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RESEARCH PAPER

Genetic assessment of combining ability for grain yield and key attributing traits in maize (*Zea mays* L.)

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Abstract Maize (*Zea mays* L.) is an important cereal crop globally, and enhancing its yield and associated traits is of paramount importance. Combining ability analysis is a valuable tool in crop improvement, allowing breeders to identify promising parent lines for developing superior hybrids. This study assessed the general and specific combining ability of ten maize inbred lines and three testers for grain yield and associated traits. A line × tester mating design was used, and thirty crosses were evaluated. Analysis of variance revealed significant differences among lines, testers, and line x testers for all studied traits, confirming the genetic diversity of the materials used. General combining ability (GCA) and specific combining ability (SCA) variances were significant, indicating the importance of both additive and non-additive gene effects. Notably, CML-425 showed significant positive GCA for grain yield, making it a potential parent for high-yielding hybrid development. Among the crosses, UMI-1200 × CML-451 exhibited desirable SCA values for grain yield. Understanding the combining ability effects of parent lines and their crosses is essential for breeding high-yielding maize hybrids. This study provides valuable insights for maize improvement programs, with the potential for significant yield enhancements.

Keywords: GCA · Hybrids · Line × Tester · Maize · SCA

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Introduction

Maize (*Zea mays* L.), ranking as the world's third most crucial cereal crop after rice and wheat, is a member of the *Poaceae* family, believed to have originated in southern Mexico. With a diploid chromosome count of 2n=20, it has earned the title "Queen of Cereals" globally due to its unparalleled genetic yield potential and the physiological advantage of being a C_4 type plant, resulting in elevated grain yields. The worldwide production of maize is substantial, with over 170 countries contributing to an aggregate output of nearly 1147.7 million metric tonnes from a cultivated area of 193.7 million hectares, achieving an average productivity of 5.75 tonnes per hectare (FAO STAT, 2020). In India, maize cultivation spans approximately 9.7 million hectares, yielding a production of 30.2 million metric tonnes (USDA, 2020). The major maize-producing states in India, including Karnatka, Uttar Pradesh, Madhya Pradesh and Maharashtra collectively contribute to over 95% of the national maize production (Economic Survey, 2020-21). The nutritional composition of maize kernels reveals their richness in carbohydrates (72-73%), protein (8-11%), ash (2% on a water-free basis), and oil (4-5%). Notably, maize oil contains minimal saturated fatty acids, with just 11% palmitic acid and 2% stearic acid, while showcasing higher levels of polyunsaturated fatty acids, particularly linoleic acid (Kling, 1991). This unique feature enables maize oil to remain in liquid form at lower temperatures, rendering it beneficial for cardiac health and earning it the moniker "nutricereal."

Maize stands apart from other cereals due to its complex of carotenoids, including carotene, cryptoxanthins, and zea carotene, all possessing Pro-vitamin A activity. Its versatility is evident as a fundamental raw material for an array of industrial products, encompassing starch, oil, protein, alcoholic beverages, food sweeteners, cosmetics, and biofuels, among others. In the context of livestock, maize plays a critical role as silage, crop residue, and grain. The maize crop has harnessed the potential of hybrid vigor, although it's essential to acknowledge that not all parental lines exhibit economically exploitable heterosis in their hybrids. This underscores the value of combining ability analysis in crop improvement, as it helps delineate the nature and extent of genetic effects governing yield and its component traits. Additionally, it aids in the identification of promising parent combinations to produce superior hybrids. The two principal types of combining abilities, namely general combining ability (GCA) and specific combining ability (SCA), provide insights into the performance of individual lines and their role in hybrid combinations, as discussed by Xiao *et al.* (2021).

Breeders have at their disposal a diverse range of biometric tools to understand the genetic control of commercially significant traits, guiding the selection of optimal breeding methodologies. The line x tester mating design, an extension of top cross analysis involving multiple testers, has been widely adopted in maize breeding and continues to play a crucial role in quantitative genetic studies of maize, as documented by Joshi *et al.* (2002) and Sharma *et al.* (2004). This design, stemming from the work of Kempthorne (1957), is a straightforward and efficient approach for evaluating a large number of inbreds or parents for their combining ability, offering fundamental insights into the combining abilities of parental inbred lines and the nature and magnitude of gene actions.

