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RESEARCH ARTICLE

Studies on combining ability for grain yield and resistance to banded leaf and sheath blight disease in maize (*Zea mays* L.) improvement

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Abstract

Twelve maize inbred lines, differing for resistance to banded leaf and sheath blight (BLSB) were crossed in a half-diallel mating design and the F$_1$s were evaluated during *kharif* 2023 at Delhi and Peddapuram. The combining ability of these inbred lines for BLSB resistance under artificial inoculation and grain yield in artificial and natural conditions was assessed. The ANOVA revealed highly significant GCA variances ($p < 0.01$) for grain yield in both conditions as well as for resistance to BLSB, indicating additive genetic variance for both traits. In addition, crosses and SCA effects also showed significant variances for both traits, suggesting the presence of significant variability among half-diallel crosses and non-additive genetic variance. Notably, the mean squares for GCA in BLSB disease resistance were much higher than those for SCA, indicating that additive genetic effects predominantly contributed to disease resistance. The results indicated that the selection for BLSB resistance under artificial epiphytotic conditions at hotspot locations would be effective in breeding programs. P5 and P7 were the most desirable inbreds for developing high-yielding, BLSB-resistant hybrids due to their higher magnitude of positive GCA effects for grain yield and higher magnitude of negative GCA effects for BLSB disease. P4×P12, P5×P7, P6×P12, and P6×P1 exhibited significant negative SCA effects for BLSB resistance and significant positive SCA effects for grain yield under artificial inoculation conditions, making them promising combinations for further breeding programs.

Keywords: Maize, BLSB, combining ability, resistance, grain yield

Introduction

Maize (*Zea mays* L.) is one of the most versatile cereal crops with wider adaptability in the world. It is cultivated across more than 170 countries in a range of climatic conditions, *viz.,* the semi-arid to irrigated environments in the tropics, subtropics, and temperate zones. It is the third most important cereal crop in India after rice and wheat. Maize is affected by more than 60 diseases, of which 16 diseases are considered major. Among these, banded leaf and sheath blight (BLSB) is a soil-borne disease caused by *Rhizoctonia solani* f. sp. *sasakii*, which is the most destructive and affects the maize yield severely. BLSB is estimated to cause yield losses ranging from 11 to 40% (Singh and Sharma 1976), with potential reduction in grain yield as high as 90% (Lal et al. 1985). The most important and sustainable BLSB management practice is the use of host plant resistance (HPR), which is still lagging due to the non-availability of BLSB disease-resistant sources. Previously, efforts have been made to identify germplasm resistance to BLSB disease in maize (Garg et al. 2005). However, the study was restricted to single-location data, limiting the understanding of the stability of the resistant reaction of the genotypes to disease pressure under artificial inoculated conditions. Furthermore, towards deployment of the resistant sources, information on combining the ability of the sources of resistance is also crucial. The breeding programs aimed at enhancing grain yield in maize along with disease tolerance necessitate a thorough understanding of the combining ability of the breeding material. The diallel cross method, introduced by Sprague and Tatum (1942), allows the examination of two important genetic parameters, namely, the general combining ability (GCA), and the specific combining ability (SCA). Griffing's (1956) graphical approach highlights gene action and the combining ability of parental lines. The GCA

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reflects the extent of additive gene action, while the SCA indicates the degree of non-additive gene action (Griffing 1956; Falconer 1981).

The information on combining ability not only helps to understand the nature and magnitude of the gene action but also aids in choosing the most effective breeding methods for further utilization. Thus, the knowledge of genetic architecture and inheritance patterns of multiple traits like yield and disease resistance enables breeders to select parental lines that are expected to result in best-performing hybrids by optimizing the resistance to diseases and yield potential. Therefore, it is crucial to comprehend both the nature and magnitude of gene action and the combining ability related to yield and disease resistance to exploit the parents to their maximum potential**.**

