RESEARCH ARTICLE :

Combining ability over environments for yield and its components in three line hybrids involving cytoplasmic genetic male sterility in rice (*Oryza sativa* L.)

■ **SREEDHAR SIDDI, T. DAYAKAR REDDY AND M.S. RAMESHA**

SUMMARY : This study was under taken to estimate the general and specific combining ability of five cytoplasmic male sterile lines and twelve restorer lines in 60 F_1 combinations for single plant yield and its important traits at three environments during *Kharif,* 2009. The pooled analysis of variance for combining ability revealed significant differences due to environments, parents, hybrids and various interactions indicating the existence of wider variability in the material studied. The ratio of *gca* to *sca* variances showed non-additive gene action was predominant in the inheritance of days to 50% flowering, number of productive tillers, number of filled grains per panicle, spikelet fertility percentage and single plant yield which suggests possibility of exploiting heterosis. The overall perusal of *sca* effects of different traits in the present investigation reveals *sca* effect and *per se* performance of the crosses was not closely related. In majority of the crosses for all the characters investigated, high *sca* was either due to high x low or low x high or low x low combining parents. The *gca* effects of the parents in pooled analysis revealed that the lines *viz.*, APMS 6A and IR-80151A and the testers *viz.,* IR-54742R, BR-827-35R, KMR-3R and IR-21567R were found to be promising general combiners for single plant yield and its components. Based on significant *sca* effects and *per se* performance, the cross combinations *viz.,* APMS 6A x IR-24R, IR-80561A x IR-32809R, IR-80151A x IR-10198R, IR-80555A x DR-714-1-2R and IR-80559A x IR-72R were identified as promising hybrids for single plant yield and other yield contributing characters.

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BACKGROUND AND OBJECTIVES

Rice is the world's most important cereal crop. The slogan "Rice is Life" aptly describes the importance of rice in food and nutritional security. It is grown worldwide over an area of 158 million hectares with an annual production of more than 497 million tones. Rice

is a staple food crop of India, providing 43 per cent of calorie requirement for more than 70 per cent of Indian population. The area grown to rice in India is the largest among all the rice growing countries and is second in production. Annually in India, 100 million tones of rice is produced in an area of 38.35 million hectares with a productivity of over two tones per hectare of milled rice.

However, currently, there is a pressing need to increase the yield of rice per unit area per unit time in order to address the continual increases in demand by the country's population that is growing. Hybrid rice technology is a key strategy for increasing rice production and addressing food security and rice self-sufficiency. Results of the hybrid rice commercialization program in the China look promising. China has been able to produce 200 million tones rice annually from 30 million hectares. Following China's success in the commercialization of hybrid rice, India was one of the countries to start applied strategic research programme on hybrid rice during 1989. In India, the area under hybrid rice cultivation is woefully low. It has to be decided to go for hybrid rice production in a big way so as to give a boost to overall production of rice in the country.

Successful development of rice hybrids by utilizing the cytoplasmic genetic male sterility and fertility restoration system mainly depends on the availability of promising male sterile and restorer lines. The choice of suitable parents with favorable alleles, which on crossing could produce heterotic hybrids, is also important. Combining ability of the parents provides useful information on their selection for better performance of hybrids besides elucidating the nature and magnitude of gene action in the inheritance of a particular character. The line x tester analysis of combining ability proposed by Kempthorne (1957) is the most commonly used method to find out the general and specific combiners and to study the nature of gene action governing the inheritance of different characters. In India, it is necessary to develop hybrids having stable yield performance over varied environments as rice is being grown under varied agro-climatic conditions. In the present study, we have assessed the combining ability of 60 hybrids and their 17 parents over three environments.

RESOURCES AND METHODS

Five elite CMS lines and 12 elite restorer lines comprised basic experimental material (Table A).

Adequate quantity of seeds of all the required 60 hybrids was obtained by hand crossing by hybridizing five CMS lines with 12 restorer lines in a line x tester mating design during *Rabi*, 2008-2009 at Research farm, Directorate of Rice Research, Rajendranagar, Hyderabad. These 60 F_1 hybrids along with their 17 parents were sown during *Kharif*, 2009 at three different locations *viz.*, Directorate of Rice Research, Hyderabad for Southern Telangana agro-climatic zone; Regional Agricultural Research Station, Warangal for Central Telangana agro-climatic zone and Regional Agricultural Research Station, Karimnagar for Northern Telangana agro-climatic zone. Each entry was planted in five rows of 1.8 m length. Single seedling was transplanted per hill by adopting a spacing of 20 x 15 cm and all recommended package of practices were followed to raise a healthy crop. At flowering and maturity stages, observations were recorded on panicle length (cm), number of productive tillers per plant, number of filled grains per plant, 1000-grain weight (g) and single plant yield (g), and randomly five plants were selected in each plot in each replication and the averages were computed. However, the data for the character, days to 50% flowering was recorded on plot basis. Plot means were computed from the data collected.

