

Estimation of combining ability and gene action in field corn (*Zea mays*) using line $\times$ tester analysis

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Abstract The study investigates the combining ability and gene action for yield and related traits in maize using a line $\times$ tester mating design. Eight inbred lines and five testers were evaluated to understand the genetic control of key agronomic traits. The analysis revealed that specific combining ability (SCA) played a more significant role than general combining ability (GCA), indicating the predominance of non-additive gene actions, particularly over-dominance. The findings suggest that heterosis breeding is a promising strategy for improving maize yield and related traits. Significant variability in SCA effects across hybrids highlighted the importance of specific parental combinations. Notably, hybrids IGI-22-58 $\times$ VL1055 and IGI-22-17 $\times$ ZL135440 demonstrated superior performance, making them strong candidates for commercial use and further breeding efforts. The study underscores the importance of selecting parental lines with desirable GCA effects while focusing on hybrid combinations with strong SCA effects to maximize breeding outcomes. This research provides valuable insights for maize breeding programs, emphasizing the need to prioritize non-additive genetic effects to achieve substantial genetic gains.

Keywords: GCA • SCA • Combining ability • line $\times$ tester

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Introduction

Maize (*Zea mays* L.) is the most widely distributed crop in the world, being a versatile crop, it adapts easily to a wide range of environments. Archaeological records suggest that domestication of maize began at least 6000 years ago, occurring independently in regions of the southwestern United States, Mexico and Central America (Mangelsdorf, 1974). In India, maize is the third most important cereal after rice and wheat that provides food, feed and serves as a source of basic raw material for the number of industrial products, viz. starch, protein, oil, alcoholic beverages, food sweeteners, cosmetics, bio-fuel, etc. The kernel can be consumed as human food, fermented to produce a wide range of foods and beverages and fed to livestock. The leaves, stalks and tassels can be fed to livestock either green (in the form of fodder or silage) or dried (in the form of Stover). The roots can be used for mulching, incorporated into the soil to improve the physical structure and burned as fuel. Maize is also considered a primary staple food in many developing countries. It has highest genetic yield potential that's why it is referred as "Queen of Cereals".

Maize belongs to the tribe Maydeae of the grass family *Poaceae*. "Zea" (zela) was derived from an old Greek name for food grass. The genus *Zea* consists of four species of which *Zea mays* L. is economically important. The other *Zea* sp. referred to as teosintes, are largely wild grasses native to Mexico and Central America (Doeblay, 1990). The number of chromosomes in *Zea mays* is $2n = 20$. Tribe Maydeae comprises seven genera that are recognized, namely old and new world groups. Old world comprises *Coix* ($2n = 10/20$), *Chionachne* ($2n = 20$), *Sclerachne* ($2n = 20$), *Trilobachne* ($2n = 20$) and *Polytoca* ($2n = 20$) and new world group has *Zea* and *Tripsacum*. Many forms of

maize are used for food, sometimes classified as various subspecies related to the amount of starch each had. They are flour corn - *Zea mays* var. *amylacea*, Popcorn - *Zea mays* var. *everta*, Dent corn - *Zea mays* var. *indentata*, Flint corn - *Zea mays* var. *indurata*, sweet corn - *Zea mays* var. *saccharata* and *Zea mays* var. *rugosa*, Waxy corn - *Zea mays* var. *ceratina*, Pod corn - *Zea mays* var. *tunicata* and striped maize - *Zea mays* var. *japonica*.

Maize is a tall, monoecious, annual C₄ plant varying in height from 1.2 to 4.0 m tall. The sexes are partitioned into separate pistillate silk and staminate (tassel) flower. It has a determinate growth habit and the shoot terminates into the inflorescences bearing staminate flowers (Dhillon and Prasanna, 2001).