Previous studies have reported that additive effects predominantly govern resistance to different diseases in maize (Vimla et al. 1988; Paterniani et al. 2000; Nuning et al. 2007; Vivek et al. 2009; Mukanga et al. 2010; Sibiya et al. 2011; Gichuru et al. 2011; Hung and Holland, 2012; Nzuve et al. 2013; Bekeko et al. 2018). The most effective strategy for the effective use of additive gene effects could be through the selection of resistant lines under artificial inoculation at hotspot locations/ environments. Identifying inbred lines exhibiting good combining ability for both high yield and strong disease resistance must involve the selection of resistant parents followed by the development of cross combinations involving resistant genotypes and their evaluation across multiple locations. Previously, studies have been carried out to identify BLSB-resistant germplasm, but the successes in combining high yield and disease resistance are meagre (Garg et al. 2005; Chen et al. 2013; Asif et al. 2017) because the combining ability and gene actions governing the resistance response have not been studied. Therefore, the development of BLSB-resistant hybrids or varieties has largely remained unrealized. Thus, the present study is conducted to identify the best hybrid combinations with an acceptable level of yield coupled with BLSB resistance by effectively involving inbred lines differing in BLSB resistance and combining ability effects.

Materials and methods

Genetic material

The genetic material comprised 12 parental genotypes (Table 1) and their 66 half-diallel crosses, generated by following a 12 × 12 half-diallel mating design during *kharif* 2022 at Winter Nursery Centre, ICAR-Indian Institute of Maize Research (IIMR), Hyderabad (17°32′58.22″N, 78°39′70.31″E). Out of the 12 parental genotypes, eight were BLSB resistant/moderately resistant and four were BLSB susceptible. Parental lines were selected during *kharif* 2021 based on their reaction to BLSB under artificially infested conditions at five BLSB hotspot locations, namely, New Delhi, Peddapuram, Kalyani, Pantnagar, and Ludhiana.

BLSB culture preparation and inoculation

For the artificial inoculation of the pathogen, *Rhizoctonia solani* was isolated aseptically from infected leaf sheaths of maize plants from the crop raised in the previous season. These infected leaf sheaths were washed thoroughly under tap water and were separately cut into small pieces of

Table 1. Details of resistant (R) and susceptible (S) inbred parents used in the present study

Entry code	Entry name	Entry identity	Disease score	Reaction to BLSB
P1	MIL 6-2123677	IC0621029	2.9	R
P2	MIL 6-2123711	IC0610222	2.8	R
P3	MIL 6-2123407	IC213078	3.2	R
P4	MIL 6-2123935	HKI-1040-7	3.7	R
P5	MIL 6-2123673	IC0621616	2.8	R
P6	MIL 6-117	LMDR-2	2.0	R
P7	MIL 6-2123932	IC613395	2.8	R
P8	MIL 6-2123662	IC0598527	6.0	S
P9	MIL 6-2123920	IC0598523	8.4	S
P10	MIL 6-2124409	EC0758213	5.8	S
P11	MIL 6-102	IC0621054	2.0	R
P12	MIL 6-2124258	IC0612797	7.1	S

about half a centimeter in size, having half healthy and half diseased areas, using a sterilized blade. Infected tissues were surface sterilized in 0.1% sodium hypochloride solution for 30 to 60 seconds, followed by rinsing in sterilized distilled water thrice. The infected pieces were placed in between two layers of sterilized blotting sheets to remove moisture and then were transferred aseptically onto solidified sterilized potato dextrose agar (PDA) plates and incubated at 27 ± 2°C. The growing mycelium from the margin of apparently distinct colonies was sub-cultured on fresh plates containing the same medium. For mass multiplication, sorghum grain, anhydrous dextrose, and water were mixed in a ratio of 1:5:1.25 (w/w/v) and boiled in the pressure cooker. The mixture was cooled to room temperature and then 200 g of such mixture was filled in 500 mL flasks. The sorghum grain preparation was sterilized in an autoclave at 15 lbs for 20 minutes. After cooling to room temperature, the flasks were inoculated with 5 mm mycelial discs of *R. solani*, and incubated in a biochemical oxygen demand (BOD) incubator at 28 ± 1°C for 10 days.

