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HETEROTIC GROUPING OF MAIZE INBRED LINES BASED ON COMBINING ABILITY EFFECTS FOR GRAIN YIELD

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ABSTRACT

In the present study, 60 inbred lines were crossed with two testers in a line × tester mating design to generate 120 F_1 crosses during *rabi*, 2019-20. These 120 F_1 hybrids along with 5 checks were evaluated in a Randomized Block Design over the three locations to estimate the general combining ability and specific combining ability for grain yield during *rabi*, 2020-21. Pooled analysis of variance revealed significant differences among genotypes, parents and crosses for all the traits indicating the presence of substantial genetic variability. The general combining ability (GCA) effects of the inbred lines for grain yield varied from -1140.83 to 1357.42. Among the testers, LM-13 exhibited a significant negative GCA effect (-68.25), whereas LM-14 recorded a significant positive GCA effect (68.25). The specific combining ability (SCA) effects for grain yield ranged from -2071.25 (PFSR-90 × LM-14) to 2071.25 (PFSR-90 × LM-13). Out of the 120 testcross hybrids evaluated, 33 hybrids exhibited significant positive SCA effects for grain yield, indicating the presence of favourable non-additive gene action and their potential utility in hybrid development programs. Based on SCA effects of testcrosses with the two testers, 17 inbred lines were assigned to heterotic group A and 16 inbred lines to heterotic group B, while the remaining 27 lines could not be assigned to either group and were therefore classified as ungrouped. The identified heterotic groups and superior combiners provide valuable genetic resources for the development of productive maize hybrids.

Keywords **:** Combining ability, Hybrid, Line × tester mating and Maize.

Introduction

Maize (*Zea mays* L.) is one of the most versatile and widely cultivated cereal crops, renowned for its remarkable adaptability across diverse agro-climatic regions. Owing to its high productivity, multiple end uses and short growth duration, it plays a pivotal role in global food, feed and industrial sectors. Cytogenetically, maize is a diploid species with a somatic chromosome number of 2n = 20 and possesses a genome size of approximately 2.3 gigabases. Taxonomically, it belongs to the family Poaceae and the tribe Maydeae, representing one of the most economically important cereal species worldwide. Globally, maize is cultivated on approximately 206.2 million hectares with a production of about 1.26 billion tonnes and an average productivity of 6.13 t ha^{-1}. In India, maize production is estimated at a record 55.09 million tonnes during 2025–26. Telangana remains one of the leading maize-producing states, with an average productivity of around 5.9 t ha^{-1} (FAO STAT, 2026).

Maize (*Zea mays* L.) is a highly cross-pollinated crop in which hybrid breeding has played a pivotal role in achieving substantial gains in productivity. The success of hybrid breeding largely depends on the identification of parental inbred lines that can produce superior hybrid combinations through the effective exploitation of heterosis. Since the performance of a hybrid is influenced by the genetic divergence between its parents, the classification of inbred lines into distinct heterotic groups has become an essential component of modern maize breeding programmes.

Heterotic grouping is an effective strategy for classifying maize inbred lines into genetically distinct groups for efficient hybrid development. The concept of heterotic grouping was described by Melchinger and Gumber (1998), who defined a heterotic group as a collection of related or unrelated genotypes that exhibit similar combining ability and heterotic responses when crossed with genotypes belonging to another genetically divergent group. The establishment of heterotic groups forms the foundation of hybrid breeding programs, as it facilitates the identification of parental combinations capable of producing superior hybrid performance.

Once heterotic groups or pools are identified, they are generally maintained as separate breeding populations to preserve their genetic divergence and ensure continued expression of heterosis (Abera *et al.*, 2018). Crosses between inbred lines derived from different heterotic pools often result in enhanced combining ability, greater heterozygosity, increased hybrid vigor and higher grain yield compared to crosses involving genetically similar lines. Consequently, heterotic grouping serves as a valuable tool for maximizing the efficiency of hybrid breeding programmes (Barata and Carena, 2006).

The classification of inbred lines into heterotic groups also assists breeders in selecting promising parental combinations while minimizing the evaluation of less productive crosses. This targeted approach reduces the resources, time and experimental space required for hybrid testing. In recent years, heterotic grouping has gained additional significance in maize improvement programmes aimed at developing climate-resilient cultivars capable of performing under diverse and challenging environmental conditions (Prasanna, 2012). As a result, continuous efforts are being made to identify and refine heterotic patterns within maize germplasm to enhance breeding efficiency and sustain long-term genetic improvement. Several researchers have classified maize inbred lines into distinct heterotic groups using a wide range of approaches, including morphological characterization, pedigree analysis, multivariate statistical techniques, mating design-based combining ability studies and molecular marker-assisted methods. These approaches have been employed to assess genetic diversity and establish heterotic patterns for the efficient development of superior hybrids (Uttam *et al.*, 2019; Elmyhun *et al*., 2020; Joshi *et al*., 2020; Kamara *et al*., 2021; Kumar *et al*., 2022 and Maazou *et al*., 2022). Based on the type of combining ability effects used for classification, one of the most widely employed heterotic grouping methods is the Specific Combining Ability for grain yield (SCA-GY) method, which assigns maize inbred lines to heterotic groups based on their specific combining ability effects for grain yield in crosses with representative testers (Menkir *et al*., 2004).