Table A: List of male sterile lines and restorer lines.	
Genotype	Source
Male sterile lines	
IR-80151A	IRRI, Philippines
IR-80555A	IRRI, Philippines
IR-80559A	IRRI, Philippines
IR-80561A	IRRI, Philippines
APMS 6A	RARS, Maruteru, India
Restorer lines	
IR-66 R	IRRI, Philippines
IR-10198 R	IRRI, Philippines
DR-714-1-2R	DRR, Hyderabad, India
IR -40750R	IRRI, Philippines
IR-72R	IRRI, Philippines
IR-24R	IRRI, Philippines
IR-21567 R	IRRI, Philippines
KMR-3	UAS, Mandya
IR-32809 R	IRRI, Philippines
IR-63883-41-3R	IRRI, Philippines
IR-54742 R	IRRI, Philippines
BR-827-35R	IRRI, Philippines

Analysis of variance for test entries was performed as a pooled analysis over environments. Analysis of variance for combining ability was carried out using mean values across environments as per Kempthorne (1957) related to method of Comstock and Robinson (1952). Standard errors for *gca* effects of female and male and *sca* effects of crosses were calculated as per Singh and Chaudhary (1977). Ratios of mean square components associated with variance of *gca* and *sca* effects were calculated as suggested by Baker (1978). In a self pollinated crop like rice, combining ability analysis is of special importance, since it leads to the identification of potential lines that can be used to develop hybrids and varieties. In recent years, yield improvement in rice achieved by exploiting heterosis. Heterotic performance of a hybrid combination depends upon the combining ability of its parents. It is therefore, necessary to access the genetic potentialities of the hybrid combination through systematic studies in relation to general and specific combining abilities which are due to additive and non-additive gene action, respectively.

Combining ability studies attempted in individual environment may not provide precise information on gene action as the environment plays an important role and influences the combining ability estimates. Hence, the estimates of general combining ability of 17 parents and specific combining ability of 60 hybrids for yield and its components were investigated across three locations and pooled analysis was attempted. The results of pooled analysis in respect of analysis of variance, ratio of *gca* to *sca* variance and estimates of *gca* and *sca* effects are discussed here.

OBSERVATIONS AND ANALYSIS

The pooled analysis of variance for combining ability over three locations represented the existence of obvious significant differences for locations for all the characters except 1000-grain weight investigated suggesting the sufficient diversity among the environments. The differences among the parents, parents vs. crosses and crosses were observed to be significant for all the characters studied; clearly indicating the considerable variability among parents and crosses, whereas significant variance due to parents vs. crosses indicated the presence of heterosis for all the characters investigated. Further, partitioning of crosses into lines, testers and lines x testers revealed that the variance due to lines were significant for all the characters except days to 50% flowering and number of productive tillers per plant, whereas for testers, all the characters were found significant, suggests wide variability existing among the genotypes. The interaction

Table 1: Pooled analysis of variance for combining ability (L × T) for yield and yield components over locations in rice

Source of variation	d.f.	Days to 50% flowering	Number of productive tillers per plant	Panicle length (cm)	Number of filled grains per panicle	Spikelet fertility percentage	1000-grain weight (g)	Single plant yield (g)
					Mean sum of squares			
Locations	2	36.642 **	38.031 **	156.643 **	14949.27 **	257.664 **	0.424	631.169 **
Replications × Locations	4	0.196	1.349	0.772	125.617	14.305	0.191	2.778
Treatments	76	311.718 **	23.842 **	14.942 **	8427.677 **	130.999 **	19.524 **	306.947 **
Parents	16	264.791 **	1.489 **	17.078 **	2161.606 **	70.975 **	34.428 **	30.189 **
Parent vs. Crosses	1	5135.646 **	576.240 **	6.706 **	99867.090 **	127.597 **	79.022 **	8612.396 **
Crosses	59	242.682 **	20.541 **	14.503 **	8577.129 **	147.334 **	14.473 **	241.229 **
Lines	4	179.744	11.807	23.366 **	15158.560 **	275.399 **	27.290**	242.810*
Testers	11	930.406 **	77.390 **	55.870 **	27786.25 **	397.911 **	53.770 **	831.909 **
Lines × Testers	44	76.473 **	7.124 **	3.355 **	3176.537 **	73.047 **	3.484 **	93.415 **
Parents × Locations	32	1.895 **	0.730	2.299 **	321.070 **	46.949 **	0.761 *	4.890
(Parent vs. Cross) × Locations	2	4.995 **	4.809 **	0.136	108.254	8.072	0.93	22.111
Crosses × Locations	118	4.308 **	3.563 **	2.882 **	1725.646 **	47.547 **	1.019 **	50.122 **
Lines × Locations	8	7.659	2.426	3.287	2953.587	134.476 *	1.106	54.414
Testers × Locations	22	4.755	6.374 **	3.656	1988.76	59.935	1.165	78.505 *
Lines × Testers × Locations	88	3.891 **	2.964 **	2.652 **	1548.237 **	36.547 **	0.974 **	42.636 **
Error	456	0.565	0.716	0.519	204.268	20.034	0.466	9.134