The fully developed pathogen culture was inoculated on a 30 to 40-day-old plant by inserting grain culture (2–4 grains that are covered with mycelium) between the stalk and the sheath at the second or third node from the ground. High humidity was maintained for the disease development by frequent watering.

Phenotyping for BLSB and grain yield

The diallel crosses were evaluated for their reaction to BLSB under both artificial inoculated as well as natural conditions at hotspot environments. *viz.,* Agricultural Research Station, ANGRAU, Peddapuram (17^{0}06′99.87″N, 82^{0}14′87.64″E) and research farm at ICAR-Indian Institute of Maize Research, New Delhi (28°64′29.17″N, 77°14′73.45″E) during *kharif* 2023. The trial was conducted in a randomized complete block design (RCBD) in two replications. Randomization of diallel crosses was carried out in the trial. Each entry in the trial was sown in one row of 3 m in length by dibbling two seeds per hill with a spacing of 75 × 20 cm between the row and plants within the row, respectively. After 10 days of germination, one seedling per hill was maintained by thinning out the extra seedling and a 95 to 100% plant stand was maintained in each plot. The BLSB disease incidence score was recorded at 35 days after inoculation by following 1–9 disease score on five random plants in each entry evaluated under artificial inoculated conditions as well as natural conditions at hotspot environments (AICMIP 1983). The grain yield data was recorded on a plot basis under artificial inoculation as well as natural conditions at each hotspot location.

Statistical analysis

Analysis of variance (ANOVA) was carried out on grain yield and BLSB disease score data for individual environments/locations. The mean values of grain yield and BLSB disease scores were subjected to Levene's test of homogeneity of variance and the analysis of variance was performed on pooled data over the environments/locations using R software by considering the crosses as fixed effects and environments/locations as random effects. Diallel analysis of variance was performed for grain yield and BLSB disease score to estimate the general and specific combining ability (GCA and SCA) by following Method II, Model B of Griffing (1956) using AGD-R software. The significance of the GCA of parents and SCA of half-diallel crosses were tested using a t-test, which was based on the standard errors of the GCA and SCA effects. The negative values of disease score and positive values of grain yield were considered desirable for further selection and use in selection.

Results and discussion

Analysis of variance (ANOVA)

The homogeneity of variance test showed no significant differences across locations for each trait (grain yield and BLSB disease score) under each condition (natural and artificial inoculation). The analysis of variance (ANOVA) of pooled data of diallel crosses is given in Table 2. The results showed that the location variances were highly significant ($p < 0.01$) for both grain yield under natural as well as artificial inoculated conditions and BLSB disease score, indicating differences in the mean value of the traits between locations. Similarly, the GCA variances were also highly significant ($p < 0.01$) for both grain yield (under natural and artificial infested conditions) and BLSB disease score, indicating the presence of additive genetic variance. The presence of additive genetic variance allows for the effective selection of the traits among the parental lines. The variances due to location × GCA were also significant for both traits,

Table 2. Analysis of variance (ANOVA) of grain yield and BLSB disease score across locations

Source of variation	DF	Mean Squares		
		Natural conditions	Artificially Inoculated	
		Grain Yield (t ha^{-1})	Grain Yield (t ha^{-1})	BLSB (1-9 scale)
Location	1	17.82 **	48.43**	8.25**
Cross	65	4.45**	6.46**	1.04**
GCA	11	6.12**	11.30**	2.71**
SCA	54	4.11**	5.48**	0.70**
Location × Cross	65	4.55**	3.67**	0.75**
Location × GCA	11	5.78**	7.88**	1.42**
Location × SCA	54	4.30**	2.81**	0.61**
Residual	110	2.97	3.19	0.31

