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Ashwani Kumar Singh
Department of Genetics and
Plant Breeding, Veer Bahadur
Singh Purvanchal University,
Jaunpur, Uttar Pradesh, India

Alok Kumar Singh
Kamla Nehru Institute of
Physical and Social Sciences,
Sultanpur, Uttar Pradesh, India

Tarkeshwar
Department of Genetics and
Plant Breeding, Acharya
Narendra Deva University of
Agriculture and Technology,
Ayodhya, Uttar Pradesh, India

Shiv Prasad Maurya
Department of Genetics and
Plant Breeding, Veer Bahadur
Singh Purvanchal University,
Jaunpur, Uttar Pradesh, India

Studies on gene action and combining ability of newly developed CMS based heterotic rice hybrids (*Oryza sativa* L.)

Ashwani Kumar Singh, Alok Kumar Singh, Tarkeshwar and Shiv Prasad Maurya

Abstract
The present study investigated the metric features resulting from the combining ability and gene activity present in CMS lines of rice (*Oryza sativa* L.) and their hybrids. In Kharif 2020, the study was carried out at Pilikothi Farm of Tilak Dhari Degree College in Jaunpur (U.P.) using a randomized block design. The observations were conducted on five competitive plants of a specific genotype that were randomly selected from a plot for every replication of the twelve features. A total of twelve metric characters recorded for the study. The analysis of variance for combining ability revealed highly significant mean squares due to lines × tester interactions representing importance of specific combining ability and non-additive gene effects for most of the characters except seedling height, panicle length, spikelets fertility (%) and harvest index. None of the CMS lines used as females had significant positive gca effects for grain yield. Among the testers, six genotypes had significant positive gca effects for grain yield per plant to emerge as good general combiner. The top five performers were Sarjoo-52 followed by AT-401, NDRK 50063, NDRK 50060 and IR64. Parents with various combinations of general combiner parents, such as high × high (H × H), high × average (H × A), high × low (H × L), average × average (A × A), average × low (A × L), and low × low (L × L), were involved in the crosses that displayed a high order of significant and desirable sca effects for different characters.

Keywords: *Oryza sativa*, gene action, GCA, SCA, combining ability, grain yield and CMS

Introduction
In India, rice is the most significant crop. At the moment, it supplies 46% of food grain production and 43% of cereal output. India, followed by China, is the country with the most area dedicated to rice cultivation, covering 49 million hectares (Kharif rice making up 43.6 Mha and Rabi rice 5.4 Mha). India is the world's second-largest producer of rice, with 118.9 million tonnes produced (MoAFW, 2020–21). On an average India produces 4.1 metric tonnes of rice per hectare (USDA study, 2022) [3].

Rice, or *Oryza sativa* L., is a major staple crop that grows from 500 North in northern Czechoslovakia on the equator to 350 South in Australia. It has been cultivated in tropical and subtropical regions of the world since ancient times. Rice is successfully grown everywhere from in the Kuttanadu district of Kerala, India, below sea level, to up to 2000 metres in the Himalayas. While *Oryza glaberrima*, the wild rice species, is found in tropical Africa, *Oryza sativa* L., the species used for cultivation, is native to South Asia's tropical regions. One of the earliest crops to be grown in India is rice (Vavilov, 1951) [20].

The annual grass known as rice (*Oryza sativa* L.) is a member of the genus *Oryza*. 22 wild species (2n=24, 48) of the genus *Oryza* correspond to 10 genetic sorts (AA, BB, CC, BBCC, CCDD, EE, FF, GG, HHJJ, and HHKK). In addition to *Oryza sativa*, *Oryza glaberrima* is also widely cultivated in Africa (Brar and Khush, 1986) [6].

It appears that the most versatile and useful genetic approach being researched to break through the rice yield barrier is hybrid rice technology. Presently, hybrid rice breeding is done using two methods: two-line systems and three-line systems. The three-line breeding method makes use of the cytoplasmic genetic male sterility (CGMS) mechanism. Yuan Long Ping, dubbed the "Father of Hybrid Rice," was the first to make it possible to produce hybrid seeds on a wide scale. China produced the first commercial rice hybrid using the CMS line, which was derived from a male sterile wild rice plant (*Oryza sativa* L. f. *spontanea*). Since then, a variety of wild and intensively farmed accessions have been used to establish a number of

Corresponding Author:
Ashwani Kumar Singh
Department of Genetics and
Plant Breeding, Veer Bahadur
Singh Purvanchal University,
Jaunpur, Uttar Pradesh, India

CMS lines. The yield of rice was greatly increased by the hybrid rice breeding that was started in China in the 1970s.

Plant breeders have found substantial benefit from the line x tester analysis because it allows for the evaluation of a larger number of lines for genetic merit through mating design. Kempthorne is credited with developing the idea of line x tester analysis (1957). It is an altered version of the top cross plan. Whereas multiple testers are utilised in the case of the line x tester cross, only one tester is used in the top cross scenario. Crossing new inbred lines to a common parent and comparing the performance of their hybrids is the first step in assessing their potential. Every new inbred line being assessed uses the same tester. Hence, the difference in the performance among the hybrids reflect differences in the general combining ability of the lines.

In practically all of the major field crops, the lines x tester analysis technique has been widely applied to estimate GCA and SCA variances and effects as well as to comprehend the nature of gene action involved in the expression of different quantitative traits.

