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COMBINING ABILITY STUDIES FOR DEVELOPING NEW RICE HYBRIDS IN BANGLADESH

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Key words: Combining ability, CMS line, hybrid rice and yield.

Abstract

Combining ability on grain yield and its components from line × tester analysis of 70 rice hybrids produced by crossing seven CMS lines and ten testers of local and exotic origin were studied. The analysis revealed higher sca variance than gca variance for all the traits indicating the prevalence of non-additive gene action. Testers played important role towards panicle length (48.18%), spikelet fertility (60.46%) and grain yield/plant (55.44%) indicating predominant of paternal influence for these traits. The contribution of interactions (line × tester) were found vital for plant height (58.55%), effective tillers/plant (51.69%), days to 50% flowering (48.95%), days to maturity (48.32%), flag leaf length (68.55%), panicles/m^2 (48.61%) and panicle weight (50.39%). D.ShanA was the only good general combiner among the female parent for earliness and dwarfness. Male parent IR64R was best general combiner for dwarfness. The crosses BRRI9A × BR168R and D.ShanA × BR168R were identified as most promising for yield and desired traits based on sca effects, per se performance and gca effects of parents for grain yield and its components in rice which could be exploited beneficially in future rice breeding program by adopting heterosis breeding strategy.

Introduction

Rice is the principal food crop and most extensively grown cereal in the tropical and subtropical regions of the world. Today, rice has special position as a source of providing over 75% of Asian population and more than three billion of world populations meal which represents 50 to 80% of their daily calorie intake (Khush 2005, Amirjani 2011). This population will increase to over 4.6 billion by 2050 (Honarnejad *et al.* 2000) which demands more than 50% of rice needs to be produced what is produced present to cope with the growing population (Ashikari *et al.* 2005, Srividya *et al.* 2010). Bangladesh is the fourth largest producer and consumer of rice in the world with an annual production ranging from 28 to 33 million tons which constitutes 94.38% of the total food grain (rice and wheat). But it is an unfortunate paradox that yield of rice, the staple food of Southeast Asia, in lowest in area where the crop has been cultured extensively since ancient times and the plant exist in its greatest varietal diversity (Jennings 1964). Development of rice hybrids with yield advantage of 30 per cent over the existing hybrids is the turning point for increasing production and productivity (Yuan 1994). In hybrid program, choice of suitable parents is of primary importance since *per se* performance of parents is not always a true indicator of its combining ability in hybrid combination (Swamy *et al.* 2003). Therefore, 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 analysis offers a powerful tool for estimating the value of a parent to produce superior hybrid. The combining ability studies of the parents provide information which helps in the selection of better parents for effective breeding. Its role is important to decide parents, crosses and appropriate breeding procedure to be followed to select desirable segregants (Salgotra *et al.* 2009). 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.

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Materials and Methods

The experiment was conducted at the experimental farm of Bangladesh Rice Research Institute (BRRI) during T. Aman season of 2009 and Boro season of 2009-10. The pre-germinated seeds of selected seven CMS and ten restorers (pollen parent) lines were sown separately during T. Aman season of 2009, in a staggered way so as to get synchronization in flowering to facilitate easy hybridization in a line (CMS line) × tester (restorer) fashion to obtain 70 hybrids. Seedlings of each of these lines were raised in bed and 21 days old seedlings were transplanted in single plant/hill in the experimental plots in three different blocks. The plots were 2.5 meter in length containing five rows. The plant spacing provided was 20 cm between rows and 15 cm between plants of the same row. In flowering stage spikelets of CMS lines were clipped off and pollinated with restorer lines. There were 7 CMS and 10 restorer lines which gave 70 F_1 hybrids in line × tester combinations. To produce sufficient amount of seeds 8 plants from each CMS lines crossed with each restorer lines. Seventy hybrids along with their corresponding parents and check varieties was grown in Boro season 2009-2010 with three replications. Individual plot size was 2 m^2 containing 50 plants in each entry with a spacing of 15 cm between plants and 20 cm between rows. Soil fertility was ensured by applying appropriate doses of fertilizer according to seasons and necessary inter culture operations and irrigation were made whenever required. Ten sample plants were randomly selected from each plot excluding the border plants and the following data were recorded: Plant height, days to 50% flowering, number of panicles/m^2, flag leaf length, panicle length, spikelet/panicle, spikelet fertility, grain yield/plot, 1000 grain weight and days to maturity. Collected data were subjected to statistical analysis using line × tester analysis by Kempthorne (1957).