**Significant at 1% level.

indicating the differences in additive genetic variance across locations. Further, the variance of crosses and SCA were also significant for both the traits, indicating the presence of sufficient variability among half-diallel crosses and the presence of non-additive genetic variance, respectively. The presence of sufficient variability and non-additive variance for both traits indicated the possibility of exploitation of favorable (less disease and higher grain yield) heterosis or hybrid vigor. The variance due to location × SCA was also significant for both traits, indicating that the differences in the BLSB reaction and grain yield of the half-diallel crosses across locations. Similar findings for significant differences among parents and crosses for grain yield and different diseases like grey leaf spot in Ethiopia (Bekeko et al. 2018), downy mildew and rust in Brazil (Paterniani et al. 2000), leaf blight, common rust, maize streak virus, ear rots, head smut, Phaeosphaeria leaf spot (Vivek et al. 2009), and BLSB (Vimla et al. 1988) have been reported.

In natural conditions, the percentage contribution of SCA was more to grain yield (76.7%) than GCA (23.3%). This indicated that specific hybrid combinations (the interaction between specific parents) had a larger influence on yield performance in natural, unmanipulated growing environments. Under artificially inoculated conditions, GCA contributed more to yield (30%) compared to the natural conditions (23.3%). However, SCA still played a major role (70.4%), indicating that specific hybrid combinations are still important for yield performance, but the overall additive genetic effects of the parents (reflected by GCA) also had a noticeable influence under stress conditions. The disease score under artificially inoculated conditions showed a significant shift in the contributions of GCA (44.1%) and SCA (56.0%). The relatively higher GCA contribution to disease resistance indicates that additive genetic effects (those contributed by individual parents) are important in determining disease resistance. This suggests that certain parents have inherent resistance to the disease, which can be passed on to their offspring. The proportion of GCA to SCA determines the predominance of additive genetic variance over non-additive genetic variance. Hence, the selection strategy largely depends on the proportion and kind of genetic variance.

In the present study, the mean squares of GCA for BLSB resistance were much higher than SCA. The proportional mean squares of GCA and SCA for grain yield under natural conditions were not much different as compared to artificial infested conditions. The results indicated that additive genetic variance was responsible for sustaining higher genetic yield under heavy BLSB infestation as compared to natural infestation. Vimla et al. (1988) reported that additive gene action is important for BLSB disease resistance. The results also indicated that the additive genetic variance was responsible for imparting BLSB resistance. Thus, simple selection for the resistance reaction under artificial epiphytotic conditions at hotspot locations would be more effective in breeding for BLSB resistance. Derera et al. (2007) reported highly significant GCA effects, contributing 90% to the total genetic variation for resistance to Phaeosphaeria leaf spot, indicating the predominance of additive gene action in the evaluated crosses. Similarly, Sibiya et al. (2011) observed both significant GCA and SCA effects, with GCA contributing 66 to 90% and SCA contributing 10 to 34% to the variation for Phaeosphaeria leaf spot resistance and grain yield. A related study by Nuning et al. (2007) on bacterial stalk rot in maize reported comparable findings, further supporting the importance of additive gene effects. Paterniani et al. (2000) also highlighted that GCA effects accounted for 70% of the variation in grain yield, while SCA effects contributed 30%. Vivek et al. (2009) reported similar results, with GCA and SCA effects contributing 65 and 35%, respectively, to total genetic variation, reinforcing the significance of both additive and non-additive gene actions in maize breeding.

General combining ability effects

In general, most of the inbred lines showed significant GCA effects for BLSB resistance and grain yield under natural as well as artificial infested conditions. However, few inbred lines, *viz.,* P2, P3 and P11 for grain yield under natural conditions; P3 and P10 for grain yield under BLSB artificial epiphytotic conditions; P1 and P9 for BLSB disease showed no significant GCA effects (Table 3). The GCA effects for BLSB disease rating ranged from 0.439 (P5) to 0.486 (P12). The variability ranged from negative value to positive value as the study material used comprised both resistant and susceptible inbred lines. Positive values for grain yield and negative values for BLSB disease resistance are desirable.