Materials and Methods

The present study was conducted at Pilikothi Farm, Tilak Dhari Post Graduate College, Jaunpur (U.P.). The experimental area, which is situated in the subtropical part of the Indo-Gangetic plain, has sandy loam soil. This position is between 25.74 °N latitude and 82.69 °E longitude, and it is 83 metres above mean sea level. District Jaunpur has scorching summers and cold winters due to its semi-arid climate. An average of 83.10 cm of rain falls annually.

For this work, 15 distinct rice genotypes were employed as testers (males) and three CMS lines with "wild abortive" (WA) cytoplasm served as the experimental material. These particular outstanding genotypes were chosen from the genetic stock collection of the rice division of the Department of Genetics and Plant Breeding at the A.N.D. University of Agriculture & Technology, Kumarganj, Ayodhya. A "line x tester" mating technique was used to construct the crosses, resulting in 45 F_1s (Kempthorne, 1957) [8].

In Kharif 2020, the final set of 45 F1s and their 18 parents were analysed using a randomised block design with three replications. On June 21, 2020, the seeds for every entry were sowed in separate plots. On July 20, 2020, thirty days later, mature seedlings were transplanted, one seedling per hill, onto three-meter-long single-row plots with a 15-cm intra-row and a 20-cm inter-row spacing. To ensure the production of an exceptional crop, all suggested cultural practices were followed.

The observations were conducted on five competitive plants of a specific genotype that were randomly selected from a plot for every replication of the twelve features. Twelve quantitative traits, including seedling height (cm), days to 50% flowering, flag leaf area (cm^2), plant height (cm), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, spikelet fertility (%), test weight (g), biological yield per plant (g), grain yield per plant (g), and harvest-index (%), were observed. For statistical analysis, the mean values of data made on five plants from each plot were used. The line x tester mating design described by Kempthorne (1957) [8] and subsequently developed by Arunachalam (1974) [4] was followed in the combining ability analysis. The average degree of dominance as determined by the Kempthorne and Curnow (1961) [9] formula. The calculation of heritability in the narrow sense (h^2n) followed Kempthorne's (1957) [8] recommendations.

Results and Discussions
Analysis of variance for line x tester

Table 1 displays the analysis of variance for sixty-three genotypes of the line tester set, which consists of 45 crossings and 18 parents. According to the analysis of variance, mean squares resulting from crosses were found to be highly significant for every character. Similarly, mean squares resulting from lines were found to be highly significant for most characters, with the exception of days to 50% flowering (6.25), spikelets fertility % (0.05), and mean squares resulting from testers. The mean squares due to lines × testers were highly significant for most of the characters except seedling height (1.52), panicle length (3.29), spikelets fertility % (3.64) and harvest index (5.56).

Table 1: Analysis of variance for combing ability for 12 traits in rice

Characters	d.f	Seedling height cm	Days to 50% flowering	Flag leaf area (cm²)	Plant height (cm)	Panicle bearing tillers per plant	Panicle length (cm)	Spikelets per panicle	Spikelets fertility (%)	Biological yield per plant (g)	Harvest index (%)	Test weight (g)	Grain yield per plant (g)
Repln	2	1.30	5.74	3.57	2.54	9.10	7.20	37.89	50.33	62.08	23.76	5.42	33.87
Cross	44	6.35**	29.08**	40.65**	178.24**	8.39**	10.37**	3059.83**	6.62**	274.97**	15.15**	5.35**	63.49**
Line(c)	2	3.00**	6.25	51.73**	35.68**	6.78**	31.26**	227.30**	2.05	25.08**	21.28**	13.16**	1.06
Test(c)	14	16.51**	70.38**	92.22**	477.13**	17.98**	21.56**	9319.55**	13.23**	722.03**	33.46**	6.79**	166.17**
Lxt (c)	28	1.52	10.06*	14.08**	38.97**	3.70**	3.29	132.29**	3.64	69.29**	5.56	4.07**	16.62**
Error	88	1.06	5.54	1.56	7.79	1.08	2.23	6.90	2.59	3.25	3.16	0.95	2.75
Total	134	2.80	13.27	14.42	63.68	3.60	4.98	1009.81	4.62	93.35	7.40	2.46	23.16

*, ** Significant at 5% and 1% probability level, respectively

Estimates of component of variance

The estimates of additive variances, dominance variances, general combining ability (gca) variances, specific combining ability (sca) variances, degree of dominance, predictability ratio and narrow-sense heritability (%) have been presented in Table 2.

For every parameter with the exception of harvest index (0.80), spikelets per panicle (41.80), panicle length (0.36), and seedling height (0.15), estimates of sca variance were larger than equivalent estimates of gca variation. With the exception of spikelets per panicle (0.75), which was less than unity and indicated partial dominance, all of the characteristics had degree of dominance values more than unity (>1). For every character, the predictability ratio was smaller than unity.

Robinson (1966) [15] divided the estimates of heredity in the narrow sense (h_2n) into three groups: high (>30%), medium (10-30%), and low (<10%). The only heredity estimate that was found to be high (60.49%) was for the number of

spikelets per panicle. Plant height (16.32), grain output per plant (13.94), flag leaf area (10.56), and biological yield per plant (17.17) all had moderate estimates of heritability in the limited sense. The narrow-sense heritability estimates for the other characteristics were low.