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

between lines and testers were significant for all the traits studied, suggesting that significant contribution of *sca* effects towards the variation among the crosses (Table 1). These results earlier have been reported by Salgotra *et al.* (2009), Rahimi *et al.* (2010), Selvaraj *et al.* (2011), Ghosh *et al.* (2012), Upadhyay and Jaiswal (2015) and Ku *et al* (2016). Furthermore, the *sca* variances were more sensitive to environmental fluctuations as evident by interaction effects of lines x testers x locations were significant for all the characters studied (Table 1). These results emphasized the importance of combining ability studies indicates the existence of wide variability in the material studied, thus justifying its use in the present investigation and there is a good scope for identifying promising parents and hybrids combinations and improving the yield through its components.

Proportional contribution of lines, testers and their interaction to the total variance indicate predominant tester influence for all the traits, whereas lines and line x tester interaction contribution was not high for any trait in pooled analysis (Table 2).

In pooled analysis, the predominant role of non-additive gene actions in the manifestation of all the traits except panicle length and 1000-grain weight was confirmed by higher values of *sca* variance than for *gca* variance, the ratio of *gca* to *sca* variance being less than

unity and the degree of dominance being greater than unity. These results indicate the presence of greater non-additive genetic variance and over dominance for high level of expression of these traits offers the scope for exploitation of the hybrid vigor through heterosis breeding. The main reason ascribed is diversified parents involved in the cross combination or involvement of uncommon genes in controlling various traits, whereas, degree of dominance less than unity was noticed for panicle length and 1000-grain weight since these traits are governed by incomplete or partial dominance (Table 3). Similar to the present findings, the role of non-additive gene action was documented by Salgotra *et al.* (2009), Rahimi *et al.* (2010), Selvaraj *et al.* (2011), Ghosh *et al.* (2012), Upadhyay and Jaiswal (2015) and Ku *et al* (2016) in rice for expression of yield and its components. However, the importance of additive components in rice were reported by Sharma and Mani (2008) for panicle length and Swain *et al.* (2003), Sanjeev Kumar *et al.* (2007) and Upadhyay and Jaiswal (2015) for 1000-grain weight which were in agreement with the present study. Yet, interestingly the role of both additive and non-additive gene action was documented by Patil *et al.* (2003) for 1000-grain weight and Kumar *et al.* (2007) for single plant yield in rice. The discrepancy among the results reported may be due to the differences in the material

Table 2 : Proportional contributions of lines, testers and their interactions to the total variance for various traits over locations in rice

Character	Contribution		
	Line (%)	Tester (%)	Line x Tester (%)
Days to 50% flowering	5.02	71.48	23.50
Number of productive tillers/Plant	3.90	70.24	25.86
Panicle length (cm)	10.92	71.82	17.25
Number of filled grains per panicle	11.98	60.39	27.62
Spikelet fertility percentage	12.67	50.35	36.97
1000-grain weight (g)	12.78	69.27	17.95
Single plant yield (g)	6.82	64.30	28.88

Table 3: Estimates of general and specific combining ability variances and proportionate gene action for yield and its components over locations in rice

Character	Source of variation			Nature of gene action	Degree of dominance
	$\sigma^2 gca$	$\sigma^2 sca$	$\sigma^2 gca/\sigma^2 sca$		$?\sigma^2 sca/\sigma^2 2gca$
Days to 50% flowering	7.2494	8.4420	0.8587	Non-additive	1.0791
Number of productive tillers/Plant	0.5732	0.7084	0.8091	Non-additive	1.1117
Panicle length (cm)	0.5115	0.3184	1.6065	Additive	0.7889
Number of filled grains per panicle	277.8647	328.9751	0.8446	Non-additive	1.0881
Spikelet fertility percentage	4.1276	5.7947	0.7123	Non-additive	1.1849
1000-grain weight (g)	0.5250	0.3459	1.5178	Additive	0.8118
Single plant yield (g)	6.8821	9.1706	0.7505	Non-additive	1.1544

used for the study.