Maize is generally protandrous, the male flower matures earlier than the female flower, each male spikelet consists of a pair of glumes that comprises of two florets, each of which is enclosed by a lemma and palea and has two lodicules, three stamens and a rudimentary pistil. The ovary ends in a thread-like structure, the silk which is actually modified style and length may vary up to 45 cm. Pollen grains per anther have been reported to range from 2000 to 7500. With the wind-borne nature of the pollen and because of the 'monoecious' condition of plant and the 'protandry' nature of flower opening, the maize is considered a highly cross-pollinated crop (> 98% cross-pollination). The position of the lodicules indicates that they represent a whorl of flower parts outside that formed by the three stamens, maize cob is a syncarpous fruit and individual maize kernel is botanically a caryopsis. Typical maize plants develop 18 to 22 total leaves. Silk in maize plant appears about 55 days after emergence and matures around 125 days after emergence (Ritchie *et al.*, 1993). The specific time interval in between stages depend on genotype, environments, planting date and location.

The germ is the source of maize vegetable oil. The total oil content of maize kernel is 4 per cent by weight. the endosperm occupies about two-thirds of a maize kernel's volume and accounts for approximately 86 per cent of its dry weight. The water-free portion of maize kernel contains starch 77 per cent, sugar 2 per cent, protein 9 per cent, fat 5 per cent, pentosans 5 per cent and ash 2 per cent. There is greater variation among different varieties of maize in the content of protein and fat. The proportion of protein may be as high as 15 per cent and low as 6 per cent. About 80 per cent of the protein is available in the endosperm of the maize kernel.

The germ though constituting only 1/10 of the kernel contains about 1/5 of the total protein. Maize kernels contain three types of proteins viz., prolamins (soluble in alcohol chiefly zein), globulins (soluble in neutral salt solutions) and glutelin. The entire protein in maize is known to be low in quality because zein is deficient in tryptophan and lysine which are essential amino acids. More than 80 per cent of the fat is concentrated in germs. Yellow maize shows more vitamin A while white kernels have a lesser quantity, which is due to 'cryptoxanthin'. Maize is fairly rich in Thiamine and more riboflavin is found in maize than rice.

Maize is the most important crop, being grown in over 166 nations throughout the world, in tropical, subtropical and temperate climates and at elevations ranging from sea level to 3000 meters above sea level. Worldwide maize grown on 207.25 million hectare (MH) with total production of 1217.31 million metric tonnes (MMT) and productivity is 5.87 metric tonnes (MT), with a greater range of soil, climate, biodiversity and management approaches, accounting for 37 per cent of global kernel production (Anonymous, 2024). The United States of America (USA) is the world's largest producer of maize, accounting for 30 per cent of global production and maize is recognized as the foundation of the US economy. In the year 2021-2022 in INDIA maize is grown on 10.04 MH with 33.62 MT production and productivity is 3349 kg/hac. (Anonymous, 2024). Gujarat contributes approximately 5 per cent of India's total production, with a total production of 6.67 lakh tonnes in the year 2020–21. The total area under cultivation was 3.88 lakh ha. giving productivity of 1716.32 kg/ha. It is grown primarily in the Panchmahal, Dahod, Chhotaudepur, Mahisagar and Arvalli district of Gujarat (Directorate of Agriculture, 2023)

In any breeding program, knowledge of gene action for yield and yield-contributing character is necessary to plan and adopt appropriate selection techniques. Combining ability analysis is crucial for identifying superior parental combinations for hybridization. GCA reflects additive gene effects, while SCA indicates non-additive genetic interactions (Hallauer *et al.*, 2010). Understanding these genetic parameters is essential for deciphering the inheritance patterns of key agronomic traits and developing effective breeding strategies aimed at enhancing crop yield and resilience. This study aims to estimate the combining ability and gene action for yield and its related traits in maize, with the goal of identifying potential parental lines

that can contribute to the development of high-yielding, climate-resilient maize varieties. The findings will provide valuable insights into the genetic mechanisms underlying key yield-contributing traits, facilitating the advancement of maize breeding programs.