Results and Discussion

Analysis of variance for yield and different yield contributing characters revealed significant variations for all the characters except for panicle weight (Table 1). The crosses also exhibited significant variations among all these characters except for effective tillers/plant and panicle weight. Similar trend of variations were observed for parents. Variance due to interaction effect of parents and crosses were highly significant for all the traits except panicle weight, which was significant at 5% level of significance. The variances due to restorer lines (tester) were found significant for all the characters except panicle weight. Variation among CMS lines was significant for all the characters studied. The ratio of gca to sca variances ranged from 0.01 to 0.38. These results indicated that the non-additive gene actions predominated over the additive gene actions for all the characters. Predominance of non additive gene action for grain yield and its components was also reported by many other workers (Satyanarayana *et al.* (2000), Rita and Motiramani (2005); Singh *et al.* (2005); Venkatesan *et al.* (2007) and Dalvi and Patel (2009).

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 important role towards panicle length (48.18%), spikelet fertility (60.46%), grain yield/plant (55.44%) indicating predominant of paternal influence for these traits. On the contrary, maternal lines contributed most (40.61%) towards 1000 grain weight. The contribution of maternal and paternal interactions (line × tester) were found vital for plant height (58.55%), effective tillers/plant (51.69%), days to 50% flowering (48.95%), days to maturity (48.32%), flag leaf length (68.55%), panicles/m^2 (48.61%) and panicle weight (50.39%). General combining ability (gca) effects are presented in Table 3.

Table 1. Analysis of variances for different yield related traits in rice.

Para-meters	df	Plant height (cm)	Effective tillers/ plant	Days to 50% flowering	Days to maturity	Flag leaf length (cm)	Panicle length (cm)	Panicle/m^2	Panicle weight (g)	Spikelet fertility	1000 grain weight	Grain yield /plot
Geno-types	86	204.30**	1.47**	92.28**	129.64**	18.18**	8.33**	4585.82**	1.12 ns	66.34**	17.23**	94328.12**
Rep	2	22.29**	0.13 ns	24.53**	23.60**	5.62**	0.32 ns	5297.37**	0.23 ns	0.03 ns	0.62 ns	165.32**
Cross	69	161.64**	1.30 ns	78.73**	114.76**	17.57**	7.05**	3564.62**	0.94 ns	61.49**	16.20**	23865.41**
Parent	16	384.70**	1.47 ns	115.89**	147.93**	19.63**	4.98**	7074.07**	1.54 ns	66.78**	18.89**	77549.48**
P vs C	1	260.74**	13.40**	648.94**	863.54**	37.25**	150.38**	35236.14**	6.33*	394.31**	61.38**	5224713.31**
Lines	6	205.46**	2.59*	347.45**	510.17**	25.52**	19.76**	15885.14**	3.02**	125.69**	75.65**	69658.97**
Testers	9	376.71**	3.07**	76.50**	114.58**	25.34**	26.03**	3453.41**	1.57 ns	285.01**	27.72**	101441.21**
L vs T	1	6530.36**	46.23**	49.25**	70.85**	15.39**	2.47 ns	2214.21**	0.61ns	17.10**	7.68**	5847.94**
Error	172	45.40	0.16	1.97	4.45	3.37	1.12	1080.58	0.10	13.05	0.93	3297.50
Variance component												
σ^2gca		0.01	0.34	0.02	0.50	0.05	0.05	15.41	0.00	0.51	0.10	205.66
σ^2sca		0.23	15.76	4.01	22.14	0.45	0.45	377.88	0.17	1.35	2.25	850.15
σ^2gca/ σ^2sca		0.02	0.02	0.01	0.02	0.12	0.12	0.04	0.02	0.38	0.04	0.24