The selection of parents based on *per se* performance may not always result in producing superior hybrids. Dhillon (1975) pointed out that combining ability of parents gives useful information on the choice of parents in terms of expected performance of their progenies. In the present investigation, the results revealed that none of the parents recorded significant *gca* effects simultaneously in the desired direction except tester, KMR-3R for all the traits studied (Table 4). The *gca* effects of the parents revealed that the line, APMS-6A was the best general combiner for most of the traits like panicle length, number of productive tillers per plant, filled grains per panicle, spikelet fertility percentage and single plant yield by exhibiting significant positive *gca* effects. This line also exhibited negative significant *gca* effect for the trait of days to 50% flowering which is considered as a desirable character, thus can use this parent for early maturity in hybrid breeding programmes. Further, the line IR-80151A contributed a large number of favorable alleles for 1000-grain weight and single plant yield as indicated by their high *gca* effects for these characters. Among the testers, IR-54742R, BR-827-35R,

KMR-3R and IR-21567R were best general combiners for majority of the important components, *i.e.*, panicle length, number of productive tillers per plant, number of filled grains per panicle, spikelet fertility percentage, 1000-grain weight and single plant yield except 1000-grain weight in case of IR-21567R and also the tester, KMR-3R exhibited high negative *gca* effects for days to 50% flowering in desired direction. Further, the tester IR-24R manifested significant positive *gca* effects for single plant yield and also exhibited significant negative *gca* effects for days to 50% flowering (Table 4).

None of the cross combinations exhibited significant and desirable *sca* effect for all the traits (Table 5) indicating that no specific combination was desirable for all the traits. These results are in conformity with the findings of Salgotra *et al.* (2009), Rahimi *et al.* (2010) and Tiwari *et al.* (2011). Single plant yield is the ultimate trait which determines the worthiness of a hybrid in hybrid rice breeding programme. For this trait, out of 60 hybrids, five best cross combinations *viz.*, IR-80561A x IR-32809R followed by IR-80555A x DR-714-1-2R, IR-80559A x 72R, IR-80559A x IR-32809R and IR-80561A x IR-40750R were identified as best specific combiners

Table 4 : Estimates of general combining ability effects of parents for various traits over locations in rice

Parents	Days to 50% flowering	No. of productive tillers/ Plant	Panicle length (cm)	No. of filled grains/panicle	Spikelet fertility percentage	1000-grain weight (g)	Single plant yield (g)
Lines							
IR-80151 A	1.08 **	-0.08	0.02	2.43	-0.83	0.23 **	0.64 *
IR -80555 A	1.20 **	-0.26 **	-0.35 **	-6.41 **	-0.31	0.02	-1.26 **
IR -80559 A	0.28 **	0.27 **	0.64 **	-0.48	1.76 **	0.70 **	0.27
IR- 80561 A	-0.74 **	-0.34 **	-0.53 **	-13.65 **	-2.05 **	-0.38 **	-1.68 **
APMS 6 A	-1.83 **	0.42 **	0.22**	18.11 **	1.44 **	-0.57 **	2.03 **
S E (Lines)	0.07	0.08	0.07	1.41	0.44	0.06	0.31
Testers							
IR- 66 R	-1.78 **	-2.11 **	-1.28 **	-39.57**	-4.74 **	-0.79 **	-6.84 **
IR -10198 R	-4.00 **	-0.21	-0.03	-7.30**	1.40 *	-0.21 *	-0.79
DR-714 -1- 2R	-2.40 **	-0.28 *	-0.61 **	-1.56	0.24	-1.55 **	0.17
IR -40750R	-5.03 **	-1.67 **	-1.26 **	-33.77 **	-3.68 **	-0.80 **	-6.34 **
IR-72R	-2.43 **	-0.88 **	-0.91 **	-18.18 **	-2.37 **	-0.15	-3.50 **
IR-24R	-0.20 *	0.09	-0.12	-1.60	-1.02	-0.19 *	1.43 **
IR-21567 R	1.61 **	0.43 **	0.29 **	13.76 **	3.06 **	-0.29 **	2.50 **
KMR-3 R	-0.40 **	1.52 **	1.14 **	32.84 **	3.18 **	0.18 *	4.74 **
IR-32809 R	-3.83 **	-0.77 **	-0.74 **	-10.69**	-2.25 **	-0.52 **	-3.19 **
IR-63883-41-3R	1.08 **	-0.001	0.12	-1.08	-1.12	0.31 **	0.78
IR-54742 R	9.28 **	2.23 **	2.54 **	38.94 **	3.65 **	2.62 **	6.22 **
BR-827-35 R	8.14 **	1.65 **	0.85 **	28.22 **	3.65 **	1.41 **	4.82 **
S E (Testers)	0.10	0.13	0.10	2.19	0.68	0.09	0.49

