COMBINING ABILITY ANALYSIS IN RICE (*Oryza Sativa* L.)

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ABSTRACT

Twenty hybrids were produced using five CMS lines viz., BRRI3A, BRRI9A, IR73328A, BRRI10A and IR78355A and four restorers viz., BRRI12R, BRRI13R, BRRI14R and BRRI15R following line x tester mating design to find out the best combination (s) in respect of their combining ability effects among the parents and hybrids at BRRI, Gazipur, Bangladesh from July 2008 to May 2009. Data were recorded from yield and yield contributing agronomic characters each entry through out the replications and mean values were subjected to line x tester analysis. The genotypes were found highly significant for all the traits which indicated that the treatments used in this study were significantly varied from each other. After the partitioning of mean sums of squares (MSS) of the treatments into parent, cross and parent vs cross. They were found highly significant except yield per plant for parent, panicle weight for crosses and leaf area index for parent vs cross. The ratio of GCA and SCA variances were found less than unity for all the characters except plant height, days to maturity and panicles per square meter. The relative contribution of line, tester and combinations of line x tester interaction of ten characters were calculated and found that panicle weight contributed the highest (69.53%) followed by thousand grain weight (63.62%), yield per plant (54.76%), panicle per meter square 51.52% in their hybrids. IR73328A was identified as good general combiner for shorter plant height (-6.09) and panicle per square meter (16.92). BRRI10A and IR78355A produced significant positive GCA for yield per plant which could be regarded as good general combiner for higher grain yield. Six hybrid combinations were found with significant and positive SCA effect of which the highest value was obtained from BRRI3A/BRRI14R (2.46) followed by IR73328A/BRRI13R (2.23) for yield per plant.

Key words: Line × tester, GCA, SCA, rice

INTRODUCTION

Bangladesh is the forth 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). Semi-dwarf high yielding modern varieties though has increased yield dramatically in many rice-growing countries, yield plateaus have been reached in many rice-growing regions. Such a situation, hybrids offer to break through the yield ceilings of semi-dwarf rice began in 1964. China is the first country to commercially exploit heterosis in rice. The discovery of CMS in rice (Athwal and Virmani, 1972) suggested that breeding could develop a commercially viable F_1 hybrid. The most promising hybrids yielded 20-30% (Lin and Yuan, 1980) and 15-20% (Yuan, 1998) higher than the best hybrids and conventional rice varieties, respectively. Line x Tester analysis is a powerful tool to discriminate the

good as well as poor combiners for choosing appropriate parental material in successful hybrid breeding program. However, the success of hybrid rice program depends upon the magnitude of heterosis which also helps in the identification of potential cross combinations to be used in the conventional breeding program to create wide array of variability in the segregating generations. Hence, the current program was undertaken to find out the best combination (s) in respect of their combining ability effects among the parents and hybrids at BRRI, Gazipur, Bangladesh from July 2008 to May 2009.

MATERIALS AND METHODS

Twenty hybrids were produced using five CMS lines viz., BRRI3A, BRRI9A, IR73328A, BRRI10A and IR78355A and four restorers viz., BRRI12R, BRRI13R, BRRI14R and BRRI15R following line x tester mating design. Thirty-day-old seedlings were transplanted at 15x20 cm spacing in RCB design with replications on January 25, 2009. Fertilizers @ 270:130:120:70:10 kg urea, TSP, MOP, gypsum and zinc per hectare of land were applied. All fertilizers along with 1/4 urea and 2/3 MP were applied at final land preparation. Remaining urea was top dressed in three equal split at first 10 February 2009 at 15 days after transplanting, second on 2 March 2009 at 35 days after transplanting, and on 21 March 2009 at PI stage. Remaining 1/3 MOP was applied during 2nd top dress of urea. Intercultural operations, irrigation were performed when necessary. Insect pest were controlled at vegetative, booting and at flowering stage with applying Malathione 57 liquid @ 1.0 L/ha, Diazenone 10G@16.5 kg/ha. Weeds were control three times during urea top dressing. Data were collected on the parameters included yield contributing agronomic characters viz. plant height (PH), days to maturity (DTM), panicle per square meter (PSM), spikelets per panicle (SPP), spikelet fertility (SF), panicle length (PL), leaf area index (LAI), panicle weight (PWT), 1000 grain weight (TGWT), yield per plant (YPP). The data were recorded from each entry through out the replications and mean values were subjected to line x tester analysis. The standard procedures developed by Kempthorne (1957) were followed to estimate the mean sum of squares (MSS) along with variances of SCA and GCA. Standard statistical tools (Singh and Choudhury, 1985) were used to analyse the combining ability effects.