$^*p < 0.05$, $^{**}p < 0.01$

Table 2. Proportional contribution (%) of CMS lines (line), restorers (tester) and their interactions (A × R) to total variance for different yield related traits in rice

Proportional contribution	Plant height	Effective tillers/ plant	Days to 50% flowering	Days to maturity	Flag leaf length	Panicle Length	Panicles /m^2	Panicle weight	Spikelet fertility	1000 grain weight	Grain yield / plant
Line	11.05	17.41	38.37	38.66	12.63	24.38	38.75	27.92	17.78	40.61	25.38
Tester	30.40	30.91	12.67	13.02	18.82	48.18	12.64	21.69	60.46	22.32	55.44
Line X tester	58.55	51.69	48.95	48.32	68.55	27.44	48.61	50.39	21.76	37.08	19.18

Table 3. Estimates of general combining ability effects of parents for yield related traits in rice.

Designation	Plant height (cm)	Effective tillers /plant	Days to 50% flowering	Days to Maturity (days)	Flag leaf length (cm)	Panicle Length (cm)	Panicles /m^2	Panicle Weight (g)	Spikelet fertility	1000 grain weight (g)	Grain yield/plant (gm)
A lines (line)											
IR 58025A	3.11*	0.35**	4.42**	5.63**	0.75*	–0.43*	42.33**	–0.57**	–0.80	–1.25**	–39.19**
II32A	–1.82	–0.04	–4.91**	–6.87**	–1.13**	–0.57**	–4.22	0.04	–0.02	0.12	20.80*
Jin 23A	1.68	0.35**	2.7**	1.73**	0.22	–0.22	6.87	–0.17**	–0.71	–2.43**	–36.65**
IR78362A	1.40	0.18*	1.22**	2.33**	–1.33**	0.55**	8.74	–0.12*	0.66	–0.92**	–2.47
D.Shan A	–4.80**	–0.27**	–3.31**	–2.87**	1.01**	0.14	-4.47	0.20**	0.46	1.26**	5.53
Gan 46A	–0.13	–0.36**	–1.78**	–1.77**	–0.15	–0.95**	–27.04**	0.30**	–3.22**	1.50**	–41.95**
BRRI 9A	0.57	–0.20**	1.56**	1.83**	0.63	1.48**	–22.20**	0.32**	3.61**	1.72**	93.93**
SE (gi)	1.739	0.103	0.363	0.544	0.474	0.273	8.488	0.083	0.933	0.248	14.827
SE (gi-gj)	2.079	0.123	0.434	0.651	0.567	0.326	10.145	0.099	1.115	0.297	17.721
R lines (testers)											
BR 827R	6.72**	0.38**	3.43**	3.67**	0.53	0.18	–20.33**	0.34**	1.09	–0.48*	9.17
BR 168R	1.52	0.66**	–2.14**	–1.76**	0.49	2.00**	–4.62	0.31**	7.07**	–1.25**	139.38**
BR6723-1-1-2R	0.46	0.39**	–1.80**	-2.19**	1.94**	0.48*	–9.27	0.25**	1.82*	–1.57**	30.13*
M.H.63R	4.03**	–0.40**	–2.28**	–3.47**	0.18	–0.94**	–4.80	0.25**	–4.02**	2.25**	–71.32**
M.H.77R	–3.42*	–0.36**	–0.38	–0.61	–0.15	–1.36**	8.16	–0.14*	–4.31**	0.24	–74.46**
Gui99R	–1.84	0.17*	–0.47	–0.61	0.31	1.30**	–9.54	–0.04	3.26**	0.50*	66.10**
IR40750R	1.55	0.04	1.24**	1.10*	–0.85*	0.47*	8.18	–0.02	1.03	–0.07	27.69*
IR64R	–8.90**	–0.37**	–0.42	–0.61	–2.39**	–1.05**	16.55*	–0.30**	–2.80**	1.33**	–56.84**
AjayaR	0.55	–0.30**	2.39**	3.53**	0.04	–1.06**	20.38**	–0.40**	–3.64**	–0.51*	–63.37**
IR44675R	–0.66	–0.20*	0.43	0.96*	–0.10	–0.02	–4.73	–0.25**	0.50	–0.45*	–6.49
SE (gi)	1.230	0.073	0.257	0.385	0.335	0.193	6.002	0.058	0.660	0.176	10.484
SE (gi-gj)	1.470	0.087	0.307	0.460	0.400	0.231	7.173	0.070	0.788	0.210	12.531

