COMBINING ABILITY OF DIFFERENT YIELD RELATED CHARACTERS IN RICE

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ABSTRACT

Combining ability for yield and yield contributing character of rice was studied using five lines IR79156A, BRRI7A, BRRI33A, BRRI21A and IR75608A and four testers BRRI20R, BRRI31R, BRRI26R and BAU521R to produce 20 F_1 in line × tester fashion. The variances due to SCA were larger than the variance due to GCA for all the characters which indicate the prevalence of non-additive gene action. BRRI7A/BRRI31R cross combination was the best specific combiner for grain yield/plant. The predominance of non-additive genetic components was observed for all the traits which indicated that the improvement of the characters with greater non-additive genetic component could be contemplated for the exploitation of heterosis. Estimates of GCA effects showed that maternal line BRRI33A and paternal tester BRRI31R was an excellent general combiner for improving yield contributing traits. The cross IR79156A/BRRI20R was found as good specific combiner for most of the yield contributing traits viz., panicle length, panicle weight, number of spikelet/panicle, spikelet fertility, 1000 grain weight, harvest index and grain yield/plant. The cross between good general combiners did not always produce the best specific crosses. Moreover, the predominance of the production of the best specific crosses from high × low and low × low combiners indicated the influence of non-additive and over dominant gene actions on the yield and yield contributing traits.

Key words: GCA, SCA, Line, Tester.

INTRODUCTION

Rice occupies 77% of total cropped area (BBS, 2011). At present rice alone constitutes about 92% of the total food grain 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). Further estimate is rather more precise to feed the

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population by the year 2025, which is about 21% higher than the population of 2000 (Bhuiyan et al., 2002). In this way breeding programs are effective and essential for improving the present varieties and increasing of yield (Nematzade and Valizade, 2002). Reduced plant height, more effective tiller, large and compact panicles, increased spikelet number/panicle, increased 1000 grain weight and higher yield are the most important rice characters to be improved in breeding programs (Paterson et al., 2005). Selection is an important technique in plant breeding and breeders use this method for improving the architecture of a crop by management of available genetic variability (Eidi Kohnaki et al., 2013). Breeding strategies based on selection of hybrids require expected level of heterosis as well as the specific combining ability. Combining ability analysis is one of the useful tools available to estimate the combining ability effects and aids in selecting the desirable parents and crosses for the exploitation of heterosis. Line $\times$ tester technique (Kempthorne et al., 1957) is useful in deciding the relative ability of female and male lines to produce desirable hybrid combinations. It also provides information on genetic components and enables the breeders to choose appropriate breeding methods for hybrid variety or cultivar development programs (Mirarab and Ahmadikhah 2010). Keeping this in view, the present investigation was carried out to study the combining ability in order to identify good combiners and superior hybrid combinations.

MATERIALS AND METHODS

The experimental material consists of nine rice genotypes viz.,IR79156A, BRRI7A, BRRI33A, BRRI21A and IR75608A were used as female (designated as lines) and four genotypes (BRRI20R, BRRI31R, BRRI26R and BAU521R) designated as tester were used as male. 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 T. Aman 2011 and Boro season 2011-12 at Research station of Bangladesh Rice Research Institute, Gazipur. In T. Aman season of 2011 Line and Tester materials were grown separately in stagger fashion with an interval of 5 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 m^2 plots in a RCBD (randomized complete block design) with three replications. In this study including traits are plant height, days to 50% flowering, days to maturity, panicle length, panicle weight, number of panicle/m^2, number of spikelet/panicle, spikelet fertility, 1000 grain weight, harvest index and grain yield/plant were evaluated based on standard evaluation rice system (Scshu, 1988). Collected data were subjected to statistical analysis using line $\times$ tester analysis following Kempthorne (1957).

