

COMBINING ABILITY FOR YIELD AND YIELD ASSOCIATED TRAITS IN RICE (*Oryza Sativa* L.)

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Abstract

Twenty hybrids developed using five CMS lines and four restorers along with their parents were evaluated for ten quantitative traits to explain the nature of gene action present in the inheritance these traits. Analysis of variance revealed significant difference among the genotype, crosses and parents. Variance of sca was higher than that of gca for all the characters suggesting the significant role of non-additive gene action on the inheritance of these character. The relative contribution of lines, testers and combination of line \times tester for all characters were calculated. It was found that lines were more important and their contribution was high for most of the traits indicated highly influence by maternal effects. The cross IR58025A/ BR9157-12-2-37-13-71-32R was the best specific combiner for grain yield. Estimates of gca effects showed that BRR113A and BR9157-12-2-37-13-15-40R were the best general combiners for improving yield and other characters. The cross BRR133A/ BR9159-8-5-49-1-1R was found to be a good specific combiner for most of the characters. It was identified as the most promising hybrid. The cross combination of good general combiner would not always produce the best specific crosses. Moreover, the predominance of production of the best specific crosses from high \times low and low \times low combiners reported the influence of non-additive and over-dominance gene action on the plant stature.

Keywords: L \times T analysis, GCA, SCA, grain yield, hybrid rice.

Introduction

Rice is a nutritious cereal crop of the world. It gives 20 percent of the calories and 15 percent protein taken by world population. Bangladesh agriculture involves food production for 163.65 million people from merely 8.75 million hectares of agricultural land (Salam *et al.*, 2014). Bangladesh is the fourth largest producer and consumer of rice in the world with an annual production ranging from 25 to 30 million tons. Rice occupies 77% of total cropped area. At present rice alone constitutes

about 92% of the total food grains produced annually in the country. It provides 75% of the calories and 55% of the proteins in the average daily diet of the people (Bhuiyan *et al.*, 2002). Compared with mid-sixties, Bangladesh has almost doubled its production during the past three decades and the higher rate of production mainly came from reallocation of land from traditional to the high yielding modern varieties. In the last few years (2009-10 to 2013-14), rice production has increased by 0.34 MT per year (BBS, 2014). According

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to Kabir *et al.* (2015), the population of Bangladesh is growing by 1.22% and the total population will be 233.2 millions in the next 40 years if the current trend continues. Therefore, Bangladesh will require more than 57.0 million tons of rice to feed its people by the year 2050.

To produce the required quantity, the only option remains open is the increase production per unit area, as there is scarcity of land, labor and water. Among the options if increasing production, the innovative genetic option of hybrid rice technology is practically feasible and readily adoptable (Viraktamath *et al.*, 2010). Performance of a F_1 hybrid depends on choice of parents. Several methods like per se performance, genetic diversity, combining ability, etc., have been attempted to select the parents. Among them combining ability is one of the powerful tools in identifying the best combiners that may be used in crosses either to exploit heterosis or to accumulate fix genes. To exploit heterosis using CMS technique in the hybrid program, one must know the combining ability of different male sterile and restorer lines. It helps know the genetic architecture of various characters that enable the breeder to design effective breeding plan for future up-grading of the existing materials. The information is also useful to breeders for genetic improvement of the existing rice genotypes on the basis of the performance in various hybrid combinations. Since the information on heterotic effect of F_1 hybrids, their genetic control and combining ability are very much limited in rice, a comprehensive study was undertaken on the basis of different agronomic and morphological characters for assessing the combining ability of selected parents and their hybrids and estimating

the nature of gene action and magnitude of heterosis.

