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Study of line x tester analysis, combining ability and *per se* performance in rice (*Oryza sativa* L.)

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Abstract
The analysis of variance for combining ability revealed significant differences due to lines and testers for all the characters indicating wide genetic diversity among lines and testers. The lines x testers' interaction components also emerged significant for all the twelve traits which indicated that combining ability contributed more in the expression of these traits. Among the CMS lines, IR 58025A having 'WA' type of cytoplasm was found to be good general combiner for grain yield and its major components. The line, NDMS 4A was poor general combiner for grain yield and most of the components but showed better ability to combine for plant height and panicle length. Among restorer lines, CR 792-B_4-2-1R was found good general combiner for grain yield and biological yield. Other good combiner was TTB 517-17-SBIR-70149-35R noticed for total number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1} and number of sterile spikelets panicle^{-1}. The higher magnitude of sca than gca variances and greater value of average degree of dominance and lower predictability ratio were observed for all the twelve characters except days to maturity, suggesting significant role of non-additive gene action for these traits which results from dominance /epistasis and various other interaction effects that are non-fixable.

Keywords: Rice, L x T, combining ability, sca, gca, degree of dominance

Introduction
The selection of proper genotypes is of great importance for desired success in a crop improvement programme. Though the performance of parental lines itself gives some indication regarding their usefulness but the long term potentialities are least known at the beginning of breeding programme. Initially the main features of breeding methodology in self pollinated crops like rice have been selection of the parents for hybridization on the basis of *per se* performance for the yield and other characters, followed by single plant selection in segregating generations. Joshi and Dhawan (1966) [6] suggested that this approach should be reviewed and reoriented so as to formulate breeding programme for yield in which the choice of parents is based not only on desirable agronomic characters but also on phenotypic stability, combining ability, genetic diversity and genetic analysis of yield and its components. The use of the concept of combining ability helps in choosing the proper parents for hybridization, which combine well to produce superior hybrids. General combining ability (gca) effects, largely involve additive genetic effects. The additive effects are mainly due to polygenes, which act in additive manner, producing fixable effects. While specific combining ability (sca) effects represent non-additive type of gene action (Griffing, 1956) [5]. Non-additive gene action results from dominance, epistasis and various other interaction effects, which are non-fixable. The choice of parents especially for heterosis breeding should be based on combining ability test and their mean performance as also suggested by Yadav and Murty (1966) [19]. In present paper, the result of combining ability on obtained from a line x tester analysis consisting 60 crosses (2 lines x 30 testers) are discussed.

Materials and methods
The investigation was conducted at Crop Research Station, Masodha, Faizabad (U.P.) during *Kharif* season. The site falls under sub tropical to semi arid region in Indo-Gangatic plains and lies between 26.47ºN latitude, 82.12ºE longitude and at an altitude of about 113 m above mean sea level.

Experimental Details
The two cytoplasmic male sterile (CMS) lines *viz*., IR 58025 A and NDMS 4A, possessing Wild Abortive (WA) type of cytoplasm, were crossed with thirty genetically diverse pollen parents viz., NDRSB-96006R, NDRSB-9730015R, NDRSB-9830099R, OR-1537-15R, OR-1543-11R, OR-1547-9-1R, OR-1564-5R, OR-1898-17R, CR-792-B_4-2-1R, IR-54112-B_2 –CR-

1-6-2R, BARO-5-1-B-6-3-34-1-1-1-1R, RAU-1411-4R, IR 31917R, TTB-517-17-SBIR-67401-17-2R, TTB-517-17-SBIR-70149-35R, CN-1035-36R, CN-1045-6R, OR-1537-6R, R-710-437-1-1R, IR 70 R, IR 600-76-IR, IR 55838-B-2-3-2-3R, IR 21567-18-3R, IR 10198-66-2R, IR 65515-47-2-1-19R, R-971-2505-2-1R, UPRI 92-79R, CSR 21R, RP 2932-2528R and JR 82-1-10R in line x tester mating fashion. A total of 60 F_1s were produced during *Kharif* 2003. The resulting set 60 F_1's their 32 parents (30 male parents + 2 female parents) and a standard check variety *i.e.* Sarjoo-52 were evaluated in Randomized Complete Block Design with three replications.