Materials and methods

In the present study, we utilized ten diverse maize inbred lines: BML-7, UMI-1200, UMI-1201, CML-72, CML-32, IML-187, DMEL-68, CML-551, LM-14, and CML-425, along with three testers: CML-451, BML-6, and LM-13. A total of thirty crosses from this set of parents were made and conducted evaluations at the Dryland Agricultural Research Station during the *kharif*-2021 season. The experimental design involved a complete randomized block design with three replications. Each experimental plot consisted of two rows, each measuring 3 meters in length, with a spacing of 60 × 20 cm.

The observations collected on various traits, included plant height (in centimeters), ear height (in centimeters), cob length (in grams), the number of kernel rows per ear, the number of kernels per row, shelling percentage (in percentage), 100-grain weight (in grams), grain yield per plant (in grams), and maturity traits (days to 50 percent tasseling and days to 50 percent silking). The various traits were recorded as follows:

Plant height (cm): Plant height was measured from the base of the plant to the tip of the tassel at the time of physiological maturity. Ten randomly selected plants from each plot were measured, and the average height was recorded.

Ear height (cm): Ear height was measured from the base of the plant to the node bearing the uppermost ear. Measurements were taken from ten randomly selected plants per plot, and the average ear height was calculated.

Cob length (cm): Cob length was measured from ten randomly selected ears per plot. Each ear was measured from the base to the tip of the cob, and the average length was recorded.

Number of kernel rows per ear: The number of kernel rows per ear was counted on ten randomly selected ears per plot. The average number of rows was then determined.

Number of kernels per row: The number of kernels per row was counted on ten randomly selected rows from ten ears per plot. The average number of kernels per row was calculated.

Shelling percentage (%): Shelling percentage was calculated by weighing the grain and the cob separately after shelling ten ears from each plot. The shelling percentage was calculated using the formula:

$$\text{Shelling percentage} = \frac{\text{Weight of grain}}{\text{Total weight of ear}} \times 100$$

100-grain weight (g): The weight of 100 randomly selected grains was measured using an electronic balance for each plot. This was repeated three times, and the average 100-grain weight was recorded.

Grain yield per plant (g): Grain yield per plant was measured by harvesting all ears from ten randomly selected plants per plot. The ears were shelled, and the grain weight was recorded. The average grain yield per plant was then calculated.

Days to 50% tasseling: The number of days from planting to when 50% of the plants in a plot had shed pollen was recorded.

Days to 50% silking: The number of days from planting to when 50% of the plants in a plot had visible silks was recorded.

To identify significant genotype differences, we initially subjected the data to separate ANOVA analyses before conducting a combined ANOVA. Combining ability analysis was then performed, following the model suggested by Kempthorne in 1957. Data analysis was carried out using Windostat (9.1) software.

Results and discussion

The results of the analysis of variance for the studied traits are presented in Table 1. The outcomes indicated significant variations among the maize lines (parents), testers, and line × tester combinations (crosses) for all the examined traits, underscoring the diverse nature of the genotypes used in this study. These findings align with those reported by Singh *et al.* (2012) for traits such as days to 50 per cent tasseling, days to 50 per cent silking, plant height (PH), ear height (EH), kernel rows per cob (KRPE), kernels per row (KPR), grain yield per plant (GYP), and 100-grain weight (GW). The variances attributed to both lines and testers were highly significant for all the traits under consideration. Similar results were reported by Kanagarasu *et al.* (2010) for traits like days to 50 per cent tasseling, days to 50 per cent silking, plant height (PH), ear height (EH), kernel rows per cob (KRPE), kernels per row (KPR), 100-grain weight (GW), and grain yield per plant (GYP). Notably, in the individual analysis, it was observed that the mean squares due to lines were more substantial than those attributed to testers for all the traits, consistent with the results reported by Abuali *et al.* (2012).

Both general combining ability (GCA) and specific combining ability (SCA) variances were found to be significant for most of the traits. The higher magnitude of σ²_SCA relative to σ²_GCA implied the greater influence of non-additive gene effects in the inheritance of traits related to maturity, grain yield per plant (GYP), and most of the component traits. The prominence of non-additive gene effects in grain yield and other traits has been reported by various researchers (Jha and Khera, 1992; Sharma and Bhalla, 1993; Vasal *et al.,* 1993; Joshi *et al.,* 1998). However, Betran *et al.* (2003) reported that the proportion of additive genetic effects in the total genetic variance for grain yield in maize was 61%.