Materials and Methods

The experimental material consists of nine rice genotypes viz, IR58025A, IR79156A, BRRI33A, BRRI13A, and BRRI7A were used as female (designated as lines) and four genotypes (BR9157-12-2-37-13-15-40R, BR9157-12-2-37-13-17-32R, BR9159-8-5-49-1-1R, and BR9159-8-5-40-13-8R) were used as male designated as tester. These parents were crossed to produce 20 F_1 hybrids according to line \times tester mating design (Kempthorne, 1957). This study was conducted in consecutive two years comprising of Boro 2015-16 and T. Aman 16 at Research Station of Bangladesh Rice Research Institute, Gazipur. In Boro season of 2015-16, Line and Tester materials were grown separately in stagger fashion with an interval of five days so as to synchronize flowering. At flowering stage, crossing was made in Line \times Tester fashion to raise 20 F_1 test hybrids. Single seedlings of each entry were transplanted at 15 \times 20 cm spacing in 3 \times 5 m² plots in a RCBD (randomized complete block design) with three replications. Data were recorded on plant height (PH) (cm), days to 50% flowering (DF) (days), days to maturity (DM) (days), panicle length (PL) (cm), panicle weight (PW) (g), number of panicle/m² (PPM), number of spikelet/panicle (SPP), spikelet fertility (SF), 1000 grain weight (TGW) (g) and grain yield (YLD) (t/ha) based on standard evaluation system of rice (Scshu, 1988). Collected data were subjected to statistical analysis using line \times tester analysis by Kempthorne (1957).

Results and Discussion

Analysis of variance

Analysis of variance for combining ability of ten characters exhibited significant differences among the genotype, crosses and parents for all the traits (Table 1). Analysis of crosses effect to its components (line, tester and parents vs crosses) expressed highly significant difference (at 1% level) among testers for all traits except panicle weight, spikelet fertility and grain yield. Similarly, among lines, most of the traits except panicle weight, spikelet per panicle, spikelet fertility, and grain yield and in parents vs crosses all traits. There was highly significant difference (at 1% level) among line \times tester for all traits. The significant differences among the lines, tester and line \times tester indicated that the genotype had wide genetic diversity among themselves for all traits. Significant mean sum of square due to lines and tester for a particular trait

indicate the prevalence of additive variance. In the present study, additive genetic variance was less than non-additive variance for all traits indicating the predominance of non-additive gene action (Table1). The variance due to sca was larger than the variance due to gca for all the character, which were lighted in σ^2 gca: σ^2 sca ratio being less than unity. This result indicated highly influenced by non-additive gene action. Similar results were reported by Hasan *et al.* (2014) and Upadhyay and Jaiswal (2015).

Proportional contribution

The proportional contribution of lines, testers and their interaction for ten characters are presented in Table 2. Results revealed that tester played very important role only for the trait panicle length and spikelets per panicle, which indicate dominance of parental influence for both the traits. Lines were more important and its contribution was high for

Table 1. Analysis of variances for different yield and yield contributing character in rice

Parameter	df	PH	DF	DM	PL	PW	PPM	SPP	SF	TGW	YLD
Genotype	28	360.48**	66.31**	83.04**	6.55**	1.68**	4887.14**	1867.05**	1450.89**	7.03**	21.10**
Replication	2	15.29**	9.98**	5.70**	1.58**	0.06	1230.81**	354.83	5.52	0.02	2.12**
Parents	8	785.06**	115.92**	142.83**	9.88**	2.34**	2337.96**	868.42**	3219.58**	4.02**	23.42**
Parents vs Crosses	1	860.74**	32.55**	14.89**	11.26**	15.55**	58917.99**	8638.73**	5959.22**	17.45**	240.71**
Crosses	19	155.38**	47.19**	61.46**	4.89**	0.67**	3116.75**	1931.13**	468.90**	7.75**	8.56**
Line	4	334.27**	122.22**	164.82**	4.51**	0.16	8843.22**	1949.03	971.47	22.42**	10.67
Tester	3	366.86**	96.46**	124.95**	20.28**	0.21	1134.04	4519.40**	143.00	8.34**	1.00
Lines \times Testers	12	42.87**	9.86**	11.12**	1.17**	0.96**	1703.60**	1278.08**	382.85**	2.71**	9.75**
Error	56	4.14	0.38	0.27	0.38	0.07	162.04	180.38	21.76	0.27	0.25
Variance Component											
σ^2 gca		3.28	1.08	1.46	0.11	-0.01	41.24	19.06	2.51	0.15	-0.04
σ^2 sca		12.91	3.16	3.61	0.26	0.29	513.85	365.90	120.36	0.81	3.16
σ^2 A		8.75	2.90	3.91	0.29	-0.02	109.98	50.82	6.69	0.39	-0.09
σ^2 D		22.95	5.62	6.42	0.47	0.53	913.51	650.49	213.97	1.44	5.62
σ^2 gca/ σ^2 sca		0.25	0.34	0.40	0.42	-0.03	0.08	0.05	0.02	0.18	-0.01