RESULTS AND DISCUSSION

The analyses of variances of the study are presented in Table 1. The genotypes were found highly significant for all the traits which indicated that the treatments used in this study were significantly varied from each other. The mean sums of squares (MSS) of the treatments were further portioned into parent, cross and parent vs cross. The results showed that all the parameters for parent, cross and parent vs cross were found highly significant except yield per plant for parent, panicle weight for crosses and leaf area index for parent vs cross (Table 1).

Similarly, the mean sum of squares for crosses was again portioned into lines, testers and line x tester components. In case of lines, significant variances were observed in six characters out of ten. On the other hand, tester was found significant for days to maturity and panicle per square meter. All the traits were observed significant for line x tester interaction studies except number of spikelet per panicle and panicle weight. The results were in confirmation with the findings of Sarker *et al.* (2002). The ratio of GCA and SCA variances were found less than unity for all the characters except plant height, days to maturity and panicles per square meter which revealed that the preponderance of

Table 1. Analysis of variance and combining ability for eight yield and its related traits in rice

Source of variation	df	PH	DTM	PSM	SPP	SF	PL	LAI	PWT	TGWT	YPP
Treatment	28	77.12**	23.20**	2443.73**	1148.21**	204.70**	6.05**	51.84**	0.52**	27.88**	20.01**
Replication	2	2.30**	0.00**	85.28**	115.80**	27.34**	7.12**	8.42**	1.42**	0.20**	4.99**
Parent (P)	8	63.36**	9.83**	2773.75**	1030.62**	307.76**	9.09**	130.21**	0.88**	47.95**	7.82^{ns}
Cross (C)	19	76.83**	17.39**	1803.05**	924.42**	158.68**	3.28**	20.64**	0.29^{ns}	15.65**	18.47**
P x C	1	192.58**	240.58**	11976.57**	6341.07**	254.66**	34.23**	17.73^{ns}	1.92**	99.62**	146.80**
Line (L)	4	330.56**	75.22**	1477.04^{ns}	1842.08*	464.94**	7.76*	42.13*	0.12^{ns}	16.49^{ns}	34.90^{ns}
Tester (T)	3	15.55^{ns}	5.53**	5883.08**	1042.02^{ns}	11.39^{ns}	1.29^{ns}	23.68^{ns}	0.41^{ns}	14.08^{ns}	6.38^{ns}
LxT	1	7.58*	1.07**	891.71**	589.13^{ns}	93.41**	2.29**	12.71*	0.32^{ns}	15.77**	16.02**
Error	56	3.14	0.02	273.06	347.90	23.17	0.31	5.68	0.19	0.22	3.76

*and ** significant at 5% and 1% level respectively
PH=plant height, DTM=days to maturity, PSM=panicle per square meter, SPP =spikelets per panicle, SF=spikelet fertility, PL=panicle length, LAI =leaf area index, PWT=panicle weight, TGWT= 1000 grain weight, YPP=yield per plant.