Understanding the combining ability effects of parents and crosses, along with individual performance, is crucial for breeders when selecting desirable lines and determining the appropriate methodology for managing segregating generations.

General combining ability (GCA) effects

The GCA effects represent the additive nature of gene action. In the present study, the general combining ability of the ten parent lines was estimated to assess their genetic potential for producing superior genotypes. The GCA effect estimates are detailed in Table 3, and a close examination of the results revealed that none of the parents exhibited significant GCA effects in the desired direction simultaneously for all the studied traits. Notably, for grain yield per plant, CML-425 displayed the most significant

Table 1. Analysis of variance for combining ability for grain yield and other character

Sources of variation	df	DA	DS	DM	PH	EH	EL	NKRE	NKR	ED	GW	SP	GYP
Replications	2	0.15	2.02	3.05	15.0	464.71*	0.33	1.64	0.32	0.21	0.08	0.07	2.01
Crosses	29	8.56**	2.14**	7.89**	371.87**	176.60**	3.41*	2.02**	15.24**	0.08	15.15**	27.43**	438.91**
Lines	9	8.13	7.78	9.35*	634.73*	380.46**	5.14**	4.50**	21.01**	0.08	14.44*	49.21*	545.21**
Testers	2	4.95*	43.65*	7.14*	772.99*	119.71	2.23	1.76	2.32	0.30**	111.59**	49.11	228.18*
Lines × Testers	18	6.78**	10.81**	12.45*	196.12	181.02**	4.71**	0.98*	23.80*	0.03*	4.88**	17.01**	409.01**
Error	29	1.04	1.06	1.44	62.10	37.736	1.81	0.42	6.86	0.01	1.12	0.10	3.31

*, *= Significant at 5 and 1 %, respectively

Where, DA= days to 50% anthesis, DS= days to 50% silking, DM= days to maturity, PH= plant height, EH= ear height, El= ear length, NKRE= No. of kernel rows per ear, NKR= No. of kernels per row, ED= ear diameter, GW= 100 grain weight, SP= shelling percentage, GYP= grain yield per plant

Table 2. Estimates of general combining ability effects of lines used in F1 crosses for grain yield and other characters in maize

LINES	DA	DS	DM	PH	EH	EL	NKRE	NKR	ED	GW	SP	GYP
BML-7	-1.61**	-1.30*	1.33	5.82	-3.81	0.70	-0.50	1.73	-0.20	1.95*	-4.02**	-9.32
UMI-1200	0.39	-1.12*	0.03	19.28**	13.22**	2.03**	-0.61*	3.91**	0.12*	0.21	-2.38**	7.93*
UMI-1201	-2.31**	-1.39**	-1.76*	-3.99**	3.42	- 0.61*	2.24**	1.62*	0.10**	-2.24**	-0.06	4.61*
CML-72	1.00	1.62**	0.45	-6.01	-5.63*	-0.81	0.30	0.13*	-0.02	-2.73**	2.29**	12.71**
CML-32	- 1.38*	0.62	-1.24**	-12.94*	-4.96*	-1.12*	-0.29**	-2.11	-0.05*	0.27	-2.02**	-7.36
IML-187	0.31	-0.22	-0.45	-16.78**	15.82**	0.54	-1.13**	-0.34*	0.21	1.53**	3.79**	-14.73**
DMEL-68	- 0.89*	-0.06	-1.43**	-1.90*	3.61	-0.05**	0.05*	-0.43	0.02**	0.14	1.87**	5.24**
CML-551	-0.61	-1.22*	0.52	2.21	0.44	-0.53	-0.15	-1.44	-0.01	-0.91*	0.38*	-2.90**
LM-14	0.78	-1.31**	2.04	0.211	3.01	-0.64	0.51*	1.36*	0.15*	0.50	2.36**	2.75**
CML-425	-0.10*	-0.22	-0.23*	5.99	6.61	-0.45	-0.36	1.33	0.12**	2.25**	1.16*	14.92 **

*, ** Significant at 5 and 1 %, respectively
Where, DA= days to 50% anthesis, DS= days to 50% silking, DM= days to maturity, PH= plant height, EH= ear height, El= ear length, NKRE= No. of kernel rows per ear, NKR= No. of kernels per row, ED= ear diameter, GW= 100 grain weight, SP= shelling percentage, GYP= grain yield per plant

