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COMBINING ABILITY FOR YIELD RELATED TRAITS OF BORO RICE (*Oryza sativa* L.)

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Abstract

An experiment was conducted following randomized complete block design with three replications during boro season of 2017-2018 to estimate combining ability for 16 agronomic traits of a 5x5 half diallel populations generated by using five selected parents of rice. Analysis of variance exhibited highly significant variability among the genotypes and combining ability variances for most of the studied traits except grain length and length-breadth ratio. The results indicated that none of the parent and hybrid combination performed better as general and specific combiner for all the traits. Performances were found to vary from trait to trait among parents and hybrid combinations. Parental genotype P_3 performed as the best general combiner for grain yield hill^{-1} (2.16**) followed by P_5 (1.43**). The hybrid combination $P_3{\times}P_5$ exhibited the best specific combiner for grain yield hill^{-1} (5.17**) followed by $P_3{\times}P_4$ (5.06**). However, the GCA : SCA ratio was less than unity for panicle length, effective tillers plant^{-1}, filled grains panicle^{-1}, straw dry weight and grain yield hill^{-1} indicating the presence of non-additive gene action. The results revealed that these traits could be improved through hybridization between the parents P_3 and P_5.

Keywords: Hybrid, half-diallel, GCA, SCA, additive and non-additive gene action, grain yield.

Introduction

Rice is the important staple food, provides about 80% daily calories consumed by more than 35% of the world's population, particularly in Asia (Sahebi *et al.,* 2018). The world population is expected to rise to eight billion within 2030, thus rice production should need to increase by at least 50 percent by this stipulated time (Abo-Yousef *et al.*, 2020). To alleviate the exact demand for rice of the growing population, it is crucial to develop stable high yielding hybrids along with superior lines/varieties with steady performance in diverse agro climatic environments. It is a great challenge for rice breeders although they are continuously trying to shift new varieties with the highest yield potential to release them as novel and high yielding varieties than the existing ones (Karthikeyan *et al.,* 2018). Generally, hybrid rice exhibits on an average yield benefit of about 15% to 20% over the inbred varieties (Abo-Yousef *et al.,* 2020). The usual

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strategies of breeding for developing varieties with high yield potential along with improved grain quality need expected level of heterosis as well as good combining ability. In breeding high yielding varieties, the breeders frequently face with the dilemma of selecting parents and crosses. Combining ability analysis is an effective approaches available for estimating the combining ability effects that can help in selecting desirable parents and hybrid combinations for the exploitation of heterosis (Denis *et al.,* 2020).

The phenotypic performance of the parents may not essentially judge them to be a good or poor combiner. Therefore, information on nature of gene action as well as their mode of expression in terms of combining ability is essential. Similarly, it also needs to explain the nature of gene action involved in the inheritance of respective characters. General combining ability (GCA) is endorsed to additive gene effects as well as additive x additive epistasis. On the contrary, specific combining ability usually attributable for non-additive gene effects may be due to prevalence of dominance or epistasis or both and is non-fixable (Begum *et al.,* 2018). The existence of non-additive genetic variance is the prime justification while initiating a hybridization program (Huseynzade *et al.,* 2020). Therefore, it is necessary to estimate yield and related characters for obtaining in depth understanding of their inheritance in order to select superior genotypes. Considering the above view, the present study was designed to estimate general and specific combining ability effects for yield and its related traits of boro rice.

Materials and Methods

Parental materials

Four boro rice varieties and one line were collected from BRRI (Bangladesh Rice Research Institute), Gazipur and BINA (Bangladesh Institute of Nuclear Agriculture), Mymensingh, and the varieties were BRRI dhan28 (P_1), BRRI dhan74 (P_2), BINA dhan10 (P_3), BRRI dhan67 (P_5) and the line was IR59418-7B-21-3 (P_4).

