

Article

Evaluation of Combining Ability and Heterosis of Popular Restorer and Male Sterile Lines for the Development of Superior Rice Hybrids

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Abstract: Twenty-four hybrids, obtained from a mating design following 6 line \times 4 testers, were evaluated to estimate the heterosis, specific, and general combining ability (SCA and GCA) of parents and hybrids to find out suitable general combiner (GC) parents and cross combinations for utilization in the future breeding program. A randomized complete block design with three replications was followed to set the experiment. Data were recorded on grain yield and 13 yield-related agronomic traits. The analysis of variance of all cross combinations had highly significant differences for most of the characters studied, which indicated a wide variation across the genotypes, parents, lines, testers, and crosses. SCA and GCA variances were significant for all studied traits except for the panicle length, indicating that both non-additive and additive gene actions were involved in these traits. The GCA variance/SCA variance for all the traits was <1 , signifying the multitude of dominant and epistatic gene actions. The GCA effects of three lines GAN46A, IR58025A, IR62629A, and a tester IR46R were significant for the majority of the agronomic traits including grain yield and might be used for improving the yield of grains in rice as parents of excellent GC. Based on the yield of grains and agronomic traits, the hybrids IR58025A \times IR46R and GAN46A \times IR46R might be considered the best hybrids and another nine hybrids could also be considered good hybrids. Similarly, based on the yield of grains and agronomic traits, the positive and significant mid-parent, better parent, and standard heterosis were obtained from 3 F_1 s, 1 F_1 , and 3 F_1 s, respectively. Heterosis and combining ability study revealed that hybrids IR58025A \times IR46R and GAN46A \times IR46R might be considered preferable hybrid cultivars.

Keywords: CMS line; restorer line; hybrids; line \times tester; GCA and SCA; agronomic traits; grain yield

1. Introduction

Rice is the staple food for more than half of the world's population. For more than 7000 years, it has been grown as the main crop [1]. The economy, foodways, and culture of numerous societies are intimately involved in rice. It can be grown at up to 1000 ft above sea level. It has wider adaptability. Rice is grown on a variety of soils due to its water holding

capacity. Approximately 80% of rice in the world is produced in India, China, Indonesia, Thailand, Vietnam, and Bangladesh. More than 90% of rice in the world is consumed and produced in Asia. Among the world's rice-growing countries, Bangladesh is the fourth for production and area. Rice covers 95% of the cereal food production in Bangladesh. In 1970, its production was <10 million tons in Bangladesh [2]. Approximately 75% of the total cropped area is occupied by rice with 94% of production. At present, about 11.42 million hectares of land are used for rice cultivation, which produces 36.61 million metric tons of rice with an average yield of 3.21 t/ha [3]. About 50% of dietary energy comes from rice. In Bangladesh, rice contributes around 80% of the required calories. It is also an essential source of protein, including globulins, albumins, glutamines, and prolamins. The highly digestible proteins easily release energy, which is essential for the body's development and growth. So, improvement of the yield of rice grain and quality are essential to feed more than one-half of the world's population.

The agricultural economy of Bangladesh is predominantly based on rice production. It is a densely populated country with a rapid rate of population increment day by day. Recently, the areas of rice are gradually declined due to industrialization, the extension of municipal areas, and housing. Furthermore, because of the decline in rice-growing areas, scarcity of water and labor, and impending intimidations of abiotic and biotic stresses [4–11], rice breeders are facing many challenges in increasing the production of rice [12]. To feed the extra population of third world countries like Bangladesh, the development of hybrid rice technology might be an innovative genetic approach for reducing the gap between rice production and demand, as well as augmentation of rice yield up to 15–20% over the existing high yielding variety [13–16]. It also breaks the yield obstruction by showing heterosis over high-yielding varieties (HYV). Despite the >15–20% yield advantage of rice hybrids over HYV inbreds, their implementation is not increasing to the desired level, owing to many causes. The adoption of hybrid rice technology is not risen to the expectable mark owing to the unexpected quality and yield benefits of hybrids, absence of favorable policies, sources of narrow base parental (CMS and restorer) lines, and discrimination in the pricing of hybrid rice. The major factors for the lower implementation of farming hybrid rice are the nonexistence of genetic divergence in the current gene pool of rice and low to medium yield potential in F_1 s [17,18].

Variability plays a key role in the selection of superior genotypes in crop improvement programs [19–21]. The extent of variability and diversity is a prerequisite for any crop breeding program. Previous literature has shown a wide range of variability and diversity across germplasm [22–33]. The magnitude of variation due to a heritable component is very important because it would be a guide for the selection of parents for crop improvement [34–37]. There are lots of quantitative and qualitative studies that were observed for evaluation of variability and diversity, such as agronomic traits [38,39], grain yield [40], proximate compositions [41,42], minerals [43,44], pigments [45–47], vitamins [48], phenolics [49,50], flavonoids content [51–53], and antioxidant activity [54]. Due to the low variability and divergence across parental lines (CMS and restorer), breeders deal with vast challenges in the development of the hybrid with the desired range of heterosis. The low to moderate yield benefits in novel hybrids might be the prime reason for narrow genetic variability and diversity in the existing rice germplasms [18]. The existing yield plateau can be overcome by using broad base germplasms through the identification of stable CMS (A) lines with greater outcrossing rate, widely diverse restorer (R) lines, and performing novel and heterotic crosses between them following cytoplasmic genetic male sterile (CGMS), which is termed as a three-line hybrid system [55]. Generally, growing hybrid rice is principally based on three stable lines, including CMS (A) line, maintainer (B) line, and restorer (R) line. The novel fertile F_1 offspring may be produced by crossing male sterile lines and restorer lines. Diverse restorer lines should be developed for respective male sterile lines to make several successful crosses. The dominant fertility restorer genes (R) from R lines restore fertility in hybrids [56–60].

Combining ability (CA) may act as a powerful tool for identification of the best combiner, utilization of appropriate crosses for the assembly of desirable genes, or achieving heterosis to get required segregates [61]. CA is ultimately helpful for the genetic understanding of the architecture of traits, which allows the breeder to plan an active program of breeding for genetic improvement of the current germplasm resources. It is also helpful to breeders for improving the current germplasm resources or genotypes based on the performance of F_1 s from the genetic point of view. The criteria of good quality hybrid development in rice to meet up the present demand is necessary to study the combining ability among the existing materials. Promising parental lines have to be identified based on their combining ability performance and superior hybrids. Hence, using line \times tester mating design, the potentials of parental lines were assessed for general combining ability (GCA) and specific combining ability (SCA) [14,62]. The present study was designed to identify potential parental lines assessing the achievement of F_1 s for yield and their agronomic traits through SCA and GCA performances and to identify the promising heterotic F_1 s for the commercial breeding program.

2. Materials and Methods

2.1. Experimental Site

This study was conducted at Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur. The site is located at 24.09° N and 90.26° E under AEZ 28.

2.2. Soil and Climate

The study site is a subtropical zone, having scarcity of rainfall, clear sunshine, low temperature in the early growing period, and moderate to high temperature in the later growing period. The soil texture was silty clay loam with acidic (pH = 6.4), low organic matter (0.87%), total nitrogen (0.09%), and exchangeable K (0.13 cmol/kg).

2.3. Materials

Six popular CMS lines of rice viz. IR58025A, BRRI1A, IR62629A, GAN46A, IR68888A, and LuhaguraA, as well as four restorer lines of rice viz. BI1R, IR46R, BU1R, and China1R were collected from the Department of Genetics and Plant Breeding, BSMRAU were used in line \times tester mating design to produce F_1 populations. During the evaluation of F_1 hybrids, six maintainer lines viz. IR58025B, BRRI1B, IR62629B, GAN46B, IR68888B, and LohaguraB, along with the popular mega rice cultivar BU dhan1, were used as a check.

2.4. Seed Germination, Pot Preparation, and Raising of Seedlings

Pure healthy seeds of parents were treated with Vitavax and germinated in the Petri-dishes. The germinated seeds were sown in the pots in four sets staggered at seven-day intervals for synchronization of flowering. Pot soil was treated with Furadan 5G before seeding.

2.5. Intercultural Operation in the Pots

Regular irrigations were provided in the pots. Fungicide (Bavistin 50 WP) was sprayed two times to avoid fungal infection.

2.6. Mainland Preparation and Transplantation

The land was prepared thoroughly by plowing 3–4 times, and then laddering. Weeds and stubbles were removed during the final land preparation. Twenty-five days old seedlings were transplanted, maintaining a distance of 20 cm \times 20 cm between lines and rows, respectively. A single seedling was transplanted into each hill.

2.7. Fertilizer Application

We applied 100 kg MP, 150 kg urea, 70 kg TSP, 10 kg zinc sulfate, and 60 kg gypsum per ha of land. Total required gypsum, TSP, zinc sulfate, and MP were applied at the time

of final land preparation. Urea was applied in three installments, such as 15 days after transplanting (DAT), 30, and 45 DAT.

2.8. Irrigation and Drainage

During the whole growing period, adequate water was ensured in the field to maintain 5–7 cm water depths up to the hard drought stage of rice. To release excess rainwater immediately, a good drainage system was also maintained.

2.9. Intercultural Operation

At the time of top dressing of urea, weeding was carried out to reduce the urea loss through denitrification. Furadan 5G was applied @ 10 kg/ha at the panicle initiation stage and active tillering to control the stem borer.

2.10. Synthesis F₁ Hybrid

All the CMS parents and four restorer lines were grown in the field. At the flowering stage, the CMS plants were transferred to an earthen pot and brought into the crossing house. Emasculation was completed in the afternoon using a vacuum emasculator to avoid injury to stigma. To avoid foreign pollen and prevent desiccation, glycine paper bags were used to cover emasculated panicles. The emasculated female plants were kept under shade. The next morning (9:00–11.00 a.m.), blooming panicles of respective restorer parents were collected and carried to the dusting room for pollination. At room temperature, panicles were placed in containers filled with water for 30 min to complete full blooming. The bloomed panicles were then dusted over the emasculated panicles. Bagging and tagging were carried out in the pollinated panicles.