*$p < 0.05$, **$p < 0.01$. Corresponding maintainer lines data for panicle weight, spikelet fertility, 1000 grain weight and grain yield/plant were taken due to CMS line is unable to produce it.

Among the CMS line IR58025A exhibited highly significant positive gca effects while D.ShanA showed significant negative gca effects for plant height. While the testers BR827R and M.H.63R showed highly significant positive gca effects but IR64R and M.H.77R had highly significant negative gca effects for plant height. From the above results, it could be suggested that the parents D.ShanA, IR64R and M.H.77R would be good general combiner for short stature of plant. The CMS line IR58025A and Jin23A considered as the best general combiner followed by BR168R, BR6723-1-1-2R and BR827R which could be utilized for evolving more tillers/plant. Richharia and Singh (1983) and Sarker (2001) reported similar sorts of results in rice.

The CMS line II32A, D.ShanA and Gan46A were good combiners for earliness due to having negative and significant gca effects for days to 50% flowering. The restorer lines M.H.63R, BR168R and BR6723-1-1-2R exhibited highly significant and negative gca effects indicating good general combiner for earliness but BR827R, AjayaR and IR40750R were regarded as poor general combiner for days to 50% flowering due to possess significant and positive gca effects. This indicated that II32A, D.ShanA and Gan46A were good general combiners for earliness and could be useful for further breeding program. The testers M.H.63R, BR6723-1-1-2R and BR168R were identified as the best general combiners for earliness due to their significant and negative gca effects. The lines D.ShanA and IR58025A showed significant positive gca effects, while IR78362A and II32A showed significant negative *gca* effects for flag leaf length. This indicated that D.ShanA and IR58025A contributed positive alleles for flag leaf length and IR78362A and II32A had some undesirable alleles for flag leaf length. Saidaiah *et al.* (2010) reported both negative and positive gca effects for flag leaf length while working with different CMS lines for developing new hybrids over environments. The restorer line BR6723-1-1-2R exhibited highly significant positive gca effects for flag leaf length.

For panicle length significant positive gca effects were found in BRRI9A and IR78362A, while significant negative gca effects were found in Gan46A, II32A and IR58025A. Positive significant gca effects were exhibited by BR168R, Gui99R, BR6723-1-1-2R and IR40750R which was considered as best general combiners for panicle length. Sharma *et al.* (2005) reported major role of non-additive gene action in rice for panicle length. The line IR58025A exhibited significant positive gca effects while Gan46A and BRRI9A showed significant negative gca effects for panicles/m^2. The restorer AjayaR and IR64R gave highly significant positive gca effects indicating some favorable alleles for this trait in them. All the CMS lines showed significant gca effects for 1000 grain weight except II32A and it ranged from –0.57 to 0.32. The restorer lines BR827R, BR168R, BR6723-1-1-2R and M.H.63R showed highly significant positive gca effects indicating presence of positive alleles for panicle weight and which could be fixed in subsequent generations.