Contemporary maize breeding has significantly advanced through the adoption of genomic selection, cutting-edge phenotyping technologies and molecular breeding techniques. These tools have greatly improved our ability to predict combining ability and heterosis with precision. When combined with collaborative breeding efforts and the global exchange of diverse germplasm these innovations offer unprecedented opportunities to develop superior hybrids tailored to specific environments and farming systems. Furthermore, identifying key yield components such as kernel number per ear and kernel per row as central drivers of heterosis has helped breeders focus their selection strategies more effectively, paving the way for enhanced hybrid performance (Bernardeli *et al.*, 2025). Despite significant progress in understanding heterosis mechanisms and combining ability concepts several challenges remain in optimizing hybrid maize breeding programs. Key difficulties include improving the accuracy of prediction models for hybrid performance across diverse environments gaining deeper insights into genotype-by-environment interactions and developing efficient breeding methods that can rapidly integrate exotic genetic material while maintaining adaptation to target growing regions. Additionally with the growing need to produce climate-resilient hybrids that exhibit enhanced stress tolerance and improved nutritional quality, it is increasingly important to evaluate both traditional agronomic traits and emerging characteristics performance, estimation of genetic parameters and analysis of combining ability effects, this research seeks to identify superior parental combinations and elucidate the genetic basis of heterosis. The findings will provide valuable insights to refine hybrid maize breeding strategies, ultimately contributing to sustainable maize production systems tailored to evolving agricultural challenges.

Materials and methods

Experimental material

The evaluation of genetic parameters was carried out through line × tester matting design, with eight lines and

five testers. The research work was carried out at MMRS, AAU, Godhra, Gujarat. Crossing of genotypes done through hand emasculation and pollination in *Kharif*-2023. Table 1 provides information regarding experimental materials utilized for study. Evaluation trial conducted during *Rabi* 2023-24, all 40 single cross hybrids along with 13 parental genotypes were planted in Randomized Complete Block Design (RBD), with three replications at MMRS, AAU, Godhra. The genotypes were grown at 60 × 20 cm spacing and two row(s) considered as a plot (row length 4.0 m). Measurements for various quantitative traits in maize were taken from five randomly selected tagged plants per plot, except for the 100 kernels weight, which was measured separately. Plant height (PH) (cm) was recorded from the base of the plant to the base of the tassel. Cob girth (CG) (cm) and cob length (CL) (cm) were measured after dehusking, with girth taken at the point of maximum diameter and length measured from the base to the tip. Cob weight (CW) (g) was determined by weighing dehusked cobs at maturity. The number of kernel rows per cob (NR) and numbers of kernels per row (NKR) were counted on five randomly selected cobs. Shelling percentage (SP) was calculated by comparing the weight of five ears to their shelled grain weight. The weight of 100 kernels was recorded using an electric balance, and kernel yield per plant (KYP) (g) was measured after drying and shelling the kernels.

Table 1. List of parents and its source

S.No.	Parents	Source
<i>Lines</i>		
1.	IGI-22-06	MMRS, Godhra
2.	IGI-22-07	
3.	IGI-22-15	
4.	IGI-22-17	
5.	IGI-22-18	
6.	IGI-22-48	
7.	IGI-22-57	
8.	IGI-22-58	
<i>Testers</i>		
1.	CML-451	Procured from CIMMYT, Hyderabad
2.	VL1055	
3.	ZL135437	
4.	ZL135440	
5.	ZL153494	

Statistical analysis

The statistical analysis was performed using a line $\times$ tester mating design, following Kempthorne's (1957) methodology. This design enabled the estimation of general combining ability (GCA) and specific combining ability (SCA), crucial for understanding gene actions in maize. Analysis of variance (ANOVA) was used to assess the significance of effects due to lines, testers, and their interactions, with the F-test applied at 5% and 1% significance levels.