Material and Methods

The experimental material comprised 60 maize inbred lines obtained from CIMMYT (International Maize and Wheat Improvement Center), Patancheru, Hyderabad; the Winter Nursery Centre (WNC) and the Maize Research Centre (MRC), Rajendranagar, Hyderabad. In addition, two well-established heterotic testers, LM-13 and LM-14, were procured from the Indian Institute of Maize Research (IIMR), Ludhiana.

The sixty-two parental genotypes were sown during *rabi*, 2019–20 at the Maize Research Centre (MRC), Rajendranagar, Hyderabad. To ensure proper synchronization of flowering between the female inbred lines and the male testers, three staggered sowings of the testers were carried out at four-day intervals. The sixty female inbred lines were crossed with the two male testers, LM-13 and LM-14, following a line × tester mating design using the hand-pollination (bagging) technique. This crossing programme resulted in the development of 120 testcross hybrids for subsequent evaluation.

The developed 120 testcross hybrids were evaluated along with 5 checks (DHM 117, DHM 121, Bio 9544, NK 6240 and KNMH 4010131) for grain yield, over the three locations representing Agro-climatic zones of Telangana *viz.*, MRC, Rajendranagar (Southern Telangana Zone), Agricultural Research Station, Karimnagar (Northern Telangana Zone) and Agricultural Research Station, Madhira (Central Telangana Zone) during *rabi*, 2020-21.

The experiment was organized as a randomized complete block design with two replications. Each entry was sown in six rows of 4m length and followed a spacing of 0.6 m × 0.2 m between row to row and plant to plant respectively. Based on recommendations of PJTAU for each site, crop management and plant protection practices were followed to maintain proper crop stand. The grain yield data was recorded on plot basis.

The grain yield data obtained from 120 testcross hybrids and 62 parental lines were subjected to combining ability analysis and based on the SCA-GY method (Menkir *et al*., 2004) in combination with two heterotic testers, potential inbred lines were identified from 60 maize inbred lines.

Statistical Analysis

Statistical analysis was carried out using the mean data recorded from five randomly selected plants in each entry across all replications. The data were analyzed using Windostat software (Version 9.3; Indostat Services). Combining ability analysis was performed following the line × tester mating design as described by Kempthorne (1957) and later adopted by Singh and Chaudhary (1985).The adjusted mean values were used to estimate general combining ability (GCA) and specific combining ability (SCA) effects for grain yield based on the line × tester model.

Results and Discussion

Pooled Analysis of Variance

The pooled analysis of variance (Table 1) demonstrated that the effects of genotype, environment (location) and genotype × environment interaction (GEI) were highly significant for grain yield. The significant genotypic effect indicated the presence of substantial genetic variability among the evaluated maize genotypes, while the significant environmental effect showed the influence of varying agro-climatic conditions across the test locations. Furthermore, the significance of the GEI component revealed that the performance of 187 maize genotypes (62 parents, 120 testcross hybrids, and 5 commercial checks) varied across environments, indicating differential responses to location-specific conditions. Similar findings highlighting the importance of genotype, environment and their interaction for grain yield in maize have been reported by Matin *et al*. (2017), Ruswandi *et al*. (2021) and Shojaei *et al.* (2021).

Mean performance

The mean grain yield performance of 62 parental lines, 120 testcross hybrids and 5 commercial checks was assessed across three locations during *rabi*, 2020-21 (Table 2). For grain yield, the parental inbred lines recorded mean values ranging from 1505 kg ha^{-1} (BML-13) to 4025 kg ha^{-1} (GP-170). While the testers LM-14 and LM-13 exhibited mean value of 4017 kg ha^{-1} and 3108 kg ha^{-1} respectively. The testcross hybrids showed a wide range of variation, with mean value varying from 4901 kg ha^{-1} (MGC-39 × LM-13) to 9915 kg ha^{-1} (PFSR-90 × LM-14). Three hybrids namely MGC-49 × LM-14, MGC-93 × LM-14 and PFSR-90 × LM-14 showed superior mean over the best check Bio 9544 (9773 kg ha^{-1}) for this trait. Similar results were reported by Hosana *et al.* (2015), Seyoum *et al.* (2016) and Kandel and Shrestha (2020) for grain yield in maize.