For spikelet fertility gca effects ranged from –3.22 to 3.61 in CMS and –4.31 to 7.07 in restorer lines. BRRI9A showed highly significant positive gca effects, while Gan46A exhibited highly significant negative gca effects. BR168R considered as best general combiner followed by Gui99R and BR6723-1-1-2R which could be utilized as parent for breeding genotype with more fertile grains per panicle. Sarker (2001) and Bashar (2002) reported either female or male parent with good general combiner for 1000-grain weight. Significant positive gca effects were found in CMS lines BRRI9A and II32A and considered as the best general combiners for yield/plant. On the other hand, significant positive gca effects was found in BR168R, Gui99R and BR6723-1-1-2R. The result indicated that BRRI9A, Jin23A, II32A, BR168R, Gui99R, BR6723-1-1-2R and IR40750R were the best general combiners for this trait. Singh and Kumar (2004) observed several hybrids having high gca effects for grain yield in rice.

Table 4. Top five crosses with high sca effects, *per se* performance and *gca* effects of parents for grain yield and its components in rice.

Character/ crosses	Mean performance	sca effect	gca effect		gca status
			Female parent	Male parent	
Days to 50% flowering					
Gan46A/Gui99R	108.33	–7.46**	–1.78**	–0.47	L × L
II32A/IR44675R	109.00	–4.57**	–4.91**	0.43	H × L
D.ShanA/IR44675R	109.33	–5.83**	–3.31**	0.43	H × L
D.ShanA/BR6723-1-1-2R	110.33	–2.60**	–3.31**	–1.80**	H × H
II32A/BR168R	110.67	–0.33*	–4.91**	–2.14**	H × H
Plant height (dwarfness)					
BRRI9A/BR168R	79.90	–21.04**	0.57	1.52	L × L
IR78362A/IR44675R	84.07	–15.52**	1.40	–0.66	L × L
D.ShanA/IR64R	85.03	–0.12	–4.80**	–8.90**	H × H
IR58025A/M.H.77R	85.22	–13.32**	3.11*	–3.42*	L × H
Jin23A/IR64R	87.00	–4.63**	1.68	–8.90**	L × H
No. of effective tillers/plant					
BRRI9A/BR168R	9.00	1.34**	–0.20**	0.66**	L × H
IR58025A/IR40750R	8.60	1.01**	0.35**	0.04	H × L
IR58025A/ BR6723-1-1-2R	8.33	0.40**	0.35**	0.39**	H × H
Jin23A/BR168R	8.20	–0.01	0.35**	0.66**	H × H
Jin23A/Gui99R	8.10	0.37**	0.35**	0.17*	H × H
Panicle length					
BRRI9A/BR168R	28.86	0.50**	1.48**	2.00**	H × H
IR78362A/BR168R	27.90	0.47**	0.55**	2.00**	H × H
BRRI9A/Gui99R	27.86	0.21	1.48**	1.30**	H × H
BRRI9A/BR6723-1-1-2R	27.79	0.96**	1.48**	0.48*	H × H
D.ShanA/BR168R	27.46	0.44**	0.14	2.00**	L × H
Panicle weight					
D.ShanA/BR168R	4.92	0.91**	0.20**	0.31**	H × H
Gan46A/BR827R	4.65	0.51**	0.30**	0.34**	H × H
Gan46A/IR40750R	4.46	0.68**	0.30**	–0.02	H × L
II32A/M.H.63R	4.35	0.57**	0.04	0.25**	L × H
BRRI9A/BR168R	4.23	0.11**	0.32**	0.31**	H × H
Spikelet fertility					
BRRI9A/BR168R	87.69	1.13**	3.61**	7.07**	H × H
Gan46A/BR168R	84.61	4.87**	–3.22**	7.07**	L × H
BRRI9A/Gui99R	84.27	1.52**	3.61**	3.26**	H × H
D.ShanA/BR168R	83.50	0.08	0.46	7.07**	L × H
BRRI9A/BR6723-1-1-2R	82.76	1.44**	3.61**	1.82*	H × H
1000 grain weight					
BRRI9A/M.H.63R	27.90	0.02	1.72**	2.25**	H × H
BRRI9A/IR64R	27.72	0.77**	1.72**	1.33**	H × H
Gan46A/IR40750R	27.64	1.15**	1.50**	–0.07	H × L
BRRI9A/Gui99R	27.30	1.17**	1.72**	0.50*	H × H
Gan46A/BR827R	27.23	2.31**	1.50**	–0.48*	H × L
Grain yield/ plant					
BRRI9A/BR168R	26.87	67.81**	93.93**	139.38**	H × H
D.ShanA/BR168R	24.23	18.84**	5.53	139.38**	L × H
BRRI9A/BR827R	24.20	58.97**	93.93**	9.17	H × L
II32A/BR168R	23.90	–14.00*	20.80*	139.38**	H × H
BRRI9A/IR40750R	23.79	18.80**	93.93**	27.69*	H × H

