



Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-2.185>

ESTIMATION OF COMBINING ABILITY IN A LINE $\times$ TESTER MATING DESIGN AMONG ELITE INBRED LINES OF MAIZE (*Zea mays* L.)

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(Date of Receiving : 17-03-2026; Date of Revision : 24-04-2026; Date of Acceptance : 25-05-2026)

ABSTRACT

Exploitation of heterosis through combining ability analysis is a cornerstone of maize improvement, as it enables the identification of superior parents and cross combinations for developing high-yielding, early and widely adapted hybrids. In the present study, 6 inbred lines were crossed with 6 testers in a line $\times$ tester mating design to generate 36 F₁ crosses during *kharif*, 2021. These thirty-six F₁ hybrids along with 12 parents were evaluated in a Randomized Block Design over the three locations to estimate the general combining ability and specific combining ability during *rabi*, 2021-22. Pooled analysis of variance revealed significant differences among genotypes, parents and crosses for all the traits indicating the presence of substantial genetic variability. Both additive and non-additive gene action were found to influence the expression of traits among the crosses. Among the parental lines, the inbred line BML-11 and the testers PFSR-151 and MGC-137 were identified as superior general combiners. While three hybrids GP-35 $\times$ MGC-137, GP-111 $\times$ PFSR-151 and BML-11 $\times$ PFSR-129 were found to be good specific combiners for earliness, grain yield and its contributing traits. The identified parents and hybrids represent valuable genetic resources for enhancing maize improvement through hybrid breeding programs.

Keywords : Combining ability, Hybrid, line $\times$ tester mating and maize.

Introduction

Maize (*Zea mays* L.) is globally recognized as one of the top three leading cereal crops, attributed to its superior yield potential and versatile adaptability. In maize breeding programmes, inbred lines are the primary genetic materials used to develop hybrids for commercial cultivation. Due to their enhanced yield potential, hybrid maize varieties are widely adopted across the globe to achieve higher grain productivity.

In plant breeding, it is essential to understand how the inbred lines or parents combine to produce superior hybrids (Amegbor *et al.*, 2017 and de Abreu *et al.*, 2019). Wegary *et al.* (2013) reported that the performance of any genetic material depends not only on its *per se* potential but also on its combining ability in hybrid combinations. Since heterosis for superior performance is mainly governed by specific combining ability (SCA), parental lines should be selected based on their SCA with suitable testers. Combining ability studies provide crucial information on the genetic

mechanisms underlying the inheritance of quantitative traits and guide the plant breeders in identifying superior parental lines for hybrid development or crop improvement (Ali *et al.*, 2012 and Saif-ul-Malook *et al.*, 2016). Understanding the nature of gene action also assists in predicting the effectiveness of selection in breeding populations. Two types of combining ability commonly evaluated in biometrical genetics are general combining ability (GCA) and specific combining ability (SCA) (Haydar and Paul, 2014). GCA refers to the average contribution of an inbred line to hybrid performance across several crosses and is largely attributed to additive gene action. In contrast, SCA reflects the performance of a specific hybrid combination relative to its expected performance based on the GCA of parental lines and is mainly due to non-additive gene action (Haydar and Paul, 2014).

In the view of above context, the present study was undertaken to assess the combining ability of 12 diverse maize inbred lines.

Material and Methods

The experimental material consisted of 49 genotypes including 36 single cross hybrids which were developed by using (6 $\times$ 6) line $\times$ tester mating design and 12 parental lines. These genotypes were evaluated for yield and yield related traits over the three locations viz., Maize Research Centre, Rajendranagar (Southern Telangana Zone), Agricultural Research Station, Karimnagar (Northern Telangana Zone) and Agricultural Research Station, Madhira (Central Telangana Zone) during *rabi*, 2021-22. The experiment was organized in a randomized complete block design with three replications. Each entry was sown in six rows of 4m length and followed a spacing of 0.6 $\times$ 0.2 m between row to row and plant to plant respectively. Based on the recommendations of PJTAU, crop management practices such as the application of 240:80:80 kg/ha of N: P₂O₅: K₂O, along with regular irrigation at critical growth stages (vegetative, tasseling and grain filling) were followed. Data were recorded on randomly selected five competitive plants from each genotype per replication

for the characters viz., plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row and 100 seed weight (g). While days to 50% tasseling, days to 50% silking, days to maturity and grain yield (kg ha⁻¹) were recorded on the plot basis. The data were statistically analyzed by utilizing Indostat services.

Results and Discussion

Pooled analysis of variance for combining ability

The pooled analysis of variance for combining ability (Table 1) revealed the presence of significant differences over the tested locations and studied maize genotypes. The source of variance partitioned into parents, hybrids and parents vs. hybrids, indicated the existence of significant differences among the inbred lines, testers, hybrids and parents vs. hybrids for eleven characters over the three locations. Existence of remarkably higher extent of genetic variability for most of the yield and its contributing traits of maize has also been reported by Mohamed, (2020), Emam *et al.* (2021) and Mousa *et al.* (2021).