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

had both the parents were poor general combiners. Other five cross combinations *viz.,* IR-80151A x IR-10198R, IR-80151A x DR-714-1-2R, IR-80151A x IR-66R, IR-80555A x IR-21567R and IR-80151A x IR-63883-41-3R were found to be good with one better combiner, while in case of APMS 6A x IR-24R, both parents were better combiners. All of these above mentioned crosses expressed significant and desirable *sca* effects for one or more component traits of seed yield per plant in which top most ranking hybrid, IR-80561A x IR-32809R exhibited significant and desirable *sca* effects for most of the important yield component traits (Table 5). Similar findings as observed in the present study were also reported by, Dalvi and Patel (2009) and Salgotra *et al.* (2009).

In the present investigation, first five top ranking hybrids that exhibited superior *per se* performance and maximum *sca* effects for single plant yield and its important traits are presented in Table 6. The overall perusal of *sca* effects and *per se* performance of different traits in the present investigation reveals that ranking based on *sca* effects of the hybrids showed reasonable deviation from *per se* performance for all the characters as parallelism between *per se* performance and *sca* effects was not existed in majority of the top five crosses. This could be expected, since the *sca* effects are only the estimates. The large *sca* effect need not necessarily result in exceptional performance of a cross. However, the *sca* effects along with *per se* performance of hybrids could give an idea about the practical utility of hybrid combinations for heterosis breeding. Thus crosses with high *per se* performance need not be the one with high *sca* effects and *vice versa*. However, some of the crosses manifesting desirable *sca* effects were also having superior *per se* performance for few of traits, thus indicating the selection of these crosses on the basis of *per se* performance will be effective. In this regard, APMS 6A x IR-24R for single plant yield, productive tillers per plant, filled grains per panicle, IR-80555A x IR-24R and APMS 6A x DR-714-1-2R for days to 50% flowering, IR-80151A x IR-63883-41-3R for spikelet fertility and IR-80151A x KMR-3R and IR-80561A x IR-54742R for 1000-grain weight were promising ones. These results are in agreement with Saleem *et al.* (2010) and Selvaraj *et al.* (2011) who reported several promising specific combiners based on high *per se* performance

and *sca* effects for grain yield and its components.

Further, in majority of the top five crosses for all the characters investigated, high *sca* was either due to high x low or low x high or low x low combining parents, which further substantiate the operation of non-additive and additive gene action (Table 6). Involvement of high x low or low x high combining parents were found in the top five cross combinations for different traits *viz.,* IR-80555A x IR-24R and APMS 6A x IR-21567R for days to 50% flowering, IR-80559A x IR-72R and APMS 6A x IR-24R for the trait of number of productive tillers per plant, IR-80559A x IR-72R and APMS 6A x DR-714-1-2R for panicle length, APMS 6A x IR-24R and IR-80555A x IR-21567R for the trait of number of filled grains per panicle, IR-80561A x IR-32809R, IR-80561A x IR-40750R and IR-80559A x IR-72R for spikelet fertility and IR-80559A x DR-714-1-2R and IR-80561A x IR-54742R for 1000-grain weight (Table 6). These results are supported by the findings of Salgotra *et al.* (2009), Bagheri and Jelodar (2010), Selvaraj *et al.* (2011) and Rumanti *et al.* (2017) for various traits. Peng and Virmani (1990) also reported the possibility of interaction between positive alleles from good combiner and negative alleles from poor combiner in high x low or low x high combiner crosses and suggested for exploitation of heterosis in F_1 generation, as their high yielding potential would be unfixable in succeeding generation.