Development of F_1 hybrids

Ten direct crosses viz. $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_4$, $P_1 \times P_5$, $P_2 \times P_3$, $P_2 \times P_4$, $P_2 \times P_5$, $P_3 \times P_4$, $P_3 \times P_5$ and $P_4 \times P_5$ were made following 5 x 5 half-diallel fashion to develop experimental materials using five selected parental genotypes in the boro season of 2017. Seeds of 10 F_1's and five parents were harvested and kept in the cold room of Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU) for growing in the following boro season.

Evaluation of experimental materials

F_1 populations along with parents were grown in the experimental field of BSMRAU in a randomized complete block (RCB) design with three replications during boro season of 2018 following recommended inputs and management operations (BRRI, 2018). Data were collected from ten randomly selected plants from each replication on 16 agronomic traits such as days to first panicle exertion (DPE), days to maturity (DMT), plant height (PHT, cm), culm length (CLT, cm), panicle length (PLT, cm), number of tillers hill^{-1} (TPP), number of effective tillers hill^{-1} (ETP), non-effective tillers hill^{-1} (NTP), filled grains panicle^{-1} (FGP), unfilled grains panicle^{-1}

(UGP), grain length (GLT, mm), grain breadth (GBD, mm), length-breadth ratio (LBR), straw weight (SDW, g), thousand grains weight (TGW, g) and grain yield hill^{-1} (YPP, g).

Statistical Analysis of Data

The preliminary statistical analysis of data was done according to the techniques developed by Snedecor and Cochran (1967) and Clark (1973). The transformed data were then exploited by the statistical software TNAUSTAR (Nadarajan *et al.,* 2016) for estimation of combining and specific ability of 5x5 half-diallel populations (parents+F_{1s}) following Griffing's approach (1956).

Results and Discussion

Analysis of Variance (ANOVA)

Analysis of variance for yield and yield components presented in Table 1 which revealed that a highly significant differences among the studied genotypes for most of agronomic characters and also for GCA and SCA. The significant variances among the genotypes indicated wider range of variability among the genotypes for most of the studied characters except plant height, grain breadth and length breadth ratio. Saha *et al.* (2019) also found similar results for tillers per hill, grains per panicle, 100-grain weight and grain yield per hill in rice. The significant general and specific combining ability (Table 1) indicated the importance of both additive and non-additive gene actions in the expression of these characters. The relative magnitude of GCA variances was higher for most of the studied characters excepts panicle length, effective tillers hill^{-1}, filled grains per panicle, straw dry weight and grain yield

Table 1. Simple analysis of variance (ANOVA) and combining ability ANOVA for 16 yield attributes of 5×5 diallel population of rice

Sources of Variation	df	DPE	DMT	PHT	CLT	PLT	TPH	ETH	NTH	FGH	UGH	GLT	GBD	LBR	SDW	TGW	YPP
Simple ANOVA																	
Replication	2	4.29	47.66	1.14	41.11	1.01	9.85	8.26	1.53	20.73	0.90	0.005	0.00	0.01	22.29	7.74	85.38
Genotypes	28	44.60**	114.70**	25.99**	22.44**	0.88ns	7.31**	3.20**	2.63**	63.60**	5.99**	1.36**	0.03ns	0.28ns	23.47**	15.55**	75.56**
Error	29	12.91	22.10	11.19	5.03	0.67	4.24	3.03	1.11	21.38	6.40	0.01	0.005	0.01	7.69	7.34	15.56
Combining Ability ANOVA																	
GCA	4	62.32**	123.13**	31.97**	14.08**	0.24ns	6.49**	0.14ns	2.08**	3.53**	4.82**	0.73ns	0.03ns	0.17ns	5.19**	7.27**	22.11**
SCA	10	6.30**	31.02**	5.41**	10.08**	0.52ns	2.52**	2.18**	1.01*	43.12**	2.26**	0.66ns	0.01ns	0.12ns	14.35**	7.98**	44.05**
Error	14	0.85	1.12	0.79	0.53	0.19	0.49	0.41	0.25	1.1	0.6	0.02	0.01	0.02	0.66	0.64	0.94
GCA:SCA		9.90	3.97	5.91	1.40	0.46	2.58	0.06	2.07	0.08	2.13	1.10	3.19	1.40	0.36	0.91	0.50