General combining ability effects

The details of GCA effects of 12 parents for all the studied characters evaluated across the three locations are represented in the Table 2.

For days to 50 % tasseling, negative GCA effects are considered as desirable, since they were observed to be associated with earliness. The GCA effects of lines ranged from -0.75 (BML-11) to 1.50 (MGC-90). Among the six inbred lines, two inbred lines viz., BML-11 (-0.75) and PFSR-51 (-0.72) were found to exhibit significant negative GCA effects. Testers showed GCA effects for this trait in the range of -3.33 (PFSR-95) to 2.63 (PFSR-129) and three testers viz., PFSR-95 (-3.33), MGC-137 (-2.33) and PFSR-151 (-0.22) showed negative GCA effects. The inbred lines and testers recorded with significant negative GCA effects were considered as good general combiners for earliness. These results are in agreement with the findings of Seyoum *et al.* (2016), Matin *et al.* (2017) and Abdulazeez *et al.* (2021).

Table 1 : Pooled analysis of variance for combining ability

Source of variation	Df	Mean sum of squares						
		Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)
Locations	2	30.96**	28.56*	61.59**	335.98**	58.35**	3.96**	3.46**
Parents	11	120.91*	119.9*	354.43**	1975.01**	456.54**	1.03**	1.70**
Lines (Females)	5	60.06*	56.58**	149.82*	1171.66**	706.60**	1.25**	1.09**
Testers (Males)	5	25.31**	23.37*	59.91**	378.89**	135.11**	0.40**	1.38**
Lines vs Tester	1	903.12*	897.12**	2850.12*	13972.34**	813.38**	3.12**	6.72 *
Crosses	35	52.56*	51.59*	268.92**	783.29**	326.15**	26.67**	9.03**

Parent vs Crosses	1	133.01*	131.05*	3078.89**	75600.37**	13529.58**	1980.16**	521.11**
Location × Parents	22	3.72 *	3.70 *	13.41**	38.43*	8.95**	0.35 *	1.44**
Location × Lines	10	3.81*	3.72*	9.84**	18.70*	4.88**	0.15 *	1.46**
Location × Testers	10	2.35**	2.21**	7.04**	43.04**	7.92**	0.45**	1.46**
Location × PAR (Lines vs Tester)	2	10.16*	10.12*	63.16**	114.05**	34.43**	0.87**	1.26 *
Location × Crosses	70	3.95*	3.22*	9.63**	35.10**	8.34**	0.49*	4.14 *
Location × Parent vs Cross	2	1.29*	1.25*	20.79**	16.50**	0.49**	0.69**	0.54**
Error	141	2.70	2.65	6.77	23.52	5.91	0.40	0.30

Table 1 (Cont.)

Source of variation	df	Mean sum of squares			
		No. of kernel rows per ear	No. of kernels per row	100 seedwt. (g)	Grain yield (kg ha ⁻¹)
Locations	2	1.12**	5.29**	5.56**	613576.71**
Parents	11	1.46**	10.10**	13.31**	594703.65**
Lines (Females)	5	1.89**	15.16**	6.46**	281556.71**
Testers (Males)	5	1.31**	5.18**	11.44**	201474.17**
Lines vs Tester	1	0.05**	9.38**	56.88**	4126585.68**
Crosses	35	12.82**	80.25**	79.80**	19410320.14**
Parent vs Crosses	1	502.64**	7926.72**	8951.34**	1530287986.96**
Location × Parents	22	0.36**	0.64**	0.75**	19198.27**
Location × Lines	10	0.16**	0.39**	0.55**	15961.76**
Location × Testers	10	0.50 *	0.81**	0.66**	22762.06**
Location × PAR (Lines vs Tester)	2	0.68**	1.01**	2.26**	17561.93**
Location × Crosses	70	0.35 *	0.93**	1.25**	150636.68**
Location × Parent vs Cross	2	0.55**	1.14**	1.90 *	118933.73**
Error	141	0.26	0.73	0.76	109470.59

*, ** Significant at 5% and 1 % level of probability respectively.

Table 2 : General combining ability effects of 12 parents across the three locations