2.11. Collection and Preservation of F₁ Seeds

The mature naked F₁ seeds were collected from the CMS parents and sun-dried. Then the seeds were oven-dried at about 30 °C temperature for three days. Seeds were treated with the malathion before storage to prevent infection of store grain pests. Finally, the labeled seeds were preserved in desiccators in the cold room.

2.12. Evaluation of Hybrids

Twenty-four F₁s, six maintainer lines, and four restorer lines were evaluated for SCA and GCA. The parent materials and hybrids obtained are shown in Table 1.

Table 1. Name of maintainer and restorer lines with their F₁s.

Maintainer Line	Restorer Line	F ₁ s
IR58025B	BI1R	IR58025A × BI1R
BRR11B	China1R	IR58025A × IR46R
IR62629B	IR46R	IR58025A × BU1R
GAN46B	BU1R	IR58025A × China1R
IR68888B		BRR11A × BI1R
LuhaguraB		BRR11A × IR46R
		BRR11A × BU1R
		BRR11A × China1R
		R62629A × BI1R
		IR62629A × IR46R
		IR62629A × BU1R
		IR62629A × China1R
		GAN46A × BI1R
		GAN46A × IR46R
		GAN46A × BU1R
		GAN46A × China1R
		IR68888A × BI1R
		IR68888A × IR46R

Table 1. Cont.

Maintainer Line	Restorer Line	F ₁ s
		IR68888A × BU1R
		IR68888A × China1R
		LuhaguraA × B11R
		LuhaguraA × IR46R
		LuhaguraA × BU1R
		LuhaguraA × China1R

2.13. Seed Germination, Pot Preparation, and Raising of F₁ Seedlings

The necked F₁ seeds, along with six respective maintainer lines, four restorer lines, and BU dhan1 as a check variety, were treated with Vitavax. Seeds were germinated in the Petri-dishes. The soil of the pot was collected from the rice field and treated with Furadan 5G and Bavistin 50 WP to avoid pest attack. Germinated seeds were placed in the pots to raise the seedlings.

2.14. Intercultural Operation in the Pots

Regular irrigations and weeding were maintained in the pots. The seedlings were sprayed twice at 10 DAS and 20 DAS with Bavistin 50 WP @ 0.2%. A synthetic insecticide (Diazinon 60 EC) was also sprayed on the seedling to prevent the attack of insects.

2.15. Main Field Preparation and Transplantation

The land was prepared thoroughly by 3–4 times plowing and then laddering. Weeds and stubbles were removed during the final land preparation. A thirty-days-old seedling was transplanted following RCBD design in three replicates maintaining the distance of 20 cm × 20 cm between lines and rows, respectively. A single seedling was transplanted into each hill. The unit plot size was 2 m × 2 m.

2.16. Fertilizer Management

Chemical fertilizer viz. MP, urea, TSP, zinc sulphate, and gypsum were applied @ 100, 150, 70, 10, and 60 kg/ha, respectively. At the time of final land preparation, the total required gypsum, TSP, zinc sulfate, and MP were applied. Urea was applied in three installments, such as 15 days after transplanting (DAT), 30, and 45 DAT.

2.17. Irrigation and Drainage

During the whole growing period, adequate water (5–10 cm water depths) was ensured in the field to maintain 5–7 cm water depths up to the hard drought stage of rice. To release excess rainwater immediately, a good drainage system was also maintained.

2.18. Data Collection

Ten randomly selected plants from each line and hybrids were used for recording data. Data were recorded on tillers per hill, plant height, panicles per hill, days to first flowering, days to maturity, days to 100% flowering, days to 50% flowering, panicle length, primary branches per panicle, secondary branches per panicle, pollen sterility (%), filled grains/panicle, 1000-grain weight, and grain yield (t/ha).

2.19. Statistical Analysis

The raw data were compiled by taking the means of all the plants taken for each treatment and replication for different traits. Statistix 8 software was used to analyze the data for analysis of variance (ANOVA) [63]. The difference across the F₁s was additionally divided into SCA and GCA following Kempthorne's method [62]. Significance tests for GCA and SCA effects were performed using a *t*-test. Mid-parent, better parent, and standard heterosis were calculated [64]. Significance tests for heterosis were performed using a *t*-test. Tests were carried out for normality and variance homogeneity.

3. Results and Discussion

The findings of the study are presented in this section. The sum of squares of the mean (MSS) of the treatment was again portioned into crosses, parents, and parents vs. crosses. Parents were also subdivided into testers, lines, and lines \times testers. The results of ANOVA for CA, estimates of GCA, and estimates of SCA were presented in Tables 2–4. The findings of these tables are discussed chronologically below.

3.1. Analysis of Variance

Table 2 represents the variance analysis (ANOVA). Except for panicle length, highly significant genotypic differences were found for all the parameters. Significant mean squares of the genotypes were observed for tillers per hill, plant height, panicles per hill, days to first, 50% and 100% flowering, days to maturity, panicle length, pollen fertility, primary branches per panicle, secondary branches per panicle, filled grains per panicle, 1000-grain, and grain yield, all of which indicated the preponderance of genetic variations across the genotypes and justified the inclusion of the genotypes under study. A wide range of variability was also reported in different rice germplasm [65–70], maize [71], and other crops [72–78]. Except for panicle length, highly significant differences were found in parents and parents vs. crosses for all the traits, which indicated a wide range of variations across parents and parents vs. crosses, which significantly differed from each other. Except for panicle length and pollen fertility (%), crosses had highly significant differences for all the traits which specified that crosses significantly differed from each other. Lines displayed a significant mean sum of the square for tillers per hill, plant height, panicles per hill, and days to 100% flowering. Testers exhibited a significant mean sum of the square for days to flowering, panicles per hill, days to maturity, secondary branches per panicle, primary branches per panicle, filled grains per panicle, grain yield, and 1000-grain weight. Lines \times testers differed significantly due to its significant mean sum of the square for all the traits except for panicles per hill, panicle length, and pollen fertility (%). Except for panicle length, the significant SCA and GCA variance was observed for all the characters studied, indicating both non-additive and additive gene action are involved in these traits.

The ratio of GCA and SCA effects was lower to unity for all the traits that indicated the prevalence of dominance and epistatic gene actions of these traits. These results were corroborative to previous findings of [64,79,80] where they stated the prevalence of dominance and epistatic gene actions for various characters of rice. For yield and the yield attributing characters, Kumar et al. [81] detected highly significant variances for SCA and GCA which specified the prevalence of both non-additive and additive gene action. They detected the multitude of additive gene actions for days to 50% flowering, plant height, harvest index, grain length, and 100-grain weight. Both non-additive and additive gene effects were correspondingly significant for grain length/breadth and grain yield per plant. For grain length and panicle length, they again reported the prevalence of dominance and epistatic gene action.

Table 2. Analysis of variance of combining ability for yield and its contributing traits.

Source of Variation	Degree of Freedom	Plant Height (cm)	Tillers Per Hill	Panicles Per Hill	Days to First Flowering	Days to 50% Flowering	Days to 100% Flowering	Days to Maturity
Replications	2	9.735	5.657	9.127	25.529	37.76	38.745 *	18.598 **
Treatments	33	426.105 **	47.873 **	38.939 **	119.052 **	80.766 **	83.782 **	65.442 **
Parents	9	521.395 **	70.596 **	53.763 **	67.219 **	56.167 **	40.241 **	55.867 **
Parents vs. crosses	1	4645.583 **	171.336 **	110.137 **	1343.086 **	345.919 **	790.850 **	502.126 **
Crosses	23	205.361 **	33.614 **	30.043 **	86.115 **	78.864 **	70.077 **	50.202 **
Lines	5	479.771 **	69.622 **	52.881 **	23.247	43.158	70.056 *	34.914
Testers	3	221.264	44.037	69.569 **	438.606 **	405.866 **	309.370 **	214.644 **
Lines × Testers	15	110.711 **	19.526 **	14.525	36.573 **	25.366 **	22.226 **	22.410 **
GCA		2.387 **	0.355 **	0.391 **	1.249 **	1.349 **	1.207 **	0.701 **
SCA		34.341 **	5.142 **	1.853 **	10.004 **	5.770 **	5.292 **	7.032 **
GCA: SCA		0.070	0.069	0.211	0.125	0.234	0.228	0.100
Error	66	7.689	4.101	8.966	6.560	8.055	6.351	1.315

Source of variation	Degree of freedom	Pollen Fertility (%)	Panicle length (cm)	Primary branches per panicle	Secondary branches per panicle	Filled grains per panicle	1000-grain weight (g)	Grain yield (t/ha)
Replications	2	54.392	4.145	2.539	2.422	34.687	0.433	0.167 **
Treatments	33	26.059 **	2.536	39.755 **	192.947 **	232.789 **	6.941 **	16.502 **
Parents	9	33.837 **	2.577	94.815 **	314.059 **	196.679 **	8.036 **	23.077 **
Parents vs. Crosses	1	184.983 **	0.162	53.088 **	744.110 **	594.648 **	16.858 **	68.852 **
Crosses	23	16.106	2.623	17.630 **	121.592 **	231.186 **	6.082 **	11.653 **
Lines	5	6.489	3.397	13.933	72.289	140.622	3.078	2.988
Testers	3	25.815	2.179	47.500 *	300.167 *	978.833 **	27.749 **	64.122 **
Lines × Testers	15	17.370	2.454	12.889 **	102.311 **	111.844 **	2.749 **	4.048 **
GCA		−0.032 **	0.004	0.120 **	0.486 **	3.010 **	0.084 **	0.192 **
SCA		2.481 **	−0.392	3.901 **	33.330 **	31.723 **	0.595 **	1.344 **
GCA: SCA		−0.013	−0.010	0.031	0.015	0.095	0.141	0.143
Error	66	9.928	3.631	1.186	2.321	16.676	0.963	0.016

GCA, general combining ability; SCA, specific combining ability; * significant at 5% level, ** significant at 1% level.