Fertilizer application

The fertilizers were applied @ 120 kg nitrogen, 60 kg phosphorus and 60 kg potash/ha through urea, di-ammonium phosphate and murate of potash recommended, for the rice crop. The full dose of phosphorus, potash and half dose of nitrogen were applied as basal and rest of nitrogen was applied in two splits as top dressing at tillering and panicle initiation stage.

Raising of CMS lines and male parents

The seeds of CMS lines were treated with 0.02 per cent mercuric chloride solution followed by subsequent washing with sterilized distilled water and then placed in petridishes holding a moist towel paper for proper germination at room temperature. Seven to ten days old seedlings were transplanted in earthen pots for their normal growth while male lines were direct seeded in nursery beds on three different dates to coincide the flowering dates of CMS lines for crossing purpose.

Production of hybrids

Each of the two cytoplasmic male sterile lines was crossed with thirty restorers, collected from diverse sources, in line x tester mating design. The seeds of F_1s obtained from these combinations were collected. Thus, a total of 93 genotypes (2 CMS lines + 30 diverse pollen parents + 60 F_1s +1 standard check-Sarjoo-52 were grown and evaluated.

Growing of F_1's and parental lines

All the crosses were attempted at Crop Research Station, Masodha, Faizabad (U.P.). The F_1's thus produced were evaluated along with their parents including standard check variety (Sarjoo-52) in Randomized Complete Block Design with three replications at Crop Research Station, Masodha, Faizabad. The seeds were sown in raised nursery beds. Twenty-five days old single seedling hill^{-1} were transplanted at a 20 cm inter and 15 cm intra-row spacing. Each test entry was raised in three rows of 3.0 m length. All the recommended cultural practices were followed to raise a good crop.

Combining ability analysis

The experimental data obtained on 12 characters were subjected to analysis of variance (Singh and Chaudhary, 1977) [13] and subsequently line x tester analysis for estimation of combining ability.

Results and discussion

Combining ability for yield and its components

The analysis of variance for combining ability revealed that significant differences existed among the lines and testers for all the characters indicating wide genetic diversity among lines and testers. Contributions of lines for all the traits were comparatively higher towards the combining ability. The line x tester interaction component also emerged significant for all the twelve traits, which indicated that the specific combining ability contributed more in the expression of these traits. Therefore, total variation among hybrids in these cases may be almost solely attributed to gca differences existing among parents.

The higher magnitude of sca than gca variance, greater values of average degree of dominance and lower predictability ratio were observed for all the twelve characters under study. This suggested significant role of non-additive gene action which resulted from dominance, epistasis and various other interaction effects and are non-fixable. Similar gene effects have been reported in rice by Mohanty and Mohapatra (1973) [7] for number of panicles, panicle length, number of grains panicle^{-1}, grain weight panicle^{-1}, 1000-grain weight and grain yield; Singh *et al.* (1979) [14] for yield and its component traits; Rao *et al.* (1980) [10] for grain yield, ear bearing tillers, panicle length, spikelets panicle^{-1}, 100-grain weight, days to flowering, plant height and spikelet sterility; Singh and Srivastava (1982) [15] for fertile tillers plant^{-1}, spikelet fertility and grain yield plant^{-1}; Mohapatra and Mohanty (1985) [8] for spikelet fertility, biological yield, harvest index and grain yield; for seedling height, ear bearing tillers, biological yield and grain yield plant^{-1}; Sardana and Borthakur (1987) [11] for days to flowering, plant height, effective tillers plant^{-1}, filled grains panicle^{-1}, 1000-grain weight and grain yield plant^{-1}; Viraktamath (1987) [18] for number of effective tillers plant^{-1}, harvest index and grain yield plant^{-1}; Bhanumati and Prasad (1991) [1] for plant height, number of filled grains and grain yield plant^{-1}; Chakraborty *et al.* (1994) [2] for plant height, panicle plant^{-1} and yield plant^{-1}; Sharma *et al.* (1996) [12] for plant height, grain weight panicle^{-1} and grain yield plant^{-1}. However, contrary to these, the predominant role of additive gene effects have been observed for yield and its component traits (Chakraborty, 1994; Vijayakumar *et al.*, 1994; Sharma *et al.*, 1996; Ram *et al.*; 1998) [2, 17, 12, 9].

