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RESEARCH ARTICLE

Identification of heterotic maize hybrids with post flowering stalk rot resistance utilizing tropical and temperate inbred lines

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Abstract

Maize (*Zea mays* L.) is a staple cereal crop contributing to global food security. The increasing demand for maize in food and feed industries necessitates enhancing the yield by utilizing diverse inbred lines with multiple stress tolerance. Forty inbred lines, including 30 tropical and 10 temperate lines, were crossed with two diverse testers, CML 286 and CML 451, during *kharif* 2021 for heterotic grouping of post-flowering stalk rot (PFSR) resistant lines with high yield potential. The heterotic group-specific and general combining ability (HSGCA) method classified them into three groups *viz.,* A of CML 286 with 19 lines, B of CML 451 with 13 lines and an undetermined group with eight lines. Six lines of group A (five tropical lines PFSR 393, PFSR 204, GP 327, PFSR 145, GP 82 and one temperate line GP 329) and five lines of group B (three tropical lines GP 36, GP 69, GP 86 and two temperate lines GP 83, GP 107) with highly significant HSGCA effects were crossed to produce 30 single cross hybrids during *Rabi* 2021-22. Screening of these 11 inbred lines from both groups A & B identified two diverse inbred lines *viz.,* tropical GP 36 and temperate GP 83 with PSFR resistance, which can be used as potential donors. The general combining ability (GCA) effects identified three tropical inbred lines, PFSR 145, PSFR 393, GP 36 and one temperate inbred GP 107 line, as good general combiners for early maturity and two temperate inbred lines, GP 329 and GP 107, as best general combiners for grain yield with moderate PFSR resistance demonstrating the potential of temperate and tropical maize lines for increased yield and PFSR resistance. The specific combining ability (SCA) effects identified five potential hybrids GP 329 × GP 83, GP 329 × GP 86, PFSR 393 × GP 107, GP 82 × GP 83 and PFSR 145 × GP 86 with high *per se* performance for grain yield for future use in maize hybrid breeding programmes with PFSR resistance.

Keywords: Maize, heterotic grouping, HSGCA, post-flowering stalk rot, temperate germplasm.

Introduction

Maize (*Zea mays* L.) is an important cereal across the globe and is being cultivated in more than 160 m ha in 166 countries under varied agro-climatic conditions with maximum production and productivity among the food cereal crops. In the world, maize is predominantly used as feed (>60%), followed by food (17%), and the rest for industrial purposes (FAO 2023). In India, maize occupies the third position among cereals and contributes nearly 9% of the overall country's food grain production. It is cultivated in an area of 10.34 m ha with productivity of 3380 kg/ha (FAO 2023). The incidence of diseases is a major constraint hindering the worldwide production of maize, with losses ranging from 12 to 80% (Harleen et al. 2016). Among them, post-flowering stalk rots (PFSR) are an important constraint in Asia, America, Australia, and Europe (Yu et al. 2017). The disease is more prevalent where there is a scarcity of irrigation, especially after the post-flowering stage of the crop. Though several management practices are available, it is difficult to control the disease. The use of improved maize genotypes with tolerance/resistance to PFSR is the most feasible and practical approach to reduce yield losses for sustainable management of PFSR in India.

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Exploiting host plant resistance requires an understanding of genetic diversity among the germplasm lines to identify and select parents for developing heterotic F_1 hybrids and to identify sources of useful alleles for introgressive hybridization (Badu-Apraku et al. 2016). One of the approaches for identifying useful parents/hybrids and developing multiple stress-tolerant hybrids is through combining ability studies (Annor et al. 2020; Elmyhun et al. 2020). However, these studies have different observations and inconsistencies reported in their gene actions, all of which will have a bearing on the inheritance of grain yield and other agronomic traits of tropical maize, thus necessitating more studies on establishing the type of gene action controlling grain yield and other related traits in maize inbreds.

To meet the growing demand for maize in India, it is important to identify heterotic groups to exploit heterosis for increased grain yield. Fan et al. (2018) have described a "heterotic group" as a group of genotypes, related or otherwise, that displayed similar combining ability and heterotic response upon crossing with genotypes from another distinct heterotic group. One approach to enhance maize yields is to derive crosses using varied germplasm to create diverse breeding populations (Abadassi and Herve 2000). Generally, in maize, tropical germplasm tends to exhibit higher genetic diversity and the temperate germplasm has a higher frequency of rare alleles (Liu et al. 2003), which can be exploited further to broaden the genetic base of maize breeding populations (Yan et al. 2009). New desirable genes from temperate germplasm can be introduced into the tropical germplasm to broaden the genetic diversity and increase heterosis in tropical maize breeding programs (Abadassi and Herve, 2000; Fan et al. 2016). In maize, the temperate germplasm is more clearly classified into heterotic groups compared to the tropical germplasm (Hallauer and Miranda 1988). Heterosis in tropical germplasm can be increased by introgression of temperate germplasm and the use of distinct heterotic patterns (Wen et al. 2012). Among the different heterotic grouping methods, a heterotic group based on specific and general combining ability effects (HSGCA) is one of the most efficient approaches for heterotic group classification (Akinwale et al. 2014).

During the past decade, the Indian maize improvement program has developed several inbred lines of different maturity groups with multiple tolerances against biotic and abiotic stresses. However, there is a lack of information on their heterotic grouping to facilitate and maximize their use in tropical hybrid breeding. Keeping this in view, the present study was conducted to classify the parental lines into heterotic groups using the HSGCA method, and to estimate the combining abilities of parental lines and hybrids and iii) to identify promising PFSR-resistant parental lines and hybrids for future maize hybrid breeding programs.

Materials and methods

Genetic materials and generation of hybrids

A total of 40 maize inbred lines, including 30 tropical and 10 temperate maize germplasm lines, out of which 14 lines were from International Wheat and Maize Improvement Centre, Mexico (CIMMYT), 15 lines were from ICAR-IIMR (ICAR-Indian Institute of Maize Research)-Winter Nursery Centre and 11 lines from Maize Research Centre (MRC), Professor Jayashankar Telangana Agricultural University (PJTSAU), Rajendranagar were used in the study (Table 1). Further, two proven heterotic testers *viz*., CML 286 and CML 451 obtained from CIMMYT-Regional Centre, Patancheru, Hyderabad, Telangana state, India, were included in the study for heterotic grouping of the inbred lines. The initial characterization of inbred lines for various morphological characters, screening for PFSR resistance, test cross hybrid development, identification of promising inbred lines and their hybridization was taken up at ICAR-AICRP (Indian Council of Agricultural Research – All India coordinated Research Programme) on Maize, MRC, PJTSAU, Rajendranagar, Hyderabad, Telangana, India.

Development of test cross hybrids

The 40 inbred lines, along with two tester lines, were sown during *kharif*, 2021, at MRC, Rajendranagar, Hyderabad. Each line was sown in six rows of 4 m length plot, with a spacing of 0.6 × 0.2 m. Three staggered sowings of the male testers were undertaken at an interval of 4 days to ensure synchronization of flowering with female lines and to produce adequate crossed seeds. The recommended package of practices and need-based plant protection measures were taken up to raise the healthy crop. The 40 inbred lines were crossed with two testers (CML286 and CML451) in line × tester pattern using the tassel bag method to develop 80 test cross hybrids.

Screening of parental lines for PFSR disease resistance

The 40 inbred lines were simultaneously screened for PFSR disease resistance along with two checks viz., KAVERI-50 (susceptible check) and JCY-2-7 (resistant check) during *Kharif* 2021 using the toothpick method (Payak and Sharma, 1985) in the PFSR screening nursery at MRC, Rajendranagar, Hyderabad. Maize plants were inoculated with mycelia of *Macrophomina phaseolina* using toothpicks at 45 to 50 days of crop growth just before the flowering stage, at the lower internodes (second) above the soil level. The disease intensity and severity were recorded following a 1 to 9 rating scale at 2 to 25 days after inoculation after the appearance of disease symptoms (Payak and Sharma 1985).