A number of studies have previously documented the significance of both additive and non-additive gene effects, with a predominance of non-additive gene effects, in the inheritance of rice grain yield and yield components (Akter *et al*., 2010; Bagheri and Jelodar, 2010; Mallikarjuna *et al*., 2014; Kishore *et al*., 2017; Sameer *et al*., 2020) [1, 5, 13, 10, 17].

Table 2: Estimates of genetic components of variance for 12 traits in rice

Estimates	Seedling height (cm)	Days to 50% flowering	Flag leaf area (cm²)	Plant height (cm)	Panicle bearing tillers per plant	Panicle length (cm)	Spikelets per panicle	Spikelets fertility (%)	Biological yield per plant (g)	Harvest index (%)	Test weight (g)	Grain yield per plant (g)
COV(HS)	0.06	0.24	0.34	1.77	0.06	0.09	37.27	0.04	2.62	0.12	0.02	0.60
COV(FS)	1.74	6.82	15.69	51.62	2.56	5.13	924.07	1.09	79.15	5.16	2.29	17.12
σ^2A	0.12	0.48	0.68	3.55	0.12	0.18	74.54	0.08	5.24	0.24	0.03	1.19
σ^2D	0.15	1.51	4.17	10.39	0.87	0.36	41.80	0.35	22.01	0.80	1.04	4.62
σ^2g (female)	0.03	-0.08	0.84	-0.07	0.07	0.62	2.11	-0.04	-0.98	0.35	0.20	-0.35
σ^2g (male)	1.67	6.70	8.68	48.68	1.59	2.03	1020.81	1.07	72.53	3.10	0.30	16.62
σ^2g (pooled)	0.31	1.05	2.14	8.05	0.32	0.86	171.89	0.15	11.27	0.81	0.22	2.48
σ^2s (sca)	0.15	1.51	4.17	10.39	0.87	0.36	41.80	0.35	22.01	0.80	1.04	4.62
A. Degree. Domi.	1.11	1.76	2.48	1.71	2.71	1.40	0.75	2.15	2.05	1.81	5.66	1.97
Predictability ratio	0.45	0.24	0.14	0.25	0.12	0.34	0.64	0.18	0.19	0.23	0.03	0.21
Narrow heritability (%)	9.21	6.43	10.56	16.32	5.74	6.53	60.49	2.51	17.17	5.81	1.60	13.94

Heritability in narrow sense
Estimates of heritability in the restricted sense that highlight the significance of additive, fixable gene effects. Only for the number of spikelets per panicle was a high estimate of narrow sense heredity found. Plant height, grain yield per plant, and flag leaf area appeared as weak indices for improvement through selection, while biological yield per plant had a low to moderate estimate of narrow sense heritability. Therefore, it is advised to use heterosis breeding to create high-yielding hybrids suitable for various environments. High to low estimates of narrow sense heritability has also been reported by Verma *et al*. (2006) [21], Seyoum *et al*. (2012) [19] and Sameer *at al*. (2020) [17] for different characters in rice.

Estimates of general combining ability effects
The estimates of general combining ability (gca) effects in respect of 18 parents (3 lines and 15 testers) for the twelve characters have been set out in Table 3, while the summary of gca effects of top five parents for different characters is presented in Table 4.

None of the CMS lines used as females had significant positive gca effects for grain yield per plant. Among the testers, six genotypes had significant positive gca effects for grain yield per plant to emerge as good general combiner. The top five performers were Sarjoo-52 followed by AT-401, NDRK 50063, NDRK 50060 and IR64. While eight testers possessed negatively significant gca effect for this trait, they were poor general combiners.

The average general combiner parents with non-significant positive value for grain yield per plant were two of the female lines i.e., IR58025A and IR79156A emerged as average general combiner for this grain yield per plant.

The first ranked general combiner for grain yield per plant, Sarjoo-52 was found to be good general combiner for seedling height, days to 50% flowering, flag leaf area, plant height, panicle bearing tillers per plant, panicle length, spikelets per panicle and biological yield per plant, while average combiner for harvest index, and poor combiner for spikelets fertility (%).

The second ranked general combiner for grain yield per plant, AT-401 was found to be good general combiner for seedling height, flag leaf area, plant height, panicle bearing tillers per plant, spikelets per panicle and biological yield per plant, while average combiner for test weight and early flowering but it was poor general combiner for spikelet fertility (%).

The third ranking parent, NDRK 50063 possessed significant gca effects for flag leaf area, plant height, panicle length, biological yield per plant and grain yield per plant in desirable direction and for spikelet fertility and test weight showed average general combing ability.

The fourth ranking parent, NDRK 50060 possessed significant gca effects in desirable directions for flag leaf area, panicle bearing tilers per plant, panicle length, biological yield per plant, test weight and grain yield per plant; and for spikelet fertility and test weight showed average general combing ability.

The fifth ranked general combiner for grain yield per plant, IR 64 was good general combiner for flag leaf area, biological yield per plant, harvest index and grain yield per plant; and for rest traits possessed it was identified as poor general combiners.

IR12T193, NDRK 50060, NDRK 50063, and IR 64 for late flowering; NDRK 50058 for panicle bearing tillers per plant are some other lines that have been discovered as good general combiners in desirable direction for traits other than grain production per plant. Although these parents are mediocre or poor general combiners for grain production, they may also be suggested for use in a hybridization programme as donors of component traits for which they turned out to be good general combiners.