General combining ability

The information regarding general combining ability (gca) effects of the parents is of prime importance as it helps in successful prediction of genetic potential of crosses, which yield desirable individuals in segregating populations of self pollinated crops. Estimates of gca effects showed that is was difficult to choose a good combiner for all the traits as the combining ability effects were not consistent for all the yield components. It might be due to low/negative association of characters. However, overall study revealed that CR 792-$B_4$2-1R proved to be the best general combiner grain yield and biological yield. TTB 517-17-SBIR-70149-35R was another good general combiner for total number of spikelets and number of fertile spikelets.

Among the CMS lines, IR 58025A having 'WA' type of cytoplasm was observed as good general combiner for grain yield and other related traits. Line NDMS-4A was poor combiner for grain yield and major yield components but it showed better combining ability for plant height and panicle length, thereby indicating the need for transferring the male sterility in to genetic back ground of local elite lines having good general combining ability for grain yield and its major components. The gca effects together with relative *per se* performance may be more useful for selecting desirable parents with favourable genes for different components of yield. The *per se* performance of the parents and their gca effects for plant height, days to 50% flowering, test weight and grain yield plant^{-1} were almost in close correspondence which indicated that the *per se* performance of parents for these traits could possibly be taken as a criterion for selection of parents, while in case of rest of the characters higher *per se* performance of pollinator lines was not necessarily associated with expression of maximum gca effects. Though the results of present finding are in agreement with the nature of gene action but not for magnitude of gene action. These differences may be due to the diversity among parents as in present case the female lines used as CMS lines possessed entirely different genetic background.

Specific combining ability effects

The specific combining ability is associated with interaction effects, which may be due to dominance and epistatic component of variation that are non-fixable in nature. In the present investigation, none of the 60 hybrids manifested consistently high sca effects for all the characters. Subramanian and Rathinam (1984) [16] and Ghosh (1993) [4] also observed that no specific combination was desirable for all the traits they studied. Almost all the crosses recorded desirable and significant sca effects for one or more than one (up to 10) characters. IR 58025A X CN 1045-6R was the hybrid which exhibited desirable as well as significant sca estimates for maximum of nine characters including grain yield. Out of 60 cross combinations, 19 crosses exhibited significant positive sca effect for grain yield plant^{-1}. Majority of the crosses which showed significant sca effect for increased yield did include at least one parent having significant gca estimates. The favourable *per se* performance and higher significant positive sca effects in relation to grain yield plant^{-1} were found in hybrid, NDMS 4A X CN 1045-6R and IR 58025A X RP 2932-2528R. These hybrids also showed favourable sca effects for more than two traits. However, the best crosses varied with the characters.

The hybrid NDMS 4A X IR 54112-B$_2$-CR-1-6-2R was good specific combination for number of fertile spikelets, number of sterile spikelets and 1000-grain weight. The hybrids such as NDMS 4A X CN 1045-6R, NDMS 4X R 710-437-1-1R and IR 58025A X IR 21567-18-3R for days to 50% flowering, NDMS 4A X R 710-437-1-1R for plant height, IR 58025A X OR 1564-5R and IR 58025A X NDRSB 96006R for ear bearing tillers plant^{-1}, NDMS 4A X OR 1543-11R, IR 58025A X BARO 5-1-B-6-3-34-1-1-1-1R and NDMS 4A X IR 65515-47-2-1-19R for panicle length and NDMS 4A X IR 54112-B$_2$-CR-1-6-2R for total number of spikelets panicle^{-1} showed better expression in relation to *per se* performance and sca effects.