Table 3. Estimates of general combining ability effects of testers used in F1 crosses for grain yield and other characters in maize

TESTERS	DA	DS	DM	PH	EH	EL	NKRE	NKR	ED	GW	SP	GY
CML-451	-1.31**	-1.42 **	1.12	-5.89*	0.7	0.42**	0.06**	0.02*	0.1*	2.73**	-1.41**	2.40**
BML-6	0.81	1.62**	1.43	-6.51*	-2.72**	-0.26*	0.32	-0.36	-0.00	1.50**	1.96**	-3.91**
LM-13	0.41	-0.21	-0.54**	0.52	2.02	-0.14	-0.33*	0.33	-0.14*	-1.27**	-0.55**	1.53**
S.E.g_i (Lines)	±0.52	±0.51	±0.63	±4.6 1	± 3.41	± 0.55	± 0.31	± 1.33	±0.11	±0.42	±0.13	±0.73
S.E.g_i g_j (Lines)	±0.71	±0.61	±0.76	±6.39	±4.82	±0.81	±0.42	±1.89	±0.16	±0.60	±0.18	±1.10
S.E. g_i (Testers)	±0.31	±0.23	±0.43	±2.51	±1.91	±0.23	±0.21	±0.73	±0.06	±0.24	±0.05	±0.42
S.E.g_i g_j (Testers)	±0.40	±0.33	±0.62	±3.53	±2.64	±0.42	±0.2	±1.03	±0.08	±0.32	±0.08	±0.60
No. of parents showing desirable gca effects	5	5	4	6	4	4	5	5	5	4	6	7

*, ** Significant at 5 and 1 %, respectively
Where, DA= days to 50% anthesis, DS= days to 50% silking, DM= days to maturity, PH= plant height, EH= ear height, El= ear length, NKRE= No. of kernel rows per ear, NKR= No. of kernels per row, ED= ear diameter, GW= 100 grain weight, SP= shelling percentage, GYP= grain yield per plant

positive GCA effect, followed by CML-72 and UMI-1200. These lines can be directly employed as parents for developing high-yielding single-cross hybrids. UMI-1201 exhibited a highly significant positive value for the number of kernel rows per ear and was a strong combiner for maturity-related traits. DMEL-68 significantly contributed to increased shelling percentage and ear diameter. For flowering traits, both BML-7 and UMI-1201 displayed highly significant negative GCA effects, which is in line with the findings of Desai and Singh (2001) who emphasized the importance of negative GCA estimates for characterizing parents as good combiners for traits like days to 50 percent tasseling and days to 50 percent silking. CML-32 and IML-187 showed desirable GCA effects for morphological traits such as plant height and ear height. UMI-1201 was identified as the best combiner for kernel rows per cob, which was also indicative of the highest and desirable combining ability for kernels per row and 100-grain weight. For 100-grain weight, CML-425 displayed the most significant positive GCA effect, followed by IML-187 and UMI-1201.

Specific combining ability (SCA) effects

The estimates of specific combining ability effects for the thirty crosses across various traits, as presented in Table 3, revealed that none of the cross combinations exhibited high SCA effects for all the traits. However, some crosses exhibited highly significant and desirable SCA effects, including BML-7 × LM-13 and DMEL-68 × BML-6 for

Table 4. Estimates of specific combining ability effects for grain yield and other characters in maize