GCA and SCA effects were calculated to evaluate overall performance and specific hybrid combinations, respectively. The relative magnitudes of GCA and SCA variances were used to determine the predominant gene actions. Higher GCA variance indicated a significant role of additive gene action, while higher SCA variance suggested the importance of non-additive effects, including dominance.

All analyses were conducted using SAS, ensuring the validity of ANOVA assumptions. The results were interpreted based on the significance of combining ability estimates, in line with established practices in plant breeding research (Griffing, 1956; Falconer 1996).

Results and discussion

Analysis of variance for combining ability (ANOVA)

Genetic variance components for combining ability were assessed through variance analysis, dividing the mean squares for hybrids into line, tester and line $\times$ tester components. The results, detailed in Table 2. Lines showed significant effects across all traits, while testers were significant for all but cob length. The line $\times$ tester interaction was highly significant for yield traits, underscoring the hybrids differs significantly. Specific combining ability (σ^2_{SCA}) was highly significant for all traits as compared to general combining ability, emphasizing the importance of non-additive variance.

The ratio of GCA to SCA variance ($\sigma^2_{GCA}/\sigma^2_{SCA}$) was less than one across all traits, including plant height, cob girth, cob length, cob weight, number of kernel rows, number of kernels per row, 100 kernel weight, shelling percentage and kernel yield per plant indicating a predominance of non-additive gene actions. The higher dominance variance across all traits suggests that their improvement would be better pursued through heterosis breeding.

Table 2. Analysis of variance for combining ability

Sources of variation	df	PH	CG	CL	CW	NR	NKR	SP	HKW	KYP
Replication	2	56.11*	0.41	4.93**	70.61*	0.03	6.36	2.10	0.43	103.8
Lines	7	649.86**	3.33**	6.12**	1908.3**	0.53**	44.21**	15.96**	93.02**	1194.17**
Testers	4	838.36**	4.91**	1.32	3069.36**	1.13**	24.84**	3.28*	44.17**	1041.71**
Lines $\times$ Testers	28	389.58**	2.89**	8.92**	1816.17**	1.08**	34.37**	8.4**	57.8**	1701.66**
Error	78	17.43	0.17	0.87	19.00	0.10	3.82	1.06	0.72	39.01
$\sigma^2_{gca}(\text{lines})$	-	17.35	0.03	-0.19	6.14	-0.037	0.66	0.50	2.35	-33.83
$\sigma^2_{gca}(\text{testers})$	-	18.7	0.08	0.32	52.22	0.002	-0.40	-0.21	-0.57	-27.50
σ^2_{gca}	-	18.18	0.06	-0.27	34.5	-0.013	0.01	0.06	0.55	-29.93
σ^2_{sca}	-	124.05**	0.91**	2.68**	599.06**	0.327**	10.1833**	2.45**	19.03**	554.22**
$\sigma^2_{gca}/\sigma^2_{sca}$	-	0.147	0.066	-0.101	0.058	-0.040	0.001	0.024	0.029	-0.054
σ^2_A	-	72.72	0.25	-1.07	137.98	-0.051	0.032	0.25	2.21	-119.74
σ^2_D	-	496.2	3.63	10.73	2396.23	1.307	40.73	9.79	2.21	-119.74
Degree of dominance	-	2.61	3.79	-	4.17	-	35.79	6.25	76.11	2216.87

*, ** Significant at 5% and 1% levels of probability, respectively, PH- Plant height (cm), CG- Cob girth (cm), CL- Cob length (cm), CW- Cob weight (g), NR- Number of rows per cob, NK- Number of kernels per row, SP- Shelling percentage, HKW- Hundred kernel Weight (g), KYP- kernel yield per plant (g)

Combining ability analysis

This study analysed combining ability (Table 3) and gene action in maize using a line by tester mating design to understand key agronomic traits. The results shed light on genetic control and the suitability of various lines and testers in breeding programs.