* $p < 0.05$, ** $p < 0.01$. PH= Plant height, DF= Days to 50% flowering, DM= Days to maturity, PL= Panicle length, PW= Panicle weight, PPM=Number of panicle/m², SPP= Number of spikelet/panicle, SF=Spikelet fertility, TGW= 1000 grain weight and YLD= Grain yield

Table 2. Proportional contribution (%) of line, tester and their interaction to total variance for different yield and yield contributing characters

Proportional contribution	PH	DF	DM	PL	PW	PPM	SPP	SF	TGW	YLD
Line	45.29	54.52	56.46	19.41	4.92	59.73	21.24	43.61	60.90	26.24
Tester	37.28	32.27	32.10	65.43	4.97	5.74	36.95	4.81	17.00	1.84
Line×Tester	17.43	13.20	11.42	15.15	90.11	34.52	41.80	51.56	22.09	71.91

PH= Plant height, DF= Days to 50% flowering, DM= Days to maturity, PL= Panicle length, PW= Panicle weight, PPM=Number of panicle/m², SPP= Number of spikelet/panicle, SF=Spikelet fertility, TGW= 1000 grain weight and YLD= Grain yield

most of the traits indicated high influence of maternal effect. The contribution of maternal and paternal interaction (line × tester) was low to high for all the traits under study. These results were in conformity with Pratap *et al.* (2013) and Saleem *et al.* (2010).

General combining ability

The line BRR17A (-7.07) was found as the best general combiner for plant height due to its significant negative gca effect. Among testers, BR9157-12-2-37-13-71-32R (-3.04) was found as good general combiner for plant height (Table 3). BRR17A showed significant negative gca value for early flowering (-3.98) and days to maturity (-4.55). Here the highest negative value is desirable for earliness. Among testers, BR9157-12-2-37-13-15-40R showed the highest significant negative value for 50% flowering (-3.56) and days to maturity (-4.15). Sharma and Mani (2008) reported similar result for days to flowering. Among CMS lines, IR58025A was the good general combiner for panicle length (0.61) and spikelets per panicle (17.26); BRR133A for panicle per meter² (42.17), spikelet fertility (8.72), and grain yield (1.50). Among testers, BR9159-8-5-49-1-1R was good general combiner for panicle length (1.50), panicles per meter² (7.65), and spikelets per panicle (13.65); BR9157-12-2-37-13-15-40R

for grain yield (0.34). The promising parents identified in terms of grain yield and earliness were BRR133A, BRR17A and BR9157-12-2-37-13-15-40R. A number of parents although had poor gca for grain yield were observed to exhibit good gca for other important traits (Table 3) and such results were in accordance with Tyagi *et al.* (2008).

Specific combining ability

Out of 20, 10 hybrids showed significant sca effects for plant height composed of five high × high and five high × low gca effect in sca analysis (Table 4). The cross combinations IR 79156A/BR9157-12-2-37-13-15-40R (-4.20), BRR133A/ BR9157-12-2-37-13-15-40R (-2.62), BRR133A/BR9159-8-5-40-13-8R (-2.63), BRR113A/BR9157-12-2-37-13-17-32R (-3.33), BRR17A/BR9157-12-2-37-13-17-32R (-2.39) and BRR17A/BR9159-8-5-40-13-8R (-3.72) showed highly significant negative sca effect for plant height indicating them as good specific combiner for dwarfness. These crosses involved parents with positive general combining ability effects for plant height. Biswas (2003) found high negative effect for crosses in which both parents with positive combiners for plant height. The excellence of low × low general combiners might be due to presence of over dominance effect.