3.2. General Combining Ability (GCA)

Negative GCA were compulsory for days flowering, plant height, and days to maturity, although positive GCA were required for other traits included in the study. Table 3 shows the parental GCA effects. None of the CMS lines was observed to be a good GC for all the traits studied. IR58025A, BRRI1A, and LuhaguraA exhibited negative and significant GCA effects for plant height indicated as good GC parents for shorter plant stature. CMS lines, LuhaguraA, and IR68888A had positive and significant GCA effects for tillers per hill. These two lines might be considered as good GC high tillering ability. Similarly, LuhaguraA could be a good general combiner (GC) for more panicles as GCA effects (3.43) for panicles per hill were significantly positive. Among lines, LuhaguraA displayed negative and significant GCA for the first and 50% flowering. IR58025A displayed negative and significant GCA for days to 50% and 100% flowering and days to maturity, and IR68888A exhibited a negative and significant GCA effect for days to maturity, indicating that these three lines could be considered good GC lines for earliness. No genotypes had positive and significant GCA effects for pollen fertility (%) and panicle length. IR62629A exhibited significant GCA effects for primary and secondary branches per panicle. Similarly, IR58025A had significant GCA effects for secondary branches per panicle. These two lines could be used as a good GC for more branching of the panicle. In the case of filled grains per panicle, only GAN46A displayed positive and significant GCA. None of the lines had significant GCA effects for 1000-grain weight. GAN46A, IR58025A, and IR62629A displayed significant GCA effects for grain yield and these three lines could be used as good GC lines for improving the grain yield of rice. Sarker et al. [82] identified good GC lines for different agronomic traits of rice that were corroborative to our present study.

Negative GCA was required for days flowering, days to maturity, and plant height, although positive GCA was necessary for other traits included in the study. No good GC testers were observed for any traits included in the study. IR46R displayed positive and significant GCA; on the other hand, BU1R displayed negative and significant GCA for plant height. So, BU1R was a useful GC for short plant stature and IR46R was a useful GC for tall plant stature. Testers BI1R and IR46R had positive and significant GCA effects for tillers per hill. These two testers might be considered good GC testers for high tillering ability. Similarly, IR46R was demonstrated as a good GC for more panicles as it displayed positive and significant GCA effects for panicles per hill. The testers BI1R and IR46R displayed positive significant general combining effects (GCA) for days to flowering and maturity designating good GC testers for long-duration rice varieties. In contrast, the testers China1R and BU1R displayed negative significant GCA effects for days to first, 50% and 100% flowering, and days to maturity. These two testers might be used as a good GC for short-duration early maturing varieties. For panicle length, no testers displayed positive and significant GCA effects. Tester IR46R displayed positive and significant GCA effects for pollen fertility (%) and might be selected as a good GC parent for pollen fertility. IR46R and BU1R exhibited significant GCA effects for secondary and primary branches per panicle. Similarly, BI1R and IR46R had significant GCA effects for secondary branches per panicle. These three testers could be used as a good GC for more branching of the panicle. Tester IR46R displayed positive and significant GCA for filled grains per panicle, 1000-grain weight, and grain yield. This tester could be used as a good GC for improving the filled grains, 1000-grain weight, and grain yield of rice. Considering grain yield and its contributing traits, the line GAN46A and tester IR46R were the best GC parents. Our present study corroborated the results of Sarker et al. [82] who identified several good GC testers for different agronomic traits of rice.

Table 3. General combining ability (GCA) effects of parents (lines and testers) for yield and its contributing traits.

Parent	PH	TH	PPH	DF (1)	DF (50)	DF (100)	DM	PF	PL	PBP	SBP	FGP	GW	GY
Lines														
IR58025A	−8.74 **	0.19	−1.15	−0.82	−2.38 **	−4.72 **	−2.76 **	1.22	0.81	0.50	1.94 **	−0.28	0.03	0.23 **
IR62629A	3.86 **	−2.39 **	−2.49 **	1.43	2.88 **	0.19	2.15 **	−0.19	−0.77	1.92 **	3.61 **	0.81	−0.23	0.27 **
BRR11A	−4.62 **	−0.81	0.18	−0.74	0.29	0.78	0.90 **	0.47	0.06	−0.83 **	−3.14 **	−1.53	0.28	−0.34 **
GAN46A	7.96 **	−2.47 **	−1.15	2.01 **	−0.29	0.44	−0.26	−0.86	−0.25	−0.08	−1.81 **	5.47 **	0.42	0.68 **
IR68888A	4.15 **	1.86 **	1.18	−0.40	1.13	1.11	−0.85 *	−0.28	0.28	−0.92 **	−0.31	0.56	0.40	−0.14 **
LuhaguraA	−2.61 **	3.61 **	3.43 **	−1.49 *	−1.63	2.19 **	0.82 *	−0.36	−0.14	−0.58	−0.31	−5.03 **	−0.90 **	−0.72 **
SE	0.800	0.585	0.864	0.739	0.819	0.728	0.331	0.910	0.550	0.314	0.440	1.179	0.283	0.036
SE (gi-gj)	1.132	0.827	1.222	1.046	1.159	1.029	0.468	1.286	0.778	0.445	0.622	1.667	0.401	0.051
Testers														
BI1R	−0.41	0.94 *	1.18	1.88 **	3.43 **	2.94 **	1.68 **	−1.11	−0.46	−0.92 **	4.42 **	−1.08	−0.59 **	−0.47 **
IR46R	4.28 **	1.50 **	2.01 **	5.99 **	4.15 **	3.50 **	3.40 **	1.61 *	−0.03	2.03 **	2.47 **	10.64 **	1.86 **	2.78 **
BU1R	−4.27 **	−2.00 **	−2.32 **	−2.74 **	−1.57 *	−1.00	−0.49	−0.67	0.12	0.53 *	−2.86 **	−3.53 **	−0.51 *	−1.28 **
China1R	0.40	−0.44	−0.88	−5.13 **	−6.01 **	−5.44 **	−4.60 **	0.17	0.37	−1.64 **	−4.03 **	−6.03 **	−0.76 **	−1.04 **
SE	0.654	0.477	0.706	0.604	0.669	0.594	0.270	0.743	0.449	0.257	0.359	0.963	0.231	0.030
SE (gi-gj)	0.924	0.675	0.998	0.854	0.946	0.840	0.382	1.050	0.635	0.363	0.508	1.361	0.327	0.042

PH, plant height (cm); TH, tillers per hill; PPH, panicles per hill; DF (1), days to first flowering; DF (50), days to 50% flowering; DF (100), days to 100% flowering; DM, days to maturity; PF, pollen fertility (%); PL, panicle length (cm); PBP, primary branches per panicle; SBP, secondary branches per panicle; FGP, filled grain per panicle; GW, 1000-grain weight (g); GY, grain yield (t/ha); * significant at 5% level, ** significant at 1% level.

Table 4. Specific combining ability (SCA) effects of crosses for yield and its contributing traits.

Crosses	PH	TH	PPH	DF (1)	DF (50)	DF (100)	DM	PF	PL	PBP	SBP	FGP	GW	GY
IR58025A × BI1R	1.60	−1.19	−2.01	−3.79*	−4.51 **	−2.61	−3.18 **	−0.89	1.41	0.67	5.50 **	−0.67	−1.32*	0.39 **
IR58025A × IR46R	6.47 **	2.92 *	4.49 *	−0.90	0.10	1.17	1.76 **	5.72 **	−0.38	2.72 **	−4.22 **	4.94 *	1.77 **	1.85 **
IR58025A × BU1R	−5.24 **	−2.25	−0.85	3.82 *	1.49	0.00	−0.01	−2.67	0.49	−2.11 **	−4.22 **	−0.56	−0.34	−1.05 **
IR58025A × China1R	−2.84	0.53	−1.63	0.88	2.93	1.44	1.43 *	−2.17	−1.52	−1.28 *	2.94 **	−3.72	−0.11	−1.20 **
IR62629A × BI1R	−9.63 **	0.06	−0.01	1.63	−0.76	1.14	2.24 **	0.53	0.59	−0.42	4.17 **	−2.42	0.57	−0.62 **
IR62629A × IR46R	−0.59	−1.50	0.49	−2.49	−0.49	−1.75	−3.49 **	1.81	−0.77	−0.36	−0.56	−4.14	−1.14 *	−1.03 **
IR62629A × BU1R	1.12	2.33*	1.49	−1.76	0.57	0.42	0.74	0.08	−0.12	1.81 **	−4.56 **	−0.64	0.26	0.56 **
IR62629A × China1R	9.10 **	−0.89	−1.96	2.63	0.68	0.19	0.51	−2.42	0.30	−1.03	0.94	7.19 **	0.31	1.09 **
BRR11A × BI1R	1.01	0.14	0.99	0.79	1.82	0.22	−1.18	0.53	0.09	0.67	8.58 **	1.92	0.40	−0.27 **
BRR11A × IR46R	6.26 **	1.25	−0.51	−2.32	0.10	−0.33	0.43	−0.86	0.03	−1.28 *	−8.14 **	4.19	0.35	0.62 **
BRR11A × BU1R	0.48	1.08	0.15	0.40	−1.18	0.50	0.65	−1.25	−0.02	−0.11	0.86	2.36	−0.15	0.53 **
BRR11A × China1R	−7.75 **	−2.47 *	−0.63	1.13	−0.74	−0.39	0.10	1.58	−0.10	0.72	−1.31	−8.47 **	−0.60	−0.87 **
GAN46A × BI1R	1.38	−1.19	−2.01	2.38	1.74	0.56	4.32 **	0.19	−0.63	0.67	5.50 **	−0.67	−1.32 *	0.39 **
GAN46A × IR46R	−8.18 **	2.92 *	4.49 *	3.26 *	3.68 *	3.67 *	0.26	−2.53	1.51	2.72 **	−4.22 **	4.94 *	1.77 **	1.85 **
GAN46A × BU1R	6.00 **	−2.25	−0.85	−3.68*	−2.60	−2.50	−3.18 **	0.42	−0.42	−2.11 **	−4.22 **	−0.56	−0.34	−1.05 **
GAN46A × China1R	0.80	0.53	−1.63	−1.96	−2.82	−1.72	−1.40 *	1.92	−0.46	−1.28 *	2.94 **	−3.72	−0.11	−1.20 **
IR68888A × BI1R	4.29 **	0.06	−0.01	−3.21 *	0.99	1.22	−3.43 **	0.61	−0.72	−0.42	4.17 **	−2.42	0.57	−0.62 **
IR68888A × IR46R	−3.54 *	−1.50	0.49	6.68 **	1.26	2.00	3.85 **	−2.44	−0.65	−0.36	−0.56	−4.14	−1.14 *	−1.03 **
IR68888A × BU1R	−4.83 **	2.33 *	1.49	0.07	1.65	1.17	1.74 *	1.50	0.09	1.81 **	−4.56 **	−0.64	0.26	0.56 **
IR68888A × China1R	4.08 *	−0.89	−1.96	−3.54 *	−3.90 *	−4.39 **	−2.15 **	0.33	1.28	−1.03	0.94	7.19 **	0.31	1.09 **
LohaguraA × BI1R	1.35	0.14	0.99	2.21	0.74	−0.53	1.24	−0.97	−0.74	0.67	8.58 **	1.92	0.40	−0.27 **
LohaguraA × IR46R	−0.42	1.25	−0.51	−4.24 **	−4.65 **	−4.75 **	−2.82 **	−1.69	0.27	−1.28 *	−8.14 **	4.19	0.35	0.62 **
LohaguraA × BU1R	2.47	1.08	0.15	1.15	0.07	0.42	0.07	1.92	−0.02	−0.11	0.86	2.36	−0.15	0.53 **
LohaguraA × China1R	−3.40 *	−2.47 *	−0.63	0.88	3.85 *	4.86 **	1.51 *	0.75	0.50	0.72	−1.31	−8.47 **	−0.60	−0.87 **
SE (sij)	1.601	1.169	1.729	1.479	1.639	1.455	0.662	1.819	1.100	0.629	0.879	2.358	0.567	0.073
SE (sij-skl)	2.264	1.654	2.445	2.091	2.317	2.058	0.936	2.573	1.556	0.889	1.244	3.334	0.801	0.103