Field evaluation of parents and 80 test cross hybrids

The 80 test cross hybrids obtained from 40 inbred parents after hybridization with two testers along with parent

Table 1. Details of the maize genotypes used in the present study

S. No.	Genotypes	Pedigree	Adaptation	Source
1	GP 1	(CM 212 × CML 189) BC3P1-⊗b⊗b⊗b-#	Tropical	CIMMYT Regional Centre, Hyderabad
2	GP 29	Tarun Ä 83-1-3-2-Ä-1-1-3-1-1	Temperate	
3	GP34	Pant12K/Trial 63/3073 OPU-1-2-2-3-1-1-1	Tropical	
4	GP 35	Tarun Ä 83-1-3-2-Ä-1-2-1 x (TarunÄ 83 x Teosinte) Ä-1-1-1-1-Ä-3	Temperate	
5	GP 36	DMRHyd/1284-Ä-1-1-1 x (DMR Hyd –1284 x Teosinte)- Ä6-1-3-1-5-3	Tropical	
6	GP 40	Pant12K/MaizePath/InbredTrial/6-Ä-1-2x (Pant12K/MaizePath/InbredTrial/6 x Teosinte) Ä-5-8-2-3-1-2	Tropical	
7	GP 41	Pant13KSCT5850Ä-1 x (Normal x Teosinte) Ä-4-2-3-1 -1-1	Tropical	
8	GP 51-1	Pant15K/BL/Sh2SCC/OP-2Ä-3-6-4-2-2-1	Tropical	
9	GP 69	Pant15K/BL/Sh2SCC/OP-2Ä-3-6-4-2-2-1	Tropical	
10	GP 77	F-720-X-87-X88-#-89-F2-#-8-3	Tropical	
11	GP 82	Population 147-F2#89-3-2-B-1-B	Tropical	
12	GP 83	Baj Pool 95 -Ä-26-8 -4-1-6-1 -1 -B-B-B (Collections from Kullu local)	Temperate	
13	GP 85	Baj Pool 98-Ä-83-10-1-6-1-1-B-B- (Collections from Katrain local)	Temperate	
14	GP 86	L173 (L118 / Chamba local, Salooni locals, CHH-71/ JH 3748/ AH 807) (This was a composite)	Tropical	
15	GP 87	[X_2Y Pool x CML 226]-B 98 R-1-1-1-Äb-Äb-Äb-Äb-Äb-Äb	Tropical	ICAR-IIMR-WNC, Hyderabad
16	GP 105	[X1Y Pool x MMH 9607]-B98k-2-1-3-1-Ä-Ä-Äb-Äb-Äb-Äb	Tropical	
17	GP 107	(VQL1///HP465-43)-⍰-⍰-⍰-⍰-⍰-⍰-⍰	Temperate	
18	GP 114	(SW92145-2EV-7-3-B*8-1/CML444)-B-3(Sel)-BBB-1-BBB	Tropical	
19	GP 114	BLS 42048-2-2-1-1-1-2	Tropical	
20	GP 153	(G32F32*POB42F258)-11-1-2-BBB	Tropical	
21	GP 173	Cuba 11J-A46-f-# (CM 117-3-2-1)	Temperate	
22	GP 186	Pob62c5HC24-5-3-2-1-B-B-2-B-B-#	Tropical	
23	GP 285	Pob25STEC1HC13-6-1-1-#-BBB-f	Tropical	
24	GP 291	LPSEQC3-H1-2-2-3-2-1-#-#-B-B	Tropical	
25	GP 321	DTPY C9-F46-3-9-1-2-2-1-3-B*10	Tropical	
26	GP 327	EY Syn-B-#-34-B-1-B	Tropical	
27	GP 329	HKI-193-2/HKI-161-13-2-3 [HQPM 4-13-2-3]	Temperate	
28	GP 330	NK125/NK128-N 09-163-1 [NK 6240-N 09-163-1]	Temperate	
29	GP 335	Pob 45c9F22-18-3-1-B*4-1-B*9	Tropical	
30	PFSR 5	Pop31 C4S5B-6-##-1-2-B*5-B1-BB-2-B*7	Temperate	MRC, PJTSAU
31	PFSR 9	Seed Tech 2324-6-2-1-1-1-1-1	Tropical	
32	PFSR 10	Temp × Trop. (HO)-84-BBB-1-1-1-1-1-1	Temperate	
33	PFSR 142	P65O6-BBB-9-BBB-1-1-1-1-1-1	Tropical	
34	PFSR 144	S00TLYWR-HG-BBB-4-BBB-35-B-1-1-1-1-1	Tropical	
35	PFSR 145	WNCQPM 10091-3-2-1-1-1-1-1	Tropical	
36	PFSR 196	WNCQPM 10501-1-2-1-1-1-1-1	Tropical	
37	PFSR 204	PFSR POOL 131155-11-2-3-2-1-1	Tropical	
38	PFSR 221	EARLY POOL 131156-3-4-3-2-1-1	Tropical	
39	PFSR 299	EARLY POOL 131156-5-2-2-2-1-1	Tropical	
40	PFSR 393	EARLY POOL 131156-13-9-2-2-1-1-1	Tropical	

lines were evaluated with three checks (NK 6240, HT 5106 and Bio 9544) for grain yield and yield component traits at two locations MRC, Rajendranagar, Hyderabad and ARS, Karimnagar during *Rabi,* 2021-22. Each entry was sown in six rows of 4 m in length and followed a spacing of 0.6 × 0.2 m between row to row and plant to plant, respectively. The experiment was conducted in a randomized complete block design with two replications. The recommended crop management and plant protection practices were followed to maintain proper crop standards. The 40 inbred lines were classified into a heterotic grouping based on the HSGCA method (Fan et al. 2009). Further, the 40 inbred lines and 80 single cross hybrids were estimated for their combining abilities.

Heterotic group's specific and general combining ability (HSGCA) computation

The HSGCA method (Fan et al. 2009) was computed as follows:

SCA = Cross mean (Xij) - line mean ($X.j$) - Tester means ($Xi.$) + Overall mean ($X..$) GCA = Line mean ($X.j$) - Overall mean ($X..$)

HSGCA = Cross mean (Xij) - Tester means ($Xi.$) = GCA + SCA

Where,

Xij = mean yield of the cross between the ith tester and jth line

$Xi.$ = mean yield of the ith tester

$X.j$ = mean yield of the jth line

Formation of heterotic groups

Using two testers (CML286 and CML451), 40 maize inbred lines were subjected to heterotic grouping following the steps mentioned below.

Step 1: The inbred lines with negative HSGCA effects were placed in the same heterotic group as their tester. An inbred line might be placed in more than one heterotic group.

Step 2: An inbred line assigned to more than one heterotic group, as in step 1, would be placed in the heterotic group, which had its HSGCA value (or largest negative value) and was removed from the other heterotic groups.

Step 3: An inbred line with a positive HSGCA effect with all the tester lines was cautiously assigned to a new heterotic group different from all the testers.

Generation of single crosses utilizing inbred lines from two heterotic groups and their field evaluation

Among the two heterotic groups, six lines from Group A and 5 lines from Group B were sown at MRC, Rajendranagar, following a spacing of 0.6 × 0.2 m during *Kharif*, 2022. All the recommended agricultural operations were followed to maintain proper crop standards. The 11 parents were crossed in a line × tester (6 × 5) mating design through controlled pollination to produce 30 single crosses at MRC, Rajendranagar, Hyderabad. The seed material of 30 single cross hybrids, along with 11 parent lines and four checks, was sown in a randomized block design with three replications following a spacing of 0.6 m between row to row and 0.2 m between plant to plant. All the recommended package of practices were followed to maintain proper crop stand and the data recorded on 11 quantitative characters of parents and hybrids along with the checks were subjected to combining ability analysis for identification of heterotic hybrids.

Data collection and statistical analyses

Data collection began at flowering stage. From each plot, field-dry harvested ears were manually shelled. The grain moisture content was determined using Kett grain moisture tester PM-450. For the determination of grain weight, a shelling percentage of 80 was assumed. The grain weight recorded per plot was adjusted to a moisture content of 15% and was converted to grain yield (kg/ha) using the following equation:

$$GY = GWT \times (100 - m/\ 85) \times 10000/A$$

Where GY = grain yield (kg/ha), GWT = grain yield at harvest moisture content per plot, m = grain moisture content at harvest, and A = plot area.