S.No.	Genotypes	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	No. of kernel rows per ear	No. of kernels per row	100 seed wt. (g)	Grain yield (kg ha ⁻¹)
	Lines											
1	GP-35	-0.27	-0.25	2.82 **	-2.90 **	-3.27**	-0.62**	-0.05	-0.52**	-1.36**	-1.84**	48.63*
2	GP-111	0.08	0.07	-1.56 **	-1.20	4.25**	-1.09 **	-0.52**	0.17	0.24	-0.54**	-2.62
3	MGC-90	1.50 **	1.48**	2.79 **	-1.37	-2.41**	-0.26*	-0.69**	-0.80**	-1.69**	-1.87**	-1401.33**
4	BML-20	0.16	0.15	0.32	4.93 **	1.28**	0.98**	0.81**	-0.35**	1.52**	2.43**	591.46**
5	BML-11	-0.75 **	-0.74 **	-2.53**	5.59**	2.39**	1.23**	0.58**	1.00**	2.21**	2.59**	704.10**
6	PFSR-51	-0.72 *	-0.71*	-1.84**	-5.04**	-2.24**	-0.23 *	-0.13	0.50**	-0.92**	-0.76 **	59.74**
	GCA (Line)	0.28	0.26	0.44	0.84	0.47	0.12	0.10	0.08	0.29	0.16	63.01
	gi - gj(Line)	0.40	0.38	0.65	1.19	0.59	0.16	0.14	0.12	0.32	0.22	90.12
	Testers											
7	PFSR-95	-3.33**	-3.28 **	-6.12**	0.70	0.83*	-1.65**	-1.21**	-0.55**	-2.75	2.15**	-1631.39**
8	PFSR-151	-0.22*	-0.23*	-2.26**	8.23**	6.03**	0.12**	0.22*	-0.02	0.30*	-0.04	93.19**
9	MGC-15	2.08**	2.01**	5.49**	-11.73**	-6.46**	-0.40**	0.19 *	-0.55**	0.27	0.37*	-118.47**
10	MGC-137	-2.33**	-2.28**	-5.81**	1.48	1.14*	2.06**	1.08**	1.25**	2.80**	2.98**	1793.24**
11	PFSR-46	1.16**	1.15**	0.82	3.87**	1.22**	-0.06	-0.35**	-0.16	-0.17	-0.26	144.24*
12	PFSR-129	2.63**	2.59**	3.35**	-2.56**	-2.77**	-0.07	0.06	0.03	-0.44**	0.90**	-280.81**
	GCA (Tester)	0.24	0.22	0.41	0.80	0.45	0.11	0.09	0.09	0.30	0.15	62.92
	gi - gj(Tester)	0.36	0.35	0.62	1.15	0.57	0.16	0.13	0.12	0.33	0.21	88.91

*, ** Significant at 5% and 1 % level of probability respectively.

For days to 50 % silking, the GCA effects of inbred lines ranged from -0.74 (BML-11) to 1.48 (MGC-90) and for testers it was ranged from -3.33 (PFSR-95) to 2.63 (PFSR-129). Significant negative

GCA effects were exhibited by the two lines viz., BML-11(-0.74) and PFSR-51(-0.71) and three testers viz., PFSR-95 (-3.28), MGC-137 (-2.28) and PFSR-151 (-0.23), indicating their earliness for this trait. Similar

results were reported by Seyoum *et al.* (2016), Sumalini *et al.* (2016) and Matin *et al.* (2017).

For days to maturity, inbred lines recorded GCA effects in the range of -2.53 (BML-11) to 2.82 (GP-35), whereas testers showed GCA effects in the range of 6.12 (PFSR-95) to 2.26 (PFSR-151). Three lines viz., BML-11 (-2.53), PFSR-51 (-1.84) and GP-111 (-1.56) and three testers viz., PFSR-95 (-6.12), MGC-137 (-5.81) and PFSR-151 (-2.26) were found to exhibit significant negative GCA effects, indicating that they were good general combiners for early maturity trait. These findings are in accordance with the results of Sumalini *et al.* (2016) and Seyoum *et al.* (2016).

The inbred lines recorded GCA effects in the range of -5.04 (PFSR-51) to 5.59 (BML-11), while the testers exhibited GCA effects in the range of -11.73 (MGC-15) to 8.23 (PFSR-151) for plant height. Two lines viz., BML-20 (4.93) and BML-11 (5.59) and two testers viz., PFSR-151 (8.23) and PFSR-46 (3.87) were identified with significant positive GCA effects. Similar findings were reported by Aminu *et al.* (2014), Talukder *et al.* (2016) and Panda *et al.* (2017).

The GCA effects of lines for ear height ranged from -3.27 (GP-35) to 4.25 (GP-111) and for testers it was ranged from -6.46 (MGC-15) to -2.77 (PFSR-129). Out of 6 inbred lines, 3 lines viz., GP-111 (4.25), BML-20 (1.28) and BML-11 (2.39) were found to exhibit significant positive GCA effects. Four testers namely PFSR-95 (0.83), PFSR-151 (6.03), MGC-137 (1.14) and PFSR-46 (1.22) showed significant positive GCA effect for ear height. Similar results were reported by Amiruzzaman *et al.* (2013) Matin *et al.* (2017) and Elmyhun *et al.* (2020) for plant height and ear height.

Significant positive GCA effect is desirable for this trait, as it directly contribute to grain yield. For ear length, inbred lines showed GCA effects in the range of -1.09 (GP-111) to 1.23 (BML-11) and for testers, it was ranged from -1.65 (PFSR-95) to 2.06 (MGC-137). Two lines viz., BML-20 (0.98) and BML-11 (1.23) and two testers viz., MGC-137 (2.06) and PFSR-151 (0.12) were observed to exhibit significant positive GCA effects. The current findings are in consonance with the reports of Matin *et al.* (2017) and Abdulazeez *et al.* (2021).