RESULTS AND DISCUSSION

Result of ANOVA (Table 1) showed that there was high significant difference among treatments, crosses and parents for all the traits indicating adequate genetic variations

among parental varieties and crosses. Analysis of crosses effect to its components (lines, tester and parents vs crosses) showed highly significant difference (at 1% level) among tester for all trait except panicle/m^2, among lines most of the traits except panicle length, panicle weight, spikelet fertility, harvest index and grain yield/plant and in parents vs. crosses all trait except panicle length. There was highly significant difference (at 1%) level among line × testers for all traits except number of spikelet/panicle. The significant differences among the lines, tester and lines × testers indicated that the genotypes had wide genetic diversity among themselves for all traits. Significant mean squares due to lines and tester for a particular trait indicate the prevalence of additive variance. However, significant difference due to interactions of line × tester for some of the characters suggested the importance of both additive and non-additive variance for these traits (Bagheri and Babaeian 2010). Thus both additive and non additive gene actions should be studied for improving yield related traits.

The variance due to SCA was larger than the variance due to GCA for all the characters which were reflected in $\sigma^2 g : \sigma^2 s$ ratio being less than unity. From this result, predominance of non-additive genetic components over the additive genetic components was revealed in the inheritance of all the traits. It could be concluded that the improvement of the characters with greater non additive genetic component could be contemplated for the exploitation of heterosis and with bi-parental mating.

Table 1: Analysis of variance (MS) for different characters in rice under line × tester method

Sources of variation	df	PH	DF	DM	PL	PW	PPM	SPP	SF	TGW	HI	GYP
Treatment	28	375.97**	31.29**	41.85**	5.42**	2.44**	2894.04**	811.17**	1353.97**	14.45**	695.83**	764.17**
Replication	2	17.17**	16.77**	11.60**	0.59	0.08	928.49**	167.71	37.70	0.01	23.19	9.20
Parents	8	801.07**	73.92**	96.70**	9.34**	4.66**	1108.37**	984.27**	2740.88**	23.41**	932.81**	1027.93**
Crosses	19	209.26**	12.09**	19.33**	3.99**	1.39**	2374.14**	667.75**	712.13**	11.35**	404.20**	475.33**
Parents vs Crosses	1	142.61**	55.23**	30.85**	1.18	4.77**	27057.58**	2151.36**	2453.66**	1.65**	4340.91**	4142.13**
Lines	4	178.29**	36.21**	58.71**	3.35	0.69	4973.55*	2061.14**	261.86	31.04**	227.31	384.08
Testers	3	741.44**	21.98**	30.37**	13.98**	4.46**	1710.08	819.45**	2646.10**	19.15**	1680.93**	1494.15**
Lines × Testers	12	86.54**	1.58**	3.44**	1.71**	0.85**	1673.69**	165.36	378.73**	2.84**	143.98**	251.04**
Error	56	3.35	0.33	0.22	0.38	0.06	136.55	103.91	27.28	0.15	8.72	9.493
Variance Component												
$\sigma^2 gca$		3.582	0.31	0.46	0.07	0.02	20.44	14.66	9.73	0.25	7.60	6.55
$\sigma^2 sca$		27.729	0.42	1.07	0.44	0.26	512.38	20.49	117.15	0.90	45.08	80.52
$\sigma^2 gca/\sigma^2 sca$		0.13	0.74	0.43	0.16	0.08	0.04	0.72	0.08	0.28	0.18	0.08

PH=Plant height, DF=Days to 50% flowering, DM=Days to maturity, PL=Panicle length, PW=Panicle weight, PPM=Number of panicle/m^2, SPP=Number of spikelet/panicle, SF= Spikelet fertility, TGW= 1000 grain weight, HI=Harvest index, GYP= grain yield/plant

Table 2: Proportional contribution of line, tester and their interaction to total variance for different characters in rice

Proportional contribution	PH	DF	DM	PL	PW	PPM	SPP	SF	TGW	HI	GYP
Lines	17.94	63.06	63.94	17.67	10.53	44.10	64.98	7.74	57.56	11.84	17.01
Tester	55.95	28.71	24.81	55.26	50.86	11.37	19.38	58.67	26.63	65.66	49.63
Line × tester	26.12	8.23	11.25	27.07	38.60	44.52	15.64	33.59	15.80	22.50	33.36