Crosses	DA	DS	DM	PH	EH	EL	NKRE	NKR	ED	GW	SP	GY
BML-7 × CML-451	2.44*	- 2.81**	-1.76	-0.91	-4.08	-0.50	0.24	2.12*	0.20	-1.40	2.53**	-9.1**
BML-7 × BML-6	-0.72	-1.19	3.06*	2.47	1.90	-0.98	-0.49	-1.48	0.10	2.19*	2.14**	8.36**
BML-7 ×LM-13	-1.80**	-1.55*	8.00**	-1.52**	-2.12**	1.47**	0.32	-0.60	-0.21	-0.80	4.67**	0.72
UMI-1200 × CML-451	-1.60	-2.92**	4.63*	9.56	-4.08	0.46	-0.27	-2.03	0.14	0.91	1.25**	23.50**
UMI-1200 × BML-6	1.80*	2.13*	-1.96*	-12.52	-2.89*	1.51	1.45	2.07*	-0.08	-0.40	0.96**	-9.12**
UMI-1200 × LM-13	-0.30	0.81	3.40**	2.97	1.12	-1.92*	-1.18*	-0.02	-0.04	-0.52	-2.21**	-14.38**
UMI-1201 × CML-451	0.10	0.11	-5.03**	0.40	-1.72	-1.98*	0.12	-2.76	0.14**	0.23	1.21**	7.37**
UMI-1201 × BML-6	0.10	2.62**	1.83	-6.21*	-4.22	1.90*	-1.06	-0.93	-0.22	-0.70	-1.04**	-12.32**
UMI-1201 × LM-13	-0.10	-2.72**	-6.43**	5.81	5.89	0.11	0.89	3.84*	0.11**	0.47	-0.17	4.97**
CML-72 × CML-451	-0.61	0.11	-0.26	5.90	-7.54*	0.71	0.20	-3.28	0.13	2.16*	3.03**	5.22**
CML-72 × BML-6	-1.21**	-2.37**	-4.20**	-0.20	2.33	-0.50	-0.58	1.44	0.12	-0.69	-1.68**	-1.82
CML-72 × LM-13	1.74*	2.30**	-2.10**	-5.70	5.12	-0.25	0.38	1.83	0.07*	-1.46*	-1.35**	-3.39**
CML-32 × CML-451	-0.60	0.61	1.64	4.23	4.09	0.50	-0.45	-0.17	-0.10	-1.21	-1.2**	-5.84**
CML-32 × BML-6	-0.70	-1.90*	0.43*	-5.38	-2.38	-0.43	-0.85	-2.91	0.04	1.25	0.91**	10.80**
CML-32 × LM-13	1.21	1.32	-1.24	1.11	-1.68	-0.05	1.28*	3.09*	0.2	-0.0	0.55*	-5.05**
IML-187 × CML-451	-0.91	-1.61*	0.46	0.73	1.33	1.14*	0.21	0.01	-0.13	0.50	-2.14*	4.18**
IML-187 × BML-6	-1.50*	-1.03	1.45*	6.63	-1.89*	-0.40	0.89	-1.10	0.02	-1.28	1.17**	-5.55**
IML-187 × LM-13	2.40*	2.62**	1.79	-7.42	-3.29	-0.75	-1.12*	1.10	0.10	0.780	-0.326	1.378*
DMEL-68 × CML451	-1.08**	0.24	1.35	-6.30	0.69	-0.18	0.79	-1.24	0.02**	-1.629*	-0.687**	-3.884**
DMEL-68 × BML-6	- 1.82**	0.80	-3.15**	-8.40	1.69	0.08	-1.60*	1.24	0.07	-0.469	1.165**	-11.526**
DMEL-68 × LM-13	-0.80	-1.13	2.18*	14.62*	-2.51	0.17	0.77	0.07	-0.08	2.096*	0.269	15.407**
CML-551 × CML451	-0.90	-1.61*	-5.00**	6.22	-0.39	-0.13	-0.96	1.48	0.10	1.700*	4.298**	4.529**
CML-551 × BML-6	2.51**	3.53	-3.22**	-3.94	4.09	-0.93	1.89**	3.76*	-0.15	-2.104*	-4.757**	-13.600**
CML-551 × LM-13	-1.62	-1.92*	5.23**	-2.41	-3.65	1.03	-0.87	-5.18**	0.04	0.432	-2.902**	9.069**
LM-14 × CML-451	-0.07	-0.12	1.09	-1.81	-2.39	0.41	0.12	2.61	-0.03	0.578	1.899**	-1.137
LM-14 × BML-6	-0.68	-0.52	-0.31	7.14	1.58	-0.73	-0.22	1.02	0.10**	1.800*	0.879**	16.720**
LM-14 × LM-13	- 0.74*	0.62	7.19**	-5.43	0.78	0.33	0.12	-3.64*	-0.05	-1.290	-0.158	-25.580**
CML-425 × CML451	-1.32	2.42**	-3.38**	-18.09*	13.89**	-0.43	-0.04	3.35*	-0.17*	-0.780	-1.496**	-13.830**
CML-425 × BML-6	0.84	-2.01*	6.42**	20.30*	-10.05**	0.50	0.69	-3.00*	0.10	1.379**	1.543**	17.980*
CML-425 × LM-13	0.43	-0.40	1.61	-2.20	-3.85	-0.08	-0.65	-0.33	0.05*	0.397	-1.547*	6.850**
SE (S_{ij})	±0.85	±0.73	+0.65	±7.91	±3.94	±0.93	±0.60	±1.52	±0.19	±0.749	±0.264	±1.279
SE ($S_{ij} – S_{ik}$)	±1.21	±1.04	1.31	±1.15	±5.49	±1.34	±0.87	±2.15	±0.28	±1.064	0.483	±1.820
No of crosses showing desirable sca effects	5	9	8	5	2	5	5	4	6	6	12	13