The choice of breeding methods and type of cultivars to be developed in a crop primarily depends upon the nature and magnitude of gene action. When additive effect forms the principal factors for genetic variance, use of pedigree method could be desirable. Comstock *et al.* (1949) [3] suggested that use of reciprocal recurrent selection would be more effective when both additive and non-additive gene effects are involved in the expression of the traits, when pronounced non-additive gene effects alongwith some additive gene effects were observed, production of hybrids, if commercial seed production is feasible, would be desirable. However, for development of pure lines, bi-parental mating approaches followed by selection of desirable recombinants from the segregating population have been suggested to be more appropriate.

Table 1: Ranking of five desirable parents on the basis of *per se* performance and gca effects

Characters	Good general combiners (gca effects)	Desirable parents (*per se*)	Best parents (*per se* performance and gca effects)
DFF	IR 21567-18-3R, JR 82-1-10R, IR 55838-B-2-3-2-3R, OR 1564-5R, RP 2932-2528R	IR 21567-18-3R, JR 82-1-10R, IR 55838-B-2-3-2-3R, RP 2932-2528R, IR 31917R	IR 21567-18-3R,JR 82-1-10R, IR 55838-B-2-3-2-3R RP 2932-2528R
PH (cm)	CSR 21R, UPRI 92-79R, R 971-2505-2-1R, JR 82-1-10R, IR 70R	IR 21567-18/-3R, IR 31917R, IR 65515-47-2-1-1-9R, JR 82-1-10R, IR 55838-B-2-3-2-3R	JR 82-1-10R
DM	IR 21567-18-3R, JR 82-1-10R, IR 55838-B-2-3-2-3R, OR-1564-5R, RP 2932-2528R	OR 1537-15R, NDMS 4A, OR 1543-11R TTB 517-17-SBIR-67401-17-2 NDSRB 9830099R	-
EBT/P	NDRSB 9830099R, OR 1564-5R, OR 1537-15R, NDRSB 96006, IR 54112-B$_2$-CR-1-6-2R	NDRSB 9830099R, OR 1537-15R IR 54112-B$_2$-CR-1-6-6-2R, NDRSB 96006R, IR 31917R	NDRSB 9830099R, OR 1537-15R, IR 54112-B$_2$-CR-1-6-6-2R, NDRSB 96006R
PL (cm)	OR 1543-11R, IR 31917R, BARO 5-1-B-6-3-34-1-1-1-1R, IR 21567-18-3R IR 10198-66-2R	OR 1537-6R, IR 65515-47-2-1-19R, NDSRB 96006R, RAU 1411-4R IR 55838-B-2-3-2-3R	-
S/P	TTB 517-17-SBIR-70149-35R, TTB 517-17-SBIR-67401-17-2R, IR 21567-18-3R CR 792-B4-2-1R, IR 600-76-1R	UPRI 92-79R, TTB 517-17-SBIR-70149-35R, RAU 1411-4R, CN 1035-36R OR 1898-17R	TTB 517-17-SBIR-90149-35R
F/P	TTB 517-17-SBIR-70149-35R, TTB 517-17-SBIR-67401-17-2R, IR 21567-18-3R CR 792-B$_4$-2-1R, IR 60-76-1R	UPRI 92-79R, TTB 517-17-SBIR-70149-35R, RAU 1411-4R, CN 1035-36R OR 1898-17R	TTB 517-17-SBIR-70149-35R
SS/P	TTB 517-17-SBIR-70149-35R, TTB 517-17-SBIR-67401-17-2R, IR 21567-18-3R CR 792-B4-2-1R, IR 600-76-1R	NDMS 4A, IR 58025A, OPRI 92-79R TTB 70149-RAU 1411-4	TTB 517-17-SBIR-70149-35R
TW (g)	IR 21567-18-3R, CR 792-B42-1R, RAU-1411-4R, NDRSB 96006R, IR 10198-66-2R	R 710-437-1-1R, UPRI 72-79R IR 70R, NDRSB 9730015	RP 2932-2528R
GY/P (g)	CR 792-B$_4$-2-1R, TTB 517-17-SBIR-70149-35R, TTB 517-17-SBIR-67401-17-2R, NDRSB 9730015R, NDRSB 96006R	CN 1035-36R, IR 31917R, CR 792-B$_4$-2-1R, NDRSB 9830099R, CSR 21R	CR 792-B$_4$-2-1R
BY/P (g)	CR 792 B$_4$-2-1R, TTB 517-17-SBIR 66401-17-2R, IR 21567-18-3R, NDRSB 96006R, NDRSB 9030099R	IR 31917R, CN 1035-36R, CR 792-B$_4$-2-1R, CSR 21R, IR 82-1-10R	CR 792-B$_4$-2-1R
HI (%)	TTB 517-17-SBIR-70149-35R, NDRSB 9730015R, JR 82-1-10R, OR 1564-5R IR 31917R	NDRSB 96006R, OR 1547-9-1R, OR 1489-17R, IR 55838-B-2-3-2-3R, NDRSB 9730015R	NDRSB 9730015R