The analysis of GCA effects for various traits in corn highlights the additive genetic potential of specific lines and testers. For PH, negative GCA effects are desirable as they contribute to shorter plants, which are often preferred in breeding programs. Lines IGI-22-18, IGI-22-58, and IGI-22-48 showed significantly negative GCA effects, marking them as good general combiners for reducing plant height. Conversely, lines IGI-22-17, IGI-22-57, and IGI-22-07 had positive GCA effects, categorizing them as poor general combiners for this trait. Among the testers, CML-451 and ZL135437 exhibited significantly negative GCA effects, making them desirable for reducing plant height, while VL1055 and ZL153494 had positive effects, identifying them as less suitable parent for reduction of plant height. For CG, lines IGI-22-17 and IGI-22-07 were good general combiners due to their positive GCA effects, whereas lines IGI-22-57, IGI-22-18, and IGI-22-48 were poor combiners with negative

effects. Similarly, testers ZL153494 and VL1055 were good general combiners, while ZL135437 and ZL135440 were poor. In terms of CL, lines IGI-22-06 and IGI-22-48 were good combiners with positive GCA effects, but IGI-22-57 and IGI-22-07 were poor combiners with negative effects. Testers ZL135440 and VL1055 showed average combining ability, while ZL135437 and ZL153494 were poor. For CW, positive GCA effects were observed in lines IGI-22-07, IGI-22-17, and IGI-22-06, making them good combiners, while IGI-22-57, IGI-22-48, and IGI-22-18 were poor. Testers VL1055, ZL135440, and ZL153494 were good combiners, while ZL135437 and CML-451 were poor. Regarding the NKR, lines IGI-22-48 and IGI-22-18 were good combiners, while IGI-22-57 was poor. Testers CML-451 and VL1055 were good, while ZL135437 was poor. For SP, lines IGI-22-18, IGI-22-06, and IGI-22-58 were good combiners, whereas IGI-22-57, IGI-22-17, and IGI-22-07 were poor. Tester ZL135437 was a good combiner, while CML-451, ZL135440, and VL1055 were poor. For HKW, lines IGI-22-58, IGI-22-57, and IGI-22-06 were good combiners, while IGI-22-18, IGI-22-48, and IGI-22-15 were poor. Testers ZL153494 and VL1055 were good, while ZL135440 and CML-451 were poor. Finally, for KYP, lines IGI-22-17, IGI-22-07, IGI-22-06, and IGI-22-58 were

Table 3. Effects of the general combining ability (gca) effects

Single Crosses	KYP	PH	CG	CL	CW	NR	NKR	SP	HKW
<i>Line</i>									
IGI-22-06	4.17*	0.60	-0.18	0.83**	10.17**	-0.18*	0.17	1.02**	0.72**
IGI-22-07	7.28**	2.78*	0.45**	-0.81**	12.59**	0.22**	-0.17	-0.77**	-0.01
IGI-22-15	-4.13*	0.74	-0.08	-0.32	1.88	-0.05	-0.70	-0.29	-3.86**
IGI-22-17	10.00**	9.92**	0.88**	-0.04	12.43**	-0.18*	0.30	-1.16**	-0.43
IGI-22-18	1.18	-11.68**	-0.42**	0.06	-6.60**	-0.18*	1.63**	1.54**	-0.69**
IGI-22-48	-4.14*	-2.71*	-0.38**	0.7**	-9.53**	0.22**	2.5**	0.05	-1.98**
IGI-22-57	-18.32**	5.30**	-0.43**	-0.86**	-18.11**	0.22**	-3.3**	-1.18**	1.74**
IGI-22-58	3.96*	-4.94**	0.16	0.42	-2.83*	-0.05	-0.43	0.78**	4.51**
S. E. (gi)±	1.61	1.08	0.11	0.24	1.13	0.08	0.50	0.27	0.22
<i>Testers</i>									
CML-451	-2.33	-7.03**	0.01	-0.08	-2.60**	0.22**	1.09**	-0.40	-1.7**
VL1055	1.60	6.49**	0.41**	0.21	10.64**	-0.28**	1.01*	-0.07	1.09**
ZL135437	-8.35**	-5.3**	-0.66**	-0.23	-18.37**	-0.12	-1.2**	0.43*	0.02
ZL135440	-0.68	1.70	-0.19*	0.29	5.65**	-0.03	-0.24	-0.29	-0.95**
ZL153494	9.77**	4.15**	0.42**	-0.19	4.69**	0.22**	-0.66	0.33	1.55**
S. E. (gi)±	1.27	1.08	0.88	0.19	0.89	0.06	0.40	0.21	0.17
Range of GCA	Min.	-18.32	-11.68	-0.66	-0.86	-18.37	-0.28	-3.30	-1.18
for parents	Max.	10.0	9.92	0.88	0.83	12.59	0.22	2.50	4.51