Thus, a preferable strategy for increasing rice yield potential would be to simultaneously improve key yield components and other related qualities in addition to grain yield. Similar results have also been reported by Mahto *et al*. (2015) [12], Kishore *et al*. (2017) [10], Madhuri *et al*. (2017) [11], Saikiran *et al*. (2018) [16] and Sameer *at al*. (2020) [17].

Table 3: Estimates of general combining ability (*gca*) effects of parents for 12 traits in rice

S. No	Crosses	Seedling height cm	Days to 50% flowering	Flag leaf area (cm²)	Plant height (cm)	Panicle bearing tillers per plant	Panicle length (cm)	Spikelets per panicle	Spikelets fertility (%)	Biological yield per plant (g)	Harvest index (%)	Test weight (g)	Grain yield per plant (g)
	Lines												
1	IR58025A (F)	0.26	0.24	1.11 **	0.57	-0.04	0.66 **	1.18 **	0.03	0.66 *	-0.78 **	0.47 **	0.07
2	PUSA6A(F)	-0.25	-0.43	-1.03 **	-1.03 *	-0.37 *	-0.94 **	-2.59 **	-0.23	-0.81 **	0.53 *	-0.59**	-0.18
3	IR79156A(F)	-0.01	0.19	-0.08	0.46	0.40 *	0.27	1.41 **	0.20	0.15	0.25	0.11	0.10
	Tester												
1	IR12T193	0.06	1.13	-3.53 **	-6.59 **	1.38 **	-0.01	79.42 **	1.96 **	10.18 **	-2.62 **	-0.86**	1.66 **
2	IR12T127	0.07	1.79 *	-1.70 **	-4.69 **	-0.43	0.15	-10.10 **	0.74	-6.76 **	-0.27	-1.09**	-3.35 **
3	NDRK 50027	0.14	-1.32	-0.85 *	-7.51 **	1.16 **	1.32 **	-22.36 **	-2.21 **	-8.65 **	1.83 **	-0.42	-2.84 **
4	NDRK 50034	-0.82 *	1.24	-3.30 **	-7.81 **	0.66	-1.38 **	-38.22 **	0.80	-9.48 **	-0.60	-1.85**	-4.46 **
5	NDRK 50035	-1.23 **	-1.32	-3.46 **	0.77	-0.70 *	-2.49 **	-18.66 **	0.79	-9.57 **	1.23 *	0.36	-3.69 **
6	NDRK 50037	-1.13 **	-3.65 **	-4.40 **	-4.26 **	-2.23 **	0.31	-25.06 **	0.74	-5.85 **	-2.92 **	0.86 **	-4.20 **
7	NDRK 50055	-1.72 **	-1.54	0.99 *	3.65 **	-2.38 **	-0.31	-6.58 **	-2.40 **	-6.58 **	2.36 **	0.39	-2.01 **
8	NDRK 50058	-0.38	0.79	3.04 **	4.40 **	0.80 *	0.89	-19.63 **	-1.36 *	-1.36 *	1.93 **	0.48	-0.01
9	NDRK 50060	0.51	4.35 **	3.02 **	13.68**	0.94 **	1.47 **	-5.13 **	-0.52	9.39 **	-2.07 **	1.44 **	2.06 **
10	NDRK 50063	-0.23	3.57 **	2.86 **	6.96 **	0.30	1.79 **	-0.68	0.31	13.71 **	-1.44 *	0.26	4.85 **
11	SARJOO-52	0.96 **	-2.43 **	3.39 **	-8.30 **	2.48 **	3.07 **	37.84 **	-0.45	12.74 **	0.82	1.04 **	8.71 **
12	AT-401	1.42 **	-0.99	3.49 **	-9.07 **	1.13 **	-0.13	53.03 **	0.07	9.63 **	1.81 **	0.30	7.46 **
13	CSR 28	3.56 **	-4.10 **	-0.68	7.00 **	-0.53	-1.26 *	-20.31 **	1.02	-3.40 **	-2.81 **	-0.12	-2.79 **
14	AT69-1	0.51	-2.32 **	-3.50 **	4.73 **	-1.70 **	-2.18 **	2.28 *	0.51	-8.60 **	1.33 *	-0.63	-3.28 **
15	IR 64	-1.71 **	4.79 **	4.62 **	7.06 **	-0.86 *	-1.23 *	-5.83 **	0.00	4.60 **	1.43 *	-0.16	1.90 **
	SE (gca line)	0.15	0.35	0.19	0.42	0.16	0.22	0.39	0.24	0.27	0.26	0.15	0.25
	SE (gca tester)	0.34	0.78	0.42	0.93	0.35	0.50	0.88	0.54	0.60	0.59	0.33	0.55
	SE (best gca lines)	0.22	0.50	0.26	0.59	0.22	0.31	0.55	0.34	0.38	0.37	0.21	0.35
	SE (best gca tester)	0.49	1.11	0.59	1.32	0.49	0.70	1.24	0.76	0.85	0.84	0.46	0.78

*, ** Significant at 5% and 1% probability level, respectively

Table 4: Ranking of five desirable parents on the basis of gca effects and their *per se* performance for 12 characters in rice