Line × tester analysis

The pooled analysis of variance for combining ability (Table 3) revealed the presence of significant differences among the parental genotypes for grain yield across the three test locations. The lines, testers, lines vs testers and crosses exhibited significant effects for grain yield. Similarly, significant differences were observed among parents, crosses and parents vs crosses, indicating the presence of substantial genetic variability among the evaluated maize genotypes for grain yield. The ratio of general combining ability (GCA) variance to specific combining ability (SCA) variance was less than unity, suggesting the predominance of non-additive gene action in the inheritance of grain yield. The greater contribution of non-additive genetic effects implies that heterosis breeding and hybrid development may be effective approaches for improving grain yield in maize. The predominance of non-additive gene action for grain yield observed in the present study is in agreement with the findings of Gemechu *et al*. (2020), Tefera *et al*. (2020), Yu *et al*. (2020), and Abdulazeez *et al*. (2021), who also reported the major role of non-additive genetic effects in the inheritance and expression of grain yield in maize.

Among the 60 inbred lines evaluated, 27 lines exhibited significant positive GCA effects for grain yield, indicating their superiority as general combiners, whereas 7 lines showed significant negative GCA effects, suggesting poor combining ability for this trait (Table 4). The GCA effects of the inbred lines varied from –1140.83 (MGC-13 and BML-30F) to 1357.42 (BML-32-2, PFSR-157 and MGC-144). Among the testers, LM-14 recorded a significant positive GCA effect (68.25), while LM-13 exhibited a significant negative GCA effect (–68.25), indicating that LM-14 was the better general combiner for grain yield. The SCA effects for grain yield ranged from -2071.25 (PFSR-90 × LM-14) to 2071.25 (PFSR-90 × LM-13) among the test cross hybrids. Out of the 120 testcross hybrids evaluated, 33 exhibited significant positive SCA effects, whereas another 33 showed significant negative SCA effects, reflecting substantial variation in specific combining ability among the crosses. These results indicate the importance of both additive and non-additive gene actions in the inheritance of grain yield. Similar findings have been reported by Mbuvi *et al.* (2018), Darshan *et al.* (2019), and Singh *et al*. (2021).

Table 1 : Pooled analysis of variance for grain yield (kg ha^{-1}) among the maize genotypes evaluated across the three locations.

Source of variation	df	Sum of squares	Mean sum of squares	F-Cal
Locations	2	2589808.66	1294904.33**	35.36
Genotypes	186	5705456888.97	31521861.26**	773.25
Locations × Genotypes	372	765046692.54	2113388.65**	51.84
Pooled error	560	22135477.67	40765.15	

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

Table 2 : Mean performance of maize genotypes for grain yield across threelocations.

S.No.	Genotypes	Grain yield (kg ha^{-1})
	Inbred lines	
1	MGC-9	2397
2	MGC-30	1964
3	MGC-32	2159
4	MGC-40	2009
5	MGC-47	1765
6	MGC-52	2109
7	MGC-68	2425
8	MGC-46	2836
9	MGC-49	2307
10	MGC-63	2316
11	MGC-13	2404
12	MGC-93	2279
13	MGC-90	3589
14	MGC-125	2686
15	MGC-39	2398
16	MGC-130	2092
17	MGC-109	2017
18	MGC-103	2373
19	MGC-114	2136
20	MGC-161	2398
21	MGC-15	3246
22	MGC-137	3587
23	MGC-144	2415
24	MGC-72	2415
25	MGC-81	2955
26	MGC-82	2238
27	PFSR-90	3020
28	PFSR-51	3561
29	PFSR-150	2425
30	PFSR-151	3255
31	PFSR-46	3237
32	PFSR-275	2550
33	PFSR-256	2298
34	PFSR-129	3204
35	PFSR-157	2530
36	PFSR-32	2686
37	PFSR-49	2415
38	PFSR-95	3177
39	PFSR-68	2056
40	GP-215	2552
41	GP-170	4025
42	GP-35	3595
43	GP-16	1777
44	GP-88	2641
45	GP-99	2552
46	GP-27	2640
47	GP-111	3547
48	GP-221	3020
49	GP-265	2594
50	BML-30F	2844
51	BML-11	3898
52	BML-51	2351
53	BML-32-2	2246
54	BML-20	3709
55	BML-10	1798
56	BML-2	1896
57	BML-13	1505
58	Z-63-45	2774
59	CM-105	1725
60	5125	1862
	Mean	2597
Range	Minimum	1505
	Maximum	4025
	Testers	
61	LM-13	3108
62	LM-14	4017
	Mean	3563
Range	Minimum	3108
	Maximum	4017

Table 2 : Contd..