Table 3. Estimates of general combining ability (gca) effects of lines and testers for yield and yield contributing traits in rice

Designation	PH	DF	DM	PL	PW	PPM	SPP	SF	TGW	YLD
A lines										
IR58025A	3.41**	3.26**	3.95**	0.61**	-0.16	-10.41**	17.26**	-11.40**	0.46**	-0.47**
IR79156A	4.28**	1.10**	1.20**	0.52**	0.03	-19.93**	-0.11	-7.78**	1.72**	-1.02**
BRR133A	3.64**	2.35**	2.61**	-0.06	0.15	42.17**	1.75	8.72**	-1.12**	1.50**
BRR113A	-4.27**	-2.73**	-3.21**	-0.91**	0.01	11.31**	-0.25	6.30**	-1.64**	0.13
BRR17A	-7.07**	-3.98**	-4.55**	-0.17	-0.04	-23.14**	-18.66**	4.16**	0.57**	-0.14
SE (gi)	0.59	0.18	0.15	0.17	0.08	3.67	3.87	1.34	0.15	0.15
SE (gi-gj)	0.83	0.25	0.21	0.25	0.11	5.19	5.48	1.90	0.22	0.21
R lines										
BR9157-12-2-37-13-15-40R	-1.63**	-3.56**	-4.15**	-1.32**	0.04	-3.45	12.15**	-0.75	-0.63**	0.34*
BR9157-12-2-37-13-71-32R	-3.04**	0.63**	1.51**	-0.18	0.13	-10.69**	-2.03	0.92	1.02**	-0.20
BR9159-8-5-49-1-1R	7.36**	0.50**	0.32*	1.50**	-0.02	7.65*	13.65**	-3.77**	-0.48**	0.05
BR9159-8-5-40-13-8R	-2.69**	2.43**	-4.15**	0.003	-0.16	6.49	-23.78**	3.60**	0.09	-0.02
SE (gi)	0.52	0.16	0.13	0.16	0.07	3.28	3.46	1.20	0.14	0.13
SE (gi-gj)	0.74	0.22	0.19	0.22	0.09	4.64	4.90	1.70	0.19	0.19

* $p < 0.05$, ** $p < 0.01$. PH= Plant height, DF= Days to 50% flowering, DM= Days to maturity, PL= Panicle length, PW= Panicle weight, PPM=Number of panicle/m², SPP= Number of spikelet/panicle, SF=Spikelet fertility, TGW= 1000 grain weight and YLD= Grain yield. Corresponding maintainer lines data for spikelet per panicle, spikelet fertility, 1000 grain weight and grain yield per plant were taken due to CMS line is unable to produce it

Table 4. Estimates of specific combining ability (sca) effects of hybrids for different yield and yield contributing traits in rice