Parents	Seedling height cm	Per se performance	Days to 50% flowering	Per se performance	Flag leaf area (cm²)	Per se performance	Plant height (cm)	Per se performance	Panicle bearing tillers per plant	Per se performance	Panicle length (cm)	per se performance
Sarjoo-52	+	18.96	+	100	+	22.81	+	98.54	+	11.05	+	22.29
AT-401	+	19.1	0	88.67	+	22.45	+	93.2	+	13.31	0	24.28
NDRK 50063	0	18.29	-	96.33	+	20.64	-	99.96	0	12.57	+	24.58
NDRK 50060	0	16.71	-	95	+	19.1	-	96.5	+	8.87	+	23.78
IR64	-	16.71	-	102.67	+	21.31	-	102.66	-	10.21	-	23.03

Continued…

Parents	Spikelets per panicle	Per se performance	Spikelets fertility (%)	Per se performance	Biological yield per plant (g)	Per se performance	Harvest index (%)	Per se performance	Test weight (g)	Per se performance	Grain yield per plant (g)	Per se performance
Sarjoo-52	+	136.11	0	90.2	+	56.35	0	38.33	+	23.34	+	21.6
AT-401	+	121.84	0	90.27	+	58.92	+	40.31	0	23.38	+	23.75
NDRK 50063	0	114.15	0	85.54	+	55.26	-	36.18	0	22.04	+	19.98
NDRK 50060	-	107.45	0	83.99	+	45.15	-	41.34	+	21.44	+	18.63
IR64	-	120.9	0	89	+	51.41	+	35.89	0	21.55	+	18.44

+ = Good combiner, - = Poor combiner, 0 = Average combiner

Specific combining ability effect: Specific combining ability (sca) effects are extremely useful for differentiating crossings based on their genetic value as breeding material. These effects are thought to be a manifestation of non-additive components of genetic variance. Table 5 provides the estimated sca impacts of 45 crosses for 12 characters. Table 6 lists the most promising specific cross pairings for various characteristics, together with their mean performance and the gca effects of their parents.

For every character in the current analysis, not a single cross displayed statistically significant sca effects in the desired direction. While some of the crossovers showed noteworthy

and appealing sca effects for one or more characters, none of them stood out as a particularly effective pairing for every character.

Three crosses, IR58025A x Sarju-52, IR79156A x Sarju-52 and PUSA6A x Sarju-52 showed significant and positive sca effects for grain yield per plant as well as some other yield components. The cross, IR58025A x Sarju-52 having highest positive and significant sca effects for grain yield per plant also recorded significant sca effects in desirable direction for flag leaf area, plant height, spikelets per panicle and biological yield per plant grain per panicle. The second ranking cross, IR79156A x Sarju-52 for higher positive and significant sca effect for grain yield per plant showed significant and desirable sca effects for plant height, panicle bearing tillers per plant, spikelet fertility (%) and biological yield per plant. The third ranking cross for significant and positive sca effects for grain yield per plant was PUSA6A x Sarju-52 which exhibited significant and positive sca effects for plant height, spikelets per panicle and biological yield per plant.

Along with good and desired significant sca effects for certain other characters, most often plant height and biological yield per plant, the three crosses that had significant and favourable sca effects for grain yield per plant also showed these effects for other characters. This implied that greater sca effects for significant yield components are associated with the appearance of sca effects for grain yield.

If Table 6 is critically examined, it can be seen that the crosses that show high order significant or non-significant sca effects in a desirable direction for different characters involved parents with all different kinds of combinations of gca effects, including general combiner parents with high × high (H × H), high × average (H × A), high × low (H × L), average × average (A × A), and low × low (L × L). The previous finding made it abundantly evident that, for the characters under investigation, there was no specific correlation between the positive and significant sca effects of crosses and the gca impacts of their parents. Gnanasekaran et al. (2006) [7], Narsimman et al. (2007) [14], Akter et al. (2010) [1], Sanghera and Hussain (2013) [22], Mallikarjuna et al. (2014) [13], Mahto et al. (2015) [12], Kishore et al. (2017) [10], Madhuri et al. (2017) [11], Saikiran et al. (2018) [16] and Sameer at al. (2020) [17].

High × high, high × average and average × average crosses give transgressive segregants and selection in early generation would be advantageous for development of pure lines as there are involvement of additive gene action, whereas, crosses having high × low, average × low and low × low general combining parents are suggested for heterosis breeding as their inheritance are controlled by non-additive and epistatic gene action.

Table 5: Estimates of specific combining ability of crosses for 12 traits in rice