The GCA effects of inbred lines for ear girth ranged from -0.69 (MGC-90) to 0.81 (BML-20), whereas the testers showed GCA effects in the range of -1.21 (PFSR-95) to 1.08 (MGC-137). Among the six inbred lines, two inbred lines viz., BML-20 (0.81) and BML-11 (0.58) showed significant positive GCA effects. The testers MGC-15 (0.19), PFSR-151 (0.22) and MGC-137 (1.08) were found to exhibit significant

positive GCA effect for ear girth. The inbred lines and testers recorded with significant positive GCA effects for this trait, were regarded as good general combiners for ear girth. Similar observations have been reported by Seyoum *et al.* (2016), Matin *et al.* (2017) and Panda *et al.* (2017) for ear girth in maize.

For number of kernel rows per ear, inbred lines exhibited GCA effects in the range of -0.80 (MGC-90) to 1.00 (BML-11). Out of 6 inbred lines, 2 lines viz., PFSR-51 (0.50) and BML-11 (1.00) recorded significant positive GCA effects. The lowest GCA effect (-0.55) was recorded by two testers (PFSR-95 and MGC-15), while the highest GCA effect (1.25) was exhibited by the tester MGC-137. Among the testers, only one tester MGC-137 (1.25) was found to exhibit significant positive GCA effect. Similar findings were reported by Seyoum *et al.* (2016), Panda *et al.* (2017) and Sugiharto *et al.* (2018).

For number of kernels per row, inbred lines showed GCA effects in the range of -1.69 (MGC-90) to 2.21 (BML-11), whereas testers recorded GCA effects in the range of -2.75 (PFSR-95) to 2.80 (MGC-137). Among the inbred lines, two inbred lines viz., BML-20 (1.52) and BML-11 (2.21) exhibited significant positive GCA effects. Out of 6 testers, 2 testers viz., MGC-137 (2.80) and PFSR-151 (0.30) showed significant positive GCA effects for this trait. In agreement with the current findings, positive GCA effects for number of kernels per row has been reported by several investigators (Seyoum *et al.*, 2016; Panda *et al.*, 2017 and Abdulazeez *et al.*, 2021).

The GCA effects of inbred lines ranged from -1.87 (MGC-90) to 2.59 (BML-11), whereas for testers it was ranged from -0.26 (PFSR-46) to 2.98 (MGC-137) for 100 seed weight (g). Significant positive GCA effects for 100 seed weight were recorded by the two lines viz., BML-20 (2.43) and BML-11 (2.59). Among the testers, four testers viz., MGC-15 (0.37), PFSR-129 (0.90), PFSR-95 (2.15) and MGC-137 (2.98) exhibited significant positive GCA effects.

The GCA effects of inbred lines for grain yield ranged from -1401.33 (MGC-90) to 704.10 (BML-11). Among the inbred lines, four lines viz., GP-35 (48.63), PFSR-51 (59.74), BML-20 (591.46) and BML-11 (704.10) were found to exhibit significant positive GCA effects. The testers showed GCA effects in the range of -1631.39 (PFSR-95) to 1793.24 (MGC-137). Out of six testers, three testers viz., PFSR-151 (93.19), PFSR-46 (144.24) and MGC-137 (1793.24) exhibited significant positive GCA effects. The inbred lines and testers recorded with significant positive GCA effects were considered as best general combiners for grain

yield and can be used for development of high yielding hybrids. These findings are similar to the reports of Rawi (2016), Seyoum *et al.* (2016) and Sugiharto *et al.* (2018).

Specific combining ability effects

The SCA effects of 36 hybrids evaluated across the three locations for eleven quantitative characters are represented in the Table 3.

For days to 50% tasseling, 7 hybrids viz., GP-111 × PFSR-46 (-3.94), GP-35 × MGC-137 (-3.25), BML-20 × MGC-15 (-2.77), GP-111 × PFSR-151 (-2.55), BML-20 × MGC-137 (-2.02), BML-11 × PFSR-129 (-2.58) and BML-11 × PFSR-95 (-1.61) showed the desired significant negative SCA effects. The SCA effects ranged from -3.94 (GP-111 × PFSR-46) to 2.80 (BML-20 × PFSR-46). These findings were in accordance with the results reported by Sumalini *et al.* (2016), Matin *et al.* (2017) and Abdulazeez *et al.* (2021).

For days to 50 % silking, the SCA effect of hybrids ranged from -3.89 (GP-111 × PFSR-46) to 2.78 (BML-20 × PFSR-46). Significant negative SCA effects for this trait were exhibited by seven hybrids namely GP-111 × PFSR-46 (-3.89), GP-35 × MGC-137 (-3.21), BML-20 × MGC-15 (-2.77), GP-111 × PFSR-151 (-2.52), BML-20 × MGC-137 (-2.01), BML-11 × PFSR-95 (-1.65) and BML-11 × PFSR-129 (-2.55). Similar findings were obtained by Sumalini *et al.* (2016), Matin *et al.* (2017) and Abdulazeez *et al.* (2021).