Table 2: Ranking of five desirable crosses on the basis of *per se* performance and sca effects in F_1 generation for twelve characters in rice

Characters	Best specific combiners	Best hybrids on the basis of *per se* performance	Best common crosses (per se performance and sca effects)
DFF	NDMS 4 X CN 1045-6R, NDMS 4A X CN-1035-36R, IR 58025 A X IR 21567-18-3R NDMS 4A X R-710-437-1-1R, IR 58025 A X IR 54112-B_2-CR-1-62R	IR 58025A X IR 21567-18-3R, NDMS 4A X R-710-437-1-1R, NDMS 4A X CN-1045-6R, NDMS 4A X IR J31917R, NDMS 4A X IR 21567-18-3R	NDMS 4A X CN 1045-6R NDMS 4A X R 710-437-1-1R IR 58025 A IR 21567-18-1R
PH (cm)	NDMS 4A X R-710-437-1-1R, NDMS 4A X IR 70R, IR 58025 A X OR-1537-6R, IR 58025 A X R600-76-1R, IR 58025 A X IR 10198-66-2R	IR 58025 A X IR 21567-18-3R, NDMS 4A X R-710-437-1-1R, NDMS 4A X CN-1045-6R, NDMS 4A X IR 31917R, NDMS 4A X IR 21567-18-3R	NDMS 4A X R 710-437-1-1R
DM	NDMS 4A X CN-1045-6R, NDMS 4A X CN-1035-36R, IR 58025 A X IR 21567-18-3R, NDMS 4A X R-710-43-1-1R, IR 58025 A X IR-54112-B2R	IR 58025 AX CSR 21R, NDMS 4A X CSR 21R NDMS 4 X R-971-2505-2-1R, IR 58025 A X JR 82-1-10R	-
EBT/P	IR 58025 A X OR-1564-5R, IR 58025 A X NDRSB-96006R, IR 58025A X IR 65515-47-2-1-19R, IR 58025 A X IR-54112-B_2-CR-1-6-2R, IR 58025 A X BARO-5-1-8-6-3-34-1-1-1-1R	IR 58025 A X NDRSB-9830099R, NDMS 4A X NDRSB-9830099R, IR 58025 A X OR-1564-5R IR 58025 A X NDRSB 96006R, IR 58025 A X OR-1537-15R	IR 58025 A X OR-1564-5R IR 58025 A X NDRSB 96006R
PL (cm)	NDMS 4A X OR-1543-11R, NDMS 4A X IR 65515-47-2-1-19R, NDMS 4A X NDRSB-9830099R, IR 58025 A X BARO-5-1-B-6-3-34-1-1-1-1R, IR 58025 A X IR 55838-B-2-3-2-3R	NDMS 4A X OR-1543-11R, IR 58025 A X BARO-5-1-B-6-3-34-1-1-1-1R, NDMS 4A X IR 65515-47-2-1-19R, IR 58025 A X IR 31917R, NDMS 4A X IR-54112-B_2-CR-1-6-2R	NDMS 4A X OR-1543-11 NDMS 4A X IR 65515-47-2-1-19R IR 58025 A X BARO-5-1-B-6-3-34-1-1-1-1R
S/P	NDMS 4A X UPRI 92-79R, IR 58025 A X IR 65515-47-2-1-19R, DMS 4A X IR 54112-B_2-CR-1-6-2R, IR 58025 A X JR 82-1-10R, IR 58025 A X RAU-1411-4	IR 58025A X R-971-2505-2-1R, IR 58025 A X IR-18-3R, IR 58025 A X IR 600-76-1R, IR 58025 A X TTB-517-17-SBIR-67401-17-2R, NDMS 4A X IR-54112-B_2-CR-1-6-2R	NDMS 4A X IR-54112-B_2-CR-1-6-2R
F/P	NDMS 4A X UPRI 92-79R, IR 58025 A X IR 65515-47-2-1-19R, NDMS 4A X IR 54112-B_2-CR-1-6-1R, IR 58025 A X JR 82-1-10R IR 58025 A X RAU 1411-4R	IR 58025 A X R 971-2505-2-1R, IR 58025 A X IR 21507-18-3R, IR 58025A X IR 600-76-1R, IR 58025 A X TTB 517-17-SBIR-67401-17-2R, NDMS 4A X IR 54112-B_2-CR-1-6-2R	NDMS 4A X IR 54112-B_2-CR-1-6-2R
SS/P	NDMS 4A X UPRI 92-79R, IR 58025 A X IR 65515-47-2-1-19R, NDMS 4A X IR 54112-B_2-CR-1-6-1R, IR 58025 A X JR 82-1-10R IR 58025 A X RAU 1411-4R	IR 58025 A X R 971-2505-2-1R, IR 58025 A X IR 21507-18-3R, IR 58025A X IR 600-76-1R, IR 58025 A X TTB 517-17-SBIR-67401-17-2R, NDMS 4A X IR 54112-B_2-CR-1-6-2R	NDMS 4A X IR 54112-B_2-CR-1-6-2R