PH, plant height (cm); TH, tillers per hill; PPH, panicles per hill; DF (1), days to first flowering; DF (50), days to 50% flowering; DF (100), days to 100% flowering; DM, days to maturity; PF, pollen fertility (%); PL, panicle length (cm); PBP, primary branches per panicle; SBP, secondary branches per panicle; FGP, filled grain per panicle; GW, 1000-grain weight (g); GY, grain yield (t/ha); * significant at 5% level, ** significant at 1% level.

3.3. Specific Combining Ability (SCA)

Negative SCA effects were required for days flowering, plant height, and days to maturity, while positive SCA effects were desirable for other traits included in the study. SCA effects of the cross combinations are shown in Table 4. None of the hybrids was observed to be a good specific combiner (SC) for all the traits studied. The cross combination IR62629A \times BI1R displayed the maximum negative and significant SCA effect for plant height and was observed as the best SC for dwarf plant stature. GAN46A \times IR46R, BRRI1A \times China1R, IR58025A \times BU1R, IR68888A \times BU1R, IR68888A \times IR46R, and LuhaguraA \times China1R displayed negative and significant SCA effects and were found to be good SC hybrids for dwarf plant stature. On the other hand, IR62629A \times China1R displayed the positive and maximum significant SCA effect for plant height and was observed as the best SC for tall plant stature. IR58025A \times IR46R, BRRI1A \times IR46R, GAN46A \times BU1R, IR68888A \times BI1R, and IR68888A \times China1R displayed positive and significant SCA effects and were found to be good SC hybrids for tall plant stature. The cross combinations IR58025A \times IR46R and GAN46A \times IR46R displayed the positive and maximum significant SCA effects for tillers per hill. These two crosses could be used as the best hybrids for tillering ability. The hybrids IR62629A \times BU1R and IR68888A \times BU1R had positive and significant SCA effects for tillers per hill and might be considered good SC hybrids. Two cross combinations IR58025A \times IR46R and GAN46A \times IR46R exhibited high positive and significant SCA effects for panicles per hill and might be considered good SC hybrids. The hybrid LuhaguraA \times IR46R displayed the highest negative significant SCA effects for days to first, 50%, and 100% flowering, and high negative significant SCA effects for days to maturity and was observed to be a good short duration hybrid. The hybrid IR62629A \times IR46R displayed negative insignificant SCA effects for days to first, 50%, and 100% flowering, but the highest negative significant SCA effects for days to maturity might be considered the best hybrid for reducing the growth duration. The hybrids IR68888A \times BI1R, GAN46A \times BU1R, IR58025A \times BI1R, and IR68888A \times China1R had high negative and significant SCA effects for days to flowering and days to maturity. These four hybrids could be used as a good short-duration hybrid. No positive and significant SCA effects were found for panicle length. The cross IR58025A \times IR46R displayed positive and significant SCA effects for pollen fertility (%) and can be used as a good SC hybrid for pollen fertility. The crosses IR58025A \times IR46R, GAN46A \times IR46R, IR62629A \times BU1R, and IR68888A \times BU1R displayed positive and significant SCA effects for primary branches per panicle. These four hybrids could be used as a good hybrid for more primary branching. Similarly, the crosses BRRI1R \times BI1R and LuhaguraA \times BI1R revealed the maximum positive and significant SCA effects for secondary branches per panicle. The crosses GAN46A \times BI1R, IR68888A \times BI1R, IR62629A \times BI1R, IR58025A \times China1R, GAN46A \times China1R, and IR58025A \times CHINA1R displayed positive and significant SCA effects for secondary branches per panicle. These eight hybrids could be used as good SC hybrids for more secondary branching of the panicle. Hybrid IR58025A \times BI1R and GAN46A \times BI1R displayed positive and significant SCA for filled grains per panicle, 1000-grain weight. These hybrids could be used as a good SC for improving the filled grains and 1000-grain weight of rice. The hybrid IR58025A \times IR46R and GAN46A \times IR46R exhibited the maximum positive and significant SCA effects for grain yield and were considered the best hybrids for grain yield and its contributing traits. These two best heterotic hybrids were produced from the high \times high GC parents, indicating additive gene actions were involved in these crosses. Nine hybrids IR68888A \times China1R, IR62629A \times China1R, LuhaguraA \times IR46R, BRRI1A \times IR46R, IR68888A \times BU1R, IR62629A \times BU1R, LuhaguraA \times BU1R, BRRI1A \times BU1R, and IR58025A \times BI1R exhibited high positive and significant SCA effects for grain yield and were considered good hybrids for grain yield and its contributing traits. Interestingly, across nine good hybrids, four hybrids, i.e., IR68888A \times China1R, IR68888A \times BU1R, LuhaguraA \times BU1R, and BRRI1A \times BU1R, were produced from the crosses of low \times low GC parents. In contrast, five good hybrid combinations, i.e., IR62629A \times China1R, LuhaguraA \times IR46R, BRRI1A \times IR46R, IR62629A \times BU1R, and IR58025A \times

BI1R, were produced from either high \times low or low \times high GC parents, indicating both additive and non-additive gene actions were involved in these cross combinations. These results were corroborative to the previous findings of Sarker et al. [82] in rice, where they reported good specific cross combinations from low \times low, high \times low, and low \times high GC parents, respectively. Similar results found from the study of Venkatesan et al. [83] set a CA study in rice using 8 lines \times 4 testers and reported dominance and epistatic gene action controlling the characters *viz.*, plant height, days to first flowering, grain yield per plant, panicle per plant, and grain L/B ratio.

3.4. Heterosis

The results of better parent (heterobeltiosis), mid-parent, and standard heterosis are given in Tables 5–7, respectively. The findings of these Tables are discussed chronologically below.

3.4.1. Mid-Parent Heterosis

The heterotic effects in F_1 generation over mid-parent are presented in Table 5. Among 24 F_1 s, 17 F_1 s displayed positive and significant heterosis for plant height. The maximum positive and significant heterosis was recorded for the combination of crosses, BRRI1A \times China1R (46.66%) followed by BRRI1A \times IR26R, BRRI1A \times BU1R, and BRRI1A \times BI1R. The heterosis of plant height ranged from -3.50% to 46.66% . Although negative heterosis was desirable for short stature high yielding rice varieties, no hybrids exhibited positive and significant heterosis for plant height. Islam et al. [84] noted eight heterotic hybrids for plant height. For tillers per hill, positive and significant heterosis was observed in eighteen hybrids. In boro rice, Islam et al. [84] reported eight heterotic crosses for tillers per hill. Cross combination IR68888A \times BI1R displayed the highest positive and most significant heterosis (38.03%), followed by IR58025A \times IR26R, IR68888A \times IR26R, IR68888A \times BU1R. The heterosis for tillers per hill ranged from -4.00% to 38.08% .