*, ** represent significant at 5% and 1% level, respectively; df= degree of freedom; ns= non-significant.

hill^{-1} indicated the predominant effect of additive gene actions for the control days to first panicle exertion (62.32**), days to maturity (123.13**), plant height (31.97**), culm length (14.08**), number of tillers hill^{-1} (6.49**), non-effective tillers hill^{-1} (2.08**), filled grains panicle^{-1} (3.53**), unfilled grains panicle^{-1} (4.82**),and grain yield per hill (22.11**). It was further supported by the ratio GCA: SCA being higher than one and degree of additive gene action. Gnanamalar and Vivekanandan (2013), also reported the predominance of additive gene actions for the control of different agronomic traits in rice.

On the other hand, higher significant contribution of SCA variances for days to maturity (31.02**), plant height (5.41**), effective tillers hill^{-1} (2.18**), filled grains per panicle (43.12**), straw dry weight (14.35**), 1000-grain weight (7.98**) and grain yield hill^{-1} (44.05**) indicated that the preponderance of non-additive gene action in the inheritance of these traits were controlled by non-additive gene action. The predominance of non-additive gene action was observed for grain yield which was illustrated by the variance of SCA was higher than variance of GCA. This result corresponds with the findings of different scholars which stated the predominance of non-additive gene action for grain yield (Saidabad *et al*., 2010; Hasan *et al*., 2013; Bano and Singh, 2019; Dianga *et al*., 2020).

DPE- Days to first panicle exertion, DMT- Days to maturity, PHT- Plant height (cm), CLT-Culm length (cm), PLT- Panicle length (cm), TPP- Tillers per hill (no.), ETH- Effective tillers per hill, NET- Non-effective tillers per hill, FGH- Filled grains per panicle, UGH- Unfilled grains per panicle, GLT- Length of grain (mm), GBD- Breadth of grain (mm), LBR- Grain length breadth ratio, SDW- Straw dry weight (g), TGW- 1000-grain weight (g), YPH- Grain yield per hill (g).

General Combining Ability Effects

The estimates of general combining ability effects are regarded as an important indicator of the potential of parental genotypes for generating superior breeding populations. Furthermore, general combining ability of the parental lines reveals the average performance of a parent in a series of crosses. In regards to significance of GCA effects in two directions in each character revealed that the parents had potential to transfer the high and low values for a trait. However, in increasing as well as decreasing the value of parental characters it would be considered positive and negative values of GCA effects, respectively. The general combining ability effect for five parental genotypes for all the traits of the study is presented in Table 2.

The negative GCA effects are desirable for earliness in case of flowering, maturity and semi dwarf type plant height in rice. In this study, P_3 was found to be early both for days to first panicle exertion and days to maturity, which showed significant and negative GCA effects (Table 2). Regarding the plant height, the parent P_2 revealed wider superiority for dwarf natured plant as possessed highly significant negative GCA effects. On the other hand, significant positive GCA effects have been recorded in P_5 and P_4 for culm length and panicle length, respectively possessing favorable gene for these traits.

Table 2. Estimates of general combining ability (GCA) effects for 16 yield related characters in a 5×5 diallel population of rice