S. No	Crosses	Seedling height cm	Days to 50% flowering	Flag leaf area (cm²)	Plant height (cm)	Panicle bearing tillers per plant	Panicle length (cm)	Spikelets per panicle	Spikelets fertility (%)	Biological yield per plant (g)	Harvest index (%)	Test weight (g)	Grain yield per plant (g)
1	IR79156A x NDRK50027	0.68	-0.90	3.47 **	-1.29	1.01	0.99	0.97	1.27	1.06	2.07 *	1.96 **	0.48
2	IR79156A x NDRK50034	0.15	0.10	4.64 **	-0.95	-1.33 *	0.05	-2.42	-0.48	-0.09	-0.45	0.73	-0.32
3	IR79156A x NDRK50035	-0.26	-0.13	-1.54 *	0.38	-0.08	-0.90	-2.25	-0.80	-1.42	1.36	0.70	0.41
4	IR79156A x NDRK50037	0.68	0.65	-1.75 *	0.75	-1.33 *	-1.33	-2.32	0.24	-0.32	1.09	0.68	-0.32
5	IR79156A x NDRK50055	-0.22	1.87	-1.93 **	-1.36	0.15	1.87 *	-2.49	-0.75	-1.74	-0.12	0.49	0.34
6	IR79156A x NDRK50058	-0.04	1.87	-0.99	-1.05	-0.37	0.75	-1.17	0.36	1.54	-0.53	-0.13	0.48
7	IR79156A x NDRK50060	-0.29	0.43	0.79	0.31	-0.74	0.60	1.02	-0.46	-1.06	-1.88	-1.44 *	-1.83
8	IR79156A x NDRK50063	0.22	1.43	-0.89	0.56	0.11	-1.14	-5.26 **	-1.26	0.90	1.15	-0.50	0.29
9	IR79156A x CSR-28	0.43	-1.46	-2.23 **	3.50 *	-1.45 *	0.06	-5.55 **	-0.58	-6.80 **	0.12	1.53 **	-3.84 **
10	IR79156A x SARJU-52	0.16	0.65	0.85	-4.77 **	1.61 **	1.23	3.55 *	1.47	7.65 **	1.13	-2.82 **	4.13 **
11	IR79156A x AT-401	-0.94	-3.68 **	-0.44	-0.67	1.31 *	-0.28	15.27 **	-0.97	0.56	-2.35 *	-1.44 *	-0.24
12	IR79156A x AT69-1	-1.60 **	-1.46	1.04	4.99 **	0.29	-1.64	3.13 *	0.75	-1.38	-1.73	-0.32	0.05
13	IR79156A x IR12T193	0.54	0.65	-1.41	0.63	1.78 **	0.61	-2.83	0.15	-0.52	-0.66	-0.03	-0.95
14	IR79156A x IR12T127	0.34	-0.13	0.26	-0.86	-0.27	-0.42	2.73	1.42	-1.92	0.44	0.32	-0.13
15	IR79156A x IR64	0.14	0.10	0.11	-0.16	-0.70	-0.45	-2.38	-0.36	3.54 **	0.35	0.27	1.45
16	PUSA6A x NDRK50027	-0.11	1.10	-1.78 *	1.07	-0.49	-0.61	-0.55	-1.09	-0.51	-0.20	-1.26 *	0.47
17	PUSA6A x NDRK50034	-0.01	-0.90	-1.92 **	1.07	0.82	0.75	3.98 *	0.55	0.22	0.08	0.03	-0.23

18	PUSA6A x NDRK50035	-0.39	0.21	1.65 *	1.52	0.44	0.60	3.68 *	1.11	1.61	0.09	-0.48	0.52
19	PUSA6A x NDRK50037	-0.76	-0.68	1.33	0.50	0.60	0.36	1.61	-1.39	0.11	-0.89	-0.31	0.17
20	PUSA6A x NDRK50055	0.59	-0.79	-1.71 *	0.88	-0.51	-1.28	2.82	0.57	2.18 *	-0.73	-0.35	0.29
21	PUSA6A x NDRK50058	0.89	-1.13	-0.30	-0.15	-0.43	-1.48	3.04 *	0.90	-0.75	1.45	0.87	0.12
22	PUSA6A x NDRK50060	0.05	-3.24 *	-0.86	0.09	0.42	0.15	-0.15	0.19	0.15	-0.75	0.74	0.64
23	PUSA6A x NDRK50063	0.20	-1.57	0.06	-1.01	-0.65	0.70	5.85 **	1.39	-1.80	-0.31	-0.44	-0.48
24	PUSA6A x CSR-28	0.25	0.54	-0.88	6.76 **	0.41	-0.52	-1.69	-0.29	-7.33 **	0.02	0.35	-2.48 *
25	PUSA6A x SARJU-52	-0.40	0.65	1.83 *	-3.39 *	0.69	0.01	4.77 **	-0.66	5.74 **	0.03	0.85	2.76 **
26	PUSA6A x AT-401	-0.24	3.32 *	0.65	-4.03 *	-0.37	0.08	-10.28 **	-0.43	0.77	0.82	1.14 *	-0.27
27	PUSA6A x AT69-1	0.27	3.87 **	1.32	-2.28	-0.11	0.71	-16.67 **	-0.26	0.84	0.74	-0.27	-0.84
28	PUSA6A x IR12T193	-0.39	-0.35	1.83 *	-0.87	-2.14 **	0.19	4.37 **	1.38	1.76	0.79	0.05	0.79
29	PUSA6A x IR12T127	-0.46	-0.13	0.16	0.25	0.22	-0.66	-3.44 *	-1.34	1.61	0.16	-0.23	0.80
30	PUSA6A x IR64	0.49	-0.90	-1.40	-0.41	1.08	1.01	2.67	-0.63	-4.58 **	-1.31	-0.69	-2.26 *
31	IR58025A x NDRK50027	-0.57	-0.19	-1.69 *	0.22	-0.52	-0.39	-0.42	-0.18	-0.55	-1.87	-0.70	-0.94
32	IR58025A x NDRK50034	-0.14	0.81	-2.72 **	-0.12	0.50	-0.80	-1.55	-0.07	-0.13	0.37	-0.77	0.54
33	IR58025A x NDRK50035	0.65	-0.08	-0.11	-1.90	-0.36	0.31	-1.43	-0.31	-0.19	-1.45	-0.21	-0.93
34	IR58025A x NDRK50037	0.07	0.03	0.42	-1.25	0.73	0.97	0.71	1.16	0.21	-0.20	-0.36	0.14
35	IR58025A x NDRK50055	-0.36	-1.08	3.64 **	0.48	0.36	-0.60	-0.33	0.18	-0.43	0.85	-0.14	-0.63
36	IR58025A x NDRK50058	-0.85	-0.75	1.29	1.20	0.80	0.73	-1.87	-1.26	-0.79	-0.92	-0.74	-0.61
37	IR58025A x NDRK50060	0.23	2.81 *	0.07	-0.40	0.32	-0.75	-0.86	0.27	0.91	2.63 *	0.70	1.19
38	IR58025A x NDRK50063	-0.43	0.14	0.83	0.45	0.53	0.44	-0.59	-0.14	0.91	-0.84	0.94	0.20
39	IR58025A x SARJU-52	-0.69	0.92	3.11 **	-10.26 **	1.04	0.46	7.24 **	0.87	14.13 **	-0.14	-1.88 **	6.31 **
40	IR58025A x CSR-28	0.24	-1.30	-2.68 **	8.16 **	-2.31 **	-1.24	-8.32 **	-0.81	-13.39 **	-1.16	1.96 **	-6.89 **
41	IR58025A x AT-401	1.18 *	0.36	-0.22	4.70 **	-0.94	0.20	-4.99 **	1.40	-1.33	1.53	0.30	0.51
42	IR58025A x AT69-1	1.33 *	-2.41	-2.36 **	-2.71	-0.18	0.94	13.54 **	-0.49	0.54	0.98	0.59	0.79
43	IR58025A x IR12T193	-0.15	-0.30	-0.42	0.24	0.36	-0.80	-1.54	-1.53	-1.24	-0.13	-0.03	0.16
44	IR58025A x IR12T127	0.12	0.25	-0.42	0.61	0.05	1.08	0.71	-0.08	0.31	-0.60	-0.09	-0.67
45	IR58025A x IR-64	-0.63	0.81	1.29	0.57	-0.38	-0.56	-0.29	0.99	1.04	0.96	0.42	0.81
	SE(sca effects)	0.60	1.36	0.72	1.61	0.60	0.86	1.52	0.93	1.04	1.03	0.56	0.96
	SE(best sca effects)	0.84	1.92	1.02	2.28	0.85	1.22	2.14	1.31	1.47	1.45	0.80	1.35