good general combiners, while IGI-22-57, IGI-22-48, and IGI-22-15 were poor. Tester ZL153494 was a good combiner, while ZL135437 was poor. These results indicated the importance of carefully selecting parental lines with desirable GCA effects to optimize breeding outcomes for specific traits in corn.

The analysis of SCA effects for various traits in corn hybrids reveals significant variability, highlighting the importance of specific parental combinations. For PH, several hybrids demonstrated desirable negative SCA effects, with IGI-22-48 × CML-451, IGI-22-57 × ZL153494, and IGI-22-15 × VL1055 being the most notable. Conversely, hybrids such as IGI-22-58 × ZL135437 and IGI-22-15 × ZL135437 exhibited undesirable positive SCA effects, categorizing them as poor combiners. Regarding CG, the cross IGI-22-17 × ZL153494 stood out with the highest positive SCA effect, making it a good specific combiner, while IGI-22-17 × ZL135437 exhibited a significant negative SCA effect, identifying it as a poor combiner. For cob length (CL), IGI-22-17 × ZL135440 and IGI-22-48 × ZL153494 were recognized as good combiners due to their positive SCA effects, while IGI-22-18 × CML-451 and IGI-22-17 × ZL153494 were poor combiners due to their negative SCA effects. In terms of CW, IGI-22-48 × ZL153494 and IGI-22-57 × CML-451 were identified as good specific combiners, exhibiting the highest positive SCA effects, whereas hybrids like IGI-22-57 × ZL153494 and IGI-22-07 × ZL135437 were poor combiners with negative SCA effects. For the NR, IGI-22-18 × VL1055 and IGI-22-15 × VL1055 were good combiners with positive SCA effects, while IGI-22-18 × ZL135437 and IGI-22-17 × VL1055 were poor combiners with negative effects. For the NKR, hybrids like IGI-22-48 × ZL153494 and IGI-22-07 × VL1055 were good specific combiners with positive SCA effects, whereas IGI-22-48 × CML-451 and IGI-22-07 × ZL135437 were poor combiners due to negative SCA effects. Regarding SP, IGI-22-07 × ZL135440 and IGI-22-17 × CML-451 were recognized as good combiners with positive SCA effects, while IGI-22-57 × ZL135440 and IGI-22-58 × ZL153494 were poor combiners. For HKW, hybrids such as IGI-22-15 × ZL153494 and IGI-22-57 × CML-451 were good combiners with significant positive SCA effects, whereas IGI-22-15 × ZL135440 and IGI-22-57 × VL1055 were identified as poor combiners due to their negative effects. Finally, for the trait KYP, IGI-22-57 × CML-451 and IGI-

22-58 × VL1055 exhibited the highest positive SCA effects, making them good combiners, while IGI-22-07 × ZL135437 and IGI-22-58 × ZL153494 were poor combiners with significant negative effects. These findings highlighted the critical role of SCA in hybrid selection to achieve desirable traits in corn.