S.No.	Genotypes	Grain yield (kg ha^{-1})
	Hybrids	
63	MGC-9 × LM-13	6589
64	MGC-30 × LM-13	6886
65	MGC-32 × LM-13	7015
66	MGC-40 × LM-13	7734
67	MGC-47 × LM-13	6028
68	MGC-52 × LM-13	7014
69	MGC-68 × LM-13	6296
70	MGC-46 × LM-13	7069
71	MGC-49 × LM-13	6019
72	MGC-63 × LM-13	8045
73	MGC-13 × LM-13	5516
74	MGC-93 × LM-13	6268

75	MGC-90 × LM-13	7819
76	MGC-125 × LM-13	6143
77	MGC-39 × LM-13	4901
78	MGC-130 × LM-13	4956
79	MGC-109 × LM-13	6816
80	MGC-103 × LM-13	6847
81	MGC-114 × LM-13	6515
82	MGC-161 × LM-13	6445
83	MGC-15 × LM-13	6758
84	MGC-137 × LM-13	6183
85	MGC-144 × LM-13	9492
86	MGC-72 × LM-13	6520
87	MGC-81 × LM-13	5849
88	MGC-82 × LM-13	7380
89	PFSR-90 × LM-13	5909
90	PFSR-51 × LM-13	7707
91	PFSR-150 × LM-13	7326
92	PFSR-151 ×LM-13	6119
93	PFSR-46 × LM-13	5868
94	PFSR-275 × LM-13	5182
95	PFSR-256 × LM-13	6503
96	PFSR-129 ×LM-13	6309
97	PFSR-157 × LM-13	7475
98	PFSR-32 × LM-13	7202
99	PFSR-49 × LM-13	6711
100	PFSR-95 × LM-13	5156
101	PFSR-68 × LM-13	6947
102	GP-215 × LM-13	7697
103	GP-170 × LM-13	7647
104	GP-35 × LM-13	6715
105	GP-16 × LM-13	8052
106	GP-88 × LM-13	7108
107	GP-99 × LM-13	7390
108	GP-27 × LM-13	5872
109	GP-111 × LM-13	5345
110	GP-221 × LM-13	6177
111	GP-265 × LM-13	7462
112	BML-30F × LM-13	7587
113	BML-11 × LM-13	8577
114	BML-51 × LM-13	7091
115	BML-32-2 × LM-13	7259
116	BML-20 × LM-13	8464
117	BML-10 × LM-13	5811
118	BML-2 × LM-13	6386
119	BML-13 ×LM-13	7930
120	Z-63-45 × LM-13	6503
121	CM-105 × LM13	7138
122	5125 × LM-13	7170
123	MGC-9 × LM-14	6069
124	MGC-30 × LM-14	6580
125	MGC-32 × LM-14	9592
126	MGC-40 × LM-14	6509
127	MGC-47 × LM-14	7202
128	MGC-52 × LM-14	9169
129	MGC-68 × LM-14	6346
130	MGC-46 × LM-14	6823
131	MGC-49 × LM-14	9790
132	MGC-63 × LM-14	8772
133	MGC-13 × LM-14	6319
134	MGC-93 × LM-14	9897
135	MGC-90 × LM-14	6509
136	MGC-125 × LM-14	6908

Table 2 : Contd..

S.No.	Genotypes	Grain yield (kg ha^{-1})
137	MGC-39 × LM-14	8041
138	MGC-130 × LM-14	7378
139	MGC-109 × LM-14	7162
140	MGC-103 × LM-14	6864
141	MGC-114 × LM-14	6972
142	MGC-161 × LM-14	8986
143	MGC-15 × LM-14	9310
144	MGC-137 × LM-14	8593
145	MGC-144 × LM-14	7340
146	MGC-72 × LM-14	8116
147	MGC-81 × LM-14	7785
148	MGC-82 × LM-14	7791
149	PFSR-90 × LM-14	9915
150	PFSR-51 × LM-14	5970
151	PFSR-150 × LM-14	7158
152	PFSR-151 ×LM-14	8609
153	PFSR-46 × LM-14	8706
154	PFSR-275 ×LM-14	7195
155	PFSR-256 × LM-14	7043
156	PFSR-129 ×LM-14	7344
157	PFSR-157 × LM-14	6298
158	PFSR-32 × LM-14	7503
159	PFSR-49 × LM-14	7632
160	PFSR-95 × LM-14	6797
161	PFSR-68 × LM-14	8846
162	GP-215 × LM-14	8091
163	GP-170 × LM-14	7410
164	GP-35 ×LM-14	5534
165	GP-16 × LM-14	7204
166	GP-88 × LM-14	6515
167	GP-99 × LM-14	7689
168	GP-27 × LM-14	8411
169	GP-111 × LM-14	8142
170	GP-221 × LM-14	5830
171	GP-265 × LM-14	7806
172	BML-30F × LM-14	6837
173	BML-11 × LM-14	7039
174	BML-51 × LM-14	7749