The heterosis for panicles per hill ranged from -26.10 to 124.32% . Out of 24 F_1 s, 3 F_1 s displayed positive and significant heterosis for panicles per hill. Sixteen hybrids exhibited negative and significant heterosis. The cross IR68888A \times BI1R had the highest heterosis value (26.98%). The range of heterosis for the character was -54.43% to 26.98% . The literature on rice has shown that heterosis ranged from -46.72 to 68.90% for panicles per hill [85]. Negative heterosis was desirable for short-duration rice varieties. Out of 24 F_1 s, 15 F_1 s displayed negative and significant heterosis for days to first flowering. IR68888A \times China1R had the highest negative heterosis (-17.85%), followed by GAN46A \times China1R, IR58025A \times China1R, IR62629A \times China1R, and GAN46A \times BU1R. The range of heterosis for this character was -17.85% to 8.15% . Out of 24 F_1 s, 14 F_1 s displayed negative and significant heterosis for days to 50% flowering. The maximum negative heterosis was detected in the hybrid IR68888A \times China1R (-18.15%), followed by GAN46A \times China1R, IR58025A \times China1R, IR62629A \times China1R, and GAN46A \times BU1R. The range of heterosis for the character was -18.15% to 8.05% . Fifteen F_1 s displayed negative and significant heterosis for days to 100% flowering. IR58025A \times China1R had the highest negative heterosis value (-17.94%) followed by the cross combination, IR68888A \times China1R, GAN46A \times China1R, IR62629A \times China1R, IR58025A \times BU1R, and IR58025A \times BI1R. The range of heterosis for the character was -17.94% to 3.25% . Negative heterosis was desirable for short-duration rice varieties. Out of 24 F_1 s, 17 F_1 s displayed negative and significant heterosis for days to maturity. IR68888A \times China1R had the maximum negative heterosis (-11.85%), followed by IR58025A \times China1R, IR58025A \times BI1R, GAN46A \times China1R, IR58025A \times BU1R, GAN46A \times BU1R, IR62629A \times China1R, and IR68888A \times BI1R. The range of heterosis for the character was -11.85% to 4.64% . Islam et al. [84] noticed fourteen hybrids for days to 50% flowering and four hybrids for days to maturity in boro rice. For pollen fertility (%), only the cross combination IR58025A \times IR26R displayed positive and significant heterosis (7.66%). Twenty-two hybrids displayed negative and significant heterosis over their mid-parents. The heterosis for the character ranged from -8.93% to

7.66%. Among the 24 F₁s, 5 hybrids displayed positive heterosis and 19 displayed negative heterosis for panicle length over their mid parent. No F₁ displayed positive and significant heterosis. The range of heterosis for panicle length was −15.83% to 10.54%. High heterosis for this trait has been noted by Khoyumthem et al. [86]. Out of 24 F₁s, 7 F₁s displayed positive and significant heterosis for primary branches per panicle. BRR1A × BU1R had the highest heterosis value (74.55%), followed by IR58025A × IR26R, BRR1A × BU1R, BRR1A × IR26R, and BRR1A × BI1R. The range of heterosis for the character was −49.55% to 74.55%. Four F₁s displayed positive and significant heterosis over their mid parent for secondary branches per panicle. BRR1A × BI1R had the highest heterosis (67.41%) over mid-parent, followed by BRR1A × China1R and IR62629A × BI1R. The range of heterosis for the character was −52.59% to 67.41%. Islam et al. [84] reported nine heterotic hybrids for primary branches per panicle and sixteen heterotic hybrids for secondary branches per panicle. Out of 24 F₁s, 13 F₁s presented positive and significant heterosis, and 4 F₁'s displayed negative and significant heterosis over their mid parent for filled grains per panicle. Six heterotic hybrids were identified in boro rice for filled grains per panicle that conformed to the present study [84]. Hybrid IR68888A × IR26R had the highest heterosis over mid parent (27.70%), followed by the hybrids IR68888A × China1R, IR58025A × IR26R, BRR1A × IR26R, BRR1A × China1R, GAN46A × IR26R, and IR62629A × IR26R. The range of heterosis for the character was −15.82% to 27.70%. Four F₁s displayed positive and significant heterosis over their mid parent for 1000-grain weight. Hybrid IR58025A × IR26R had the highest heterosis value (10.11%) over mid-parent, followed by IR68888A × IR26R, GAN46A × IR26R, and IR62629A × IR26R. The heterosis over mid-parent ranged from −14.64% to 10.11%. Rao et al. [87] found highly heterotic crosses, IR62829A × IR2797-105R and IR58025A × IR2797-105R, for grain weight/plant. Three F₁s displayed positive and significant heterosis and twenty F₁s displayed negative and significant mid-parent heterosis for grain yield. IR58025A × IR26R had the highest heterotic value (31.32%) over its mid-parent, followed by IR68888A × IR26R and GAN46A × IR26R. Islam et al. [84] identified 13 heterotic hybrids for grain yield per hill that corroborated the present study. The range of heterosis for the character was −65.53% to 31.32%.

Table 5. Estimates of mid-parent heterosis of 24 crosses for yield and its contributing traits.

Crosses	Plant Height (cm)	Tillers Per Hill	Panicles Per Hill	Days to First Flowering	Days to 50% Flowering	Days to 100% Flowering	Days to Maturity
IR58025A × BI1R	10.85 **	−6.33	−37.50 **	−12.68 **	−10.24 **	−11.11 **	−9.71 **
IR58025A × IR26R	20.02 **	27.50 **	10.59 **	−5.74 **	−4.50 **	−7.22 **	−3.58 **
IR58025A × BU1R	−0.75	−38.27 **	−54.43 **	−9.13 **	−9.23 **	−13.20 **	−8.39 **
IR58025A × China1R	4.50	−8.43	−50.62 **	−16.22 **	−14.62 **	−17.94 **	−10.96 **
BRR 1A × BI1R	28.36 **	−13.16 **	−3.57	1.96	8.05 **	3.25 **	4.64 **
BRR1A × IR26R	37.62 **	−23.08 **	−9.71 **	0.86	7.05 **	−0.75	0.00
BRR1A × BU1R	35.12 **	−20.51 **	−23.64 **	−6.96 **	3.17*	−2.85	2.04 *
BRR1A × China1R	46.66 **	−35.00 **	−47.37 **	−7.53 **	−4.55 **	−9.87 **	−2.18 *
IR62629A × BI1R	11.77 **	−26.92 **	−9.52 *	−3.97 *	0.79	−2.18	−3.88 **
IR62629A × IR26R	21.09 **	−18.10 **	−19.10 **	−6.17 **	−0.98	−3.06 *	−0.42
IR62629A × BU1R	6.61 *	−39.62 **	−39.76 **	−12.08 **	−8.88 **	−6.86 **	−3.62 **
IR62629A × China1R	1.37	−51.85 **	−36.47 **	−15.88 **	−15.44 **	−14.18 **	−7.91 **
GAN46A × BI1R	21.35 **	−32.50 **	−11.11 **	−1.46	−0.59	−2.00	−1.23
GAN46A × IR26R	16.20 **	−8.64 **	−2.94	2.87	1.95	1.08	−2.49 **
GAN46A × BU1R	21.18 **	−31.71 **	−38.71 **	−14.11 **	−11.76 **	−10.31 **	−8.69 **
GAN46A × China1R	27.29 **	−37.51 **	−16.64 **	−17.45 **	−16.31 **	−13.74 **	−9.62 **
IR68888A × BI1R	23.03 **	38.03 **	26.98 **	−1.96	0.79	−0.36	−7.84 **
IR68888A × IR26R	19.46 **	27.78 **	17.65 **	8.15 **	1.38	0.18	0.28
IR68888A × BU1R	9.45 **	9.59 **	−6.45	−5.22 **	−4.54 **	−5.43 **	−4.84 **
IR68888A × China1R	20.62 **	−4.00	−9.38 *	−17.85 **	−18.15 **	−17.79 **	−11.85 **
LuhaguraA × BI1R	2.14	−5.08	−2.97	5.07 **	2.93	0.93	−1.53
LuhaguraA × IR26R	4.35	−27.73 **	−33.96 **	−1.13	−3.53*	−4.06 **	−2.80 **
LuhaguraA × BU1R	−0.96	−48.33 **	−36.00 **	−2.99	−4.38 **	−3.14*	−3.78 **
LuhaguraA × China1R	−3.50	1.64	−3.92	−6.36 **	−7.35 **	−4.90 **	−6.41 **

Table 5. Cont.

Crosses	Pollen fertility (%)	Panicle length (cm)	Primary branches per panicle	Secondary branches per panicle	Filled grains per panicle	1000-grain weight (g)	Grain yield (t/ha)
CD (0.05)	5.591	10.124	9.173	3.076	3.111	2.59	1.822
CD (0.01)	7.587	13.74	12.449	4.174	4.222	3.516	2.473
IR58025A × BI1R	−3.35 **	5.53	16.13 *	7.18	3.10	−14.64 **	−30.16 **
IR58025A × IR26R	7.66 **	−7.48	52.24 **	−25.96 **	24.46 **	10.11 **	31.32 **
IR58025A × BU1R	−3.40 **	−14.01	1.59	−42.45 **	−4.59	−9.66 **	−58.70 **
IR58025A × China1R	−3.53 **	−15.72	−13.85 *	−15.05 *	−2.21	−10.79 **	−60.30 **
BRR1A × BI1R	−2.80 **	10.54	37.04 **	67.41 **	9.54 **	−5.26 **	−34.05 **
BRR1A × IR26R	0.74	−14.36	51.65 **	16.25 *	23.88 **	−2.36	−4.76
BRR1A × BU1R	−1.33	−14.36	74.55 **	−5.80	2.96	−5.65 **	−28.24 **
BRR1A × China1R	−4.85 **	4.07	15.79 *	39.29 **	20.62 **	−7.56 **	−23.15 **
IR62629A × BI1R	−3.50 **	7.21	−4.48	30.06 **	1.31	−5.78 **	−49.48 **
IR62629A × IR26R	−1.48 *	−9.39	−2.78	−38.27 **	18.18 **	6.02 **	0.85
IR62629A × BU1R	−3.55 **	−11.93	0.00	−26.51 **	−5.70 *	−7.14 **	−49.36 **
IR62629A × China1R	−1.10	−6.02	−14.29*	−27.14 **	−12.49 **	−11.08 **	−65.53 **
GAN46A × BI1R	−7.05 **	−8.50	−44.00 **	−52.59 **	9.77 **	−3.86 *	−30.65 **
GAN46A × IR26R	−6.55 **	0.00	−7.50	−10.82	21.10 **	8.64 **	14.60 **
GAN46A × BU1R	−4.95 **	−4.09	21.05 **	−39.57 **	5.02	−6.07 **	−35.17 **
GAN46A × China1R	−1.67 *	−0.98	6.65	−39.81 **	11.06 **	−10.61 **	−32.89 **
IR68888A × BI1R	−6.31 **	−4.83	−11.39	−26.21 **	7.11 *	−6.05 **	−37.29 **
IR68888A × IR26R	−6.16 **	−11.56	0.00	−20.00 **	27.70 **	9.27 **	17.79 **
IR68888A × BU1R	−3.47 **	−9.14	−35.00 **	−26.32 **	−0.97	−2.35	−49.34 **
IR68888A × China1R	−5.40 **	−7.42	−34.15 **	−26.78 **	25.62 **	1.01	−12.08 *
LuhaguraA × BI1R	−8.93 **	−7.30	−37.04 **	−34.48 **	6.15 *	−11.23 **	−29.93 **
LuhaguraA × IR26R	−6.28 **	5.09	−34.51 **	−15.15 **	13.01 **	−8.08 **	−15.80 **
LuhaguraA × BU1R	−3.99 **	−5.69	−35.78 **	−38.72 **	−8.21 **	−10.27 **	−52.38 **
LuhaguraA × China1R	−5.88 **	−15.83	−49.55 **	−46.41 **	−15.82 **	−14.11 **	−72.7 **
CD (0.05)	1.386	22.508	13.772	12.437	5.267	3.025	11.397
CD (0.01)	1.882	30.546	18.689	16.874	7.148	4.105	15.467

CD = critical difference, * significant at 5% level, ** significant at 1% level.