Table 3. GCA effects for grain yield and BLSB disease reactions

Parents	Natural conditions	Artificially inoculated	
	Grain Yield (t ha^{-1})	Grain Yield (t ha^{-1})	BLSB (1-9 scale)
P1	-0.168 **	0.113**	-0.024
P2	0.048	0.434**	-0.066**
P3	-0.002	-0.091	-0.058**
P4	0.318**	-0.441**	0.070**
P5	0.296**	0.312**	-0.439**
P6	0.166**	-0.349**	-0.370**
P7	0.504**	1.302**	-0.183**
P8	-0.302**	-0.403**	0.217**
P9	-0.972**	-0.645**	-0.014
P10	0.293**	0.041	0.106**
P11	0.056	0.158**	0.274**
P12	-0.237**	-0.430**	0.486**

** Significant at 1% level.

Statistically significant desirable GCA effects for BLSB disease resistance were observed in five BLSB-resistant/moderately resistant inbred lines, namely, P2, P3, P5, P6 and P7. Since P1 to P7 and P11 parents were resistant/moderately resistant to BLSB, it was expected that all the resistant/moderately resistant inbred lines should show negative GCA effects. Similar results were reported in other studies. For example, Sibiya et al. (2013) used the maize line A1220-4 in their study which exhibited significant negative GCA effects for resistance to Phaeosphaeria leaf spot. Similarly, Nzuve et al. (2013) and Eisele et al. (2020) reported significant negative GCA effects in some of the lines evaluated for resistance to grey leaf spot. Vivek et al. (2009) in their study reported negative GCA effects for Phaeosphaeria leaf spot resistance in maize line CML395.

In the present study, two resistant/moderately resistant inbred lines (P4 and P11) to BLSB showed statistically significant but undesirable positive GCA effects for BLSB resistance, whereas rest all resistant/moderately resistant inbred lines except P1 showed a significant negative GCA effect. On the contrary, three out of four BLSB susceptible inbred lines showed significant undesirable positive GCA effects as per expectation, and the remaining one inbred line, P9 showed desirable negative GCA effects, but the value was not statistically significant. The results of the present study also indirectly corroborate the resistance reaction of six of the eight resistant inbred lines, identified based on screening across five BLSB hotspot locations under artificial epiphytotic conditions.

The range of GCA effects for grain yield under natural conditions ranged from -0.972 to 0.504, whereas it ranged from -0.645 to 1.302 under artificial epiphytotic conditions. The higher magnitude of positive GCA effects for grain yield under epiphytotic conditions could be useful to realize higher grain yield under BLSB disease conditions. However, there is a need to consider both BLSB disease resistance and grain yield to realize maximum yield potential under disease pressure.

The inbred lines with a higher magnitude of GCA effects are good general combiners depending on the direction of GCA effects and the trait of interest. In the present study, both grain yield and higher BLSB disease resistance were desirable. The most desirable inbred lines are the ones with a higher magnitude of GCA effects for both the traits, namely grain yield and BLSB resistance, but with negative GCA effects for BLSB and positive GCA effects for grain yield are the best desirable combinations. Vieira et al. (2009) also demonstrated in their study that the lines with high GCA effects for yield and resistance traits could serve as reliable sources for developing multiple disease-resistant hybrids. Based on the GCA effects value, it was possible to classify the inbred lines into different categories. However, the most desirable and useful inbred lines for the development of high-yielding and BLSB disease-resistant combinations were P5 and P7. The present study revealed that the utility of other inbred lines in the breeding program could be contextual. Therefore, both P5 and P7 could serve as important source materials to develop high-yielding and BLSB-resistant cross combinations. Both the inbred lines have a relatively higher magnitude of positive GCA effects for grain yield and a higher magnitude of negative GCA effects for BLSB disease. Vivek et al. 2009 highlighted in their study that the significance of identifying and utilizing parental lines with specific GCA attributes is critical to improving resistance to multiple traits or diseases.