The analysis of variance was performed using PROC GLM in SAS (SAS 2012) using a RANDOM statement with the TEST option (SAS, 2012) where block nested within replicate × environments, replicate within environments, and environments were random effects while genotypes were fixed effects. The means derived from each ANOVA procedure were utilized for the line × tester analysis, following the method outlined by Singh and Chaudhary (1985). The GCA and SCA for grain yield and other measured traits were estimated using SAS (2012) by partitioning the hybrid mean squares for each trait into line, tester, and line × tester components, whereas the hybrid × environment was partitioned into line × environment, tester × environment, and line × tester × environment. Based on the performance of each of the two testers with all 40 lines (females) in a hybrid, their GCA effect was calculated and similarly, for each line, it was determined based on the performance in combination with the two testers. The GCA and SCA effects were determined for each trait. The general linear model for line × tester mating design is:

$$Y_{ijbkl}=\mu+A_l+áb_{(k)}+\Gamma_{k(l)}+g_i+g_j+s_{ij}+(Av)_{ijl}+E_{ijbkl}$$

Where Y_{ijbkl} = observed value of the progeny between the ith line and the jth tester in the bth block within the kth replication in the lth environment, μ = population mean, A_l = average effect due to environment, $áb_{(k)}$ = effect of block nested

Table 2. Analysis of variance for grain yield for heterotic grouping of maize inbred lines during *kharif* 2021

Source of Variation	df	Sum of squares	Mean sum of squares
Genotypes	121	4140224424.0	34216730.8**
Lines	39	52045828.8	1334508.4*
Testers	1	212051.0	212051.0
Parents *vs.* Crosses	1	3085272319.4	3085272319.4**
Crosses	79	1002548385.5	12690485.9*
Line effect	39	599022523.4	15359551.9
Tester effect	1	21404713.7	21404713.7
Line ×Tester effects	39	382121148.5	9797978.2*
Error	121	285697901.0	2361139.7
Var. GCA		133779.5	
Var. SCA		95530290.0	
GCA / SCA		0.001	

*Significance at 5% probability, **Significance at 1% probability

within replication, $\Gamma_{k(l)}$ = effect of replication nested within environment, g_i = general combining ability (GCA) of the i^{th} line, g_j = general combining ability (GCA) effect of the j^{th} tester, s_{ij} = specific combining ability (SCA) of the ij^{th} testcross, $(Av)_{ijl}$ = effect of interaction between the ij^{th} testcross and l^{th} location, and E_{ijbkl} = residual effect. The relative importance of GCA and SCA sums of squares for measured traits was determined according to the method proposed by Baker (1978). The HSGCA values were estimated as HSGCA = Cross mean (X_{ij}) + Tester mean (X_i) = GCA + SCA (Fan et al. 2009), where X_{ij} is the mean yield of the cross between i^{th} tester and j^{th} line, X_j is the mean yield of the i^{th} tester.

Results

Analysis of variance for grain yield

Analysis of variance showed that the effect of genotypes on grain yield was highly significant ($p < 0.01$) (Table 2). The contrast between the parents vs crosses was also highly significant for grain yield ($p < 0.01$). The effects of lines, crosses and the interactive effect of lines × testers on grain yield were also significant ($p < 0.05$) (Table 2). These indicated that there was sufficient variability in the material evaluated in the study to make valid experimentation and inferences.

Evaluation of maize inbred lines

Forty maize inbred lines were evaluated for earliness (days to 50% tasselling, DFT; days to 50% silking, DFS and days to maturity, DM), grain yield, plant height and resistance to post-flowering stalk rot (PFSR) (Table 3). The inbred lines varied with respect to both DFT and DFS, with line GP 36 attaining tasselling and silking in 47 and 49 days, respectively. Two inbred lines, PFSR 144 and PFSR 9, reached tasselling and silking in 66 and 69.50 days, respectively. The grain yield ranged from 2752.20 (GP 335) to 5749.30 kg/ha (GP 327). Out of the 40 inbred lines evaluated for PFSR resistance, nine were moderately resistant, 20 were moderately susceptible and nine were susceptible to the disease. Only two inbred lines GP 36 and GP 83 were resistant to PFSR with disease scores of 2.8 and 3.0, respectively (Table 3).

Heterotic grouping based on HSGCA effects for grain yield

Heterotic grouping of 40 maize inbred lines using two diverse tester lines CML 286 (denoted as group A) and CML 451 (denoted as group B) was performed for grain yield using the HSGCA method (Table 3 and Supplementary Table S1). The inbred lines showing a negative HSGCA effect with a particular tester were placed in the corresponding tester group. In the event of an inbred line showing negative HSGCA effects with both the testers, they were assigned to the tester group with which it had the smallest value (largest negative value). The inbred lines showing positive HSGCA effect with both the testers were placed in the undetermined group. Out of the 40 inbred lines, 19 lines showed negative HSGCA effects with CML 286 and were placed in heterotic group A, while 13 lines showing negative HSGCA effects with CML 451 were placed in group B (Table 3). Eight inbred lines were assigned to the undetermined group.

Identification of parental lines, generation of single crosses and screening for PFSR resistance

Out of the 40 inbred lines, 11 maize inbred lines were resistant to moderately resistant to PFSR disease (Table 3). Six inbred lines belonging to HSGCA heterotic group A (CML 286) were characterized by high grain yield and short to medium plant height and were identified as female parents (lines) *viz.,* five tropical lines PFSR 393, PFSR 204, GP 327, PFSR 145 and GP 82 and one temperate line GP 329. Five inbred lines of HSGCA heterotic group B (CML 451) were characterized by medium to tall plant height and earliness and were used as male parents (testers) *viz.,* three tropical germplasm lines GP 36, GP 69 and GP 86 and two temperate lines GP 83, and GP 107 (Table 3).

The 11 inbred parents were crossed in a line × tester (6 × 5) mating system and 30 single crosses were generated (Table 4). All the crosses were resistant to moderately resistant to PFSR disease except for one single cross, PFSR 393 × GP 86, which was moderately susceptible to PFSR disease. The single cross hybrid GP 329 x GP 83 was the most resistant, followed by the crosses PFSR 145 × GP 83, PFSR 145 × GP 36, PFSR 393 × GP 36, PFSR 393 × 69, GP 329 × GP 36, GP 327 × GP 36 and PFSR 145 × GP 86, which were resistant to PFSR (Table 4).

Table 3. Evaluation of maize inbred lines for yield and related traits and their heterotic grouping based on the HSGCA effects for grain yield using two diverse testers during *kharif* 2021