175	BML-32-2 × LM-14	5379
176	BML-20 × LM-14	5732
177	BML-10 × LM-14	8143
178	BML-2 × LM-14	7120
179	BML-13 × LM-14	7421
180	Z-63-45 × LM-14	7575
181	CM-105 × LM14	7266
182	5125 × LM-14	8134
	Mean	7148
Range	Minimum	4901
	Maximum	9915
	Checks	
183	DHM 117	8879
184	DHM 121	9330
185	Bio 9544	9773
186	NK 6240	9733
187	KNMH 4010131	9043
	Grand mean	5669
Range	Minimum	1403
	Maximum	9915
	CV	15.66
	SEM	887.36
	CD @ 5%	1750.58

Table 3 : Pooled analysis of variance for combining ability

Source of variation	df	Sum of squares	Mean sum of squares	F-Cal
Locations	2	2589808.66	1294904.33 **	35.36
Parents	61	424356295.61	6956660.58**	190.00
Lines (Females)	59	421613712.12	7145995.12**	195.17
Testers (Males)	1	2262008.33	2262008.33**	61.78
Lines *vs* Testers	1	480575.16	480575.16**	13.12
Crosses	119	3696150580.91	31060088.92**	848.31
Parents *vs* Crosses	1	2112909209.62	2112909209.62**	57707.54
Location × Parents	122	7111015.92	58287.02**	1.59
Location × Lines	118	6971723.98	59082.41**	1.61
Location × Testers	2	72735.17	36367.58**	0.99
Location × PAR (Lines *vs* Testers)	2	66556.77	33278.39**	0.90
Location × Crosses	238	6889471.06	28947.36**	0.79
Location × Parents *vs* Crosses	2	201705.02	100852.51**	2.75
Error	543	19881451.16	36614.09	
σ^2 GCA	-	160812.65		
σ^2 SCA	-	460053.29		
σ^2 GCA / σ^2 SCA	-	0.35		

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

Heterotic grouping

The heterotic grouping of maize inbred lines was carried out following the procedure proposed by Menkir *et al.* (2004) with suitable modifications. The classification was based on the specific combining ability effects of the inbred lines when crossed with the two testers, LM-13 and LM-14. Inbred lines that showed significant positive SCA effects with tester LM-13 and negative SCA effects with tester LM-14 were assigned to heterotic group A. Conversely, lines exhibiting significant positive SCA effects with tester LM-14 and negative SCA effects with tester LM-13 were placed in heterotic group B. Out of the 60 maize inbred lines evaluated, 17 lines exhibited significant positive specific combining ability (SCA) effects when crossed with tester LM-13 and were consequently assigned to heterotic group A. Similarly, 16 inbred lines showed significant positive SCA effects with tester LM-14 and were classified into heterotic group B. The remaining inbred lines did not display significant positive SCA effects with either tester and therefore, remained unassigned to any heterotic group (Table 5). The present findings are in agreement with several earlier studies that employed the line × tester mating design for heterotic grouping in maize. Fan *et al*. (2001) classified six maize inbred lines into three heterotic groups using the SCA-GY (Specific Combining Ability for Grain Yield) method. Similarly, Xingming *et al.* (2001) evaluated ten QPM lines and assigned them to four heterotic groups (A, B, C, and D) based on SCA effects. Librando and Magulama (2008) utilized two heterotic testers (CML 254 and CML 247) and classified 11 of 21 inbred lines into two heterotic groups, while the remaining ten lines remained unclassified. Likewise, Gurung *et al.* (2009) developed

40 test crosses using four testers and established three heterotic groups (A, B, and AB) based on SCA effects.