Specific combining ability effects

The SCA effects of half-diallel crosses for grain yield under natural as well as artificial infested conditions and BLSB disease were statistically significant in most of the cross combinations (Table 4). The number of cross combinations with statistically significant SCA effects for grain yield under natural conditions, grain yield under artificial infested conditions and BLSB disease was 43 (~65%), 37 (~56%) and 51 (~77%), respectively. On the contrary, the number of crosses with statistically significant positive SCA effects for grain yield under natural conditions, grain yield under artificial infested conditions and negative SCA effects for BLSB disease was 23 (~35%), 18 (27%), and 27 (~41%), respectively. Thus, the proportion of crosses with desirable SCA effects reduced to almost half as compared to the total number of crosses with significant SCA effects.

The statistical significance of SCA effects indicates the presence of non-additive genetic variance on all three parameters. Since the study material comprised contrasting genotypes in their reaction to BLSB, the highest percentage

Table 4. SCA effects for grain yield (t ha^{-1}) and BLSB disease reactions (1-9 scale) under Natural (N) and Artificial Inoculated (AI) conditions

Cross	N C	A I		Cross	NC	AI		Cross	NC	AI	
	Grain yield	Grain yield	Disease score		Grain yield	Grain yield	Disease score		Grain yield	Grain yield	Disease score
P2 × P3	-0.670**	-0.094	-0.223**	P3 × P9	-1.697**	0.145	-0.340**	P10 × P11	0.201	-0.788**	0.510**
P2 × P4	-2.823**	-3.241**	0.393**	P4 × P9	0.716**	-0.489**	0.235**	P2 × P12	1.260**	2.127**	-0.563**
P3 × P4	-0.701**	-2.981**	0.560**	P5 × P9	1.167**	0.477**	0.049	P3 × P12	0.051	0.114	-0.105
P2 × P5	-0.591**	0.176	0.058	P6 × P9	-0.398	-0.494**	-0.009	P4 × P12	0.298	1.170**	-0.363**
P3 × P5	1.154**	0.360	0.016	P7 × P9	0.035	-1.381**	-0.119	P5 × P12	-1.215**	-1.123**	0.468**
P4 × P5	0.915**	1.985**	0.174**	P8 × P9	-0.367	0.361	0.027	P6 × P12	-0.526**	0.963**	-0.233**
P2 × P6	0.521**	-0.415	-0.309**	P2 × P10	0.707**	0.151	0.433**	P7 × P12	-0.423	-1.866**	0.158**
P3 × P6	0.846**	0.591**	0.566**	P3 × P10	0.351	0.180	-0.359**	P8 × P12	-0.038	-1.105**	-0.155**
P4 × P6	-1.050**	-0.716**	-0.234**	P4 × P10	-0.019	-0.119	-0.868**	P9 × P12	1.468**	-0.064	-0.722**
P5 × P6	0.687**	0.454	-0.112	P5 × P10	-1.235**	-0.173	-0.203**	P10 × P12	0.650**	0.202	0.593**
P2 × P7	-0.721**	-0.327	0.331**	P6 × P10	0.189	-0.318	-0.128	P11 × P12	-0.918**	-1.307**	-0.403**
P3 × P7	1.552**	1.092**	0.331**	P7 × P10	-0.313	-0.946**	-0.388**	P2 × P1	1.004**	-0.082	-0.234**
P4 × P7	0.738**	0.850**	0.156**	P8 × P10	1.873**	1.187**	0.508**	P3 × P1	-0.271	0.215	-0.443**
P5 × P7	-0.671**	1.356**	-0.347**	P9 × P10	-0.868**	2.124**	0.274**	P4 × P1	1.626**	1.405**	0.174**
P6 × P7	0.794**	0.049	-0.172**	P2 × P11	1.355**	0.211	-0.146**	P5 × P1	-0.833**	-0.734**	0.047
P2 × P8	-0.229	1.532**	0.310**	P3 × P11	-0.638**	0.231	0.271**	P6 × P1	0.208	1.016**	-0.362**
P3 × P8	0.023	0.146	-0.273**	P4 × P11	0.493**	1.313**	-0.112	P7 × P1	-0.125	0.246	0.403**
P4 × P8	-0.192	0.823**	-0.115	P5 × P11	0.961**	-1.448**	-0.282**	P8 × P1	-0.010	-0.199	-0.242**
P5 × P8	-0.338	-1.330**	0.133	P6 × P11	-1.820**	0.372	0.477**	P9 × P1	0.483**	-1.196**	0.149**
P6 × P8	0.549**	-1.501**	0.516**	P7 × P11	0.716**	0.880**	-0.008	P10 × P1	-1.535**	-1.500**	-0.370**
P7 × P8	-1.581**	0.045	-0.344**	P8 × P11	0.311	0.041	-0.363**	P11 × P1	0.062	-0.068	-0.448**
P2 × P9	0.186	-0.037	-0.048	P9 × P11	-0.724**	0.554**	0.504**	P12 × P1	-0.608**	0.890**	1.326**