PH=Plant height, DF=Days to 50% flowering, DM=Days to maturity, PL=Panicle length, PW=Panicle weight, PPM=Number of panicle/m^2, SPP=Number of spikelet/panicle, SF= Spikelet fertility, TGW= 1000 grain weight, HI=Harvest index, GYP= grain yield/plant

The proportional contribution of lines, testers and their interaction for yield and yield contributing characters are presented in table 2. It is evident from the table that testers played an important role toward for plant height (55.95%), panicle length (55.26%), panicle weight (50.86%), spikelet fertility (58.76%), harvest index (65.66%) and grain yield/plant (49.63%) indicating predominant parental influence for these traits. The lines contributed 63.06%, 63.94%, 44.10%, 64.98% and 57.56% towards days to 50% flowering, days to maturity, number of panicle/m^2, number of spikelet/panicle and 1000 grain weight respectively. The smaller contribution of interactions of the line × tester than tester for all traits except for number of panicle/m^2 indicated higher estimates of variances due to general combining ability Contribution of interactions of line × tester was higher than lines for plant height (26.12%), panicle length (27.07), panicle weight (38.60), spikelet fertility (33.59), harvest index (22.50) and grain yield (33.36), exhibiting higher estimates of GCA variances for interaction. Rissi et al. (1991) observed higher estimates of GCA variance due to tester in rice.

General Combining Ability Effects

Among the female parent BRRI33A and BRRI21A showed significant positive GCA effect while IR75608A had significant negative effects for plant height (Table 3). Among male parent BRRI20R and BRRI26R showed positive GCA effect while, BRRI31R and BAU521R showed negative GCA effect. BRRI21A had positive significant effect on days to flowering while IR75608A had significant negative significant effect for days to 50% flowering. In case of days to maturity IR79156A, BRRI7A and BRRI33A exhibited positive significant effect while BRRI21A and IR75608A showed significant negative effect. Paternal line BRRI20R and BRRI31R exerted significant negative effect and on the other hand BRRI26R and BAU521R showed significant positive effect for this trait. BRRI20R and BRRI31R showed significant negative effect while BRRI26R showed significant positive effect for days to maturity. Significant negative GCA effects on plant height and growth duration are useful for the development of early dwarf variety. From above result it is evident that IR75608A and BRRI31R was the good general combiner for plant height and growth

duration. The result suggested that IR75608A and BRRI31R could be used to contribute for shorter plant height and growth duration (Table 3).

For panicle length BRRI7A and BRRI26R exhibited good combining ability effect due to their positive significant effect. BRRI33A and BRRI20R showed positive significant GCA value 0.23 and 0.75 respectively on panicle weight. The line BRRI33A had significant positive effect on number of panicles/m^2 while BRRI7A and BRRI21A showed significant negative effect. In case of tester BRRI31R showed significant positive effect and BAU521R showed significant negative effect for same trait. For the number of spikelet/panicle BRRI33A exhibited good combining ability effects. In case of spikelet fertility BRRI33A and BRRI21A showed good GCA effect but paternal effect of BRRI20R and BRRI31R was also significantly positive. All the parental line showed poor GCA effect for 1000 grain weight except BRRI7A which was a good combiner for that trait. Among the testers BRRI20R and BRRI31R are good general combiner and the other two are poor combiner for this trait.

Table 3: Estimate of general combining ability (GCA effects of parents for different traits in rice