Lines	Mean					HSGCA effects		Heterotic group
	DFT	DFS	PH (cm)	GY (kg/ha)	PFSR disease score (Reaction)	CML 286 (A)	CML 451 (B)	
GP 1	53.0	54.5	175.5	3260.5	5.8 (MS)	-735.7	1786.8	A
GP 29	53.0	54.5	108.0	3068.8	8.2 (S)	-1513.5	-4907.5	B
GP34	56.0	61.0	158.8	4069.2	6.2 (MS)	-4457.9	-2240.9	A
GP 35	54.0	57.5	150.5	4518.6	8.4 (S)	-3238.4	-2046.5	A
GP 36	47.0	49.0	142.5	2865.9	2.8 (R)	431.0	-1518.7	B
GP 40	61.0	63.0	132.2	4466.5	6.6 (MS)	-2291.2	-1185.4	A
GP 41	53.0	61.0	123.8	5018.0	6.0 (MS)	-735.7	-963.1	B
GP 51-1	52.0	55.5	108.0	3182.3	6.0 (MS)	-457.9	675.7	A
GP 69	52.0	55.0	167.5	3818.0	3.2 (MR)	2375.4	-1879.8	B
GP 77	63.0	65.0	108.0	2920.9	7.4 (S)	1181.0	-3213.2	B
GP 82	49.0	51.0	157.5	5017.5	3.8 (MR)	-430.1	814.6	A
GP 83	50.0	52.0	160.0	3949.8	3.0 (R)	792.1	-4213.1	B
GP 85	49.0	52.5	160.5	3886.7	5.2 (MS)	-888.4	-852.1	A
GP 86	55.0	58.0	132.5	3614.5	4.4 (MR)	-2791.2	-6185.3	B
GP 87	47.0	58.5	166.3	3685.2	5.8 (MS)	-3319.0	-1046.5	A
GP 105	54.0	57.5	139.7	2991.6	8.2 (S)	-1346.8	4092.3	A
GP 107	49.0	51.0	150.0	3290.9	3.6 (MR)	1542.1	-963.2	B
GP 111	61.0	65.5	131.3	3358.4	7.0 (MS)	347.7	-1407.6	B
GP 114	59.0	64.5	158.0	3525.0	8.2 (S)	3403.2	1175.7	UN
GP 153	55.0	62.0	138.8	5191.2	9.0 (S)	-124.6	786.8	A
GP 173	55.0	58.0	138.0	3157.3	9.0 (S)	-3707.9	-1213.2	A
GP 186	56.0	64.0	170.5	4985.5	6.4 (MS)	-1402.3	1425.7	A
GP 285	58.0	60.5	123.8	3652.2	6.8 (MS)	1486.5	286.8	UN
GP 291	53.0	56.5	118.0	4016.0	6.2 (MS)	28.2	-4685.3	B
GP 321	47.0	59.0	109.7	2782.8	5.7 (MS)	-2624.6	259.1	A
GP 327	51.0	53.0	122.5	5749.8	3.8 (MR)	-430.1	592.4	A
GP 329	57.0	59.0	132.5	5358.4	4.6 (MR)	-1791.2	-1740.9	A
GP 330	61.0	65.5	147.2	3985.6	5.3 (MS)	931.0	759.1	UN
GP 335	59.0	61.0	139.7	2752.3	6.4 (MS)	153.2	-296.5	B
PFSR 5	60.0	66.0	131.3	2821.7	6.4 (MS)	1208.7	1564.6	UN
PFSR 9	63.0	69.5	127.2	4852.2	5.8 (MS)	931.0	-5435.3	B
PFSR 10	61.0	69.0	156.3	4414.7	8.2 (S)	2986.5	536.8	UN
PFSR 142	65.0	66.5	161.3	4385.6	5.2 (MS)	208.8	2870.1	UN
PFSR 144	66.0	68.5	172.2	3958.3	6.2 (MS)	5292.1	786.8	UN
PFSR 145	53.0	55.0	145.0	4182.8	4.2 (MR)	-207.9	1814.6	A
PFSR 196	64.0	66.0	122.2	4052.1	6.1 (MS)	-207.9	1786.8	A
PFSR 204	49.0	51.0	132.5	3652.2	4.2 (MR)	-1513.4	1481.3	A
PFSR 221	63.0	65.5	144.7	4252.1	5.3 (MS)	-402.4	-3268.7	B

PFSR 299	64.0	66.0	119.7	3682.8	8.4 (S)	1403.2	1592.4	UN
PFSR 393	49.0	51.0	125.0	5549.3	3.4 (MR)	-6318.9	-3852.0	A
CML 286	64	66	122	3985.0	5.2 (MR)			
CML 451	66	69	125	3525.0	5.0 (MR)			
CV:	8.10	8.80	12.5	13.50	22.1			
CD (0.05)	2.5	3.1	18.6	156.6	1.5			

DFT = Days to 50% tasselling; DFS = Days to 50% Silking; PH = Plant Height (cm); GY = Grain yield (kg/ha); HSGCA = Heterotic grouping based on specific and general combining ability; A = Heterotic Group A (Tester group CML 286), B = Heterotic Group B (Tester group CML 451), UN = Undetermined group (Ungrouped under both the testers), R = Resistant (Score:≤3.0), MR = Moderately Resistant (Score: 3.1-5.0), MS- Moderately Susceptible (Score: 5.1-7.0) and S = Susceptible (Score: ≥7.0)

Table 4. Evaluation of 11 inbred parent lines of two heterotic groups and their 30 cross combinations for post-flowering stalk rot resistance during *rabi* 2022-23

S. No.	Cross combination	Mean disease score and disease reaction	S. No.	Inbred parent	Mean disease score and disease reaction
1	PFSR 393 × GP 36	2.6 (R)	1	PFSR 393 (Female)	3.4 (MR)
2	PFSR 393 × GP 69	2.6(R)	2	PFSR 204 (Female)	4.2 (MR)
3	PFSR 393 × GP 83	3.2(MR)	3	GP 329 (Female)	4.6(MR)
4	PFSR 393 × GP 86	6.2(MS)	4	GP 327 (Female)	3.8(MR)
5	PFSR 393 × GP 107	3.1(MR)	5	PFSR 145 (Female)	4.4(MR)
6	PFSR 204 × GP 36	3.6(MR)	6	GP 82 (Female)	3.6(MR)
7	PFSR 204 × GP 69	3.6(MR)	7	GP 36 (Male)	2.8(R)
8	PFSR 204 × GP 83	3.2(MR)	8	GP 69 (Male)	3.0 (R)
9	PFSR 204 × GP 86	3.2(MR)	9	GP 83 (Male)	3.0 (R)
10	PFSR 204 × GP 107	4.2(MR)	10	GP 86 (Male)	5.4 (MR)
11	GP 329 × GP 36	2.6(R)	11	GP 107 (Male)	3.6 (MR)
12	GP 329 × GP 69	4.4(MR)		Kaveri-50 (Susceptibe Check)	8 (S)
13	GP 329 × GP 83	2.2(R)		JCY-2-7 (Resistant Check)	3.4 (MR)
14	GP 329 × GP 86	4.0(MR)		CV	15.1
15	GP 329 × GP 107	4.2(MR)		CD @ 5%	1.25
16	GP 327 × GP 36	2.8(R)			
17	GP 327 × GP 69	3.4(MR)			
18	GP 327 × GP 83	3.2(MR)			
19	GP 327 × GP 86	3.8(MR)			
20	GP 327 × GP 107	4.6(MR)			
21	PFSR 145 × GP 36	3.4(MR)			
22	PFSR 145 × GP 69	2.6(R)			
23	PFSR 145 × GP 83	2.4(R)			
24	PFSR 145 × GP 86	3.0(R)			
25	PFSR 145 × GP 107	4.0(MR)			
26	GP 82 × GP 36	4.6(MR)			
27	GP 82 × GP 69	3.4(MR)			
28	GP 82 × GP 83	4.6(MR)			
29	GP 82 × GP 86	4.4(MR)			
30	GP 82 × GP 107	4.8(MR)			

R = Resistant (Score:≤3.0), MR = Moderately Resistant (Score:3.1-5.0), MS = Moderately Susceptible (Score:5.1-7.0) and S = Susceptible (Score:≥7.0).

Table 5. Promising general and specific combiners in maize identified for various quantitative characters

S. No.	Genotypes	Characters
	Inbred lines	
1	PFSR 145	Days to 50% tasselling, days to 50% silking, days to maturity, plant height (cm) and ear height (cm)
2	GP 329	Ear girth, number of kernels per ear, number of kernels per row, 100 kernel weight and grain yield
3	GP 107	Days to 50% tasselling, days to 50% silking, days to maturity and number of kernels per ear
4	PFSR 393 and	Days to 50% tasselling, days to 50% silking and days to maturity
5	GP 36	Days to 50% tasselling, days to 50% silking and days to maturity
	Hybrids	
1	PFSR 204 × GP 36	Days to 50% tasselling, days to 50% silking, days to maturity, number of kernels per ear and number of kernels per row
2	PFSR 393 × GP 83	Number of kernels per ear, number of kernels per row, 100 kernel weight
3	PFSR 145 × GP 36	Ear length and number of kernels per ear
4	GP 82 × GP 83	Days to 50% tasselling, days to 50% silking, days to maturity, number of kernels per ear and grain yield

Table 6. Top five maize hybrids with desirable SCA effects along with per se performance and GCA effects of their inbred parents