*, **Significant at 5% and 1% probability level, respectively

Table 6: Most promising cross combinations for different characters with their *per se* performance, sca effects and gca effects of parents

Characters	Crosses with significant effects	*per se* performance	sca effects	Gca effects of parents
Seedling height (cm)	IR58025A x AT69-1	21.48	1.33	A X A
	IR58025A x CSR 28	18.74	1.18	A X H
Days to 50% flowering	IR79156A x AT-401	87.33	-3.68	A X L
	PUSA6A x NDRK 50060	88.00	-3.24	L X L
Flag leaf area (cm²)	IR79156A x NDRK 50034	26.00	4.64	L X L
	IR58025A x NDRK 50055	22.05	3.64	H X H
	IR79156A x NDRK 50027	23.00	3.47	A X L
	IR58025A x Sarju-52	27.99	3.11	H X H
	PUSA6A x NDRK 50035	21.71	1.65	L X L
Plant height	IR58025A x Sarju-52	99.35	-10.26	A X H
	PUSA6A x AT 401	82.12	-4.03	H X H
	IR79156A x Sarju-52	98.23	-4.77	A X H
	PUSA6A x Sarju-52	98.02	-3.39	H X H
Panicle bearing tillers per plant	IR79156A x IR12T193	14.01	1.78	H X H
	IR79156A x Sarju-52	14.67	1.61	H X H
	IR79156A x AT 401	16.55	1.31	H X H
Panicle length (cm)	IR79156A x NDRK 50055	23.04	1.78	A X A
Spikelets per panicle	IR79156A x AT-401	198.79	15.27	H X H
	IR58025A x AT69-1	212.48	13.54	H X H
	IR58025A x Sarju-52	148.01	7.24	H X H
	PUSA6A x NDRK 50063	125.68	5.85	L X A
	PUSA6A x Sarju-52	145.99	4.77	L X H
Spikelet fertility (%)	IR79156A x Sarju-52	90.45	1.47	A X A
	IR79156A x IR12T127	90.61	1.42	A X A
	PUSA6A x NDRK 50063	88.46	1.39	A X A
	IR79156A x NDRK 50027	91.91	1.27	A X L
	IR58025A x NDRK50037	90.81	1.16	A X A
Biological yield per plant (g)	IR58025A x Sarju 52	76.03	14.13	H X H
	IR79156A x Sarju-52	74.38	7.65	A X H
	PUSA6A x Sarju 52	71.00	5.74	L X H
	IR79156A x IR64	61.16	3.54	A X H
	PUSA6A x NDRK 50055	44.15	2.18	L X L
Harvest-index (%)	IR58025A x NDRK 50060	47.78	2.63	L X L
	IR79156A x NDRK 50027	41.21	2.07	A X H
	IR79156A x NDRK 50027	25.55	1.96	A X A
Test weight (g)	IR58025A x CSR 28	26.31	1.96	H X A
	IR79156A x CSR 28	25.18	1.53	A X A
	PUSA6A x AT 401	25.56	1.14	L X A
Grain yield per plant (g)	IR58025A x Sarju 52	31.58	6.31	A X H
	IR79156A x Sarju 52	31.01	4.13	A X H
	PUSA6A x Sarju 52	29.95	2.76	A X H

H = High (significant and positive),
L= Low (significant and negative),
A= Average (non-significant).