Sl. No.	Designation	PH	DF	DM	PL	PW	PPM	SPP	SF	TGW	YLD
1	IR58025A/BR9157-12-2-37-13-15-40R	-2.03	-0.60	0.32	-0.25	-0.12	8.91	-17.93*	-0.24	1.38**	-0.17
2	IR58025A/BR9157-12-2-37-13-17-32R	0.65	-2.47**	-3.02**	0.39	0.73**	15.98*	24.20**	12.78**	-0.52	2.70**
3	IR58025A/BR9159-8-5-49-1-1R	0.48	1.67**	1.85**	0.33	-0.19	5.48	2.42	-4.35	0.22	-0.37
4	IR58025A/BR9159-8-5-40-13-8R	0.90	1.40**	0.85**	-0.47	-0.41**	-30.4**	-8.70	-8.20**	-1.09**	-2.16**
5	IR79156A/BR9157-12-2-37-13-15-40R	-4.20**	0.90**	0.40	-0.43	-0.77**	22.43**	-36.7**	-6.35*	0.43	-0.95**
6	IR79156A/BR9157-12-2-37-13-17-32R	0.68	-1.63**	-0.93**	0.14	0.48**	4.25	8.54	10.40**	-0.39	1.73**
7	IR79156A/BR9159-8-5-49-1-1R	1.08	0.50	1.27**	0.47	-0.58**	-12.92	3.20	-18.84**	-0.27	-2.43**
8	IR79156A/BR9159-8-5-40-13-8R	2.43*	0.23	-0.73*	-0.18	0.87**	-13.77	24.92**	14.80**	0.23	1.66**
9	BRR133A/BR9157-12-2-37-13-15-40R	-2.62*	-0.68	-0.35	0.05	0.13	-22.5**	10.88	-1.55	-0.18	-0.65*
10	BRR133A/BR9157-12-2-37-13-17-32R	4.39**	2.12**	1.65**	0.05	-0.35*	1.31	1.26	-12.19**	0.04	-1.08**
11	BRR133A/BR9159-8-5-49-1-1R	0.65	0.58	0.52	0.39	0.32*	-14.44	-12.97	11.04**	0.77*	0.74*
12	BRR133A/BR9159-8-5-40-13-8R	-2.63*	-2.02**	-1.82**	-0.48	-0.104	35.63**	0.83	2.69	-0.64*	0.99**
13	BRR113A/BR9157-12-2-37-13-15-40R	0.92	0.40	0.82**	0.66	0.48**	1.68	22.66**	2.98	-0.21	1.22**
14	BRR113A/BR9157-12-2-37-13-17-32R	-3.33**	2.53**	2.15**	0.09	-0.48**	-18.25*	-15.36	-2.11	-0.54	-1.39**
15	BRR113A/BR9159-8-5-49-1-1R	-0.60	-1.67**	-1.98**	-0.62	0.35*	-10.33	6.54	8.02**	-0.08	1.23**
16	BRR113A/BR9159-8-5-40-13-8R	3.02*	-1.27**	-0.98**	-0.14	-0.35*	26.90**	-13.84	-8.89**	0.83**	-1.06**
17	BRR17A/BR9157-12-2-37-13-15-40R	7.92**	-0.02	-1.18**	-0.03	0.28	-10.52	21.05**	5.16	-1.42**	0.56
18	BRR17A/BR9157-12-2-37-13-17-32R	-2.39*	-0.55	0.15	-0.68	-0.38*	-3.29	-18.65*	-8.88**	1.41**	-1.96**
19	BRR17A/BR9159-8-5-49-1-1R	-1.80	-1.08**	-1.65**	-0.57	0.09	32.21**	0.81	4.13	-0.65*	0.82**
20	BRR17A/BR9159-8-5-40-13-8R	-3.72**	1.65**	2.68**	1.28**	0.01	-18.39*	-3.21	-0.41	0.66*	0.57
	SE (Sij)	1.17	0.36	0.30	0.35	0.15	7.34	7.75	2.69	0.30	0.29
	SE (Sij-Ski)	1.66	0.50	0.42	0.50	0.21	10.39	10.96	3.81	0.43	0.41

$P < 0.05$, $p < 0.01$. PH= Plant height, DF= Days to 50% flowering, DM= Days to maturity, PL= Panicle length, PW= Panicle weight, PPM=Number of panicle/m², SPP= Number of spikelet/panicle, SF=Spikelet fertility, TGW= 1000 grain weight and YLD= Grain yield

Among 20 crosses, 12 crosses showed significant sca effects composed of seven high \times low and five low \times low gca effects for earliness (days to 50% flowering). Dominance \times dominance gene action was observed in these specific cross combinations (Table 5).