(2021).

Early maturing type of hybrids are suitable to the areas with short rainy season, since they will help to escape the moisture stress encountering during grain filling stage or late in the season. Among 36 crosses, 11 crosses viz., GP-111 × PFSR-151(-10.10), GP-111 × PFSR-46 (-8.99), GP-35 × MGC-137 (-7.40), GP-35 × PFSR-129 (-4.57), BML-20 × MGC-137 (-4.90), BML-20 × PFSR-95 (-4.10), BML-20 × MGC-15 (-3.21), GP-35 × MGC-15 (-2.71), PFSR-51 × MGC-137(-2.24), BML-11 × PFSR-129 (-2.21) and BML-11 × PFSR-95 (-1.07) recorded significant negative SCA effect for days to maturity. The SCA effects ranged from -10.10 (GP-111 × PFSR-151) to 8.98 (GP-111 × MGC-137). These results are in accordance with the findings of Sumalini *et al.* (2016), Seyoum *et al.* (2016) and Panda *et al.* (2017). The significant positive SCA effects for plant height were exhibited by 12 crosses viz., GP-35 × PFSR-151 (4.15), GP-35 × MGC-15 (4.95), GP-35 × MGC-137 (4.23), GP- 111 × PFSR-151 (4.95), GP-111 × MGC-15 (7.26), MGC-90 × PFSR-151(7.62), MGC-90 × MGC-15 (12.59), MGC-90 × MGC-137 (12.20), BML-20 × PFSR-95(15.51), BML-11 × PFSR-129 (10.29), PFSR-51 × PFSR-95 (8.65), PFSR-51 × PFSR-46 (21.31). The SCA effects ranged from -18.18 (MGC-90 × PFSR-95) to 21.31 (PFSR-51 × PFSR-46). Similar results were reported by Amiruzzaman *et al.* (2013), Matin *et al.* (2017) and Abdulazeez *et al.* (2021).

Table 3 : Specific combining ability effects

S. No.	Crosses	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	No. of kernel rows per ear	No. of kernels per row	100 seed wt. (g)	Grain yield (kg/ha)
1	GP-35 × PFSR-95	2.41**	2.39**	7.23**	-4.98**	-2.42**	-0.56*	-0.22	0.41	-1.60**	0.01	-536.16**
2	GP-35 × PFSR-151	1.97 **	1.95 **	1.84	4.15 *	3.71 ***	0.48	0.66 **	0.88 **	1.00**	-0.76 *	-195.24
3	GP-35 × MGC-15	-0.66	-0.63	-2.71*	4.95 *	-0.11	0.68 *	0.85**	0.07	1.19**	0.48*	1751.08**
4	GP-35 × MGC-137	-3.25**	-3.21**	-7.40**	4.23*	3.77**	1.70**	1.13**	0.77**	2.67**	3.37**	1759.53**
5	GP-35 × PFSR-46	-0.58	-0.55	5.62 **	-5.15*	-2.97**	-1.31**	-1.08**	-0.97***	-2.19**	-3.04**	-1359.63**
6	GP-35 × PFSR-129	0.11	0.98	-4.57**	-3.21	-1.97 *	-0.98***	-1.33**	-1.17**	-1.07**	-0.06	-1419.57**
7	GP-111 × PFSR-95	0.55	0.52	-0.71	-4.68*	-2.94**	-0.43	0.24	0.71**	-3.38**	-1.95**	-317.24**
8	GP-111 × PFSR-151	-2.55**	-2.52**	-10.10**	4.95*	-3.64**	2.95**	1.46**	1.35**	5.22**	4.93**	1725.50*
9	GP-111 × MGC-15	2.13**	2.11**	4.00**	7.26**	6.19**	2.15**	0.49 *	0.71**	1.75**	2.51**	959.33*
10	GP-111 × MGC-137	2.22**	2.15**	8.98**	0.71	1.57	-1.48**	-1.22**	-2.25***	-4.94***	-5.59**	-1642.21**
11	GP-111 × PFSR-46	-3.94**	-3.89**	-8.99**	-5.68**	1.16	-1.34**	-0.28	-0.67**	1.03**	-0.51	-354.55**
12	GP-111 × PFSR-129	1.58*	1.55*	6.81**	-2.56	-2.33**	-1.84**	-0.69**	0.13	0.31	0.62	-370.82**
13	MGC-90 × PFSR-95	-0.02	-0.01	-2.07	-18.18**	-11.11**	-2.09**	-0.08	-0.47*	-1.44**	-1.12 **	297.64
14	MGC-90 × PFSR-151	-1.13	-1.12	0.53	7.62**	5.35**	-0.54	0.30	0.16	-0.66	-0.73	1143.89**
15	MGC-90 × MGC-15	-1.11	-1.12	-1.01	12.59**	12.19**	1.48**	0.99**	0.85**	5.03**	4.51**	1323.39**
16	MGC-90 × MGC-137	2.30**	2.25**	4.12**	12.20**	3.74**	-0.48	-0.39	0.05	1.00**	2.06**	-1695.66**
17	MGC-90 × PFSR-46	0.97	0.95	0.31	-11.68**	-6.33**	1.15**	-0.61*	-0.69**	-2.02**	-2.18**	-739.32*
18	MGC-90 × PFSR-129	-1.00	-1.00	-1.88	-2.56	-3.83**	0.48	-0.19	0.1	-1.91**	-2.54 ***	-329.94*
19	BML-20 × PFSR-95	-1.19	-1.18	-4.10**	15.51**	8.52**	1.31**	0.07	1.24**	-0.32	0.23	755.17**
20	BML-20 × PFSR-151	1.52*	1.52*	7.17**	-4.01	0.16	-0.12	-0.36	-1.28**	0.44	0.45	-592.07**