3.4.2. Better-Parent Heterosis

The estimation of better-parent heterosis is shown in Table 6. Negative heterosis was desirable for short stature high yielding rice varieties but no hybrids exhibited negative and significant heterosis for plant height. Among the 24 F₁'s, GAN46A × BI1R displayed the highest positive and significant heterosis (29.61%), followed by IR68888A × BI1R, GAN46A × BI1R, BRR1A × CHINA 1R, BRR1A × IR26R, and IR62629A × IR26R. Hybrid IR58025A × BU1R displayed the highest negative and significant heterosis (−1.57). The range of better-parent heterosis for plant height was −1.57% to 29.61%. Islam et al. [84] noted 12 heterotic cross combinations for plant height. Suresh et al. [88] reported the highest positive heterosis for plant height. Among the 24 F₁s, 4 hybrids displayed positive and significant heterobeltiosis for tillers per hill. Islam et al. [84] reported seven heterotic crosses for tillers per hill. IR68888A × China1R displayed the highest positive and significant heterobeltiosis (30.23%), followed by IR58025A × IR26R and IR68888A × BI1R. The range of heterobeltiosis for tillers per hill was −60.76% to 30.23%. Twenty-one F₁s displayed negative and significantly better parent heterosis for panicles per hill. Only one hybrid displayed positive and significant heterosis over better parents. Seven heterotic hybrids were reported for panicles per hill in boro rice [84]. IR68888A × China1R had the highest heterobeltiosis value (28.95%). The heterobeltiosis for this character ranged from −60.53% to 28.95%.

Negative heterobeltiosis was desirable for short-duration rice varieties. Out of 24 F₁s, 12 F₁s displayed negative and significant heterobeltiosis for days to first flowering. GAN46A × China1R had the highest negative heterobeltiosis (−15.90%), followed by IR68888A × China1R, IR62629A × China1R, IR58025A × China1R, and GAN46A × BU1R. The heterobeltiosis for this character ranged from −15.90% to 13.43%. Eight F₁s displayed negative and significant better-parent heterosis for days to 50% flowering. The highest negative heterobeltiosis (−18.15%) was observed in the hybrid GAN46A × China1R, followed by IR68888A × China1R, IR62629A × China1R, and IR58025A × China1R. The heterobeltiosis

for the character ranged from -17.90% to 13.66% . Eleven F_1 s displayed negative and significant heterobeltiosis for days to 100% flowering. IR68888A \times China1R and IR58025A \times China1R had the highest negative heterobeltiosis value (-16.30%), followed by the cross combination, GAN46A \times China1R, IR62629A \times China1R, IR58025A \times BU1R, BRR11A \times China1R, and IR58025A \times BI1R. The heterobeltiosis for this character ranged from -16.30% to 4.87% . Out of 24 F_1 s, 12 F_1 s displayed negative and significant heterobeltiosis for days to maturity. IR68888A \times China1R had the highest negative heterobeltiosis (-11.11%), followed by IR58025A \times China1R, GAN46A \times China1R, IR58025A \times BI1R, GAN46A \times BU1R, and IR58025A \times BU1R. The heterobeltiosis for this character ranged from -11.11% to 11.76% . Islam et al. [84] noticed 25, 1, and heterotic hybrids for days to 50% and 100% flowering, and seven for days to maturity in boro rice. Negative heterobeltiosis was desirable for short-duration rice varieties. Out of 24 F_1 s, 2 F_1 s displayed positive and significant heterobeltiosis for pollen fertility. IR58025A \times IR26R had the highest pollen fertility, followed by IR58025A \times BI1R. The heterobeltiosis for the character ranged from -9.57% to 3.60% . Among the 24 F_1 s, no F_1 displayed the highest positive and significant heterobeltiosis. The heterobeltiosis for panicle length ranged from -24.13% to 5.95% . Out of 24 F_1 s, 5 F_1 s displayed positive and significant heterobeltiosis for primary branches per panicle. Hybrid BRR11A \times BU1R had the highest heterobeltiosis value (71.43%), followed by GAN46A \times BU1R, IR58025A \times IR26R, and BRR11A \times IR26R. The range of heterobeltiosis for the character was -65.43% to 71.43% . Two F_1 s displayed positive and significant heterobeltiosis for secondary branches per panicle. GAN46A \times BU1R and GAN46A \times China1R had the highest heterobeltiosis value (126.40%) for this trait. The range of heterobeltiosis for this character was -56.00% to 126.30% . Islam et al. [84] reported five heterotic hybrids for primary branches per panicle, and twelve heterotic hybrids for secondary branches per panicle. Among 24 F_1 s, 5 F_1 s displayed positive and significant heterobeltiosis and 6 F_1 s displayed negative and significant heterobeltiosis for filled grains per panicle. IR68888A \times IR26R had the highest better parent heterosis (26.89%), followed by BRR11A \times IR26R, IR68888A \times China1R, and IR58025A \times IR26R. Four heterotic hybrids were identified in boro rice for filled grains per panicle that conformed to the present study [84]. The range of heterobeltiosis for this character was -76.58% to 26.89% . Only one F_1 displayed positive and significant heterobeltiosis for 1000-grain weight. On the other hand, 20 hybrids exhibited negative and significant heterobeltiosis. L4 \times T4 alone displayed significantly positive heterosis for 100-grain weight found by Suresh et al. [88]. Out of 24 F_1 s, only one F_1 (IR58025A \times IR26R) displayed positive and significant heterobeltiosis and 23 F_1 s presented negative and significant heterobeltiosis for grain yield. The heterobeltiosis for the character ranged from -78.65% to 5.37% . The better-parent heterosis for yield was corroborative to the results of Islam et al. [84]. Rao et al. [87] identified seven heterotic hybrids for grain yield per hill that corroborated the present study. They performed 5 line \times 4 tester analysis to study the CA and heterosis for rice yield and its agronomic traits and reported IR62829A and IR58025A as good GC for grain yield/plant, spikelet fertility, grains/panicle, and per day productivity. MangalaA \times IR2797-105R and Pushpa A \times IR2797-105R displayed a significant and high degree of SCA for spikelet fertility, grain yield/plant, grains/panicle, and per day productivity. PushpaA \times ARC11353R displayed a significant heterotic effect over standard and better parents for productive tillers/panicle. IR62829A \times IR2797-105R and IR58025A \times IR2797-105R were extremely heterotic for grain weight/plant.

Table 6. Estimates of better parent heterosis (heterobeltiosis) of 24 crosses for yield and its contributing traits.

Crosses	Plant Height (cm)	Tillers Per Hill	Panicles Per Hill	Days to First Flowering	Days to 50% Flowering	Days to 100% Flowering	Days to Maturity
IR58025A × BI1R	9.08 **	−7.50	−41.86 **	−9.87 **	−6.94 **	−6.87 **	−9.34 **
IR58025A × IR26R	18.61 **	27.50 **	9.30	−4.17 *	−1.61	−3.75 *	−3.31 *
IR58025A × BU1R	−1.57	−39.02 **	−58.14 **	−6.41 **	−6.10 **	−9.77 **	−8.26 **
IR58025A × China1R	5.47 **	−11.63 **	−53.49 **	−14.64 **	−13.62 **	−16.30 **	−10.71 **
BRR1A × BI1R	14.08 **	−15.38 **	−27.03 **	3.54	12.33 **	3.45*	11.76 **
BRR1A × IR26R	27.12 **	−25.00 **	−26.19 **	3.98	13.66 **	0.77	8.05 **
BRR1A × BU1R	19.27 **	−24.39 **	−41.67 **	−5.31 **	7.49 **	−1.92	8.36 **
BRR1A × China1R	27.52 **	−39.53 **	−60.53 **	−4.87 *	1.76	−7.28 **	4.33 **
IR62629A × BI1R	16.31 **	−41.54 **	−19.15 **	−1.29	4.08 *	2.67	−5.45 **
IR62629A × IR26R	25.45 **	−33.85 **	−23.40 **	−5.00 **	1.61	0.75	0.56
IR62629A × BU1R	10.03 **	−50.77 **	−46.81 **	−9.83 **	−6.10 **	−3.01 *	−2.54
IR62629A × China1R	2.77	−60.00 **	−42.55 **	−14.64 **	−14.79 **	−12.32 **	−6.48 **
GAN46A × BI1R	29.61 **	−34.15 **	−24.32 **	1.72	3.27	2.67	−0.55
GAN46A × IR26R	23.55 **	−9.76	−21.43 **	4.58 *	5.24 **	4.87 **	−2.49
GAN46A × BU1R	28.34 **	−31.71 **	−47.22 **	−11.54 **	−8.54 **	−6.77 **	−8.56 **
GAN46A × China1R	23.42 **	−37.21 **	−21.05 **	−15.90 **	−17.90 **	−14.13 **	−10.50 **
IR68888A × BI1R	28.68 **	25.64 **	8.11	−0.44	4.08 **	4.20 **	−6.94 **
IR68888A × IR26R	24.40 **	15.00 **	−4.76	11.50 **	4.03 **	3.75 **	0.56
IR68888A × BU1R	13.54 **	−2.44	−19.44 **	−3.54	−1.63	−1.88	−4.44 **
IR68888A × China1R	12.83 **	30.23 **	28.95 **	−15.49 **	−17.51 **	−16.30 **	−11.11 **
LuhaguraA × BI1R	18.71 **	−29.11 **	−23.44 **	13.43 **	5.58 **	3.44*	0.57
LuhaguraA × IR26R	20.69 **	−45.57 **	−45.31 **	8.46 **	−0.43	−2.55	−1.42
LuhaguraA × BU1R	14.08 **	−60.76 **	−50.00 **	4.98 **	−1.72	−1.50	−2.27
LuhaguraA × China1R	8.99 **	−21.52 **	−23.44 **	2.49	−2.58	−4.73 **	−4.55 **
CD (0.05)	3.70	11.03	9.45	3.60	3.64	2.78	2.62
CD (0.01)	5.02	14.97	12.82	4.89	4.94	3.77	3.56