Designation	PH	DF	DM	PL	PW	PPM	SPP	SF	TGW	HI	GYP
A lines (line)											
IR79156A	-0.01	0.33	2.00[**]	0.24	0.07	0.41	-2.02	-1.42	0.18	-0.77	1.93[**]
BRRI7A	-0.04	0.33	0.33[*]	0.57[**]	0.09	-13.68[**]	1.91	-5.88[**]	2.62[**]	-4.22[**]	-2.96[**]
BRRI33A	4.80[**]	1.42[**]	1.58[**]	0.08	0.23[*]	33.89[**]	20.88[**]	5.23[**]	-1.67[**]	7.37[**]	9.10[**]
BRRI21A	1.17[*]	0.92[**]	-0.33[*]	-0.03	0.02	-17.72[**]	-6.67[*]	4.29[**]	-0.58[**]	-0.92	-3.92[**]
IR75608A	-5.92[*]	-3.00[**]	-3.58[**]	-0.86[**]	-0.41[**]	-2.90	-14.11[**]	-2.22	-0.55[**]	-1.47	-4.16[**]
SE(gi)	0.53	0.17	0.13	0.18	0.07	3.37	2.94	1.51	0.11	0.85	0.89
SE(gi-gj)	0.75	0.23	0.19	0.25	0.10	4.77	4.16	2.13	0.16	1.20	1.26
R lines (tester)											
BRRI20R	3.55[**]	-1.10[**]	-1.42[**]	0.24	0.75[**]	0.31	4.91	11.80[**]	1.23[**]	9.95[**]	11.02[**]
BRRI31R	-3.64[**]	-0.90[**]	-0.88[**]	-0.20	0.06	14.71[**]	-10.96[**]	10.62[**]	-0.54[**]	8.26[**]	5.80[**]
BRRI26R	7.87[**]	1.43[**]	1.72[**]	1.14[**]	-0.48[**]	-4.97	3.82	-14.82[**]	0.60[**]	-10.37[**]	-9.47[**]
BAU521R	-7.78[**]	0.57[**]	0.58	-1.18[**]	-0.33[**]	-10.04[**]	2.22	-7.59[**]	-1.29[**]	-7.84[**]	-7.35[**]
SE (gi)	0.47	0.15	0.12	0.16	0.06	3.01	2.63	1.35	0.10	0.76	0.80
SE (gi-gj)	0.66	0.21	0.17	0.23	0.09	4.27	3.72	1.91	0.14	1.08	1.13

PH=Plant height, DF=Days to 50% flowering, DM=Days to maturity, PL=Panicle length, PW=Panicle weight, PPM=Number of panicle/m^2, SPP=Number of spikelet/panicle, SF= Spikelet fertility, TGW= 1000 grain weight, HI=Harvest index, GYP= grain yield/plant

In case of harvest index, the line BRRI33A and tester BRRI20R and BRRI31R exhibited significant positive GCA effects while BRRI7A, BRRI26R and BAU521 had significant negative effects. BRRI33A, IR79156A, BRRI20R and BRRI31R were identified as good combiners for grain yield/plant because for most of the traits of these genotypes showed desirable combining ability effects. On the contrary BRRI7A, BRRI21A, IR75608A, BRRI26R and BAU521R had poor combining ability effects for grain yield.

Specific Combining Ability Effects

Out of 20 crosses, 13 crosses showed significant SCA effects for plant height composed of one high × high, ten high × low and four low × low GCA effects (Table 5). The cross combination IR79156A/ BRRI31R, IR79156A/BAU521R, BRRI7A/BAU521R, BRRI33A/BRRI20R, BRRI21A/BRRI20R and IR75608A/ BRRI26R exhibited highly significant negative SCA effects for Plant height indicating them as good specific combiner crosses for dwarfness (Table4). These crosses involved positive general combiners for plant height. Biswas (2003) found high negative effect for a cross in which both parents were positive combiners for plant height. The superiority of low × low general combiners might be due to presence of over dominance effect.

For earliness (days to flower) the best cross combinations were IR79156A/BRRI31R (0.93), BRRI7A/BAU521R (0.73) and BRRI33A/BRRI20R (0.82) which showed significant negative SCA effect and these were considered as the best specific combiners for earliness. Whereas BRRI7A/BRRI20R (0.93), BRRI33A/BAU521R (0.85) and BRRI21A/ BRRI31R (0.82) identified as the poor specific combiner for this trait. This result was also in agreement with the findings of Hossain (2008).