** Significant at 1% level.

of diallel crosses showed significant SCA effects for their reaction to BLSB (Table 4). Thus, the results implicitly indicate the appropriateness of genetic material used for the study. Even though additive genetic variance plays a major role in determining the BLSB resistance, but higher percentage of diallel cross combinations with statistically significant SCA effects underline the importance of non-additive gene effects as well.

It is also imperative to investigate the number of cross-combinations with desirable SCA effects for both traits. The crosses with a higher magnitude of positive SCA effects under both conditions, along with a higher magnitude of negative SCA effects for BLSB disease, were the best combinations that could directly be considered for the development of heterotic hybrids with higher grain yield with resistance to BLSB. Out of 66 half-diallel crosses, only one cross combination, P2 × P12, showed highly significant positive SCA effects for grain yield under both conditions and highly significant negative SCA effects for BLSB under artificial inoculated conditions. It is interesting to note here that this cross involved one each of resistant and susceptible genotypes. However, there were other cross combinations that showed negative SCA effects with or without statistical significance under either or both conditions and also negative SCA effects for BLSB disease with or without statistical significance. Such cross combinations include P2 × P11, P2 × P12, P3 × P8, P3 × P10, P3 × P12, P4 × P11, P4 × P12, P5 × P6, P6 × P7, P6 × P1, P7 × P11, and P8 × P11. Out of 12 such crosses, six crosses include both resistant parents, whereas the remaining six crosses include one each of resistant and susceptible parents. Further, out of six crosses, two crosses include P4 as one of the parents, which showed a positive GCA effect for BLSB disease. Sibiya et al. (2011) also reported significant and negative specific combining ability (SCA) effects for *Phaeosphaeria* leaf spot disease scores across different environments in their study. Further, the number of crosses with significant negative SCA effects for BLSB as well as significant positive SCA effects for grain yield under artificial inoculated conditions are four (P4 × P12, P5 × P7, P6 × P12, P6 × P1). Mukanga et al. (2010) and Eisele et al. (2020) also observed resistance reaction in hybrid crosses, which were made between susceptible (S) and resistant (R) parental lines, indicating the effectiveness of specific parental combinations in enhancing disease resistance. In the present study, some additional promising crosses were obtained, which can be further used in the breeding program to develop high-yielding heterotic hybrid combinations with resistance to BLSB by selectively exploiting SCA effects for grain yield and BLSB disease reactions (Table 4).

Authors' contribution

Conceptualization of research (SR, AVR, CGK, KRY, DVR); Designing of the experiments (SR, AVR, CGK, KRY, DVR); Contribution of experimental materials (CGK, SR, KRY, JK, SRJ, SP); Execution of field/lab experiments and data collection (DVR, CGK, KRY, MRR, HK, RPS, PBC, RG, KSH, OK); Analysis of data and interpretation (DVR, CGK); Preparation of the manuscript (DVR, CGK, SR, KRY, PLK).

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