Crosses	Pollen fertility (%)	Panicle length (cm)	Primary branches per panicle	Secondary branches per panicle	Filled grains per panicle	1000-grain weight (g)	Grain yield (t/ha)
IR58025A × BI1R	1.17 *	2.04	2.86	4.67	−3.62	−18.36 **	−44.3 **
IR58025A × IR26R	3.60 **	−11.46	45.71 **	−27.36 **	15.22 **	6.96 **	5.37 *
IR58025A × BU1R	−6.23 **	−19.36	−8.57	−44.55 **	−6.16	−13.10 **	−66.99 **
IR58025A × China1R	−7.80 **	−20.37	−20.00 **	−22.55	−12.32 **	−15.05 **	−69.47 **
BRR1A × BI1R	−7.47 **	0.76	37.04 **	5.61	9.09	−11.89 **	−54.25 **
BRR1A × IR26R	−2.16 **	5.95	43.75 **	−12.26	21.49 **	−6.00 **	−23.98 **
BRR1A × BU1R	−4.76 **	−24.13 *	71.43 **	−40.91 **	−1.84	−11.76 **	−50.11 **
BRR1A × China1R	−9.57 **	−7.16	10.00	−7.14	14.88 *	−14.40 **	−48.09 **
IR62629A × BI1R	−6.76 **	−1.65	−20.00 **	−0.93	−7.85	−10.57 **	−56.90 **
IR62629A × IR26R	−4.32 **	−17.68	−12.50	−10.71	6.48	2.18	−13.32 **
IR62629A × BU1R	−5.49 **	−21.51 *	−15.00	−44.55 **	−9.90	−11.36 **	−56.66 **
IR62629A × China1R	−4.61 **	−15.65	−25.00 **	−8.93	−23.55 **	−15.97 **	−71.74 **
GAN46A × BI1R	−8.54 **	−15.78	−56.25 **	−56.00 **	3.31	−9.51 **	−46.58 **
GAN46A × IR26R	−7.55 **	−8.84	−22.92 **	−17.60	12.87	3.82	−11.16 *
GAN46A × BU1R	−5.13 **	−14.23	47.92 **	126.40 **	−75.55 **	−11.10 **	−49.92 **
GAN46A × China1R	−5.67 **	−10.56	14.58	126.40 **	−76.58 **	−16.62 **	−51.60 **
IR68888A × BI1R	−7.47 **	−10.94	−32.69 **	−28.97 **	6.67	−14.80 **	−59.27 **
IR68888A × IR26R	−6.83 **	−18.06	−50.00 **	−22.64 **	26.89 **	0.55	−23.19 **
IR68888A × BU1R	−3.65 **	−17.45	−50.00 **	−30.00 **	−6.34	−10.96 **	−67.04 **
IR68888A × China1R	−9.57 **	−13.83	−34.62 **	−9.52	20.59 **	−15.18 **	−48.37 **
LuhaguraA × BI1R	−9.25 **	−9.54	−58.02 **	−39.20 **	−1.43	−14.40 **	−42.99 **
LuhaguraA × IR26R	−6.45 **	1.49	−54.32 **	−21.60*	3.93	−9.96 **	−31.02 **
LuhaguraA × BU1R	−5.02 **	−10.77	−56.79 **	−42.40 **	−10.36*	−12.97 **	−61.14 **
LuhaguraA × China1R	−6.38 **	−19.77	−65.43 **	−55.20 **	−25.00 **	−17.54 **	−78.65 **
CD (0.05)	1.32	21.15	16.65	19.43	10.19	2.29	8.85
CD (0.01)	1.79	28.71	22.60	26.36	14.68	3.97	12.00

CD, critical difference; * significant at 5% level, ** significant at 1% level.

3.4.3. Standard Heterosis

The heterotic effects in F₁ generation over BU dhan1 are presented in Table 7. Negative and significant standard heterosis is desirable for the development of short-statured high-yielding rice varieties. Four cross combinations, i.e., IR58025A × BU1R, IR62629A × China1R, IR58025A × China1R, and IR62629A × BU1R, exhibited negative heterosis over

BU dhan1, which could be used for semi-dwarf varieties. On the other hand, 12 F_1 s having positive and significant heterosis over BU dhan1 could be used to develop tall varieties. Eight hybrids presented positive and significant heterosis over BU dhan1. The maximum standard heterosis (67.57%) was observed in the cross combination LuhaguraA \times China1R, followed by LuhauraA \times BI1R, IR58025A \times IR26R, IR68888A \times BI1R, IR68888A \times BU1R, IR68888A \times IR26R, IR62629A \times IR26R, and LuhaguraA \times IR26R. The standard heterosis for the character over BU dhan1 ranged from -29.73% to 67.57% . Ten hybrids displayed positive and significant heterosis over BU dhan1. The highest standard heterosis (81.48%) was observed in the cross combinations LuhaguraA \times China1R and LuhaguraA \times BI1R, followed by IR58025A \times IR26R, IR68888A \times BI1R, IR68888A \times IR26R, LuhaguraA \times BI1R, IR62629A \times BI1R, IR62629A \times IR26R, LuhaguraA \times IR26R, and GAN46A \times IR26R. The standard heterosis over BU dhan1 for the character ranged from -44.44 to 81.48% . Negative standard heterosis was desirable for short-duration rice varieties. Out of 24 F_1 s, 22 F_1 s displayed negative and significant heterosis over BU dhan1 for days to first flowering. IR68888A \times China1R had the highest negative standard heterosis over BU dhan1 (-25.10%), followed by GAN46A \times China1R, IR62629A \times China1R, IR58025A \times China1R, and LuhaguraA \times China1R. The range of heterosis over BU dhan1 for the character was -25.10% to -1.18% . All the F_1 s displayed negative and significant standard heterosis over BU dhan1 for days to 50% flowering. The highest negative heterosis (-25.18%) was observed in the hybrid GAN46A \times China1R, followed by IR68888A \times China1R, IR62629A \times China1R, IR58025A \times China1R, and GAN46A \times BU1R. The range of standard heterosis for the character was -25.18% to -7.45% . Patil et al. [89] observed high heterotic hybrids for days to 50% flowering, which was corroborative to the present findings. All the F_1 s displayed negative and significant standard heterosis over BU dhan1 for days to 100% flowering. Hybrids IR68888A \times China1R and IR58025A \times China1R had the highest negative heterosis over BU dhan1 (-23.00%), followed by the cross combination, GAN46A \times China1R, IR58025A \times BU1R, IR62629A \times China1R, BRRI1A \times China1R, and IR58025A \times BI1R. The range of heterosis for the character was -23.00% to -6.67% . These results conformed with the results of Sarker et al. [82], who reported high heterotic hybrids for days to 100% flowering. Negative standard heterosis was desirable for short-duration rice varieties. All the F_1 s displayed negative and significant heterosis over BU dhan1 for days to maturity. IR68888A \times China1R had the highest negative heterobeltiosis (-13.51%), followed by GAN46A \times China1R, IR58025A \times China1R, IR58025A \times BI1R, IR58025A \times BU1R, IR62629A \times China1R, GAN46A \times BU1R, and IR58025A \times BU1R. The range of heterosis for the character was -2.16% to -13.51% . Out of 24 F_1 s, one F_1 s, i.e., IR58025A \times IR26R, displayed positive and significant heterosis over BU dhan1 for pollen fertility. The range of heterosis for the character was -6.25% to 5.88% . Among the 24 F_1 s, four hybrids displayed significant heterosis over BU dhan1 for panicle length. BRRI1A \times IR26R displayed the maximum positive and significant heterosis (39.26%) over BU dhan1, followed by LuhaguraA \times IR26R, IR58025A \times BI1R, and LuhaguraA \times BU1R. The range of heterosis for panicle length was 4.09% to 39.26% . Khoyumthem et al. [86] reported high heterotic hybrids over the standard check, which conformed to the present findings. Out of 24 F_1 s, 9 F_1 s displayed positive and significant heterosis over BU dhan1 for primary branches per panicle. IR58025A \times IR26R had the highest heterosis value (59.38%) over BU dhan1, followed by BRRI1A \times BU1R, BRRI1A \times IR26R, and GAN46A \times BU1R. The range of heterosis for the character was -34.38% to 59.38% . Three F_1 s displayed positive and significant heterosis over BU dhan1 for secondary branches per panicle. BRRI1A \times BI1R had the highest heterosis value (17.71%) over BU dhan1, followed by IR58025A \times BI1R and IR62629A \times BI1R for this trait. The range of heterosis for the character was -47.92% to 17.71% . Among 24 F_1 s, no F_1 s displayed positive and significant heterosis over BU dhan1. In contrast, 13 F_1 s displayed negative and significant standard heterosis for filled grains per panicle. The range of heterosis for the character was -30.00% to 6.00% . Three F_1 s displayed positive significant heterosis for 1000-grain weight. On the other hand, 20 hybrids exhibited negative and significant heterosis. The highest significant and positive heterosis over

standard check BU dhan1 was observed in the hybrid IR58025A \times IR26R, followed by hybrids GAN46A \times IR26R and IR62629A \times IR26R. The standard heterosis ranged from -14.17% to 8.89% . Out of 24 F_1 s, three F_1 s were found heterotic over standard variety BU dhan1. The highest positive and significant standard heterosis was observed in the hybrid IR58025A \times IR26R, followed by GAN46A \times IR26R, and IR62629A \times IR26R. In contrast, 18 F_1 s displayed negative and significant heterosis for grain yield. The range of heterosis for the character was -66.61% to 46.62% . Similar related findings were found by Sathya et al. [90] to evaluate the nature and degree of heterobeltiosis, heterosis, and standard heterosis for yield and its agronomic traits in a line \times tester design. They reported that the hybrids, such as IR62829A \times IR50R, IR62829A \times AS90043R, and IR58025A \times AS89090R, were declared the best for manipulation of standard heterosis, applied to grain yield per plant. These two combinations displayed significant standard heterosis for productive tillers per plant and grain yield.