The negative significant SCA effect estimated for days to maturity in IR79156A/BRRI26R (-1.13). BRRI7A/BAU521R (-0.67), BRRI33A/BRRI31R (-0.78), BRRI21A/BRRI20R (-1.67), BRRI21A/BAU521R (-0.67) and IR75608A/BRRI20R (-1.08) indicate the hybrids had good specific combining ability for earliness. The cross combination BRRI21A/BRRI20R and IR75608/BRRI20R showed negative significant SCA effects due to having low × low parental GCA effect. Generally, low × low general combiner parents produced the best and early hybrids with highly significant negative SCA effects (Table 5). This result indicated that dominant × dominant type of gene action was responsible for the cross combination for earliness. Bashar (2002) reported the similar result in rice.

For panicle length the cross combination BRRI7A/BRRI26R (1.12) and IR79156A/BRRI20R (1.03) showed significant positive SCA effects due to evolved from high × high and medium × medium parental GCA effects indicating additive and over dominant gene action for this trait (Table 4 & 5). For panicle weight, the cross combinations IR79156A/BRRI20R, BRRI7A/ BRRI31R, BRRI33A/BRRI26R and BRRI21A/BRRI26R showed significant positive SCA effects while IR79156A/BRRI31R, IR79156A/BRRI26R, BRRI7A/BRRI26R, BRRI21A/ BRRI20R and IR75608A/BRRI26R had significant negative SCA effects.

Table 4: Estimate of specific combining ability (SCA) effects of hybrids for different traits in rice

Designation	PH	DF	DM	PL	PW	PPM	SPP	SF	TGW	HI	GYP
IR79156A/BRRI20R	3.73**	0.60	1.33**	1.03**	0.87**	-25.47**	13.92*	10.28**	0.91**	4.05*	6.65**
IR79156A/ BRRI31R	-3.31**	-0.93**	-0.53	-0.33	-0.38**	-18.13**	-7.93	-10.44**	0.57	-4.42*	-8.44**
IR79156A/BRRI26R	3.52**	-0.27	-1.13**	-0.14	-0.42**	7.56	-3.98	-4.04	-1.45**	-4.08*	-4.53*
IR79156A/BAU521R	-3.94**	0.60	0.33	-0.56	-0.07	36.04**	-2.01	4.19	-0.02	4.45*	6.31**
BRRI7A/BRRI20R	2.76*	0.93**	1.00**	-0.93*	-0.10	12.77	-7.21	-0.11	0.23	3.16	0.29
BRRI7A/ BRRI31R	5.29**	0.07	0.13	0.73	0.57**	13.54	-0.35	16.31**	-0.36	9.68**	11.97**
BRRI7A/BRRI26R	-1.85	-0.27	-0.47	1.12**	-0.40**	-1.44	1.94	-8.60**	-0.26	-6.82**	-5.02**
BRRI7A/BAU521R	-6.20**	-0.73*	-0.67*	-0.93*	-0.06	-24.87**	5.62	-7.60**	0.38	-6.02**	-7.24**
BRRI33A/BRRI20R	-3.48**	-0.82*	0.42	0.02	-0.16	-12.29	-2.68	-5.61	0.01	-4.98**	-5.87**
BRRI33A/ BRRI31R	0.12	-0.35	-0.78**	-0.22	-0.23	-20.77**	-7.61	-6.61*	0.32	-5.21**	-8.45**
BRRI33A/BRRI26R	3.01**	0.32	-0.05	0.15	0.58**	26.91**	5.67	8.85**	0.45	7.49**	8.60**
BRRI33A/BAU521R	0.36	0.85*	0.42	0.05	-0.18	6.15	4.61	3.37	-0.78**	2.70	5.71**
BRRI21A/BRRI20R	-5.82**	-0.32	-1.67**	-0.08	-0.76**	-2.00	-0.85	-13.57**	-1.24**	-4.68**	-10.00**
BRRI21A BRRI31R	-1.56	0.82*	1.13**	-0.20	-0.14	13.83*	7.14	0.43	-0.31	-0.95	3.33
BRRI21A/BRRI26R	4.20**	0.15	1.20**	-0.47	0.67**	-15.07**	-2.10	16.24**	1.95**	9.98**	10.16**
BRRI21A/BAU521R	3.18**	-0.65	-0.67*	0.76	0.23	3.33	-4.17	-3.10	-0.40	-4.35*	-3.48
IR75608A/BRRI20R	2.81*	-0.40	-1.08**	-0.03	0.15	27.09**	-3.16	8.99**	0.10	2.45	8.92**
IR75608A/ BRRI31R	-0.53	0.40	0.05	0.01	0.19	11.52	8.75	0.32	-0.23	0.90	1.59
IR75608A/BRRI26R	-8.87**	0.07	0.45	-0.66	-0.42**	-17.96*	-1.53	-12.45**	-0.68**	-6.57**	-9.21**
IR75608A/BAU521R	6.60**	-0.07	0.58*	0.69	0.08	-20.65**	-4.06	3.14	0.81**	3.22	-1.31
SE (sij)	1.06	0.33	0.27	0.36	0.14	6.74	5.88	3.01	0.22	1.71	1.77
SE (sij-skl)	1.49	0.50	0.38	0.50	0.20	9.54	8.32	4.26	0.31	2.41	2.52