*, ** Significant at 5 and 1 %, respectively
Where, DA= days to 50% anthesis, DS= days to 50% silking, DM= days to maturity, PH= plant height, EH= ear height, El= ear length, NKRE= No. of kernel rows per ear, NKR= No. of kernels per row, ED= ear diameter, GW= 100 grain weight, SP= shelling percentage, GYP= grain yield per plant

days to 50 percent tasseling, UMI-1200 × CML-451, BML-7 × CML-451, CML-72 × BML-6 for days to 50 percent silking, UMI-1201 × LM-13 and UMI-1201 × CML-451 for days to maturity, BML-7 × LM-13, UMI-1201 × BML-6, and CML-425 × CML-451 for plant height, BML-7 × LM-13, UMI-1200 × BML-6, CML-72 × CML-451, IML-187 × BML-6, and CML-425 × BML-6 for ear height, BML-7 × LM-13, UMI-1200 × BML-6, and IML-187 × CML-451 for ear length, CML-32 × LM-13 and CML-551 × BML-6 for kernel rows per cob, BML-7 × CML-451, UMI-1200 × BML-6, UMI-1201 × LM-13, CML-32 × LM-13, CML-551 × BML-6, and

CML-425 × CML-451 for kernels per row, UMI-1201 × CML-451, UMI-1201 × LM-13, CML-72 × LM-13, DMEL-68 × BML-6, LM-14 × BML-6, and CML-425 × LM-13 for ear diameter, BML-7 × BML-6, CML-72 × CML-451, DMEL-68 × LM-13, CML-551 × CML-451, and LM-14 × BML-6 for 100-grain weight, BML-7 × LM-13, UMI-1200 × CML-451, UMI-1200 × BML-6, UMI-1201 × CML-451, CML-72 × CML-451, CML-32 × BML-6, IML-187 × BML-6, CML-551 × CML-451, CML-32 × LM-13 for shelling percentage, and BML-7 × BML-6, UMI-1200 × CML-451, UMI-1201 × CML-451, UMI-1201 × LM-13, CML-72 × CML-451, CML-32 × BML-6, IML-187 × CML-451, IML-187 × LM-13, DMEL-68 × LM-13 for grain yield per plant.

In assessing the performance of parents based on general combining ability, it was noted that many of the specific cross combinations resulted from crosses between low × high, low × low, low × average, high × high, or high × average general combiners. Among these crosses, CML-425 × LM-13 and LM-14 × BML-6, which exhibited the highest positive SCA effect for yield, involved high × low combiners, while UMI-1201 × LM-13 involved high × high combiners, and CML-32 × LM-13 involved low × high combiners, suggesting that the involvement of at least one strong general combiner is crucial for achieving favorable specific combinations. These results are consistent with the findings of several researchers (Dass *et al.,* 1997; Aguiar *et al.,* 2003; Asif *et al.,* 2007), emphasizing the superiority of crosses involving high × high, high × average, and average × average combiners as parents, possibly due to the concentration and interaction of favorable alleles contributed by the parents. Crosses involving low × high or low × average combiners as parents may result in the interaction between positive alleles from good or average combiners and negative alleles from poor combiners, leading to high yields. Cross combinations involving low × low general combiners could be attributed to overdominance and epistasis. In conclusion, our findings demonstrate significant differences among lines and line × testers for all the traits, indicating the potential for selection to improve yield and yield-related traits. Among the parents, CML-425, followed by CML-72 and DMEL-68, exhibited highly desirable GCA effects for grain yield per plant and are promising candidates for the development of hybrids. Notably, crosses such as UMI-1200 × CML-451 demonstrated superior combinations with highly significant and positive SCA values, followed by CML-425 × BML-6 for grain yield per plant, making them valuable for future hybrid breeding programs aimed at achieving a substantial improvement in maize production.