Furthermore, involvement of low x low combining parents produced superior specific combining hybrids as evident among the top five cross combinations for different traits *viz.,* IR-80151A x IR-21567R for days to 50% flowering, IR-80561A x IR-32809R*,* IR-80151A x DR-714-1-2R and IR-80555A x DR-714-1-2R for the trait of number of productive tillers per plant, IR-80151A x IR-24R, IR-80561A x IR-32809R and IR-80555A x IR-63883-41-3R for panicle length, IR-80561A x IR-32809R, IR-80559A x IR-72R and IR-80559A x IR-32809R for number of filled grains per panicle, IR-80151A x IR-63883-41-3R and IR-80555A x IR-72R for spikelet fertility and IR-80561A x IR-32809R and APMS 6A x IR-40750for 1000-grain weight. It is observed from the above results that the superiority of low x low combinations might be due to dominance x dominance interaction or concentrations and interaction between favorable genes contributed by parents, which have also been suggested by Dalvi and Patel (2009). Gupta (1981) also observed that *gca* of the parents in general had no

Table 5: Estimates of specific combining ability effects for yield and its components over locations in rice

Cross	Days to 50% flowering	No. of productive tillers/plant	Panicle length (cm)	No. of filled grains /panicle	Spikelet fertility percentage	1000-grain weight (g)	Single plant yield (g)
IR- 80151Ax IR- 66 R	-0.22	0.68*	0.48*	12.39*	-0.09	-0.13	2.95**
IR -80151Ax IR -10198 R	1.91**	0.81**	0.67**	19.54**	1.95	-0.04	3.58**
IR -80151Ax DR-714 -1-2R	0.44	1.04**	0.17	12.55*	2.59	0.14	3.44**
IR -80151Ax IR -40750R	-0.49*	-0.14	0.32	-2.51	-6.99**	-0.27	-0.76
IR- 80151Ax IR-72R	2.09**	-0.95**	-0.52*	-23.50**	-3.58*	-0.64**	-2.71*
IR- 80151Ax IR-24R	3.53**	-0.09	1.20**	-8.32	-0.75	-0.32	1.99
IR-80151Ax IR-21567 R	-4.62**	-0.37	-0.09	7.63	2.37	0.33	-1.52
IR -80151Ax KMR-3 R	1.51**	-0.15	0.16	-17.04**	-0.15	2.28**	-1.04
IR- 80151Ax IR-32809 R	-1.84**	-1.37**	-1.37**	-28.59**	-5.89**	-1.24**	-6.82**
IR- 80151Ax IR-63883-41-3R	1.36**	0.93**	-0.72**	13.32**	6.69**	-0.31	2.37*
IR- 80151Ax IR-54742 R	-1.51**	-0.37	0.18	9.78*	2.72	0.67**	-0.85
IR- 80151Ax BR-827-35 R	-2.16**	-0.02	-0.49*	4.74	1.14	-0.47*	-0.63
IR- 80555Ax IR- 66 R	-0.23	0.12	0.20	4.30	-1.50	0.21	0.92
IR- 80555Ax IR -10198 R	-1.54**	0.36	-0.43	-6.59	0.84	0.66**	-0.48
IR- 80555Ax DR-714 -1-2R	1.77**	0.96**	-0.21	21.04**	2.45	0.10	4.50**
IR- 80555Ax IR -40750R	-1.05**	0.01	-0.29	3.20	0.63	0.15	0.24
IR- 80555Ax IR-72R	-1.92**	0.32	-0.42	4.95	4.93**	0.01	0.18
IR -80555Ax IR-24R	-6.81**	0.32	0.36	3.97	0.78	0.59**	-0.18
IR- 80555Ax IR-21567 R	11.92**	-0.30	0.42	22.33**	-1.04	-0.25	2.93**
IR- 80555Ax KMR-3 R	0.28	0.08	-0.39	-12.79**	-1.35	-0.57**	-0.03
IR- 80555Ax IR-32809 R	-0.85**	-1.64**	-0.21	-33.55**	-1.72	-0.04	-6.60**
IR- 80555Ax IR-63883-41-3R	0.12	-0.63*	1.02**	-2.99	-1.91	-0.01	-2.98**
IR -80555Ax IR-54742 R	-0.96**	-0.01	-0.03	9.85*	-1.45	-0.62**	1.62