PH=Plant height, DF=Days to 50% flowering, DM=Days to maturity, PL=Panicle length, PW=Panicle weight, PPM=Number of panicle/m^2, SPP=Number of spikelet/panicle, SF= Spikelet fertility, TGW= 1000 grain weight, HI=Harvest index, GYP= grain yield/plant

For number of panicle/m^2 out of 20 cross combinations four crosses, IR79156A/BAU521R (36.04), BRRI33A/BRRI26R (26.91), BRRI21A/ BRRI31R (13.83) and IR75608A/BRRI20R (27.09) showed positive significant effect and those were considered as good specific combiners. The poorest specific combiners were IR79156A/BRRI20R (-25.47), IR79156A/BRRI31R (-18.13), BRRI7A/BAU521R (-24.87), BRRI33A/BRRI31R (-20.77), BRRI21A/BRRI26R (-15.07), IR75608A/ BRRI26R (-17.96), and IR75608A/BAU521R (-20.65) for this trait. Generally, high × medium, high × low and medium × medium general combiner parents produced good specific combination crosses with positive SCA effects for panicle/m^2. It indicated additive ×additive and additive × 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. For the number of spikelet/panicle, only one IR79108A/BRRI20R combination (13.92) showed specific good combining ability. Spikelet fertility exhibited significant SCA effects for eleven crosses in which near about to half of the crosses showed positive effects and the rest half showed negative effects (Table 4).

Based on parental GCA effects specific cross combinations are divided into three types of interactions viz., high × high, high × medium and low × low interactions (Table 5).

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						
		H×H	H×M	H×L	M×M	M×L	L×L	Total
PH	+	2	3	2	0	1	1	9
	0	0	1	3	0	0	1	5
	-	2	0	1	0	3	0	6
DF	+	1	0	0	0	1	0	2
	0	3	3	5	0	2	2	15
	-	0	1	1	0	1	0	3
DM	+	0	0	3	0	1	1	5
	0	2	2	4	0	0	1	9
	-	1	1	1	0	1	2	6
PL	+	1	0	0	1	0	0	2
	0	0	4	1	5	5	1	16
	-	0	1	1	0	0	0	2
PW	+	0	1	1	1	1	0	4
	0	1	2	2	1	4	1	11
	-	0	1	0	1	2	1	5
PPM	+	0	1	1	1	1	0	4
	0	0	2	2	1	3	1	9
	-	1	1	0	2	2	1	7
SPP	+	0	0	0	1	0	0	1
	0	0	3	1	5	8	2	19
	-	0	0	0	0	0	0	0
SF	+	0	2	3	0	0	0	5
	0	2	1	3	0	3	0	9