Table 2. Combining ability variances of 10 characters in rice

Variance	PH	DTM	PSM	SPP	SF	PL	LAI	PWT	TGWT	YPP
GCA	12.26	2.91	206.54	63.18	10.72	0.17	1.50	-0.004	-0.04	0.34
SCA	1.48	0.35	206.22	80.41	23.41	0.66	2.34	0.044	5.18	4.09
GCA : SCA	8.29	8.35	1.00	0.79	0.46	0.25	0.64	-0.10	-0.01	0.08

PH=plant height, DTM=days to maturity, PSM=panicle per square meter, SPP =spikelets per panicle, SF=spikelet fertility, PL=panicle length, LAI =leaf area index, PWT=panicle weight, TGWT= 1000 grain weight, YPP=yield per plant.

non-additive gene action governing the traits concerned, conversely, additive gene action might be prevailed for plant height, days to maturity (Table 2). But for panicles per square meter both additive and non-additive gene actions suppose to playing the role of controlling the trait. This was also reported by Annadurai and Nadaranjan (2001), Bobby and Nadaranjan (1993), Singh *et al.,* (1996) and Ganesen and Rangaswamy (1997).

The relative contribution of line, tester and combinations on line x tester interaction of ten (10) characters are presented in Table 3. Among the ten characters studied six of them were considered to contributing the highest by lines ranged from 41.95 to 91.09 which indicated that lines contributed more positive alleles for those characters having prevalence of additive gene action. Only the panicle per meter square tester contributed 51.52% in their hybrids. In the other three yield related characters: viz. panicle weight (69.53%), thousand grain weight (63.62%) and yield per plant (54.76%) line x tester interaction contributed the highest proportion in their respective hybrid. This indicated that the concerned characters were influenced by non-additive gene action. In case of yield per plant similar result was also reported by Hossain *et al.* (2009).

Table 3. Proportional contribution of CMS lines (line), restorer and their interaction to total variances for 8 yield and its related traits in rice

Contributor	PH	DTM	PSM	SPP	SF	PL	LAI	PWT	TGWT	YPP
Lines	90.58	91.09	17.25	41.95	61.69	49.78	42.97	8.64	22.18	39.78
Tester	3.20	5.02	51.52	17.80	1.13	6.20	18.12	21.84	14.20	5.46
LxT	6.23	3.89	31.24	40.25	37.18	44.02	38.91	69.53	63.62	54.76

PH=plant height, DTM=days to maturity, PSM=panicle per square meter, SPP =spikelets per panicle, SF=spikelet fertility, PL=panicle length, LAI =leaf area index, PWT=panicle weight, TGWT= 1000 grain weight, YPP=yield per plant.

General combining ability (GCA) effects

GCA effects of ten yield and yield related traits of the present study are presented in Table 4. The table showed that BRRI3A and BRRI9A both were produced highly significant GCA for plant height, days to maturity, number of spikelet per panicle, leaf area index and 1000 grain weight, therefore these two CMS lines were considered as the best general combiner for the respective traits. Similarly, IR73328A was identified as good general combiner for shorter plant height (-6.09) and panicle per square meter (16.92). Significant negative GCA effects for plant height and growth duration are useful for the development of early dwarf variety. Hossain *et al*. (2009) also mentioned similar report with the same parents. Results also showed that among the parental lines used in this study only BRRI10A and IR78355A produced significant positive GCA for yield per plant which could be regarded as good general combiner for higher grain yield. On the other hand, for restorer, positive and significant GCA effects were found in BRRI14R for plant height (1.47), days to maturity (0.28), number of spikelet per square meter (16.05) and leaf area index (1.58). The results wre in agreement with the findings of Hossain *et al*. (2009), Rashid *et al*. (2007) and Singh and Kumer (2004). Desirable GCA effects were also observed in BRRI15R for plant height (-0.22), days to maturity (-0.85), and 1000-grain weight. Considering the exhibition of useful GCA effects by the restorers were identified as good general combiners for the traits concerned. However, none of parents was observed significant and positive GCA effect for panicle weight. These results were in accordance with the findings of Hossain *et al*. (2009). However, none of the restorer line was found under significant GCA effect for yield per plant. It could be mentioned that the parents with significant and positive GCA values might be

contributed positive alleles in their hybrid due to its additive nature of gene action for the respective traits.