Genotypes	DPE	DMT	PHT	CLT	PLT	TPH	ETH	NTH	FGH	UGH	GLT	GBD	LBR	SDW	TGW	YPH
P1	-0.61ns	-1.9ns	1.6ns	-1.67*	0.01ns	1.23**	0.02ns	0.86**	0.66**	1.23**	0.1**	-0.09**	0.09**	-0.71**	1.71**	-1.82**
P2	2.28**	2.87*	-3.38**	-0.99ns	-0.28ns	0.02ns	-0.07ns	0.02ns	-0.97**	-0.03ns	0.51**	-0.02ns	0.24**	0.74**	-0.79**	-1.61**
P3	-4.89**	-6.52**	-0.66ns	0.41ns	0.03ns	0.61ns	2.24**	0.05ns	0.26ns	0.05ns	-0.08*	0.07**	-0.12**	-0.87**	-0.56**	2.16**
P4	2.29**	3.29*	1.89ns	0.24ns	2.21**	-0.72ns	-0.11ns	-0.55ns	-0.5**	-1.11**	0.05ns	0.07**	-0.08**	1.05**	0.16**	-0.15*
P5	0.93ns	2.27ns	0.55ns	2.01**	0.24ns	-1.14**	-1.08**	-0.38**	0.56**	-0.13*	-0.37**	-0.02ns	-0.12**	-0.21**	-0.52**	1.43**
SE (gi)	0.85	1.12	0.79	0.53	0.19	0.59	0.41	0.25	1.10	0.6	0.02	0.06	0.02	0.66	0.64	0.94

*, ** represent significant at 5% and 1% level, respectively; df= degree of freedom; ns= non-significant.

The parent P_3 was a good combiner for effective tillers hill^{-1}, grain breadth and grain yield hill^{-1} as revealed highly significant and positive GCA effects for all these characters. The parent P_1 had significant positive GCA effects for number of tillers plant^{-1} (0.86**), filled grains panicle^{-1} (0.66**), larger grain size (0.10**) and thousand grain weight (1.71**) where it revealed a good combiner for these traits but in case of grain yield hill^{-1} (-1.82**), it showed significant negative effects which might not desirable for rice breeding. Although parental genotype P_5 exhibited non-significant and negative GCA effects for most of the traits, it would be a good general combiner for filled grains panicle^{-1} (0.56**) along with grain yield hill^{-1} (1.43**) as it showed positive and significant GCA effects for these characters. Parental genotypes P_1 and P_2 would be a good general combiner for comparatively longer grain with lesser breadth that is slender type grain.

DPE- Days to first panicle exertion, DMT- Days to maturity, PHT- Plant height (cm), CLT-Culm length (cm), PLT- Panicle length (cm), TPP- Tillers per hill (no.), ETH- Effective tillers per hill, NET- Non-effective tillers per hill, FGH- Filled grains per panicle, UGH- Unfilled grains per panicle, GLT- Length of grain (mm), GBD- Breadth of grain (mm), LBR- Grain length breadth ratio, SDW- Straw dry weight (g), TGW- 1000-grain weight (g), YPH- Grain yield per hill (g).

Maximum positive and significant GCA effects were recorded in P_4 for straw dry weight (1.05**). Whereas, parents P_1 and P_4 exhibited the highest significant positive GCA values for thousand grain weight (1.71** and 0.16**, respectively) and grain yield hill^{-1} in

P_3 and P_5 (2.16** and 1.43**, respectively) (Table 2). Hasan *et al.* (2017) also reported similar results for most of the yield related traits in rice. From the above findings, it can be concluded that none of the parents have desirable GCA effects for all of the studied traits. Thus, no parent contains favorable gene for all the characters. So, multiple crossing among the parents may produce desirable traits including yield. Moreover, the parental genotypes may also serve as valuable donors in hybridization or multiple crossing schemes for producing high yielding genotypes or in the process of selection of transgressive segregates for obtaining pure line varieties using background selection. Therefore, simultaneous improvement for grain yield hill^{-1} is possible by enhancing yield attributes in rice.

Specific Combining Ability Effects

The specific combining ability (SCA) effects for 10 rice hybrids for studied agronomic traits are presented in Table 3. Based on the SCA effects, it was observed that none of the cross combination produced desirable and significant SCA effects for all the traits. These results are similar with that of many other studies on combining ability analysis of rice (Abo-Yousef *et al.,* 2020; Devi *et al.,* 2017). Generally, yield is considered as ultimate goal in rice breeding program. Estimates of SCA effects revealed that hybrids $P_3×P_4$, $P_3×P_5$, $P_1×P_4$ had higher positive and significant SCA effects for grain yield hill^{-1} (5.06**, 5.17, 4.93**, respectively). In addition, these crosses also exhibited significant positive SCA effects for thousand grain weight (Table 3).