References

Abuali, A. I., Abdelmulla, A. A., Khalafalla, M. M., Idris, A. E. & Osman, A. M. (2012). Combining ability and heterosis for yield and yield components in maize (*Zea mays* L.). *Australian Journal of Basic and Applied Sciences,* **6**(10): 36-41.

Asif, M. I., Nehvi, F. A., Wani, S. A., Qadir, R. & Dar, Z. A. (2007). Combining ability for grain yield and yield related traits in maize. (*Zea mays* L.). *International Journal of Agricultural Sciences,* **27**: 101-105

Aguiar, A. M., Carlini-Garcia, L. A., Silva, A. R. Santos, M. F., Garcia, A. A. F. & Souja, J. R. (2003). Combining ability of inbred lines of maize and stability of their respective single-crosses. *Scientia Agricricola,* **60**: 83-89.

Betran, F. J., Beck, D., Banziger & Edmeades, G. O. (2003). Genetic analysis of Inbred and hybrid grain yield under stress and non-stress environments in Tropical maize. *Crop Science*, **43**: 807-817.

Dubey, R. S. (1975). Combining ability in cigar filter tobacco. *Indian Journal of Genetics,* **35**: 76-82.

Dass, S., Ahuja, V. P. & Singh, M. (1997). Combining ability for yield in maize. *Indian Journal of Genetics and Plant Breeding,* **57**(1): 98-100.

Economic Survey of the year. (2020-2021). Top Maize-Producing States in India: Production, Uses, and Global Comparison.

FAO STAT. (2020). Food and Agriculture Organization Corporate Statistical Database (FAOSTAT) online database.

Joshi, V. N., Dubey, R. B. & Marker, S. (2002). Combining ability for polygenic traits in early maturity hybrids of maize (*Zea mays* L.). *Indian Journal of Genetics and Plant Breeding,* **62**: 312-315.

Joshi, V. N., Pandiya, N. K. & Dubay, R. B. (1998). Heterosis and combining ability for quality and yield in early maturity single cross hybrids in maize (*Zea mays* L.). *Indian Journal of Genetics and Plant Breeding*, **58**(4): 519-524.

Jha, P. B. & Khehra, A. S. (1992). Evaluation of maize inbred lines derived from two heterotic populations. *Indian Journal of Genetics and Plant Breeding*, **52**(2): 126-131.

Kempthorne, O. (1957). An Introduction to Genetic Statistics. John Wiley and Sons, Inc. New York, USA, pp 468-473.

Kanagarasu, S., Nallathambi, G. & Ganesan, K. N. (2010). Combining ability analysis for yield and its component traits in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding,* **1**(4): 915-920.

Kling, I. G. (1991). Quality and Nutrition of Maize; IITA Research Guide 33. Ibadan: *International Institute of Tropical Agriculture,* pp 9–21.

Sharma, J. K. & Bhalla, S. K. (1993). Combining ability for some drought tolerant characters in maize (*Zea mays* L.) *Indian Journal of Genetics and Plant Breeding*, **53**(1): 79-84.

Sharma, S., Narwal, R., Kumar, M. S. & Dass, S. (2004). Line x tester analysis in maize (*Zea mays* L.). *Forage Research,* **30**: 28-30.

Singh, P. K., Singh, A. K., Shahi, J. P. & Ranjan, R. (2012). Combining ability and heterosis in quality protein maize. *The Bioscan,* **7**(2): 337-340.

United States Department of Agriculture, (2020). Foreign Agricultural Services. World Agricultural Production. https://www.fas.usda.gov

Vasal, S. K., Srinivasan, G., Gonzalez, C. F., Beck, D. L. & Crossa, J. (1993). Heterosis and combining ability of CIMMYT's quality protein maize germplasm II. Subtropical. *Crop Science,* **33**(1): 51-57.

Xiao, Y., Jiang, S., Cheng, Q., Wang, X., Yan, J., Zhang R., Qiao, F., Ma, C., Luo, J., Li, W., Liu, H., Yang, W., Song, W., Meng, Y., Warburton, L. M., Zhao, J., Wang, X. & Yan, J. (2021). The genetic mechanism of heterosis utilization in maize improvement (*Zea mays* L.). *Genome Biology,* **22**(1): 1-29.