74**	1.32**	-0.27	11.88**	5.90**	-1.89**	9.70**
MT 20-1-1	-3.45**	-1.89**	-6.40**	-2.13**	-1.11**	-1.73**	-12.76*8	-0.82	-1.45**	-0.36
NDR 507	2.60**	2.33**	1.16	-0.73*	-1.34**	0.28	-17.25**	3.30**	-0.14	-2.31**
NDRK 5027	0.05	-7.11**	-3.40**	-1.79**	-2.72**	0.53**	-12.39**	1.78**	1.60**	-3.16**
S.E.(sij)±	0.37	0.43	0.67	0.33	0.25	0.39	1.33	0.56	0.32	0.43
S.E.(gi-gj)±	0.52	0.60	0.96	0.47	0.35	0.55	1.88	0.79	0.46	0.61
<b>Females</b>										
IR 58025A	2.07**	0.56*	3.46**	0.59**	0.79**	0.43	24.99**	-1.78**	-0.09	-1.09**
PMS 8A	-0.48*	0.51*	-5.71**	-1.80**	-1.15**	-0.05	-7.70*8	0.75**	-0.25	-1.57**
PMS 10A	-1.61*8	-1.07**	2.25**	1.21**	0.36	0.27	-17.29**	53**	0.34	2.65**
S.E.(sij)±	0.23	0.26	0.41	0.20	0.2	0.24	0.81	0.34	0.20	0.29
S.E.(gi-gj)±	0.32	0.37	0.58	0.29	0.21	0.34	1.15	0.48	0.28	0.37

where, \* and \*\* indicate significance of value at P=0.05 and 0.01, respectively.

*al.* (2004) and Vanaja *et al.* (2003).

### Proportional contribution :

The proportional contribution of lines, testers and their interaction for ten traits is presented in Table 2. It was evident from the finding that males showed higher per cent contribution than female lines for all the traits and they played very important role for all the traits indicated dominance of parental influence for the traits. Lines were more important but their contribution was not too high, revealed low influence of maternal effect for all traits. The contribution of maternal and paternal interaction (line x tester) were more than 60 % for five characters grain yield per plant (86.42%), panicle length (74.58%), panicle bearing tillers per plant (69.99%), total spikelet fertility (67.14%) and number of total tillers per plant (60.56%). These results are in confirmity with those of Saleem *et al.* (2010) and Rashid *et al.* (2007).

### General combining ability :

The significant and positive GCA effects for grain yield per plant were exhibited only by 3 males namely, Swarna (9.70), NDRK 5026 (2.17) and NDRK 5032 (1.19) and 1 female, PMS 10A (2.65) and these lines also showed favorable and significant GCA effects for most of traits under study as showed in Table 3. These lines serve as valuable donors for hybridization programme or multiple crossing programmes for obtaining high yielding hybrid varieties or in selection of transgressive segregants for developing pure line varieties of aromatic and non-aromatic rice through background selection. Hence, simultaneous improvement for yield, yield component and other associated traits is possible and also very important for enhancing yield potential in rice. The additive gene effects were fixable nature for grain yield and most of other yield component traits suggested that these traits are amenable to improvement through background selection in early generations. The