	-	2	1	0	0	1	2	6
TGW	+	0	1	1	0	0	1	3
	0	2	0	5	0	2	4	13
	-	0	1	2	0	0	1	4
HI	+	0	1	2	0	2	0	5
	0	0	3	2	0	1	0	6
	-	2	2	0	0	3	2	9
GYPP	+	1	0	5	0	0	1	7
	0	0	0	3	0	0	2	5
	-	3	0	2	0	0	3	8
Total	+	5	9	18	4	7	4	47
	0	10	21	31	12	28	15	117
	-	11	9	8	3	13	12	56

H= High GCA, L= Low GCA, M= Medium GCA

'+'= significant positive SCA, '0'= non-significant SCA, '-'= significant negative SCA

PH=Plant height, DF=Days to 50% flowering, DM=Days to maturity, PL=Panicle length, PW=Panicle weight, PPM=Number of panicle/m^2, SPP=Number of spikelet/panicle, SF= Spikelet fertility, TGW= 1000 grain weight, HI=Harvest index, GYP= grain yield/plant

Seven cross combinations found to have significant SCA effects in which three were IR79156A/BRRI20R (0.91), BRRI21A/BRRI26R (1.95) and IR75608A/BAU521R (0.81) positive which were considered as the best specific combiners and rest four were   IR79156A/BRRI26R   (-1.45),   BRRI33A/BAU521R   (-0.78), BRRI21A/BRRI20R (-1.24) and IR75608A/BRRI26R (-0.68) considered as the poorest specific combiners for thousand grain weight (Table 4). Generally, the above crosses involving high × medium, high × low and low × low general combiner parents produced good or best specific combination of crosses with positive SCA effects for 1000 grain weight (Table 5). It indicated that additive × additive, additive × dominant and dominant × dominant types of gene actions were involved for the crosses. Similar finding was also reported by Pradhan and Singh (2008).

Fourteen crosses showed significant SCA effects for harvest index in which IR79156A/BRRI20R (4.05) (medium × high), IR79156A/BAU521R (4.45) (medium × low), BRRI7A/ BRRI31R (9.68) (low × high), BRRI33A/BRR26R (7.49) (high × low) and BRRI21A/BRRI26R (9.98) (medium × low). IR75608A/BRRI31R (-4.42) (medium ×high), IR75608A/BRRI26R (-4.08) (medium × low), BRRI7A/BRRI26R (-6.82) (low ×low), BRRI7A/BAU521R (-6.02) (low × low), BRRI33A/BRRI20R (-4.98)   (high × high), BRRI33A/ BRRI31R (-5.21) (high × high), BRRI21A/BRRI20R (-4.68) (medium × high) and BRRI21A/BAU521R(-4.35) (medium × low) , IR75608A/BRRI26R (-6.57) (medium × low) produced significant

negative SCA effects for harvest index (Table 4). The predominance of best specific crosses from high × low and low ×low general combiners indicated the non-additive and over dominant gene actions in improving the harvest index for high grain yield.

Out of 20 cross combinations 7 crosses expressed significant positive SCA effects and 8 crosses showed significant negative SCA effect for grain yield/plant. Out of seven crosses best performing crosses was IR79156A/BRRI20R (6.65) (was high × high for grain yield/plant and the rest were either with high × low or low × low combination. Petchiammal and Kumar (2007) and Hossain (2008) also obtained high SCA effects for grain yield from high × low and low ×low general combiners in rice (Table 5). The superiority of low × low general combiner might be due to over dominance effect. Such crosses were expected to generate transgressive segregation for exploiting super high yielding genotypes. Importantly, BRRI7A/ BRRI31R cross combination was the best specific combiner for grain yield/plant (highest positive SCA value of 11.97).

CONCLUSION

From above results predominance of non-additive genetic components over the additive genetic components was revealed in the inheritance of all the traits. It could be concluded that the improvement of the characters with possess greater non-additive genetic components could be contemplated for the exploitation of heterosis and with bi-parental mating. BRRI33A and BRRI31R was an excellent general combiner for improving yield contributing traits. The cross IR79156A/BRRI20R was the good specific combiner for most of the yield contributing characters. BRRI7A/ BRRI31R cross combination was the best specific combiner for grain yield/plant.

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