Table 3: Contributions of females, males, females X males to different characteristics and their genetic components in rice

S. N.	Characters	Per cent contributions of			gca variance	sca variance	Average degree of	Predictability ratio
		Lines (F)	Testers (M)	Lines x Testers (F x M)	σ^2 g	σ^2 s	dominance (σ^2 s/2 σ^2 g)	$2\sigma^2{}_{g/}\ 2\sigma^2{}_{g}+\sigma^2$ s
1.	DFF	6.95	37.24	55.81	3.09	6.18	3.39	0.32
2.	PH (cm)	10.32	67.10	22.59	6.57	13.13	3.92	0.39
3.	DM	6.32	36.76	56.92	2.50	5.01	3.63	0.29
4.	EBT/P	21.77	72.53	5.69	0.43	0.87	1.94	0.19
5.	PL (cm)	10.35	35.30	54.36	1.56	3.11	2.31	0.34
6.	S/P	12.17	8.61	27.22	30.70	61.39	2.87	0.48
7.	F/P	12.20	6.59	27.21	22.45	44.91	2.86	0.50
8.	SS/P	12.17	8.61	27.22	0.79	15.7	2.86	0.18
9.	TW (g)	11.87	50.21	37.91	0.71	1.42	2.50	0.18
10.	GY/P (g)	14.36	57.97	327.69	11.21	22.42	2.37	0.45
11.	BY/P (g)	9.57	57.63	32.81	23.07	46.15	3.65	0.46
12.	HI (%)	8.70	51.48	39.82	0.96	1.91	3.61	0.17

Conclusion

Among 60 hybrids studied, none of the crosses exhibited high sca effects for all the characters. However, the most promising combinations were NDMS 4A X CN 1045-6R and IR 58025 A X RP 2932-2528R which expressed highly significant and positive sca effects with better *per se* performance, significant high gca effects for both or one of the parents and higher standard heterosis for grain yield plant^{-1}. The relative contribution of males x females was higher than that of males and females for the expression of all the characters except total number of spikelets and number of fertile spikelets. Males exhibited maximum contribution for ear bearing tillers plant^{-1}.

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