Table 4 : GCA and SCA effects of parents and hybrids

S.No.	Inbred lines	GCA effects
1	MGC-9	293.92
2	MGC-30	329.67
3	MGC-32	934.47*
4	MGC-40	838.42**
5	MGC-47	616.93*
6	MGC-52	1033.42**
7	MGC-68	-737.57**
8	MGC-46	-111.82
9	MGC-49	527.43
10	MGC-63	1350.18*
11	MGC-13	-1140.82**
12	MGC-93	902.47*
13	MGC 90	1024.17**
14	MGC-125	-532.57
15	MGC-39	-111.82
16	MGC-130	112.92
17	MGC-109	62.92
18	MGC-103	763.97**
19	MGC-114	293.92
20	MGC-161	-314.82**
21	MGC-15	975.92**
22	MGC-137	1244.67**
23	MGC-144	1357.43*
24	MGC-72	-314.82
25	MGC-81	-241.07**
26	MGC-82	527.43
27	PFSR-90	-219.82**
28	PFSR-51	853.67**
29	PFSR-150	527.43
30	PFSR-151	932.47**
31	PFSR-46	228.92*
32	PFSR-275	391.22
33	PFSR-256	380.72
34	PFSR-129	886.22**
35	PFSR-157	1357.42**
36	PFSR-32	293.93
37	PFSR-49	112.93
38	PFSR-95	485.97*
39	PFSR-68	838.43
40	GP-215	835.67**
41	GP-170	470.42
42	GP-35	380.72*
43	GP-16	569.68
44	GP-88	-247.07**
45	GP-99	480.93
46	GP-27	487.92
47	GP-111	756.47**
48	GP-221	593.93*
49	GP-265	575.68
50	BML-30F	-1140.82**
51	BML-11	749.92**
52	BML-51	361.68
53	BML-32-2	1357.43*
54	BML-20	660.22**
55	BML-10	63.47
56	BML-2	480.93
57	BML-13	616.93*
58	Z-63-45	329.67**
59	CM-105	143.68
60	5125	593.93*
	S.E (GCA for lines)	532.42
61	LM-13	-68.25*
62	LM-14	68.25**
	S.E (GCA for testers)	69.31

Table 4 : Contd..

S.No.	Hybrids	SCA effects
63	MGC-9 × LM-13	191.25
64	MGC-30 × LM-13	221.75
65	MGC-32 × LM-13	-518.50
66	MGC-40 × LM-13	680.50*
67	MGC-47 × LM-13	-518.50
68	MGC-52 × LM-13	-1009.50*
69	MGC-68 × LM-13	-43.50
70	MGC-46 × LM-13	191.25
71	MGC-49 × LM-13	-317.75*
72	MGC-63 × LM-13	-295.75*
73	MGC-13 × LM-13	-333.25**
74	MGC-93 × LM-13	-518.50*
75	MGC-90 × LM-13	-1746.75**
76	MGC-125 × LM-13	314.00**
77	MGC-39 × LM-13	-191.25**
78	MGC-130 × LM-13	43.50
79	MGC-109 × LM-13	-35.12
80	MGC-103 × LM-13	-440.25**
81	MGC-114 × LM-13	-160.25
82	MGC-161 × LM-13	160.25
83	MGC-15 × LM-13	1344.00**
84	MGC-137 × LM-13	1272.75**
85	MGC-144 × LM-13	1144.50**
86	MGC-72 × LM-13	160.25
87	MGC-81 × LM-13	900.00**
88	MGC-82 × LM-13	-137.50
89	PFSR-90 × LM-13	800.75**
90	PFSR-51 × LM-13	-2071.25**
91	PFSR-150 × LM-13	-317.75
92	PFSR-151 ×LM-13	1313.25**
93	PFSR-46 × LM-13	1487.50**
94	PFSR-275 × LM-13	-137.50

95	PFSR-256 × LM-13	193.63
96	PFSR-129 ×LM-13	900.00**
97	PFSR-157 × LM-13	1144.50**
98	PFSR-32 × LM-13	-82.50
99	PFSR-49 × LM-13	392.00
100	PFSR-95 × LM-13	752.50**
101	PFSR-68 × LM-13	645.50**
102	GP-215 × LM-13	-1219.25**
103	GP-170 × LM-13	186.50
104	GP-35 × LM-13	-658.75**
105	GP-16 × LM-13	492.25**
106	GP-88 × LM-13	365.00**
107	GP-99 × LM-13	-81.50
108	GP-27 × LM-13	-84.50
109	GP-111 × LM-13	-1466.50**
110	GP-221 × LM-13	242.00
111	GP-265 × LM-13	-104.25
112	BML-30F × LM-13	333.25**
113	BML-11 × LM-13	-1009.50**
114	BML-51 × LM-13	-260.25
115	BML-32-2 × LM-13	-900.00*
116	BML-20 × LM-13	-1434.25**
117	BML-10 × LM-13	-15.87
118	BML-2 × LM-13	-81.50
119	BML-13 ×LM-13	323.00
120	Z-63-45 × LM-13	1272.75**
121	CM-105 × LM13	4.75
122	5125 × LM-13	-413.50*
123	MGC-9 × LM-14	-191.25
124	MGC-30 × LM-14	-221.75
125	MGC-32 × LM-14	518.50
126	MGC-40 × LM-14	-680.50**
127	MGC-47 × LM-14	518.50
128	MGC-52 × LM-14	1009.50*
129	MGC-68 × LM-14	43.50
130	MGC-46 × LM-14	-191.25
131	MGC-49 × LM-14	317.75*
132	MGC-63 × LM-14	295.75*
133	MGC-13 × LM-14	333.25**
134	MGC-93 × LM-14	518.50**
135	MGC-90 × LM-14	1746.75**
136	MGC-125 × LM-14	-314.00**
137	MGC-39 × LM-14	191.25**
138	MGC-130 × LM-14	-43.50
139	MGC-109 × LM-14	35.12
140	MGC-103 × LM-14	440.25**

Table 4 : Contd..