The cross combination $P_1×P_3$ revealed significant and positive SCA effects for

Table 3. Estimation of specific combining ability (SCA) effects for different plant characteristics in a 5×5 diallel cross of rice

Genotypes	DPE	DMT	PHT	CLT	PLT	TPH	ETH	NTH	FGH	UGH	GLT	GBD	LBR	TGW	YPH	SDW
P1×P2	-0.92ns	0.14ns	3.18**	4.17**	0.74**	1.19**	0.04ns	0.18**	1.35**	2.24**	0.32**	-0.07**	0.26**	-3.37**	-2.88*	3.58**
P1× P3	1.39*	-4.02*	0.02ns	1.98**	0.68**	0.1ns	1.47**	0.45**	2.77**	-0.09ns	-1.36**	-0.02ns	-0.54**	2.62**	-10.64**	0.28ns
P1×P4	3.89**	6.14**	-0.89*	-0.65*	-0.54**	1.43**	-0.53**	0.52**	6.18**	0.41*	-1.31**	-0.06**	-0.48**	5.25**	4.93**	0.12ns
P1×P5	1.43*	1.63ns	-0.19ns	3.37**	0.62**	2.34**	1.24**	0.75**	-0.93*	0.69**	0.68**	-0.03*	0.32**	0.74**	-8.29**	2.72**
P2×P3	-2.09**	-6.94**	0.89*	3.85**	0.47*	1.31**	0.47**	0.69**	-2.39**	-2.14**	0.17**	-0.07**	0.15*	0.84**	3.59**	-0.79*
P2×P4	-1.18*	-4.08*	-1.66**	-2.83**	0.6**	-1.36**	1.19**	-1.21**	10.91**	0.47*	0.13**	-0.06**	0.14*	-1.36**	-6.29**	5.79**
P2×P5	2.63**	2.5ns	0.59*	1.04**	-0.05ns	0.06ns	1.03**	-1.04**	-8.64**	1.64**	0.13**	-0.05**	0.11*	0.86**	3.22**	-0.33ns
P3×P4	-1.35*	8.65**	-0.18ns	0.92*	-0.51**	-0.34ns	1.11**	-0.82**	-2.86**	0.49*	-0.13**	-0.08**	0.05ns	-3.56**	5.06**	3.13**
P3×P5	0.9ns	-6.05**	-2.88**	-2.45**	0.05ns	-0.53*	-0.27*	-1.31**	8.63**	-1.44**	0.64**	-0.01ns	0.26**	-2.43**	5.17**	2.89**
P4×P5	1.94*	0.52ns	-3.13**	-0.33ns	-0.88**	1.5**	1.62**	-0.34**	1.89**	0.12ns	0.16**	-0.12**	0.22**	-0.52*	4.05**	0.91*
SE (Sij)	1.10	1.45	1.03	0.69	0.25	0.63	0.53	0.32	1.42	0.78	0.03	0.02	0.03	0.83	1.21	0.85

*, ** represent significant at 5% and 1% level, respectively; df= degree of freedom; ns= non-significant.

days to maturity (1.39**), panicle length (0.68**), effective tillers hill^{-1} (1.47**), filled grains panicle^{-1} (2.77**), and 1000-grain weight (2.62**). These traits may be used for increasing hybrid vigor in rice. The cross combination $P_2 \times P_3$ revealed as a good specific combiner for traits like days to first panicle exertion (-2.09**), days to maturity (-6.94**) their SCA effects were negative and significant for these traits. This cross combination also be a good specific combiner for panicle length (0.47**), tillers per hill (1.31**), effective tillers hill^{-1} (0.47**), grain length breadth ratio (0.15**), 1000-grain weight (0.84**) and grain yield hill^{-1} (3.59**) as their SCA effects were positive and significant. The cross combination $P_1 \times P_4$ revealed as a good specific combiner for shorter plant height (-0.89**), culm length (-0.65**), shorter panicle (-0.54**) with higher tillers hill^{-1} (1.43**), increasing filled grains panicle^{-1} (6.18**), increasing thousand grain weight ()5.25** and grain yield hill^{-1} (4.93**).