Table 4. General combining ability (GCA) effects for 10 yield and its related traits in rice

Patrent	PH	DTM	PSM	SPP	SF	PL	LAI	PWT	TGWT	YPP
BRRI3A	-3.28**	-2.60**	-4.50^{ns}	14.67**	-5.87**	-0.27^{ns}	2.01**	-0.05^{ns}	0.43**	-2.44**
BRRI9A	-1.22*	-2.85**	-6.00^{ns}	12.08**	-2.78^{ns}	-0.18^{ns}	2.05**	-0.09^{ns}	1.71**	-1.02^{ns}
IR73328A	-6.09**	1.40**	16.92**	-11.08*	-3.62*	-0.52**	-1.47*	0.06^{ns}	0.04^{ns}	0.51^{ns}
BRRI10A	3.75**	2.15**	-11.25*	-5.92^{ns}	9.63**	-0.45**	-1.68*	0.15^{ns}	-1.15**	1.53**
IR78355A	6.84**	1.90**	4.83^{ns}	-9.75^{ns}	2.63^{ns}	1.42**	-0.91^{ns}	-0.07^{ns}	-1.03**	1.42*
SEgi L	**0.51**	**0.04**	**4.77**	**5.38**	**1.39**	**0.16**	**0.69**	**0.13**	**0.14**	**0.56**
SE gi-gj L	**0.72**	**0.06**	**6.75**	**7.61**	**1.96**	**0.23**	**0.97**	**0.18**	**0.19**	**0.79**
BRRI12R	-0.38^{ns}	0.55*	-20.82**	2.18^{ns}	-1.18^{ns}	0.05^{ns}	-1.32^{ns}	0.17^{ns}	-0.92**	0.37^{ns}
BRRI13R	-0.87^{ns}	0.02^{ns}	17.78**	1.85^{ns}	0.55^{ns}	-0.42*	-0.61^{ns}	-0.20^{ns}	-0.60**	-0.98^{ns}
BRRI14R	1.47**	0.28**	16.05**	7.78^{ns}	0.75^{ns}	0.12^{ns}	1.58*	0.09^{ns}	0.27^{ns}	0.33^{ns}
BRRI15R	-0.22^{ns}	-0.85**	-13.02**	-11.82*	-0.12^{ns}	0.25^{ns}	0.36^{ns}	-0.07^{ns}	1.24**	0.29^{ns}
SEgjT	**0.46**	**0.04**	**4.27**	**4.82**	**1.24**	**0.14**	**0.62**	**0.11**	**0.12**	**0.50**
SE gi-gj T	**0.65**	**0.06**	**6.03**	**6.81**	**1.76**	**0.20**	**0.87**	**0.16**	**0.17**	**0.71**

* and ** significant at 5% and 1% level respectively
PH=plant height, DTM=days to maturity, PSM=panicle per square meter, SPP =spikelets per panicle, SF=spikelet fertility, PL=panicle length, LAI =leaf area index, PWT=panicle weight, TGWT= 1000 grain weight, YPP=yield per plant.

Specific combining ability (SCA) effects

Specific combining ability (SCA) of a cross is the estimation and the understanding of the effect of non additive gene action for a trait. Non-additive gene action of a trait is an indicator for the selection of a hybrid combination. Therefore, a highly significant SCA effect is desirable for a successful hybrid breeding program. The results of SCA effect of the present study are given in the Table 5. The results showed that out of 20 hybrid combinations three of them viz. BRRI10A/BRRI15R (-2.47), IR78355A/BRRI12R (-2.34) and BRRI9A/BRRI14R (-2.13) produced significant and negative SCA effect for shortening plant height. Similarly, for growth duration eight combinations possessed significant and negative SCA which were desirable for early maturity hybrid. In case of number of panicles per square meters considerable magnitude of SCA effects were observed in six crosses having significant and positive SCA effect ranged from 11.77 to 28.63 where the hybrid combination IR78355A/BRRI13R produced the highest SCA effect. This combination could be selected for further evaluation for high yield heterosis. Four combinations possessed significant and positive SCA effect for spikelets per panicle. The combination BRRI9A/BRRI15R (18.32) produced the highest SCA effect followed by BRRI3A/BRRI12R (16.07), IR73328A/BRRI13R (14.48) and BRRI10A/BRRI12R (13.98) for the trait. Significant and positive SCA effects were observed in five hybrid combinations for spikelet fertility in which BRRI10A/BRRI13R gave the highest (10.37) value.