S.No.	Hybrids	SCA effects
141	MGC-114 × LM-14	160.25
142	MGC-161 × LM-14	-160.25
143	MGC-15 × LM-14	-1344.00**
144	MGC-137 × LM-14	-1272.75**
145	MGC-144 × LM-14	-1144.50*
146	MGC-72 × LM-14	-160.25
147	MGC-81 × LM-14	-900.00**
148	MGC-82 × LM-14	137.50
149	PFSR-90 × LM-14	-800.75**
150	PFSR-51 × LM-14	2071.25**
151	PFSR-150 × LM-14	317.75
152	PFSR-151 ×LM-14	-1313.25**
153	PFSR-46 × LM-14	-1487.50**
154	PFSR-275 ×LM-14	137.50
155	PFSR-256 × LM-14	-193.63
156	PFSR-129 ×LM-14	-900.00**
157	PFSR-157 × LM-14	-1144.50**
158	PFSR-32 × LM-14	82.50
159	PFSR-49 × LM-14	-392.00
160	PFSR-95 × LM-14	-752.50**
161	PFSR-68 × LM-14	-645.50*
162	GP-215 × LM-14	1219.25**
163	GP-170 × LM-14	-186.50
164	GP-35 ×LM-14	658.75**
165	GP-16 × LM-14	-492.25*
166	GP-88 × LM-14	-365.00**
167	GP-99 × LM-14	81.50
168	GP-27 × LM-14	84.50
169	GP-111 × LM-14	1466.50**
170	GP-221 × LM-14	-242.00
171	GP-265 × LM-14	104.25
172	BML-30F × LM-14	-333.25**
173	BML-11 × LM-14	1009.50**
174	BML-51 × LM-14	260.25
175	BML-32-2 × LM-14	900.00*
176	BML-20 × LM-14	1434.25**
177	BML-10 × LM-14	15.87
178	BML-2 × LM-14	81.50
179	BML-13 × LM-14	-323.00
180	Z-63-45 × LM-14	-1272.75**
181	CM-105 × LM14	-4.75
182	5125 × LM-14	413.50*
	SE (Sij-Skl)	1315.16
	SE (Sij-Sik)	1082.74

Comparable results were reported by Kanyamasoro *et al.* (2012) who assigned 23 and 24 inbred lines to heterotic groups A and B, respectively, while five lines were placed in both groups. Hosana *et al.* (2015) successfully classified nine of twenty-five inbred lines into two heterotic groups using two testers, whereas sixteen lines remained undetermined. Similarly, Keno *et al.* (2016) established three heterotic groups (A, B, and AB) from ten inbred lines and seven testers. Thakur *et al*. (2016) classified twenty-seven inbred lines into two heterotic groups, with thirteen lines in group A and fourteen lines in group B. Ejigu *et al*. (2017) grouped sixteen white maize inbred lines into two tester-based heterotic groups using divergent testers 1368 and CML 444. Hundera (2017) classified thirty-two inbred lines into three groups, including a separate group of lines exhibiting non-significant SCA effects with both testers. Similarly, Singode *et al*. (2017) reported that among thirty-one inbreds with positive GCA effects, fifteen were assigned to heterotic group A and sixteen to heterotic group B based on their SCA responses with testers CML474 and V373, respectively. Likewise, Abera *et al.* (2018) assigned three OPVs to heterotic group A, two to group B, and fourteen to group AB. Fan *et al*. (2018) classified twenty-four inbred lines into the Suwan1, Reid, and non-Reid heterotic groups using the SCA-GY approach. Uttam *et al*. (2019) categorized eight of eleven inbred lines into two tester groups, while three remained unclassified due to non-significant SCA effects. More recently, Elmyhun *et al*. (2020) classified eight inbred lines into two heterotic groups of four lines each and emphasized that crosses between different heterotic groups are valuable for hybrid development, whereas superior combiners within the same group may be utilized for synthetic variety development.