The cross combinations IR58025A/BR9157-12-2-37-13-17-32R (-2.47), IR79156A/BR9157-12-2-37-13-17-32R (-1.63), BRRI33A/BR9159-8-5-40-13-8R (-2.02), BRRI13A/BR9159-8-5-49-1-1R (-1.67) and BRRI7A/BR9159-8-5-49-1-1R (-1.08) were

Table 5. Distribution of crosses in relation to GCA effects of parents and SCA effects of crosses for yield and yield contributing characters in rice

Characters	SCA status of cross	GCA status of parent						Total
		H \times H	H \times M	H \times L	M \times M	M \times L	L \times L	
PH	+	2	0	2	0	0	0	4
	0	1	0	6	0	0	3	10
	-	3	0	3	0	0	0	6
DF	+	0	0	3	0	0	3	6
	0	2	0	3	0	0	3	8
	-	0	0	3	0	0	3	6
DM	+	2	0	2	0	0	3	7
	0	0	0	4	0	0	1	5
	-	2	0	4	0	0	2	8
PL	+	0	0	0	1	0	0	1
	0	2	6	3	3	4	1	19
	-	0	0	0	0	0	0	0
PW	+	0	0	0	6	0	0	6
	0	0	0	0	7	0	0	7
	-	0	0	0	7	0	0	7
PPM	+	0	2	1	0	1	1	5
	0	2	1	3	0	3	2	11
	-	0	1	1	0	1	1	4
SPP	+	0	2	1	0	1	0	4
	0	1	4	2	3	2	1	13
	-	1	1	0	0	1	0	3
SF	+	0	0	3	0	2	0	5
	0	2	4	1	0	1	1	9
	-	1	2	1	0	1	1	6
TGW	+	1	1	1	0	1	1	5
	0	2	1	5	0	0	3	11
	-	0	1	2	0	1	0	4
GY	+	0	3	0	2	3	0	8
	0	0	1	1	1	1	0	4
	-	1	1	1	3	2	0	8
Total	+	5	8	13	9	8	8	51
	0	12	17	28	14	11	15	97
	-	8	6	15	10	6	7	52

PH= Plant height, DF= Days to 50% flowering, DM= Days to maturity, PL= Panicle length, PW= Panicle weight, PPM=Number of panicle/m², SPP= Number of spikelet/panicle, SF=Spikelet fertility, TGW= 1000 grain weight and YLD= Grain yield

good specific combiner for earliness (Table 4). Crosses which recorded good sca for high yield (t/ha), earliness and quality may be utilized for commercial production of hybrid. On the contrary IR58025A/BR9159-8-5-49-1-1R (1.67), IR58025A/BR9159-8-5-40-13-8R (1.40), IR79156A/BR9157-12-2-37-13-15-40R (0.90), BRR133A/BR9157-12-2-37-13-17-32R (2.12), BRR113A/ BR9157-12-2-37-13-17-32R (2.53) and BRR17A/BR9159-8-5-40-13-8R (1.65) identified as the poor specific combiner for days to 50% flowering. This result was also in compliance with the findings of Hossain *et al.* (2009).

Among crosses, seven crosses had significant positive sca effects for days to maturity. The negative significant sca effect estimated for days to maturity in IR58025A/BR9157-12-2-37-13-17-32R (-3.02), IR79156A/BR9157-12-2-37-13-17-32R (-0.93), IR79156A/BR9159-8-5-40-13-8R (-0.73), BRR133A/BR9159-8-5-49-1-1R (-1.82), BRR113A/BR9159-8-5-49-1-1R (-1.98), BRR113A/BR9159-8-5-40-13-8R (-0.98), BRR17A/BR9157-12-2-37-13-15-40R (-1.18) and BRR17A/ BR9159-8-5-49-1-1R (-1.65) indicated that the hybrids had good specific combining ability for earliness. The cross combinations IR58025A/ BR9157-12-2-37-13-17-32R and IR79156A/ BR9157-12-2-37-13-17-32R exhibited negative significant sca effects due to having low \times low parental gca effect. Generally parents with low \times low general combining ability produced the best and early hybrids with highly significant negative sca effects (Table 5). This result indicated that dominant \times dominant type of gene action was responsible for the expression of earliness. Hasan *et al* (2015) reported similar result in rice. None of the crosses