Characters and crosses	per se	SCA effects	GCA effects		GCA status
			Line	Tester	
Days to maturity					
PFSR 204 × GP 36	86	-9.73**	0.34	-2.83**	L × H
PFSR 145 × GP 86	88	-8.55**	-2.48**	0.49	H × L
PFSR 393 × GP 107	87	-8.01**	-1.78**	-1.08*	H ×H
PFSR 393 × GP 36	86	-7.10**	-1.78**	-2.83**	H ×H
GP 329 × GP 83	87	-6.36**	-0.50	1.00*	L × L
Ear length (cm)					
PFSR 145 × GP 36	20.9	1.40*	-0.16	-0.10	L × L
PFSR 204 × GP 83	20.8	1.18	-0.14	-0.22	L × L
GP 329 × GP 83	21.3	1.14	0.50	-0.22	L × L
PFSR 393 × GP 86	21.1	1.00	0.10	0.38	L × L
GP 327 × GP 36	21.3	0.92	0.00	-0.10	L × L
Ear girth (cm)					
GP 327 × GP 83	15.2	0.53	-0.20	-0.10	L × L
PFSR 393 × GP 83	15.5	0.50	0.13	-0.10	L × L
PFSR 204 × GP 86	14.9	0.48	-0.52**	-0.03	L × L
GP 82 × GP 83	15.4	0.38	0.18	-0.10	L × L
PFSR 145 × GP 36	15.3	0.37	-0.02	0.03	L × L
Number of Kernels per ear					
GP 82 × GP 83	555.3	62.15**	5.31	21.88**	L × H
GP 329 × GP 86	612.6	57.07**	56.74**	-2.75	H× L
PFSR 393 × GP 83	533.6	45.55**	2.10	21.88**	L × H
PFSR 145 × GP 36	467.3	39.03**	-32.11**	-16.51**	L × L
PFSR 204 × GP 36	457.7	31.99*	-20.97**	-16.51**	L × L

Number of kernels per row					
PFSR 393 × GP 83	35.5	2.52*	-0.25	-0.62	L × L
PFSR 204 × GP 36	34.9	1.96*	-0.00	-0.39	L × L
PFSR 393 × GP 69	34.9	1.71*	-0.25	0.14	L × L
GP 327 × GP 107	34.9	1.56	0.28	-0.24	L × L
PFSR 145 × GP 86	35.2	1.41	-0.70	1.12**	L × H
100 kernel weight (g)					
PFSR 393 × GP 83	38.2	3.65**	-0.31	0.12	L × L
PFSR 204 × GP 107	35.5	3.06**	-0.38	0.27	L × L
PFSR 145 × GP 69	35	2.30*	-0.07	0.09	L × L
PFSR 145 × GP 86	35.4	1.69	-0.07	0.40	L × L
GP 327 × GP 107	34.3	1.46	-0.11	0.27	L × L
Grain yield (kg ha^{-1})					
GP 82 × GP 83	12711.78	1333.11**	-334.59*	-168.39	L × L
PFSR 145 × GP 69	12697.38	768.94**	-98.37	145.16	L × L
GP 329 × GP 83	12772.2	686.76*	372.16*	-168.39	H × L
GP 327 × GP 36	12259.16	597.72*	48.26	-268.47*	L × L
PFSR 204 × GP 107	12479.13	543.32*	-171.84	225.99*	L × H

*Significance at 5% probability, **significance at 1% probability

Promising general and specific combiners based on estimation of GCA and SCA effects

Among the 11 inbred lines, two lines, PFSR 393 and PFSR 145 and two testers, GP 36 and GP 107, had highly significant ($p < 0.01$) and negative GCA effects for earliness, indicating their significance in developing early maturing hybrids (Supplementary Table S3). Line GP 329 and tester GP 107 had positive GCA effects for grain yield. The SCA effects of 30 single cross hybrids revealed that eight hybrids (PFSR 393 × GP 36, PFSR 393 × GP 107, PFSR 204 × GP 36, GP 329 × GP 83, GP 327 × GP 83, GP 327 × GP 86, PFSR 145 × GP 86 and GP 82 × GP 83) had highly significant and negative SCA effects for earliness indicating their usefulness in developing short-duration hybrids (Supplementary Table S4). Four hybrids, PFSR 204 × GP 107, GP 329 × GP 83, GP 327 × GP 36, PFSR 145 × GP 69 and GP 82 × GP 83 showed highly significant ($p < 0.01$) to significant ($p < 0.05$) positive SCA effects for grain yield and could be used in maize improvement program for high yields (Supplementary Table S4).

Based on estimated GCA effects, five inbred lines, PFSR 145, GP 329, GP 107, PFSR 393 and GP 36 were identified as promising general combiners for various yield attributes and maturity traits (Supplementary Table S3 and Table 7). Four hybrids, PFSR 204 × GP 36, PFSR 393 × GP 83, PFSR 145 × GP 36 and GP 82 × GP 83 were found to be good specific combiners for grain yield and other characters (Table 5). The hybrid GP 82×GP 83 had significant and desirable SCA effects for earliness, grain yield and related traits.

Estimated SCA effects of top five maize hybrids with per se performance and GCA status

The top five best cross combinations based on the desirable SCA effects, *per se* performance and GCA effects of their parents are presented in Table 6 along with their GCA status, i.e., low (L) to high (H). For days to maturity, the best specific combiners were the result of all possible GCA statuses of the parent inbred lines L × H, H × L, H × H and L × L. The best crosses for ear length, ear girth, number of kernels per row and 100 kernel weight involved low combiners except for PFSR 145×GP 86 (L × H, number of kernels per row). The crosses GP 82×GP 83, PFSR 145×GP 69 and GP 327×GP 69 involved L × L combiners as parents for grain yield, while the crosses PFSR 204× GP 107 and GP 329×GP 83 had L × H and H × L general combiners, respectively.

Discussion

Breeding for hybrids is a prime example of agricultural advancement that has a direct bearing on enhancing crop productivity. It majorly involves developing stable, trait-specific inbred parental lines and selecting appropriate parents for heterosis breeding (Mukri et al. 2021). Maize is one of the most successful examples of crops where heterosis has been utilized to improve agricultural production (Duvick, 2001). Genetic variability is the most important criterion for selecting inbred lines for maize improvement (Yu et al. 2020). In the present study, 40 promising inbred lines were evaluated for yield and related traits. The analysis of variance indicated the presence of high genetic variability among the genotypes for grain yield, allowing for the selection of high-yielding hybrids (Belay 2018; Mukri et al. 2022). Significant differences for yield in parents *vs.* hybrids and line × tester reflected interaction between the male and female parents that generated variable SCA effects, which might be associated with the wide genetic variability among the parental lines. The 40 inbred lines used were diverse with tropical or temperate backgrounds and had different maturity groups ranging from extra-early (7 lines), early (7 lines), medium (14 lines) and long duration (12 lines). Both the testers CML 286 and CML 451 of CIMMYT are also diverse long-duration lines. The combined genetic diversity of inbred lines and testers aided in a comprehensive evaluation of grain yield potential across different genetic profiles and may have contributed to the grain yield variance in the hybrids (Das et al. 2021; Gaballah et al. 2022).

In this study, two diverse tester lines CML 286 and CML 451, were used to classify the 40 inbred lines using the HSGCA method for grain yield. Many researchers have found the HSGCA method to be more efficient compared to the SCA method and even the markers-based techniques (Fan et al. 2009; Akinwale et al. 2014; Badu-Apraku et al. 2015b; Mahato et al. 2021). Recently, Kumar et al. (2022) used the HSGCA method to classify 26 baby corn inbred lines into heterotic groups for baby corn yield and found the HSGCA heterotic grouping method to be more efficient and effective for baby corn yield compared to the SCA method. The two diverse tester lines, CML 286 and CML 451 used in the present study effectively classified the 40 inbred lines into heterotic group A (19 lines), heterotic group B (13 lines) and undetermined group (8 lines), indicating the potential of these inbred lines to develop high-yielding hybrids and synthetic varieties (Annor et al., 2020). In their study, Kumar et al. (2022) used the baby corn inbred lines from opposite HSGCA heterotic groups to develop crosses with more productive hybrids. In the present study, in addition to the HSGCA heterotic grouping for grain yield, PFSR resistance and earliness traits were also considered to identify potential lines and testers to develop early maturing, PFSR resistant high yielding single cross hybrids. In maize, PFSR is a serious biotic stress affecting maize production worldwide and hence it is important to develop maize hybrids resistant to the disease so that the true potential of these hybrids is protected especially when grown in regions that favor the occurrence of PFSR, such as state of Telangana, India where the present study has been conducted. The PFSR-resistant lines identified in the present study can be used as resistant sources in population improvement (Mir et al. 2018). By incorporating resistance to stalk rots into breeding programs, these lines can serve as valuable sources for developing improved open-pollinated varieties with enhanced PFSR resistance, which in turn can be directly deployed in resource-poor regions where stalk rots are a significant threat to maize production. Such an approach can improve the resilience of maize in these regions and contribute to food security. The PFSR-resistant lines can also be used in maize hybrid breeding. In this study, all 11 inbred parents and 29 single cross hybrids were found to be resistant to moderately resistant to PFSR disease, which could be due to the additive gene action for the inheritance of PFSR resistance in maize hybrids (Mir et al. 2018). The inbred parents identified in this study can be studied for their GCA effects on PFSR and be further exploited to develop a range of hybrid combinations suitable for specific environments.