Conclusion
The estimates of sca variance were higher than the corresponding estimates of gca variance for all the characters except seedling height, panicle length, spikelets per panicle and harvest index. Parents with various combinations of general combiner parents, such as high × high (H × H), high × average (H × A), high × low (H × L), average × average (A × A), average × low (A × L), and low × low (L × L), were involved in the crosses that displayed a high order of significant and desirable sca effects for different characters. The top five performers were Sarjoo-52 followed by AT-401, NDRK 50063, NDRK 50060 and IR64. Three hybrids i.e., IR58025A x Sarju-52, IR79156A x Sarju-52 and PUSA6A x Sarju-52 exhibited significant and positive sca effects for grain yield per plant as well as some other yield components.

References
1. Akter A, Hasan M, Begum J, Kulsum HMU, Hossain MK. Combining ability analysis in rice (*Oryza sativa* L.). Bangladesh J Pl Breed Genet. 2010;23(2):07-13.
2. Anonymous. Ministry of Agriculture and Farmers Welfare; c2020-21; c2021.
3. Anonymous. USDA report; c2022.
4. Arunachalam V. The fallacy behind the use of modified Line X Tester design. Ind. J Genet. 1974;34:280-287.
5. Bagheri N, Jelodar NB. Heterosis and combining ability analysis for yield and related-yield traits in hybrid rice. Int. J Biol. 2010;2(2):222-231.
6. Brar BS, Khush GS. Wide hybridization and chromosome manipulation in cereals. In: Evans BH, Sharp WR, Ammirato PV, editors. Handbook of Plant Cell Culture, Vol. 4, Techniques and Applications. New York (USA): Mac Millan Publishers; c1986. p. 221-263.
7. Gnanasekaran M, Vivekananda P, Muthuramu S. Combining ability and heterosis for yield and quality in two-line rice (*Oryza sativa* L) hybrids. Ind. J Genet.

2006;66(1):6-9.

8. Kempthorne O. An Introduction to Genetical Statistics. New York, USA: John Wiley and Sons, Inc.; c1957.

9. Kempthorne O, Curnow RN. The partial diallel cross. Biometrics. 1961;17:229-250.

10. Kishore SN, Praveenkumar G, Pallavi M, Kamalakar J, Shahana F, Tagore KR, *et al*. Combining ability analysis for yield and related traits in rice (*Oryza sativa* L.). Agriculture Update. 2017;12(TECHSEAR-6):1573-1577.

11. Madhuri R, Shivakumar N, Bindhu KG, Lohithaswa HC, Pavan R. Gene action and combining ability estimates of newly developed CMS based heterotic rice hybrids (*Oryza sativa* L.). J Appl. Nat Sci. 2017;9(3):1557-1565.

12. Mahto SK, Sahu PK, Prajapati V, Sharma D, Chandrakar PK. Gene action and combining ability analysis using CMS based hybrid breeding system in rice (*Oryza sativa* L.). Trends Biosci. 2015;8(18):4881-4886.

13. Mallikarjuna BP, Shivakumar N, Devendrappa J, Sheela VD, Bharamappa G, Halikatti G, *et al*. Combining ability analysis for grain yield and its attributes in rice (*Oryza sativa* L.). SAARC J Agri. 2014;12(1):01-08.

14. Narsimman R, Kumar TS, Eswarn R, Sampath K, Pravin C, Anandan A, *et al*. Combining ability and heterosis for grain yield and its component characters in rice (*Oryza sativa* L). Crop Improvement. 2007;34(1):16-18.

15. Robinson HF. Quantitative genetics in relation to breeding on the centennial of Mendelism. Indian J Genet. 1966;26(A):171-187.

16. Saikiran V, Krishna L, Mohan YC, Shankar VG. Studies on gene action and combining ability analysis in hybrid rice (*Oryza sativa* L.). Int. J Curr. Microbiol. App. Sci. 2018;7(11):101-107.

17. Sameer SK, Reddy VR, Srinivas B, Madhavi M. Study on gene action and combining ability of yield and quality components in rice (*Oryza sativa* L). Int. J Curr. Microbiol. App. Sci. 2020, 9(11).

18. Sanghera GS, Hussain W. Heterosis and combining ability estimates using line x tester analysis to develop rice hybrids for temperate conditions. Notulae Scientia Biologicae. 2012;4(3):131-142.

19. Seyoum M, Alamerew S, Bantte K. Genetic variability, heritability, correlation coefficient, and path analysis for yield and yield-related traits in upland rice (*Oryza sativa* L.). J Plant Sci. 2012;7(1):13-22.

20. Vavilov NI. The origin, variation, immunity and breeding of cultivated plants. Chronica Botanica. Waltham, Mass, USA; c1951.

21. Verma GP, Prasad G, Chauhan MP, Bahadur R. Combining ability analysis in hybrid rice. Ann Plant Physiol. 2006;20(2):270-274.

22. Sanghera GS, Hussain W. Gene Action and Combining Ability Studies Using CMS System for Developments of Hybrid Rice under Temperate Conditions. American Journal of Agricultural Science and Technology. 2013;1:27-44.