On the other hand, five significant and positive values were found in five combinations for panicle length. Similar trends of positive and significant SCA effects were also observed in six combinations for LAI. In case of panicle weight only two crosses and for thousand grain weight only six crosses were found to have under significant and positive SCA effect which range from 0.89 to 2.76. The highest SCA effect produced by IR78355A/BRRI15R (2.76) followed by IR78355A/BRRI14R (2.34) for the trait. For yield per plant six hybrid combinations were found with significant and positive SCA effect of which the highest value was obtained from BRRI3A/BRRI14R (2.46) followed by IR73328A/BRRI13R (2.23). These combinations might be used for further evaluation. The results were confirmed with the findings of Ganesen and

Rangaswamy (1997), Roy and Mondal (2001), Singh and Kumar (2004) and Rashid *et al.* (2007).

Table 5. Specific combining ability (SCA) effects for 10 yield and its related traits in rice

Cross	PH	DTM	PSM	SPP	SF	PL	LAI	PWT	TGWT	YPP
BRRI3A/BRRI12R	-0.26^{ns}	0.20^{**}	3.90^{ns}	16.07^{**}	2.93^{*}	-0.06^{ns}	-0.75^{ns}	0.44^{**}	0.24^{ns}	1.77^{**}
BRRI3A/BRRI13R	-0.66^{ns}	0.07^{ns}	-5.70^{ns}	-12.93^{**}	-4.13^{**}	-1.05^{**}	-2.33^{**}	-0.49^{**}	-1.11^{**}	-4.82^{**}
BRRI3A/BRRI14R	0.40^{ns}	0.13^{**}	-9.97^{*}	5.80^{ns}	-0.33^{ns}	0.21^{ns}	1.69^{*}	0.16^{ns}	0.89^{**}	2.46^{**}
BRRI3A/ BRRI15R	0.52^{ns}	-0.40^{**}	11.77^{*}	-8.93^{ns}	1.53^{ns}	0.91^{**}	1.39^{*}	-0.10^{ns}	-0.02^{ns}	0.59^{ns}
BRRI9A/BRRI12R	0.92^{ns}	-0.55^{**}	-4.27^{ns}	8.32^{ns}	4.52^{**}	0.85^{**}	1.63^{*}	0.13^{ns}	1.29^{**}	-0.82^{ns}
BRRI9A/BRRI13R	0.44^{ns}	0.98^{**}	13.13^{**}	-14.68^{**}	-8.22^{**}	-0.61^{**}	-0.26^{ns}	-0.34^{**}	0.42^{**}	-0.54^{ns}
BRRI9A/BRRI14R	-2.13^{**}	-0.28^{**}	3.20^{ns}	-11.95^{*}	1.92^{ns}	0.18^{ns}	-0.74^{ns}	0.07^{ns}	-1.72^{**}	0.84^{ns}
BRRI9A/ BRRI15R	0.76^{ns}	-0.15^{**}	-12.07^{ns}	18.32^{**}	1.78^{ns}	-0.42^{*}	-0.63^{ns}	0.14^{ns}	0.01^{ns}	0.52^{ns}
IR73328A/BRRI12R	-0.67^{ns}	0.20^{**}	-1.18^{ns}	-14.85^{**}	-3.32^{*}	-0.82^{**}	-1.49^{*}	-0.11^{ns}	1.88^{**}	-0.33^{ns}
IR73328A/BRRI13R	0.55^{ns}	-1.27^{**}	-16.12^{**}	14.48^{**}	-2.05^{**}	0.92^{**}	-1.41^{*}	0.09^{ns}	1.49^{**}	2.23^{**}
IR73328A/BRRI14R	0.85^{ns}	0.47^{**}	14.28^{**}	7.55^{ns}	7.08^{***}	-0.22^{ns}	0.60^{ns}	0.02^{ns}	-0.67^{**}	0.47^{ns}