The potential for heterosis in the six lines (female parents) and five testers (male parents) was determined by combining ability studies to understand the nature and extent of gene effects controlling quantitative traits (Basbag et al. 2007). Genotypes with superior GCA and SCA for various traits can be used to generate more heterotic populations for developing high-yielding hybrids (Akinwale et al. 2014). In the present study, both positive and negative GCA effects were observed for earliness, NKR, NKE, KW and grain yield. Several other researchers also observed similar GCA effects for grain yield and yield component traits (Yu et al., 2020; Kumar et al. 2022; Mukri et al. 2022). Lines PFSR 393 and PFSR 145 and testers GP 36 and GP 107 showed significant negative GCA effect for all the three earliness traits (DFT, DFS and DM) and are good general combiners for these traits can be used to develop early maturing hybrids. While the tester GP 36 showed significant negative GCA effects for grain yield and yield component traits, the tester GP 107 showed significant positive GCA effects for these traits, indicating that GP 36 is a good general combiner for developing early maturing hybrids but a poor combiner for grain yield and on the other hand GP 107 is a good general combiner for developing high yielding early maturing hybrids. These findings are comparable to those of Talukder et al., (2016) and Murtadha et al. (2018), showing the importance of additive gene action for these traits. The evaluated lines and testers can thus be effective for developing early maturing and/or high-yielding maize hybrids. Three out of the five top cross hybrids obtained in this study *viz.,* GP 82 × GP 83, GP 329 × GP 83 and PFSR 204 × GP 107, with high grain yield performance and high significant positive SCA effects had parents each belonging to tropical and temperate germplasm. In addition, other hybrids such as PFSR 393 × GP 83, GP 329 × GP 69, PFSR 393 × GP 107 and PFSR 145 × GP 107 derived from crosses between tropical and temperate maize germplasm lines were also superior with high mean grain yields over the commercial checks, which might be due to temperate genes introgressed into the tropical lines thereby increasing breeding efficiency and heterosis (Abadassi and Herve, 2000; Fan et al. 2016).

Previous studies by Musundire et al. (2019) and Kulka et al. (2018) reported high genetic diversity in hybrids developed from intercrosses of tropical and temperate maize inbred lines compared to crosses developed from either tropical or temperate germplasm lines *per se*. This is important because the maize hybrid breeding program in India is constrained by narrow genetic base, thus limiting yield improvement. To meet the increasing demand for maize in the world in general and specifically in India, it is essential to broaden the genetic base and in this context, introgression of exotic germplasm into locally adapted germplasm offers tremendous scope to improve maize productivity (Fan et al. 2009).

Among the 30 single cross hybrids, different SCA effects were seen in all the evaluated traits. In the present study, the inconsistent association between the GCA of the parents and SCA in specific crosses for evaluated traits suggested complex gene interaction governing these quantitative traits (Su et al. 2017). For instance, crosses PFSR 393 × GP 36 and PFSR 393 × GP 107 showed promising performance for earliness with significant negative SCA effect and all the three parent lines are good general combiners for earliness, suggesting the role of cumulative effects of additive × additive interaction of positive alleles (Singh et al. 2018; Fasahat et al. 2016). The cross PFSR 204 × GP 36 (poor general combiner × good general combiner) showed positive performance for earliness, which may be attributed to good combiner parent depicting favorable additive effects and poor combiner parent displaying epistatic effects (Singh et al. 2018; Fasahat et al. 2016). At the same time, crosses like GP 327 × GP 83 and GP 327 × GP 86, despite involving both the parents with GCA in a desirable direction, had low SCA effects for earliness, which might be due to the absence of any interaction among the positive alleles of genes (Singh et al. 2019). This clearly indicates the importance of both GCA and SCA in a selection of elite parents for the development of heterotic hybrids.

While the roles of heterosis and combining ability in maize breeding are widely recognized, a thorough understanding of the genetic basis is still lacking. Molecular diversity of the inbred lines using markers like simple sequence repeats might give better insights into understanding the genetic base of the inbred lines (Andorf et al. 2019). Several studies have utilized genetic distances based on phenotypic and genotypic data to understand genetic variation and predict heterosis. However, contrasting findings ranging from no correlation to positive or negative correlation of genetic distances with the SCA effects of several traits were reported in maize (Wegary et al., 2013) and pearl millet (Gupta et al. 2018). Additional investigation using diverse sets of large numbers of molecular markers spanning the entire genome along with different selections of parental germplasm across multiple environments might provide valuable insights into the intricate genetic mechanisms underlying heterosis and combining ability in maize. The 40 inbred lines and 2 testers used in this study belonged to different maturity groups. While the study focused on how the genetic potential of the inbred lines influences grain yield and attributes, its combined effect with maturity groups can be investigated further for the identification of specific lines that perform well within certain maturity groups. By exploring various genetic backgrounds under diverse environmental conditions, we can further refine our strategies for maize breeding and ultimately contribute to the development of high-yielding hybrids with improved traits. Overall, the present study demonstrated the successful utilization of diverse maize germplasm to identify the best crosses that exploited the yield potential of temperate germplasm while simultaneously maintaining the PFSR resistance of tropical germplasm for future quality hybrid breeding in maize to develop superior hybrids with stable PFSR resistance.

Supplementary material

Supplementary Tables S1 to S3 are presented which can be accessed at www.isgpb.org.

Authors' contribution

Conceptualization of research (NBD, BVV, MVNK, VR, NS, DB, BM and AM); Designing of the experiments (NBD, MVNK, DB and AM); Contribution of experimental materials (NBD, BVV, MVNK and NS); Execution of field/lab experiments and data collection (NBD, MVNK, DB and BM); Analysis of data and interpretation (NBD, BVV, MVNK, VR and AM); Preparation of the manuscript (NBD, DVV, MVNK, DB and VR).

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Supplementary Table S1. Yield performance of 40 maize inbred lines and two testers evaluated at two locations during Kharif 2021

S. No.	Inbred	Grain yield (kg ha^{-1})		
		Maize Research Centre, Rajendranagar	Agricultrural Research Station, Karimnagar	Mean
1	GP 1	3358.2	3162.7	3260.45
2	GP 29	3016.9	3120.6	3068.75
3	GP34	4166.3	3972.0	4069.15
4	GP 35	4470.6	4566.6	4518.6
5	GP 36	2963.2	2768.7	2865.95
6	GP 40	4566.4	4366.6	4466.5
7	GP 41	4916.0	5120.0	5018
8	GP 51-1	3102.5	3262.1	3182.3
9	GP 69	3916.0	3720.0	3818
10	GP 77	3019.1	2822.6	2920.85
11	GP 82	4816.0	5219.0	5017.5
12	GP 83	3900.3	3999.3	3949.8
13	GP 85	3785.5	3987.8	3886.65
14	GP 86	3568.0	3661.0	3614.5
15	GP 87	3882.6	3487.7	3685.15
16	GP 105	2943.3	3039.9	2991.6
17	GP 107	3187.9	3393.8	3290.85
18	GP 111	3258.3	3458.4	3358.35
19	GP 114	3600.0	3450.0	3525
20	GP 153	5137.6	5244.8	5191.2
21	GP 173	2954.3	3360.3	3157.3
22	GP 186	5080.5	4890.5	4985.5
23	GP 285	3450.2	3854.2	3652.2
24	GP 291	4110.0	3922.0	4016
25	GP 321	2732.7	2832.9	2782.8
26	GP 327	5647.3	5852.3	5749.8
27	GP 329	5206.3	5510.4	5358.35
28	GP 330	3787.5	4183.6	3985.55
29	GP 335	2832.3	2672.2	2752.25
30	PFSR 5	2920.8	2722.6	2821.7
31	PFSR 9	4950.2	4754.2	4852.2
32	PFSR 10	4258.6	4570.8	4414.7
33	PFSR 142	4688.5	4082.7	4385.6
34	PFSR 144	4060.3	3856.2	3958.25
35	PFSR 145	4580.7	3784.8	4182.75
36	PFSR 196	4002.0	4102.2	4052.1
37	PFSR 204	3850.2	3454.2	3652.2
38	PFSR 221	4348.1	4156.1	4252.1
39	PFSR 299	3980.7	3384.9	3682.8