IR -80555Ax BR-827-35 R	-0.72**	0.41	-0.01	-13.71**	-0.67	-0.23	-0.13
IR- 80559Ax IR -66 R	2.03**	-0.56	-0.70**	-2.34	0.11	-0.04	-1.72
IR- 80559Ax IR -10198 R	-0.62**	-1.19**	-0.75**	-29.44**	-3.29*	-0.15	-2.65*
IR-80559Ax DR-714 -1- 2R	0.92**	-0.66*	-0.26	-21.89**	-1.47	0.85**	-3.18**
IR- 80559Ax IR -40750R	1.76**	-0.31	0.18	-4.93	0.32	-0.08	-1.88
IR- 80559Ax IR-72R	-1.99**	1.15**	0.85**	28.35**	2.98	-0.05	4.49**
IR- 80559Ax IR-24R	0.56*	-0.03	-1.03**	0.73	2.23	-0.25	0.16
IR- 80559Ax IR-21567 R	-2.15**	0.57	0.48*	10.32*	0.31	-0.24	0.74
IR- 80559Ax KMR-3 R	0.43	-0.23	0.66**	17.85**	0.35	-0.47*	1.10
IR -80559Ax IR-32809 R	-2.37**	0.48	0.14	25.39**	1.45	0.02	3.01**
IR -80559Ax IR-63883-41-3R	1.61**	0.42	0.36	-0.08	-0.57	0.29	1.38
IR- 80559Ax IR-54742 R	-0.04	0.88**	-0.21	-6.57	-0.44	0.11	-0.13
IR- 80559Ax BR-827-35 R	-0.13	-0.52	0.28	-17.39**	-1.98	0.00	-1.31
IR- 80561Ax IR- 66 R	-2.72**	-0.18	0.50*	4.05	0.78	-0.36	-0.07
IR- 80561Ax IR -10198 R	-2.14**	-0.20	0.33	1.87	0.43	-0.12	-1.53
IR- 80561Ax DR-714 -1- 2R	0.06	-1.87**	-0.41	-22.47**	-2.34	-0.72**	-6.82**
IR -80561Ax IR -40750R	0.12	0.63*	-0.40	12.37*	3.74*	-0.51*	2.49*
IR- 80561Ax IR-72R	2.81**	-0.45	-0.21	-7.21	-3.50*	0.44*	-1.29
IR- 80561Ax IR-24R	1.81**	-1.85**	-0.71**	-23.72**	-4.23**	-0.35	-5.71**
IR- 80561Ax IR-21567 R	-1.23**	0.89**	-0.37	-11.80*	-0.70	-0.01	1.03
IR- 80561Ax KMR-3 R	-2.10**	0.31	0.12	19.76**	1.89	-0.24	1.95
IR- 80561Ax IR-32809 R	2.10**	2.27**	1.08**	40.85**	4.00**	0.72**	8.40**
IR -80561Ax IR-63883-41-3R	-1.14**	-0.17	-0.73**	-8.82	-3.33*	-0.06	-0.36
IR- 80561Ax IR-54742 R	0.77**	0.36	0.18	-13.27**	1.05	0.78**	-0.02
IR- 80561Ax BR-827-35 R	1.68**	0.27	0.64**	8.40	2.23	0.43*	1.93
APMS 6Ax IR- 66 R	1.15**	-0.07	-0.47*	-18.40**	0.70	0.32	-2.07
APMS 6Ax IR -10198 R	2.39**	0.22	0.18	14.62**	0.08	-0.35	1.08
APMS 6Ax DR-714 -1-2R	-3.19**	0.53	0.71**	10.77*	-1.23	-0.37	2.06
APMS 6Ax IR -40750R	-0.34	-0.19	0.18	-8.12	2.31	0.72**	-0.08
APMS 6Ax IR-72R	-0.99**	-0.07	0.30	-2.59	-0.82	0.23	-0.67
APMS 6Ax IR-24R	0.90**	1.65**	0.18	27.34**	1.98	0.33	3.74**
APMS 6Ax IR-21567 R	-3.92**	-0.77**	-0.44	-28.47**	-0.94	0.18	-3.19**
APMS 6Ax KMR-3 R	-0.12	-0.01	-0.54*	-7.78	-0.73	-0.99**	-1.99
APMS 6Ax IR-32809 R	2.97**	0.26	0.36	-4.11	2.15	0.54**	2.01
APMS6Ax IR-63883-41-3R	-1.94**	-0.55	0.07	-1.42	-0.88	0.08	-0.41
APMS 6Ax IR-54742 R	1.75**	-0.87**	-0.12	0.20	-1.89	-0.94**	-0.62
APMS 6Ax BR-827-35 R	1.33**	-0.14	-0.42	17.96**	-0.72	0.26	0.14
SE (Crosses)	0.23	0.29	0.23	4.90	1.52	0.20	1.10

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

bearing on the *sca* effects of the cross *i.e.*, the cross involving parents with high *gca* recorded less *sca* effects, while the parents with poor *gca* effect exhibited high *sca* effects. This may be due to genetic diversity in the form of number of heterozygous loci in the parents as reported by Pathak *et al*. (1993).