exhibited significant sca effect for panicle length (Table 4). For panicle weight the cross combination IR58025A/ BR9157-12-2-37-13-17-32R, IR79156A/ BR9157-12-2-37-13-17-32R, IR79156A/ BR9159-8-5-40-13-8R, BRR113A/ BR9157-12-2-37-13-15-40R exhibited significant positive sca effects while IR58025A/BR9159-8-5-40-13-8R, IR79156A/BR9157-12-2-37-13-17-32R, IR79156A/BR9159-8-5-49-1-1R, BRR133A/ BR9157-12-2-37-13-17-32R, BRR113A/ BR9157-12-2-37-13-17-32R, BRR113A/ BR9159-8-5-40-13-8R and BRR17A/ BR9157-12-2-37-13-17-32R had significant negative sca effects. The sca effects from all medium \times medium parental gca effects indicating dominant gene action for this trait (Table 4 and 5).

For panicle number per meter², five crosses IR58025A/ BR9157-12-2-37-13-17-32R (15.98), IR79156A/ BR9157-12-2-37-13-15-40R (22.43), BRR133A/ BR9159-8-5-40-13-8R (35.63), BRR113A/ BR9159-8-5-40-13-8R (26.90) and BRR17A/ BR9159-8-5-49-1-1R (32.21) exhibited positive significant sca effects and those were considered as good specific combiners. The poor specific combiners were IR58025A/ BR9159-8-5-40-13-8R (-30.37), BRR133A/ BR9157-12-2-37-13-15-40R (-22.50), BRR113A/ BR9157-12-2-37-13-17-32R (-18.25) and BRR17A/BR9159-8-5-40-13-8R (-18.39) for this trait. Generally, high \times medium, high \times low, medium \times low and low \times low general combiner produced good specific combinations with positive sca effects for panicle per meter². It indicated additive \times dominant type of gene action for the crosses (Table 5). Parental gca effects for individual traits and its expression in sca hybrid combinations determine high, medium and low status of cross combinations.

Seven crosses showed significant sca effects in which four combinations displayed positive and three crosses demonstrated negative sca effects for spikelets per panicle (Table 4). The cross combinations IR58025A/ BR9157-12-2-37-13-17-32R (24.20), IR79156A/ BR9159-8-5-40-13-8R (24.92), BRR13A/ BR9157-12-2-37-13-15-40R (22.66) and BRR17A/ BR9157-12-2-37-13-15-40R (21.05) indicated the presence of dominance alleles in them for spikelets per panicle. Good specific combination for this trait was evolved from high \times medium, high \times low and medium \times low general combiner parents (Table 5). Additive \times additive and additive \times dominance gene action were observed in good specific cross combinations. Saidaiah *et al.* (2010) mentioned that the combinations with significant specific combining ability effects were due to the combination of parents both of which were good or poor general combiners or any one was a good general combiner. The crosses IR58025A/ BR9157-12-2-37-13-17-32R (12.78), IR79156A/ BR9157-12-2-37-13-17-32R (10.40), IR79156A/ BR9159-8-5-40-13-8R (14.80), BRR13A/ BR9159-8-5-49-1-1R (11.04) and BRR13A/ BR9159-8-5-49-1-1R (8.02) exhibited significant positive sca effects whereas IR58025A/ BR9159-8-5-40-13-8R (-8.20), IR79156A/ BR9157-12-2-37-13-15-40R (-6.35), IR79156A/ BR9159-8-5-49-1-1R (-18.84), BRR13A/ BR9157-12-2-37-13-17-32R (-12.19), BRR13A/ BR9159-8-5-40-13-8R (-8.89) and BRR17A/ BR9157-12-2-37-13-17-32R (-8.88) showed significant negative sca effects for spikelet fertility. Based on parental gca effects specific cross combinations were divided into three types of interactions, viz. high \times high, high \times medium and low \times low interaction (Table 5).