40	PFSR 393	5747.3	5351.3	5549.3
41	CML 286	4181.5	3788.5	3985
42	CML 451	3722.0	3328.0	3525
	Mean	4260.0	3948.0	4104
Range	Minimum	2732.7	2672.2	2702.45
	Maximum	5647.3	5852.3	5749.8

Supplementary Table S2. Yield performance of 80 test cross hybrids evaluated at two locations during Rabi 2021-22

S. No.	Test cross Hybrid	Grain yield (kg ha^{-1})		
		Maize Research Centre, Rajendranagar	Agricultrural Research Station, Karimnagar	*Mean*
1	GP 1 × CML 286	11606.6	10226.6	10916.6
2	GP 29 × CML 286	12970.1	13979.1	13474.6
3	GP34 × CML 286	9680.8	10596.8	10138.8
4	GP 35 × CML 286	6408.7	7146.7	6777.7
5	GP 36 × CML 286	7417.4	6971.2	7194.3
6	GP 40 × CML 286	9697.4	9191.6	9444.5
7	GP 41 × CML 286	8482.4	8345.2	8413.8
8	GP 51-1 × CML 286	9451	9826.6	9638.8
9	GP 69 × CML 286	11597.3	12569.1	12083.2
10	GP 77 × CML 286	10688.1	9645.4	10166.75
11	GP 82 × CML 286	9644.1	9077.9	9361
12	GP 83 × CML 286	11262.7	9737.7	10500.2
13	GP 85 × CML 286	11540.4	10292.8	10916.6
14	GP 86 × CML 286	10309.3	11134.9	10722.1
15	GP 87 × CML 286	11646.1	10742.5	11194.3
16	GP 105 × CML 286	9656.6	7778.6	8717.6
17	GP 107 × CML 286	10439.6	12004.6	11222.1
18	GP 111 × CML 286	13012.7	11987.1	12499.9
19	GP 114 × CML 286	11920.5	12968.1	12444.3
20	GP 153 × CML 286	8424.9	6519.3	7472.1
21	GP 173 × CML 286	10075.9	11451.7	10763.8
22	GP 186 × CML 286	5747.8	5252	5499.9
23	GP 285 × CML 286	12324.8	13230.5	12777.65
24	GP 291 × CML 286	13647.2	15574.8	14611
25	GP 321 × CML 286	9452.9	11158.1	10305.5

26	GP 327 × CML 286	16530.2	15025	15777.6
27	GP 329 × CML 286	13646.1	12742.5	13194.3
28	GP 330 × CML 286	9958.3	11385.9	10672.1
29	GP 335 × CML 286	12568.5	11431.3	11999.9
30	PFSR 5 × CML 286	15576.9	14534.2	15055.55
31	PFSR 9 × CML 286	12078.5	13643.5	12861
32	PFSR 10 × CML 286	12227.7	10827.7	11527.7
33	PFSR 142 × CML 286	12623.2	13598.8	13111
34	PFSR 144 × CML 286	9998.8	8973.2	9486
35	PFSR 145 × CML 286	14846	13321	14083.5
36	PFSR 196 × CML 286	8609.8	7362.2	7986
37	PFSR 204 × CML 286	8791.9	9707.9	9249.9
38	PFSR 221 × CML 286	10130.9	10868.9	10499.9
39	PFSR 299 × CML 286	14038.5	13072.3	13555.4
40	PFSR 393 × CML 286	8513.8	9513.8	9013.8
41	GP 1 × CML 451	13761.8	12515.8	13138.8
42	GP 29 × CML 451	11284.2	12660	11972.1
43	GP34 × CML 451	12163.5	11197.3	11680.4
44	GP 35 × CML 451	7221.4	6778.7	7000.05
45	GP 36 × CML 451	9390.5	8665.5	9028
46	GP 40 × CML 451	11575.3	12313.3	11944.3
47	GP 41 × CML 451	10736.2	11708.0	11222.1
48	GP 51-1 × CML 451	11780.7	12773.9	12277.3
49	GP 69 × CML 451	9403.0	10319.0	9861
50	GP 77 × CML 451	10567.3	9321.3	9944.3
51	GP 82 × CML 451	13335.8	11830.6	12583.2
52	GP 83 × CML 451	13012.9	11875.7	12444.3
53	GP 85 × CML 451	11317.6	12293.2	11805.4
54	GP 86 × CML 451	10902.9	11874.7	11388.8
55	GP 87 × CML 451	12799.2	11756.5	12277.85
56	GP 105 × CML 451	6412.2	6087.2	6249.7
57	GP 107 × CML 451	15262.5	14014.9	14638.7
58	GP 111 × CML 451	11809.3	12634.9	12222.1

59	GP 114 × CML 451	13090.6	12187.0	12638.8
60	GP 153 × CML 451	8987.7	8400.9	8694.3
61	GP 173 × CML 451	10156.3	11321.3	10738.8
62	GP 186 × CML 451	14734.9	13709.3	14222.1
63	GP 285 × CML 451	13670.5	14718.1	14194.3
64	GP 291 × CML 451	16369.3	14463.7	15416.5
65	GP 321 × CML 451	11361.0	12361.0	11861
66	GP 327 × CML 451	14097.4	15013.4	14555.4
67	GP 329 × CML 451	16575.3	17313.3	16944.3
68	GP 330 × CML 451	13224.7	11719.5	12472.1
69	GP 335 × CML 451	12012.9	10875.7	11444.3
70	PFSR 5 × CML 451	14632.5	13589.8	14111
71	PFSR 9 × CML 451	13550.7	15115.7	14333.2
72	PFSR 10 × CML 451	15699.9	14299.9	14999.9
73	PFSR 142 × CML 451	13734.3	14709.9	14222.1
74	PFSR 144 × CML 451	14123.8	13098.2	13611
75	PFSR 145 × CML 451	15734.9	14209.9	14972.1
76	PFSR 196 × CML 451	9040.4	7792.8	8416.6
77	PFSR 204 × CML 451	12597.4	13513.4	13055.4
78	PFSR 221 × CML 451	12908.6	13646.6	13277.6
79	PFSR 299 × CML 451	5816.4	4850.2	5333.3
80	PFSR 393 × CML 451	8596.1	7071.1	7833.3
	Checks			
	NK 6240	11572.9	13500.5	12536.7
	Hi-Tech-5160	13574.1	12436.9	13005.5
	Hi-Tech-5106	12535	11492.3	12013.65
	Bio 9544	13198.2	14763.2	13980.7
	Mean	11296.6	11172.1	11234.4
Range	Minimum	5816.4	4850.2	5333.2
	Maximum	16575.3	17313.3	16944.2
	CV			16.8
	SEM			1069.7
	CD @ 5%			2997.6

Supplementary Table S3. General combining ability effects of 11 parents across evaluated during *Rabi* 2022-23