Table 5 : Heterotic grouping based on SCA effects for grain yield

S.No.	Inbred lines	SCA effects		Heterotic group
		LM-13 (Heterotic group A)	LM-14 (Heterotic group B)	
1	MGC-9	191.25	-191.25	-
2	MGC-30	221.75	-221.75	-
3	MGC-32	-518.50	518.50	-
4	MGC-40	680.50*	-680.50*	A
5	MGC-47	-518.50	518.50	-
6	MGC-52	-1009.50*	1009.50*	B
7	MGC-68	-43.50	43.50	-
8	MGC-46	191.25	-191.25	-
9	MGC-49	-317.75*	317.75*	B
10	MGC-63	-295.75*	295.75*	B
11	MGC-13	-333.25**	333.25**	B
12	MGC-93	-518.50*	518.50**	B
13	MGC 90	-1746.75**	1746.75**	B
14	MGC-125	314.00**	-314.00**	A
15	MGC-39	-191.25**	191.25**	B
16	MGC-130	43.50	-43.50	-
17	MGC-109	-35.12	35.12	-
18	MGC-103	-440.25**	440.25**	B
19	MGC-114	-160.25	160.25	-
20	MGC-161	160.25	-160.25	-
21	MGC-15	1344.00**	-1344.00**	A
22	MGC-137	1272.75**	-1272.80**	A
23	MGC-144	1144.50**	-1144.50*	A
24	MGC-72	160.25	-160.25	-
25	MGC-81	900.00**	-900.00**	A
26	MGC-82	-137.50	137.50	-
27	PFSR-90	800.75**	-800.75**	A
28	PFSR-51	-2071.25**	2071.25**	B
29	PFSR-150	-317.75	317.75	-
30	PFSR-151	1313.25**	-1313.30**	A
31	PFSR-46	1487.50**	-1487.50**	A
32	PFSR-275	-137.50	137.50	-
33	PFSR-256	193.63	-193.63	-
34	PFSR-129	900.00**	-900.00**	A
35	PFSR-157	1144.50**	-1144.50**	A
36	PFSR-32	-82.50	82.50	-
37	PFSR-49	392.00	-392.00	-
38	PFSR-95	752.50**	-752.50**	A
39	PFSR-68	645.50*	-645.50*	A
40	GP-215	-1219.25**	1219.25**	B
41	GP-170	186.50	-186.50	-
42	GP-35	-658.75**	658.75**	B
43	GP-16	492.25**	-492.25*	A
44	GP-88	365.00**	-365.00**	A
45	GP-99	-81.50	81.50	-
46	GP-27	-84.50	84.50	-
47	GP-111	-1466.5**	1466.50**	B
48	GP-221	242.00	-242.00	-
49	GP-265	-104.25	104.25	-
50	BML-30F	333.25**	-333.25**	A
51	BML-11	-1009.50**	1009.50**	B
52	BML-51	-260.25	260.25	-
53	BML-32-2	-900.00*	900.00*	B
54	BML-20	-1434.25**	1434.25**	B
55	BML-10	-15.87	15.87	-
56	BML-2	-81.50	81.50	-
57	BML-13	323.00	-323.00	-
58	Z-63-45	1272.75**	-1272.80**	A
59	CM-105	4.75	-4.75	-
60	5125	-413.50*	413.50*	B

Therefore, the classification of 17 inbred lines into heterotic group A and 16 inbred lines into heterotic group B in the present study, while leaving the remaining lines ungrouped due to non-significant SCA effects with either tester, is consistent with the heterotic grouping patterns reported in previous maize breeding studies. This further validates the effectiveness of the line × tester approach and SCA-based classification for identifying genetically divergent parental lines suitable for hybrid breeding programmes.

Conclusion

The pooled analysis of variance revealed highly significant differences among the genotypes for grain yield, indicating the presence of substantial genetic variability among the maize inbred lines and their testcrosses. Among the evaluated testcross hybrids, MGC-49 × LM-14, MGC-93 × LM-14, and PFSR-90 × LM-14 exhibited superior grain yield performance and out-yielded the best commercial check, Bio 9544 (9,773 kg ha^{-1}). General combining ability analysis identified 27 out of 60 inbred lines as good general combiners for grain yield, indicating their potential utility in hybrid breeding programmes. Similarly, specific combining ability analysis revealed that 33 out of 120 testcrosses were good specific combiners for grain yield, suggesting the existence of favorable non-additive gene action for this trait. Based on the SCA effects with the two testers, 17 inbred lines were assigned to heterotic group A and 16 inbred lines to heterotic group B, while the remaining lines could not be assigned to either group and were therefore categorized as ungrouped. These findings provide valuable information for the identification of promising parental lines and heterotic patterns, which can be effectively utilized in the development of high-yielding maize hybrids.

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