S. No.	Crosses	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	No. of kernel rows per ear	No. of kernels per row	100 seed wt. (g)	Grain yield (kg/ha ⁻¹)
21	BML-20 × MGC-15	-2.77**	-2.77**	-3.21 **	-4.04	-2.17 *	0.23	-1.00**	1.07**	0.47	0.21	-968.58
22	BML-20 × MGC-137	-2.02**	-2.01**	-4.90**	-11.09**	-5.78**	-0.90**	-0.56*	0.60**	-1.21**	-1.23**	-587.63**
23	BML-20 × PFSR-46	2.80**	2.78**	3.12**	0.01	-4.36**	-1.76**	0.71**	-0.14	-2.41**	-1.31**	417.53**
24	BML-20 × PFSR-129	1.66*	1.65 *	1.92	3.62	3.63**	1.23**	1.13**	-1.50**	3.03**	1.65**	975.58**
25	BML-11 × PFSR-95	-1.61 *	-1.60*	-1.07*	3.68	5.57**	1.06**	-0.03	-0.28	5.47**	3.73**	-591.63**
26	BML-11 × PFSR-151	0.44	0.42	2.53*	0.15	1.05	-0.70*	-1.31**	-1.64**	-3.74**	-1.87**	-1266.88**
27	BML-11 × MGC-15	2.47**	2.41**	0.98	-8.20**	-8.61**	-3.84**	-1.61**	-2.11**	-7.38**	-6.12**	-3104.21**
28	BML-11 × MGC-137	1.38*	1.38*	2.45*	-7.09**	-3.56**	1.15**	0.32**	0.92**	0.57*	1.56**	1011.10*
29	BML-11 × PFSR-46	-0.11	-0.09	-1.68	1.18	-0.97	1.98**	1.77**	2.49**	2.89**	2.34**	2389.89**
30	BML-11 × PFSR-129	-2.58**	-2.55**	-2.21*	10.29**	6.52**	2.65**	0.85**	2.46**	3.33**	3.48**	2683.94**
31	PFSR-51 × PFSR-95	-0.13	-0.12	1.73	8.65**	2.38*	0.70*	0.02	-1.61 **	1.28**	-0.90*	392.22**
32	PFSR-51 × PFSR-151	-0.25	-0.23	-1.99	-12.87**	-6.64**	-2.06**	-0.75**	0.52*	-2.27**	-2.01**	-815.19*
33	PFSR-51 × MGC-15	-0.05	-0.03	1.95	-12.56**	-7.47**	-0.70*	0.27	-0.61**	-1.07**	-1.59**	38.97
34	PFSR-51 × MGC-137	-0.63	-0.62	-2.24*	1.04	0.24	2.31**	0.71**	1.74**	3.06**	2.95**	2277.08**
35	PFSR-51 × PFSR-46	0.86	0.83	1.62	21.31**	13.49**	1.29**	-0.50 *	-0.01	2.69**	4.70**	-353.91*
36	PFSR-51 × PFSR-129	0.22	0.21	-0.07	-5.56**	-2.00*	-1.54**	0.24	-0.03	-3.69**	-3.15**	-1539.19
	SCA	0.69	0.69	1.07	2.06	0.99	0.28	0.24	0.21	0.37	0.38	154.13
	Sij – Skl	0.98	0.98	1.51	2.91	1.40	0.40	0.34	0.30	0.53	0.54	217.97
	Sij – Sik	1.06	1.06	1.64	3.14	1.51	0.43	0.37	0.33	0.57	0.59	235.43

The SCA effects for ear height ranged from -11.11 (MGC-90 × PFSR-95) to 13.49 (PFSR-51 × PFSR-46). Out of 36 crosses, 12 crosses namely GP-35 × PFSR-151(3.71), GP-35 × MGC-137 (3.77), GP-111 × MGC-15 (6.19), MGC-90 × PFSR-151 (5.35), MGC-90 × MGC-15 (12.19), MGC-90 × MGC-137 (3.74), BML-20 × PFSR-95 (8.52), BML-20 × PFSR-129 (3.63), BML-11 × PFSR-95 (5.57), BML-11 × PFSR-129 (6.52), PFSR-51 × PFSR-95 (2.38) and PFSR-51 × PFSR-46 (13.49) were found to exhibit significant positive SCA effect for this trait. These findings were in confirmation with the results of Amiruzzaman *et al.* (2013), Matin *et al.* (2017) and Abdulazeez *et al.* (2021).