Table 7. Estimates of standard heterosis of 24 crosses for yield and its contributing traits.

Crosses	Plant Height (cm)	Tillers Per Hill	Panicles Per Hill	Days to First Flowering	Days to 50% Flowering	Days to 100% Flowering	Days to Maturity
IR58025A \times BI1R	−3.44	0.00	−7.41	−17.65 **	−19.15 **	−18.67 **	−10.81 **
IR58025A \times IR26R	4.99 **	37.84 **	74.07 **	−9.80 **	−13.48 **	−14.33 **	−5.41 **
IR58025A \times BU1R	−12.86 **	−32.43 **	−33.33 **	−14.12 **	−18.09 **	−20.00 **	−10.00 **
IR58025A \times China1R	−6.64 **	2.70	−25.93 **	−20.00 **	−21.28 **	−23.00 **	−12.16 **
BRR 1A \times BI1R	−2.23	−10.81 *	0.00	−8.24 **	−9.57 **	−10.00 **	−2.43 **
BRR11A \times IR26R	9.87 **	−18.92 **	14.81	−7.84 **	−8.51 **	−12.33 **	−5.68 **
BRR11A \times BU1R	3.85 *	−16.22 **	−22.22 **	−16.08 **	−13.48 **	−14.67 **	−5.41 **
BRR11A \times China1R	14.98 **	−29.73 **	−44.44 **	−15.6 **	−18.09 **	−19.33 **	−8.92 **
IR62629A \times BI1R	−0.33	2.70	40.74 **	−9.80 **	−9.57 **	−10.33 **	−6.22 **
IR62629A \times IR26R	8.43 **	16.22 **	33.33 **	−10.59 **	−10.6 **	−10.33 **	−3.51 **
IR62629A \times BU1R	−4.20 **	−13.51 *	−7.41	−17.25 **	−18.09 **	−14.00 **	−6.49 **
IR62629A \times China1R	−7.34 **	−29.73 **	0.00	−20.00 **	−22.34 **	−19.33 **	−10.27 **
GAN46A \times BI1R	11.07 **	−27.03 **	3.70	−7.06 **	−10.28 **	−10.33 **	−2.70 **
GAN46A \times IR26R	6.78 **	0.00	22.22 **	−1.57	−7.45 **	−6.67 **	−4.59 **
GAN46A \times BU1R	11.75 **	−24.32 **	−29.63 **	−18.82 **	−20.21 **	−17.33 **	−10.54 **
GAN46A \times China1R	11.28 **	−27.03 **	11.11	−21.18 **	−25.18 **	−21.00 **	−12.43 **
IR68888A \times BI1R	10.28 **	32.43 **	48.15 **	−11.76 **	−9.57 **	−9.00 **	−9.46 **
IR68888A \times IR26R	7.52 **	24.32 **	48.15 **	−1.18	−8.51 **	−7.67 **	−2.16 **
IR68888A \times BU1R	−1.15	8.11 **	7.41	−14.51 **	−14.18 **	−13.00 **	−7.03 **
IR68888A \times China1R	10.81 **	−2.70 **	7.41	−25.10 **	−24.82 **	−23.00 **	−13.51 **
LuhaguraA \times BI1R	1.73	51.35 **	81.48 **	−10.59 **	−12.77 **	−9.67 **	−4.32 **
LuhaguraA \times IR26R	4.32 **	16.22 **	29.63 **	−14.51 **	−17.7 **	−13.33 **	−6.22 **
LuhaguraA \times BU1R	−0.68	−16.22 **	18.52 *	−17.25 **	−18.79 **	−12.67 **	−7.03 **
LuhaguraA \times China1R	−1.73	67.57 **	81.48 **	−19.22 **	−19.50 **	−12.67 **	−9.19 **
CD (0.05)	3.511	10.342	10.278	2.816	2.547	2.242	1.481
CD (0.01)	4.177	15.55	20.149	3.462	3.125	2.769	1.901
Crosses	Pollen fertility (%)	Panicle length (cm)	Primary branches per panicle	Secondary branches per panicle	Filled grains per panicle	1000-grain weight (g)	Grain yield (t/ha)
IR58025A \times BI1R	−4.41 **	31.26 **	12.50	16.67 **	−11.33	−14.17 **	−21.14 **
IR58025A \times IR26R	5.88 **	16.37	59.38 **	−19.79 **	6.00	8.89 **	46.62 **
IR58025A \times BU1R	−5.88 **	10.64	0.00	−36.46 **	−13.67 **	−9.72 **	−53.60 **
IR58025A \times China1R	−4.41 **	7.53	−12.50 *	−17.71 **	−19.33 **	−9.86 **	−52.25 **
BRR 1A \times BI1R	−4.41 **	29.62	15.63 **	17.71 **	−12.00 **	−7.36 **	−35.19 **
BRR11A \times IR26R	−4.00 **	39.26 **	43.75 **	−3.13	−2.00	−4.31 **	5.78
BRR11A \times BU1R	−4.41 **	4.09	50.00 **	−32.29 **	−12.67 **	−8.33 **	−29.87 **
BRR11A \times China1R	−6.25 **	25.37	3.13	−18.75 **	−7.33 **	−9.17 **	−18.82 **
IR62629A \times BI1R	−3.68 **	26.51	0.00	10.42*	−10.00 **	−5.97 **	−38.95 **
IR62629A \times IR26R	−2.21 **	8.18	9.38	−47.92 **	4.00	4.03 **	20.61 **
IR62629A \times BU1R	−5.15 **	7.69	6.25	−36.46 **	−12.00 **	−7.92 **	−39.07 **
IR62629A \times China1R	−1.10	13.91	−6.25	−46.88 **	−25.33 **	−10.83 **	−55.80 **
GAN46A \times BI1R	−5.51 **	8.35	−34.38 **	−42.71 **	−6.33 **	−4.86 **	−24.33 **
GAN46A \times IR26R	−5.51 **	19.80	15.63 **	7.29	2.33	5.69 **	23.61 **
GAN46A \times BU1R	−4.78 **	17.68	43.75 **	−26.04 **	−5.67	−7.64 **	−29.60 **
GAN46A \times China1R	−2.21 **	20.79	12.50 **	−42.71 **	−5.67	−11.53 **	−24.30 **

Table 7. Cont.

IR68888A × BI1R	−4.41 **	14.57	9.38	−20.83 **	−14.67 **	−10.42 **	−42.31 **
IR68888A × IR26R	−4.78 **	7.69	31.25 **	−14.58 **	0.67	2.36	6.88
IR68888A × BU1R	−2.94 **	13.26	−18.75 **	−19.79 **	−16.67 **	−7.50 **	−53.67 **
IR68888A × China1R	−3.31 **	14.40	−15.63 **	−30.21 **	−4.33	−3.19 *	−12.63 *
LuhaguraA × BI1R	−6.25 **	16.37	6.25	−20.83 **	−8.00	−10.00 **	−19.25 **
LuhaguraA × IR26R	−4.04 **	33.39 *	15.63 **	2.08	−3.00	−8.33 **	−4.03
LuhaguraA × BU1R	−2.57 **	22.42 *	9.38	−25.00 **	−16.33 **	−9.58 **	−45.37 **
LuhaguraA × China1R	−2.94 **	8.35	−12.50 *	−41.67 **	−30.00 **	−12.50 **	−66.61 **
CD (0.05)	1.116	28.837	9.596	8.862	4.595	2.849	11.968
CD (0.01)	1.464	37.469	13.026	11.401	5.03	3.999	16.246

CD, critical difference; * significant at 5% level, ** significant at 1% level.

4. Conclusions

Significant SCA and GCA variances were obtained for all traits except for panicle length, indicating both non-additive and additive gene action are involved in these traits. The ratio of GCA and SCA effects was lower to unity for all the traits that indicated the predominance of non-additive gene actions of these traits. Across lines, GAN46A, IR58025A, and IR62629A displayed significant GCA for grain yield and the majority of agronomic traits can be used as good GC lines for improving the grain yield of rice. Across testers, IR46R displayed significant GCA effects for grain yield, and the majority of agronomic traits can be used as good GC testers for improving the grain yield of rice. The best hybrids for grain yield and its contributing traits were hybrid IR58025A × IR46R and GAN46A × IR46R. Nine hybrids, i.e., IR68888A × China1R, IR62629A × China1R, LuhaguraA × IR46R, BRRI1A × IR46R, IR68888A × BU1R, IR62629A × BU1R, LuhaguraA × BU1R, BRRI1A × BU1R, and IR58025A × BI1R, were considered as being good hybrids for grain yield and its contributing traits. The F₁s IR58025A × IR26R, IR68888A × IR26R, and GAN46A × IR26R displayed positive and significant heterosis over mid-parent for grain yield and the majority of agronomic traits. The hybrid IR58025A × IR26R displayed positive and significant heterobeltiosis for grain yield. Three hybrids, IR58025A × IR26R, GAN46A × IR26R, and IR62629A × IR26R, were found heterotic over standard check variety BU dhan1. The hybrids IR58025A × IR26R and GAN46A × IR26R demonstrated high heterosis over standard check, as well as high specific CA effects that could be selected for the most preferable hybrids.

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