S. No.	Genotypes	Characters										
		Days to 50% tasselling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernels per row	Number of Kernel per ear	100 kernel weight (g)	Grain yield (kg ha^{-1})
	Lines											
1	PFSR 393	-2.31**	-2.33**	-1.78**	-0.00	1.25	0.10	0.13	-0.25	2.1	-0.31	184.37
2	PFSR 204	0.28	0.30	0.34	0.24	2.09	-0.14	-0.52**	-0.02	-20.97**	-0.38	-171.84
3	GP 329	-0.52	-0.52	-0.50	3.10	0.23	0.50	0.43*	1.43**	56.74**	1.38**	372.16*
4	GP 327	1.25 **	1.23**	1.01*	0.55	1.86	0.00	-0.20	0.28	-11.06	-0.11	48.26
5	PFSR 145	-0.78 **	-0.80**	-2.48**	-3.44*	-3.44**	-0.16	-0.02	-0.7	-32.11**	-0.07	-98.37
6	GP 82	0.52 *	0.56*	3.41**	-0.45	-2.00	-0.30	0.18	-0.75*	5.31	-0.49	-334.59*
	GCA (Line)	0.25	0.25	0.47	2.12	1.05	0.27	0.18	0.37	5.65	0.40	106.62
	gi-gj (Line)	0.36	0.35	0.67	3.00	1.49	0.38	0.26	0.53	8.0	0.57	150.79
	SE	0.342	0.327	1.851	1.221	0.470	0.220	0.146	0.411	4.052	0.556	180.619
	Testers											
1	GP 36	-1.39 **	-1.36 **	-2.83**	3.10	1.24	-0.10	0.03	-0.39	-16.51*	-0.90*	-268.47 *
2	GP 69	0.97 **	0.71 **	2.41**	-2.33	-1.54	-0.34	0.04	0.14	-13.54*	0.09	145.16
3	GP 83	0.97 **	1.02 **	1.00*	-4.63 *	0.50	-0.22	-0.10	-0.62	21.88**	0.12	-168.39
4	GP 86	0.97 **	0.99 **	0.49	0.57	-1.37	0.38	-0.03	1.12**	-2.75	0.40	65.70
5	GP 107	-1.52 **	-1.36 **	-1.08 *	3.28	1.16	0.28	0.06	-0.24	10.94*	0.27	225.99 *
	GCA (Tester)	0.2359	0.2322	0.43	1.93	0.96	0.25	0.17	0.34	5.16	0.37	97.3362
	gi-gj (Tester)	0.3337	0.3283	0.61	2.74	1.36	0.35	0.24	0.48	7.3	0.52	137.6542
	SE	0.306	0.292	1.656	1.092	0.421	0.196	0.130	0.368	3.624	0.497	161.551

*Significance at 5% probability, **significance at 1% probability

Supplementary Table S4. **Specific Combining ability effects of 30 hybrid combinations evaluated during *Rabi* 2022-23**

S. No.	Single cross hybrids	Characters										
		Days to 50% tasselling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernels per row	Number of Kernel per ear	100 kernel weight (g)	Grain yield (kg ha^{-1})
1	PFSR 393×GP 36	-3.57**	-3.66**	-7.10**	-4.82	-1.00	-0.70	-0.44	-2.41**	-11.34	-0.94	-287.15
2	PFSR 393×GP 69	-1.10	-1.08	4.48**	1.41	-1.41	-1.42*	0.14	1.71*	9.51	-1.31	-474.97*
3	PFSR 393×GP 83	3.39**	3.44**	4.39**	-3.62	-1.13	0.80	0.50	2.52**	45.55**	3.65**	275.33
4	PFSR 393×GP 86	4.39**	4.63**	6.24**	8.03	5.71*	1.00	-0.33	0.76	-3.78	1.07	127.17
5	PFSR 393×GP 107	-3.10**	-3.33**	-8.01**	-1.00	-2.16	0.31	0.13	-2.59**	-39.94**	-2.46**	359.621
6	PFSR 204× GP 36	-6.01**	-5.96**	-9.73**	2.92	2.48	-0.65	0.14	1.96*	31.99*	0.95	133.31
7	PFSR 204× GP 69	1.461*	1.78**	2.68*	-2.84	-1.12	0.17	0.06	-0.8	-3.34	-1.74	-216.19
8	PFSR 204× GP 83	1.12	1.14*	2.09	-3.40	-2.21	1.18	-0.64	-1.69*	-16.19	-0.61	-624.18*
9	PFSR 204× GP 86	1.79**	1.83**	1.94	-0.05	0.90	-0.27	0.48	0.31	-13.4	-1.65	163.74
10	PFSR 204× GP 107	1.62**	1.20*	3.01**	3.37	-0.04	-0.43	-0.05	0.21	0.93	3.06**	543.32*
11	GP 329×GP 36	-0.07	0.3	2.94**	-1.12	-0.38	-1.77**	-0.24	-2.06*	-78.52**	-2.28*	-1182.41**
12	GP 329×GP 69	0.56	0.71	-3.80**	0.30	3.34	0.14	0.34	0.93	6.94	0.61	22.63
13	GP 329×GP 83	-3.43*	-3.52*	-6.36**	2.57	-1.68	1.14	-0.13	-0.16	-15.44	1.07	686.76**
14	GP 329×GP 86	1.89**	1.43*	2.05	0.19	-1.73	-0.19	0.36	1.18	57.07**	0.90	373.83
15	GP 329×GP 107	-0.93	-1.03	-0.80	-1.94	0.45	0.67	-0.33	0.11	29.95*	-0.30	99.17
16	GP 327× GP 36	3.68**	3.43**	10.93**	2.21	0.11	0.92	0.19	1.08	22.88	1.08	597.72*
17	GP 327×GP 69	0.49	0.51	-3.65**	4.28	-0.85	0.47	-0.98*	-0.95	2.11	-0.34	-50.79
18	GP 327× GP 83	-2.67**	-2.28**	-5.40**	-2.28	-0.51	-1.41*	0.53	-0.15	-41.74**	-1.64	-417.39
19	GP 327× GP 86	-2.17**	-1.92**	-4.05**	-1.19	0.86	-0.49	0.29	-1.54	17.11	-0.55	-82.11
20	GP 327× GP 107	0.66	0.26	2.18*	-3.03	0.39	0.51	-0.03	1.56	-0.37	1.46	-47.41
21	PFSR 145×GP 36	2.22**	1.96**	2.74*	2.37	-0.64	1.40*	0.37	0.46	39.03**	0.17	414.13
22	PFSR 145×GP 69	0.52	0.88	1.84	3.27	4.08	-0.01	0.3	-0.2	1.96	2.30*	768.94**
23	PFSR 145×GP 83	2.36***	2.07**	2.43*	-4.18	-1.00	-1.47*	-0.64	-1.66	-34.32**	-2.92**	-1253.63**

24	PFSR 145×GP 86	-6.47**	-6.72**	-8.55**	-2.53	0.67	0.57	-0.18	1.41	-1.06	1.69	315.36
25	PFSR 145×GP 107	1.36*	1.80**	1.51	1.06	-3.10	-0.48	0.15	-0.01	-5.62	-1.24	-244.79
26	GP 82×GP 36	3.75**	3.93**	0.19	-1.57	-0.55	0.80	-0.02	0.95	-4.05	1.03	324.40
27	GP 82×GP 69	-1.93**	-2.81**	-1.552	-6.44	-4.02	0.64	0.12	-0.68	-17.19	0.49	-49.60
28	GP 82×GP 83	-2.77**	-2.95**	-3.13**	10.92*	6.55**	-0.24	0.38	1.15	62.15**	0.46	1333.11**
29	GP 82×GP 86	0.56	0.73	2.37*	-4.45	-6.43**	-0.62	-0.62	-2.13*	-55.95**	-1.47	-898.01**
30	GP 82×GP 107	0.39	1.1	2.11*	1.54	4.45	-0.58	0.14	0.7	15.05	-0.51	-709.90**
	SCA	0.57	0.56	1.05	4.74	2.36	0.61	0.42	0.84	12.64	0.916	238.42
	Sij - Skl	0.81	0.80	1.49	6.71	3.34	0.86	0.59	1.19	17.88	1.29	337.18
	Sij - Sik	0.96	0.95	1.77	7.94	3.96	1.02	0.70	1.4	21.16	1.53	398.95
	SE	0.685	0.653	3.702	2.441	0.941	0.439	0.292	0.822	8.103	1.111	361.238

*Significance at 5% probability, **significance at 1% probability