Significant positive SCA effects for ear length were observed in 15 crosses viz., GP-35 × MGC-15 (0.68), PFSR-51 × PFSR-95 (0.70), BML-11 × PFSR-95 (1.06), MGC-90 × PFSR-46 (1.15), BML-20 × PFSR-129 (1.23), PFSR-51 × PFSR-46 (1.29), BML-20 × PFSR-95 (1.31), MGC-90 × MGC-15 (1.48), GP-35 × MGC-137 (1.70), BML-11 × PFSR-46 (1.98), BML-11 × MGC-137(1.15), GP-111 × MGC-15 (2.15), PFSR-51 × MGC-137 (2.31), BML-11 × PFSR-129 (2.65) and GP-111 × PFSR-151 (2.95). The lowest SCA effect (-3.84) was recorded by the cross BML-11 × MGC-15 and highest significant SCA effect (2.95) for this trait was exhibited by the cross GP-111 × PFSR-151. Several researchers (Sumalini *et al.*, 2016; Matin *et al.*, 2017 and Abdulazeez *et al.*, 2021) reported similar results for ear length.

Among 36 crosses, 12 crosses namely GP-111 × MGC-15 (0.49), GP-35 × PFSR-151 (0.66), BML-20 × PFSR-46 (0.71), PFSR-51 × MGC-137 (0.71), GP-35 × MGC-15 (0.85), BML-11 × PFSR-129 (0.85), BML-11 × MGC-137 (0.32) MGC-90 × MGC-15 (0.99), GP-35 × MGC-137 (1.13), BML-20 × PFSR-129 (1.13), GP-111 × PFSR-151(1.46) and BML-11 × PFSR-46 (1.77) exhibited significant positive SCA effects for ear girth. The SCA effects ranged from -1.61 (BML-11 × MGC-15) to 1.77 (BML-11 × PFSR-46). These results were in conformity with the research findings of Sumalini *et al.* (2016) Matin *et al.* (2017) and Panda *et al.* (2017).

The SCA effects ranged from -2.25 (GP-111 × MGC-137) to 2.49 (BML-11 × PFSR-46) for number of kernel rows per ear. Out of 36 crosses, 14 crosses viz., PFSR-51 × PFSR-151(0.52),BML-20 × MGC-137 (0.60), GP-111 × PFSR-95 (0.71), GP-111 × MGC-15 (0.71), GP-35 × MGC-137 (0.77), MGC-90 × MGC-15 (0.85), GP-35 × PFSR-151 (0.88), BML-20 × MGC-15(1.07), BML-20 × PFSR-95 (1.24), GP-111 × PFSR-151 (1.35), PFSR-51 × MGC-137 (1.74), BML-11 × MGC-137 (0.92), BML-11 × PFSR-129 (2.46) and BML-11 × PFSR-46 (2.49) showed significant positive SCA effect. Similar observations have been reported by Sumalini *et al.* (2016) and Abdulazeez *et al.* (2021).

For number of kernels per row, 16 crosses namely GP-35 × PFSR-151 (1.00), MGC-90 × MGC-137 (1.00), GP-111 × PFSR-46 (1.03), GP-35 × MGC-15 (1.19), PFSR-51 × PFSR-95 (1.28), GP-111 × MGC-15 (1.75), GP-35 × MGC-137 (2.67), PFSR-51 × PFSR-

46 (2.69), BML-11 $\times$ PFSR-46 (2.89), BML-11 $\times$ MGC-137 (0.57), BML-20 $\times$ PFSR-129 (3.03), PFSR-51 $\times$ MGC-137 (3.06), BML-11 $\times$ PFSR-129 (3.33), MGC-90 $\times$ MGC-15 (5.03), GP-111 $\times$ PFSR-151 (5.22) and BML-11 $\times$ PFSR-95 (5.47) exhibited significant positive SCA effects. The highest and lowest SCA effects were exhibited by the crosses BML-11 $\times$ PFSR-95 (5.47) and BML-11 $\times$ MGC-15 (-7.38) respectively. The current findings are in accordance with the results reported by Seyoum *et al.* (2016), Panda *et al.* (2017) and Matin *et al.* (2017).