**Table 4 : Estimates of specific combining ability (SCA) effects of hybrids for 10 characters in rice**

Crosses	Seedling growth	Days to 50% flowering	Plant height (cm)	No. of total tillers/plant	Panicle bearing tillers/plant	Panicle length (cm)	Total spikelets / panicle	Spikelet fertility %	Test weight (g)	Grain yield / plant (g)
IR 58025A x NDRK 5026	-0.07	5.11**	11.24**	3.74**	3.05**	2.91**	7.26**	6.56**	0.74	18.28**
IR 58025A x NDRK 5023	6.05**	-4.89**	-3.29**	-4.01**	-3.77**	1.52*	-2.35	3.08**	-0.22	-12.97**
IR 58025A x NDRK 5031	-1.11	2.44**	2.85*	1.56**	1.36**	2.59**	37.70**	-17.82**	2.27**	1.09
IR 58025A x NDRK 5032	-1.86**	2.78**	3.18**	-2.84**	-0.74	-3.27**	39.63**	-5.57**	-0.97	-12.08**
IR 58025A x Swarna	-1.18	0.78	0.64	-0.38	-0.59	-2.22**	-5.18*	4.47**	0.06	11.52**
IR 58025A x MT 20-1-1	0.57	5.56**	-0.92	-2.31**	-2.99**	-0.76	-12.13**	10.03**	0.28	11.48**
IR 58025A x NDR 507	-0.48	0.67	-0.71	4.09**	2.07**	-0.76	-36.64**	-0.23	-0.73	-16.41**
IR 58025A x NDRK 5027	-1.93**	-2.22**	-12.99*	0.15	1.62**	-0.01	-18.56**	-0.79	-1.43*	-10.89**
PMS 8A x NDRK 5026	-0.87	6.60**	-4.26**	-1.55**	-3.22**	-1.77**	-1.68	-4.21**	-0.74	-7.79**
PMS 8A x NDRK 5023	-0.78	1.82**	6.71**	5.87**	5.01**	0.00	15.08**	-0.54	-0.65	20.34**
PMS 8A x NDRK 5031	-2.07**	3.51**	-6.53**	-1.47*	-2.12**	-1.39*	-19.65**	10.51**	-1.07	-10.93**
PMS 8A x NDRK 5032	1.01	-2.85**	-7.48**	2.95**	5.04**	3.29*	-8.59*	-1.13	2.18*	11.73**
PMS 8A x Swarna	6.02**	-3.18**	12.48**	2.69**	-3.31	-0.71	-15.66**	0.33	0.65	20.69
PMS 8A x MT 20-1-1	-1.24	-1.01*	1.69	0.45	0.72	0.73	6.65**	-4.48**	0.87	-13.54**
PMS 8A x NDR 507	-1.67**	-0.63	-8.79**	-2.89**	-2.32**	-1.28	32.72**	1.83	-1.31*	8.83**
PMS 8A x NDRK 5027	-0.38	2.82**	6.18**	-0.67*	0.20	1.14	1.13	-2.03*	1.06	12.75**
PMS 10A x NDRK 5026	0.94	-1.49**	-6.97**	-2.20**	0.17	-1.14	8.95**	-02.35**	0.00	-10.39**
PMS 10A x NDRK 5023	-5.27**	3.07**	-3.42**	-1.86**	-1.24**	-1.51	-12.73**	-2.53**	0.86	-7.38**
PMS 10A x NDRK 5031	3.18**	1.07*	3.69**	-0.09	0.76	-1.20	-18.05**	7.31**	-1.218	9.86**
PMS 10A x NDRK 5032	0.85	0.08	4.28**	-0.11	-4.31**	-0.02	-20.89**	6.60**	-1.21*	0.38
PMS 10A x Swarna	-4.84**	2.40**	-13.12**	3.07**	3.91**	2.92**	20.86**	-5.06**	0.29	9.17**
PMS 10A x MT 20-1-1	0.67	-4.48**	-0.77	1.86**	2.27**	0.04	5.48*	-5.19**	-1.15*	-7.93**
PMS 10A x NDR 507	2.15**	-0.04	9.50*8	-1.20*	0.25	2.04**	-1.08	-1.58	2.04**	8.18**
PMS 10A x NDRK 5027	2.32*8	-0.60	6.80**	0.52	-1.81**	-1.13	17.44**	2.82**	0.37	-1.86
S.E.(sij)±	0.64	0.46	1.17	0.57	0.43	0.67	2.31	0.97	0.56	0.76
S.E.(gi-gj)±	0.91	1.04	1.65	0.81	0.61	0.95	3.26	1.37	0.79	1.05

where, \* and \*\* indicate significance of values at P=0.05 and 0.01, respectively

considerable improvement in status of grain yield and important yield attributes in rice can still be achieved by following conventional breeding procedures by the use of suitable donor with superior restorer parents in autogamous crops leading to development of high yielding varieties.

### Specific combining ability effects :

The specific combining ability (SCA) effects, which are supposed to be manifestation of non-additive components of genetic variance, were highly valuable for discrimination of crosses for their genetic worth as breeding materials. Among 24 hybrids studied, none of the hybrids exhibited high SCA effects for all 10 characters (Table 4). However, hybrid IR58025A x NDRK 5026 and PMS 8A x NDRK 5032 showed highly significant favourable SCA effects in respect of 6 characters. The best cross IR 58025A x NDRK 5026 exhibited high significant and positive SCA effects for grain yield per plant (18.28), total spikelets per panicle (7.26) total tillers per plant (3.74), panicle bearing tillers per plant (3.05), panicle length (2.91), and spikelets fertility % (6.56). Cross PMS8A x NDRK 5032 was best specific combiner for panicle bearing tillers per plant (5.04), panicle length (3.29) and also good specific combiner for grain yield per plant (11.73), number of tillers per plant (2.95), days to 50% flowering (-2.85) and plant height (-7.48). However, best specific combiner for grain yield per plant was PMS 8A x Swarna (20.69) followed by PMS 8A x NDRK 5023 (20.34). Best specific combiner for seedling growth and days to 50% flowering was IR58025A x NDRK 5023 (6.05 and -4.89, respectively), for plant height PMS 10A x Swarna (-13.12), for number of total tillers per plant PMS 8A x NDRK5023 (5.87), for total spikelets per panicle IR 58025A x NDRK 5032 (39.63), for spikelet fertility PMS 8A x NDRK5031 (10.51) and for test weight IR 58025A x NDRK 5031 (2.27).

The predominance of non-additive gene effects represented non-fixable dominance and epistatic components of genetic variance indicated that maintenance of heterozygosity would be highly fruitful for improving the traits. Hence, the suitable breeding strategy for attaining high yield would be the full or partial exploitation of hybrid vigour through development of fully extended hybrid, synthetic or composite cultivars.

In general, the crosses showing significant and desirable SCA effects were associated with better *per se* performance for respective traits. Therefore, both *per se* performance along with SCA effects should be considered for evaluating the superiority of a cross, if development of hybrids is the ultimate objective.

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