The highest significant positive SCA effects were found in the cross combinations $P_4 \times P_5$, $P_1 \times P_3$, $P_1 \times P_5$ and $P_3 \times P_4$ for effective tillers hill^{-1} (1.62**, 1.47**, 1.24** and 1.11**, respectively) whereas undesirable SCA effects were found non-effective tillers hill^{-1} in the crosses combinations $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_4$, $P_1 \times P_5$ and $P_2 \times P_3$ revealed as poor specific combinations for this trait. The cross combinations of $P_2 \times P_4$, $P_3 \times P_5$, $P_1 \times P_4$ and $P_1 \times P_3$ performed as good specific combiners for filled grains panicle^{-1} (10.91**, 8.63**, 6.18** and 2.77**, respectively) as revealed higher significant positive SCA value. On the contrary, the cross combinations $P_1 \times P_2$ and $P_2 \times P_5$ revealed undesirable significant positive SCA effects for number of unfilled grains panicle^{-1} (2.24** and 1.64**, respectively) and would not be effective if selected for improving grain numbers.

It can be inferred that, most of the cross combination exhibited significant positive SCA effects for grain length and negative SCA effects for grain breadth indicated longer grain with shorter breadth. The cross combination $P_1 \times P_2$ had maximum SCA effects for straw dry weight (3.58**). The crosses $P_1 \times P_4$ and $P_3 \times P_5$ revealed as a good specific combiner for thousand grain weight and grain yield hill^{-1} (5.25** and 5.17**, respectively) (Table 3). Veeresha *et al.* (2015) and Ghidan *et al.* (2019) reported similar findings of combining ability effects for days to maturity, tillers per hill, panicle length, filled grains per hill, 1000-grain weight and grain yield per hill in rice. However, the most of the cross combinations, showed significant SCA effects that revealed both good and poor specific combiners for respective characters indicates involvement of additive and non-additive type gene actions in the expression of the traits under study.

DPE- Days to first panicle exertion, DMT- Days to maturity, PHT- Plant height (cm), CLT-Culm length (cm), PLT- Panicle length (cm), TPP- Tillers per hill (no.), ETH- Effective tillers per hill, NET- Non-effective tillers per hill, FGH- Filled grains per panicle, UGH- Unfilled grains per panicle, GLT- Length of grain (mm), GBD- Breadth of grain (mm), LBR- Grain length breadth ratio, SDW- Straw dry weight (g), TGW- 1000-grain weight (g), YPH- Grain yield per hill (g).

Conclusion

Highly significant GCA and SCA variances for all the characters except grain breadth and length breadth ratio indicated wide range of variability among the genotypes. None of the parents and cross combinations revealed desirable GCA and SCA values for all the characters. Rather, their performances varied significantly from trait to trait. The GCA effects revealed that parent P_3 would be a good combiner for days to panicle exertion, days to maturity, effective tillers plant^{-1} and grain yield hill^{-1}. The parental genotype P_5 revealed non-significant and negative GCA effects for most of the characters except filled grains panicle^{-1} and grain yield hill^{-1}. The cross combination $P_2 \times P_3$ revealed as the best specific combinations for effective tillers hill^{-1}, grain length, grain breadth, 1000-grain weight and grain yield hill^{-1} followed by $P_2 \times P_5$. Thus, theses combinations may be a good resource for specific combinations in rice breeding.

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