Besides these interactions, both parents were found to be the best general combiners in the top five cross combinations which could be ascribed due to predominance of additive x additive type of gene action

for different traits *viz*., IR-80561A x IR-66R and APMS 6A x DR-714-1-2R for days to 50% flowering, IR-80151A x KMR-3R for 1000-grain weight and APMS 6A x IR-24R for single plant yield. Salgotra *et al*. (2009) also reported on the interactions between positive and positive alleles in crosses involving high x high combiners which can be fixed in subsequent generations for effective selection, if no repulsion phase linkages are involved.

In the present investigation, it can be emphasized

Table 6 : Top five crosses on the basis of high *per se* performance, *sca* effects and *gca* effects of parents for single plant yield (g) and its components over locations in rice.

Character	*Per se* performance	*sca* effect	*gca* status of parents
Days to 50% flowering	APMS 6A x DR-714-1-2R	IR-80555A x IR-24R	Low x High
	IR-80561A x IR-10198 R	IR-80151A x IR-21567R	Low x Low
	IR-80559 A x IR-32809 R	APMS 6A x IR-21567R	High x Low
	IR-80555 A x IR-24 R	APMS 6A x DR-714-1-2R	High x High
	IR-80559 A x IR-10198 R	IR-80561A x IR-66R	High x High
Productive tillers per plant	IR-80559 A x IR-54742 R	IR-80561A x IR-32809R	Low x Low
	IR-80561 A x IR-54742 R	APMS 6A x IR-24R	High x Low
	APMS 6A x IR-24 R	IR-80559A x IR-72R	High x Low
	IR-80555 A x IR-54742 R	IR-80151A x DR-714-1-2R	Low x Low
	APMS 6A x BR-827-35R	IR-80555A x DR-714-1-2R	Low x Low
Panicle length (cm)	IR-80559 A x IR-54742 R	IR-80151A x IR-24R	Low x Low
	IR-80151 A x IR-54742 R	IR-80561A x IR-32809R	Low x Low
	APMS 6A x IR-54742 R	IR-80555A x IR-63883-41-3R	Low x Low
	IR-80559 A x KMR-3 R	IR-80559A x IR-72R	High x Low
	IR-80561 A x IR-54742 R	APMS 6A x DR-714-1-2R	High x Low
Filled grains per panicle	APMS 6A x BR-827-35R	IR-80561A x IR-32809R	Low x Low
	APMS 6A x IR-54742 R	IR-80559A x IR-72R	Low x Low
	IR-80151A x IR-54742 R	APMS 6A x IR-24R	High x Low
	IR-80559 A x KMR-3R	IR-80559A x IR-32809R	Low x Low
	APMS 6A x IR-24 R	IR-80555A x IR-21567R	Low x High
Spikelet fertility percentage	IR-80559 A x KMR-3R	IR-80151A x IR-63883-41-3R	Low x Low
	IR-80559 A x IR-21567 R	IR-80555A x IR-72R	Low x Low
	IR-80559 A x IR-54742 R	IR-80561A x IR-32809R	High x Low
	IR-80151 A x IR-63883-41-3R	IR-80561A x IR-40750R	High x Low
	IR-80151 A x IR-21567 R	IR-80559A x IR-72R	High x Low
1000-grain weight (g)	IR-80151 A x IR-54742 R	IR-80151A x KMR-3R	High x High
	IR-80559 A x IR-54742 R	IR-80559A x DR-714-1-2R	High x Low
	IR-80561 A x IR-54742 R	IR-80561A x IR-54742R	Low x High
	IR-80151 A x KMR-3R	IR-80561A x IR-32809R	Low x Low
	IR-80559 A x BR-827-35R	APMS 6A x IR-40750 R	Low x Low
Single plant yield (g)	APMS 6A x IR-54742 R	IR-80561A x IR-32809R	High x Low
	APMS 6A x IR-24 R	IR-80555A x DR-714-1-2R	Low x Low
	APMS 6A x BR-827-35R	IR-80559A x IR-72R	Low x Low
	IR-80555 A x IR-54742 R	APMS 6A x IR-24R	High x High
	IR-80559 A x IR-54742 R	IR-80151A x IR-10198R	High x Low

that among the lines, APMS 6A and IR-80151A and the testers, IR-54742R, BR-827-35R, KMR-3R and IR-21567R were proved to be good combiners for single plant yield and its components by exhibiting high *gca* effects for majority of the yield and yield contributing traits. Hence, these female and male parents could be considered as potential donors in improving single plant yield and its components need to be exploited in future breeding programme. Among the hybrids, APMS 6A x IR-24R, IR-80561A x IR-32809R, IR-80151A x IR-10198R, IR-80555A x DR-714-1-2R and IR-80559A x IR-72R manifested the desired significant *sca* effects and *per se* performance for yield and its important components.

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