H= High gca effect; L= Low gca effect

Crosses with desirable sca effects for various traits along with mean performance and gca effects of parents involved in the crosses are listed in the Table 4. The crosses BRRI9A × BR168R and D.ShanA × BR168R expressed significant sca effects as well as high *per se* performance for grain yield per plant and some other traits. However, II32A × BR168R and D.ShanA × BR6723-1-1-2R for days to 50% flowering (earliness), D.ShanA × IR64R for plant height (dwarfness), Jin23A × BR168R and IR58025A × BR6723-1-1-2R for number of effective tillers, BRRI9A × BR168R and BRRI9A × Gui99R for panicle length, BRRI9A × BR168R and Gan46A × BR827R for panicle weight, BRRI9A × BR168R and BRRI9A × Gui99R for spikelet fertility, BRRI9A × M.H.63R and BRRI9A × IR64R for 1000 grain weight had high mean performance and highly significant mean values. These desirable cross combinations involved high × high type of general combiners. Kalitha and Upadhaya (2000), Shivani *et al.* (2009) and Salgotra *et al.* (2009) also reported about interaction between positive and positive alleles in crosses involving high × high combiners which can be fixed in subsequent generations if no repulsion phase linkages are involved.

The desirable performance of combinations like high × low may be ascribed to the interaction between dominant alleles from good combiners and recessive alleles from poor combiners (Dubey 1975). Such combinations were observed in the hybrids; II32A × IR44675R and D.ShanA × IR44675R for days to 50% flowering (earliness), Jin23A × IR64R and IR58025A × M.H.77R for plant height (dwarfness), BRRI9A × BR168R and IR58025A × IR40750R for number of effective tillers, D.ShanA × BR168R for panicle length, Gan46A × IR40750R and II32A × M.H.63R for panicle weight, Gan46A × BR168R and D.ShanA × BR168R for spikelet fertility, Gan46A × BR827R and Gan46A × IR40750R for 1000 grain weight, D.ShanA x BR168R and BRRI9A × BR827R for grain yield per plant. Peng and Virmani (1990) also reported the possibility of interaction between positive alleles from good combiner and negative alleles from poor combiner in high × low cross combination and suggested for the exploitation of F_1 generation, as their high yielding potential would be unfixable in succeeding generation.

Involvement of both the poor combiners also produced superior specific combining hybrids as evidenced from the combinations: Gan46A × Gui99R for days to 50% flowering (earliness) and BRRI9A × BR168R and IR78362A × IR44675R for plant height (dwarfness). Involvement of both the combiners with low gca has been attributed to over dominance and epistasis interaction, which has been suggested by Amrithadevarathinam (1983), Singh *et al.* (2005) and Dalvi and Patel (2009). In majority of the crosses, high *sca* was mainly either due to high × low or low × low combining parents, which further substantiate the operation of non-additive gene action (additive × dominance and dominance × dominance epistatic interaction).

The crosses BRRI9A × BR168R and BRRI9A × BR827R were identified as most promising for yield based on sca effects. Hence these could be used for the exploitation of heterosis for yield and related characters. These best combiners could be utilized in hybrid development breeding program.

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