IR73328A/ BRRI15R	-0.73^{ns}	0.60^{**}	3.02^{ns}	-7.18^{ns}	-1.72^{ns}	0.12^{ns}	2.29^{**}	0.01^{ns}	-2.71^{**}	-2.37^{**}
BRRI10A/BRRI12R	2.35^{**}	0.45^{**}	12.98^{**}	-16.02^{**}	-3.578	-0.15^{ns}	2.45^{**}	-0.35^{**}	1.66^{**}	0.72^{ns}
BRRI10A/BRRI13R	-0.22^{ns}	-0.02^{ns}	-19.95^{**}	13.98^{**}	10.37^{**}	1.39^{**}	1.05^{ns}	0.66^{***}	-0.77^{**}	1.91^{**}
BRRI10A/BRRI14R	0.34^{ns}	-0.28^{**}	-11.55^{*}	2.05^{ns}	-4.17^{**}	-0.02^{ns}	-1.62^{*}	-0.27^{*}	-0.85^{**}	-2.02^{**}
BRRI10A/ BRRI15R	-2.47^{**}	-0.15^{**}	18.52^{**}	-0.02^{ns}	-2.63^{ns}	-1.22^{**}	-1.88^{**}	-0.03^{ns}	-0.04^{ns}	-0.61^{ns}
IR78355A/BRRI12R	-2.34^{**}	-0.30^{**}	-11.43^{ns}	6.48^{ns}	-0.57^{ns}	0.18^{ns}	-1.84^{**}	-0.10^{ns}	-5.06^{**}	-1.34^{*}
IR78355A/BRRI13R	-0.11^{ns}	0.23^{**}	28.63^{**}	4.03^{**}	-0.85^{**}	-0.64^{**}	2.93^{**}	0.09^{ns}	-0.03^{ns}	1.22^{*}
IR78355A/BRRI14R	0.55^{ns}	-0.03^{ns}	4.03^{ns}	-3.45^{ns}	-4.50^{**}	-0.15^{ns}	0.07^{ns}	0.02^{ns}	2.34^{**}	-1.75^{**}
IR78355A/ BRRI15R	1.91^{**}	0.10^{*}	-21.23^{**}	-2.18^{ns}	1.03^{ns}	0.62^{**}	-1.17^{ns}	-0.01^{ns}	2.76^{**}	1.87^{**}
SE_{sij}	0.51	0.04	4.77	5.38	1.39	0.16	0.69	0.13	0.14	0.56
SE_{sij-lm}	1.45	0.13	13.49	15.23	3.93	0.45	1.95	0.36	0.39	1.58

* and ** significant at 5% and 1% level respectively

PH=plant height, DTM=days to maturity, PSM=panicle per square meter, SPP =spikelets per panicle, SF=spikelet fertility, PL=panicle length, LAI =leaf area index, PWT=panicle weight, TGWT= 1000 grain weight, YPP=yield per plant.

All the yield contributing characters except panicle per square meter were found under less than unity of GCA:SCA ration which might be influenced by non-additive gene action and may be impressive in favor of hybrid development. The two CMS lines BRRI 3A and BRRI 9A identified as good general combiner in respect of plant height and maturity with significant and negative GCA effects due to its additive nature of gene action and might be useful to develop hybrid variety with shorter plant height and earliness. The three hybrid combinations: BRRI9A/BRRI14R, BRRI10A/BRRI15R and IR78355A/BRRI12R could be selected also for shorter plant height. Hybrid BRRI3A/BRRI14R and IR78355A/BRRI13R was selected as good specific combiner for yield per plant. These combinations could be used for exploitation of heterosis in further hybrid breeding program.

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