Thousand grain weight is one of the important character for grain yield. For this trait, IR58025A/ BR9157-12-2-37-13-15-40R (1.38) (high \times low), BRR13A/ BR9159-8-5-49-1-1R (0.77) (low \times low), BRR13A/ BR9159-8-5-40-13-8R (0.83) (low \times medium), BRR17A/ BR9157-12-2-37-13-17-32R (1.41) (high \times high) and BRR17A/ BR9159-8-5-40-13-8R (0.66) (high \times medium) showed significant positive sca effect and IR58025A/ BR9159-8-5-40-13-8R (-1.09) (high \times medium), BRR17A/ BR9157-12-2-37-13-15-40R (-1.42) (high \times low) and BRR17A/ BR9159-8-5-49-1-1R (-0.65) (high \times low) were regarded as the poorest specific combiners. This result indicated that additive \times additive, additive \times dominant and dominant \times dominant type of gene action was responsible for the cross combination of thousand grain weight. Similar results were observed by Hossain *et al.* (2016). The combination BRR13A/ BR9159-8-5-49-1-1R showed significant positive sca effect for panicle weight, spikelet fertility, thousand grain weight and yield (t/ha).

Yield is the cumulative function of different components, the contribution of components for yield is through component compensation mechanism. It was proved in some of the crosses IR58025A/ BR9157-12-2-37-13-17-32R (2.70), IR79156A/ BR9159-8-5-49-1-1R (1.73), IR79156A/ BR9159-8-5-40-13-8R (1.66), BRR13A/ BR9159-8-5-40-13-8R (0.99), BRR13A/ BR9157-12-2-37-13-15-40R (1.22), BRR13A/ BR9159-8-5-49-1-1R (1.23), and BRR17A/ BR9159-8-5-49-1-1R (0.82), which were characterized by significant positive sca effect for grain yield. The cross combinations with poor sca effects were IR58025A/ BR9159-8-5-40-13-8R

(-2.16), IR79156A/ BR9157-12-2-37-13-15-40R (-0.95), IR79156A/ BR9159-8-5-49-1-1R (-2.43), BRR133A/ BR9157-12-2-37-13-15-40R (-0.65), BRR133A/ BR9157-12-2-37-13-17-32R (-1.08), BRR113A/ BR9157-12-2-37-13-17-32R (-1.39), BRR113A/ BR9159-8-5-40-13-8R (-1.06), and BRR17A/ BR9159-8-5-49-1-1R (-1.96) for grain yield. High \times medium, medium \times medium, and low \times medium general combiners produced good specific combinations with positive sca effects for grain yield. It reported additive \times dominance and dominance \times dominance types of gene action for the crosses (Table 5). Several hybrids having high sca effects for grain yield in rice were reported by Petchiammal and Kumar (2007). In general, the gca effects of the parents were reflected in the sca effects of the crosses in most of studied traits. This is in line with the results of Hussain *et al.* (2003). Besides, Deitos *et al.* (2006) reported that parents with good general combining ability does not show high sca effects in their hybrid combinations. On the contrary, Paul and Duara (1991) obtained high estimates of sca effects from the parents with high gca effects in their study.

Conclusion

The sense of gene action is very useful to a plant breeder in the selection of parents for hybridization. GCA as well as sca variance were found to be significant in the findings. GCA effects suggested that the parents BRR133A and BR9157-12-2-37-13-15-40R were good for general combiner for grain yield and BRR113A, BRR17A, BR9157-12-2-37-13-15-40R, and BR9159-8-5-40-

13-8R for earliness, BRR113A, BRR17A, BR9157-12-2-37-13-15-40R, BR9157-12-2-37-13-17-32R and BR9159-8-5-40-13-8R for short statured plant. The crosses IR58025A/ BR9157-12-2-37-13-17-32R, IR79156A/ BR9157-12-2-37-13-17-32R, IR79156A/ BR9159-8-5-40-13-8R, BRR133A/ BR9159-8-5-49-1-1R, BRR133A/ BR9159-8-5-40-13-8R, BRR113A/ BR9157-12-2-37-13-15-40R, BRR113A/ BR9159-8-5-49-1-1R, and BRR17A/ BR9159-8-5-49-1-1R showed high sca effects for grain yield. These could be used in hybrid development after further evaluation. The crosses showing high sca effects involving high \times high general combiners could be utilized for the purpose of developing high yielding genotypes and obtaining transgressive segregants in F_2 generation.

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