Significant positive SCA effects for 100 seed weight were exhibited by 13 crosses namely BML-20 $\times$ PFSR-129 (1.65), MGC-90 $\times$ MGC-137 (2.06), BML-11 $\times$ PFSR-46 (2.34), GP-111 $\times$ MGC-15 (2.51), PFSR-51 $\times$ MGC-137 (2.95), GP-35 $\times$ MGC-15 (0.48), GP-35 $\times$ MGC-137 (3.37), BML-11 $\times$ PFSR-129 (3.48), BML-11 $\times$ MGC-137 (1.56), BML-11 $\times$ PFSR-95 (3.73), MGC-90 $\times$ MGC-15 (4.51), PFSR-51 $\times$ PFSR-46 (4.70) and GP-111 $\times$ PFSR-151 (4.93). The SCA effect ranged from -6.12 (BML-11 $\times$ MGC-15) to 4.93 (GP-111 $\times$ PFSR-151). Similar results for 100 seed weight have been reported by Sumalini *et al.* (2016), Panda *et al.* (2017) and Owusu *et al.* (2017).

The SCA effects ranged from -3104.21 (BML-11 $\times$ MGC-15) to 2683.94 (BML-11 $\times$ PFSR-129) for grain yield (kg ha^{-1}). Out of 36 crosses, 14 crosses viz., PFSR-51 $\times$ PFSR-95 (392.22), BML-20 $\times$ PFSR-46 (417.53), BML-20 $\times$ PFSR-95 (755.17), GP-111 $\times$ MGC-15 (959.33), BML-20 $\times$ PFSR-129 (975.58), MGC-90 $\times$ PFSR-151 (1143.89), MGC-90 $\times$ MGC-15 (1323.39), GP-111 $\times$ PFSR-151 (1725.50), GP-35 $\times$ MGC-15 (1751.08), GP-35 $\times$ MGC-137 (1759.53), PFSR-51 $\times$ MGC-137 (2277.08), BML-11 $\times$ MGC-137 (1011.10), BML-11 $\times$ PFSR-46 (2389.89) and BML-11 $\times$ PFSR-129 (2683.94) recorded significant positive SCA effect for this trait. These findings were equivalent to those of Sumalini *et al.* (2016), Owusu *et al.* (2017) and Suyadi *et al.* (2021).

Promising general and specific combiners for eleven quantitative characters

The general combining ability effects of 12 parents revealed that the two inbred lines (BML-11 and PFSR-51) and three testers (PFSR-95, PFSR-151 and MGC-137) exhibited significant negative GCA effects for maturity determining traits like days to 50 % tasseling, days to 50 % silking and days to maturity, indicating their usefulness for development of early maturing cross combinations. Two lines (BML-20 and BML-11) and two testers (PFSR-151 and MGC-137) were found to be good general combiners for grain yield and most of the yield related traits. Whereas the

inbred line BML-11 and two testers (PFSR-151 and MGC-137) were regarded as good general combiners for earliness, grain yield and its contributing traits. Hence, they could be utilized in hybrid breeding programs for development of superior hybrids with earliness. Similarly, Seyoum *et al.* (2016), Matin *et al.* (2017) and Abdulazeez *et al.* (2021) also identified good general combiners for earliness, yield and its components in maize.

The specific combining ability effects of 36 crosses revealed that seven hybrids (GP-35 $\times$ MGC-137, GP-111 $\times$ PFSR-151, GP-111 $\times$ PFSR-46, BML-20 $\times$ MGC-15, BML-20 $\times$ MGC-137, BML-11 $\times$ PFSR-95 and BML-11 $\times$ PFSR-129) were found to have significant negative SCA effects for days to 50 % tasseling, days to 50 % silking and days to maturity indicating their usefulness in hybrid breeding programs to develop short duration hybrids.

Ten hybrids (GP-35 $\times$ MGC-15, GP-35 $\times$ MGC-137, GP-111 $\times$ PFSR-151, GP-111 $\times$ MGC-15, MGC-90 $\times$ MGC-15, BML-20 $\times$ PFSR-129, BML-11 $\times$ PFSR-46, BML-11 $\times$ MGC-137, BML-11 $\times$ PFSR-129 and PFSR-51 $\times$ MGC-137) were found to be good specific combiners for grain yield and its related traits. Whereas the hybrids GP-35 $\times$ MGC-137, GP-111 $\times$ PFSR-151 and BML-11 $\times$ PFSR-129 were found to be good specific combiners for earliness, grain yield and its contributing traits. Hence, these hybrids can be exploited to isolate the superior genotypes with respective traits in subsequent generations. Similarly, Sumalini *et al.* (2016), Owusu *et al.* (2017) and Suyadi *et al.* (2021) reported good specific combiners for earliness, grain yield and its related traits.

Conclusion

The pooled analysis revealed substantial genetic variability among maize genotypes, with non-additive gene action predominantly governing grain yield and its related traits. Parents such as BML-11, BML-20, PFSR-151 and MGC-137 were identified as superior general combiners, while crosses including GP-35 $\times$ MGC-137, GP-111 $\times$ PFSR-151 and BML-11 $\times$ PFSR-129 showed outstanding specific combining ability. Therefore, these potential hybrids can be utilized for the development of high-yielding maize hybrids in future breeding programmes."

Acknowledgment

The authors are grateful to PJTAU, Maize Research Centre (Rajendranagar) and the Agricultural Research Stations at Karimnagar and Madhira for providing the resources necessary to conduct the experiment.

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