Gene actions

The gene action study (Table 2) revealed key insights into the genetic control of maize traits. For PH, the significant SCA variance (124.05) compared to GCA variance (18.18) and the low $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio (0.147) indicated predominant non-additive gene action and over-dominance, these results agreed with Abdulhamed *et al.* (2021) and Keerthana *et al.* (2023). Similarly, CG exhibited significant SCA variance (0.91) relative to GCA variance (0.06), with a ratio of 0.066 and an average degree of dominance (3.79), suggesting non-additive gene action and over-dominance (Bakala *et al.* 2018). Cob length showed significant SCA variance (2.68) and a negative GCA variance (-0.27), confirming non-additive gene action and over-dominance due to the higher σ^2D (10.73) compared to σ^2A (Keerthana *et al.* 2023). In CW, the significant SCA variance (599.06) and low $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio (0.058) indicated non-additive gene action with over-dominance, supported by a high average degree of dominance (4.17) and greater σ^2D (Panwar *et al.*, 2013). The number of kernels rows per cob had significant SCA variance (0.327) compared to GCA variance (-0.013), with an average degree of dominance indicating over-dominance (Dar *et al.* 2018). For the number of kernels per row, significant SCA variance (10.18) and a low $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio (0.001) suggested non-additive gene action and strong over-dominance (Mutlag *et al.* 2018). Shelling percentage showed significant SCA variance (2.45) over GCA variance (0.06), with a low $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio (0.024) indicating non-additive gene action and over-dominance (Dar *et al.* 2018). For HKW, significant SCA variance (19.03) and a low $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio (0.029) indicated non-additive genetic variance with over-dominance, as reflected by a high average degree of dominance (5.86) (Keerthana *et al.* 2023). Lastly, kernel yield per plant demonstrated significant SCA variance (554.22) over GCA variance (-29.93), with a negative GCA and a low $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio (-0.054) pointing to non-additive gene action and over-dominance (El Ghonemy *et al.* 2023).

Table 3. Effects of the specific combining ability (sca) effects

Single crosses		KYP	PH	CG	CL	CW	NR	NKR	SP	HKW
IGI-22-06 × CML-451		-4.78	7.92**	0.57*	1.32*	-15.88**	0.18	2.71*	-0.82	-5.81**
IGI-22-06 × VL1055		25.4**	-0.67	-0.17	0.93	12.08**	-1.32**	-0.88	0.24	1.02*
IGI-22-06 × ZL135437		5.74	-3.21	0.23	0.59	25.16**	0.52**	1.33	-1.7**	1.34**
IGI-22-06 × ZL135440		-23.47**	-2.17	-0.41	-0.73	-17.87**	0.43*	-2.63*	0.6	3.94**
IGI-22-06 × ZL153494		-2.89	-1.87	-0.22	-2.11**	-3.50	0.18	-0.54	1.68**	-0.50
IGI-22-07 × CML-451		-6.90	2.05	0.02	-0.09	0.18	-0.22	-1.96	-0.12	1.91**
IGI-22-07 × VL1055		6.63	-0.03	-0.21	0.01	-19.53**	0.28	4.46**	-2.32**	2.96**
IGI-22-07 × ZL135437		-39.65**	-2.31	-1.1**	-1.66**	-36.05**	0.12	-6.33**	-1.5*	-5.13**
IGI-22-07 × ZL135440		26.68**	-1.48	1.25**	-0.22	32.59**	0.03	2.38*	3.34**	2.06**
IGI-22-07 × ZL153494		13.23**	1.77	0.04	1.96**	22.82**	-0.22	1.46	0.60	-1.8**
IGI-22-15 × CML-451		23.25**	10.39**	-0.27	0.79	20.57**	0.05	2.91*	-1.75**	2.14**
IGI-22-15 × VL1055		-29.69**	-15.29**	1.39**	-0.84	-1.13	0.55**	-1.34	1.04	2.32**
IGI-22-15 × ZL135437		16.1**	16.42**	0.18	-0.36	4.06	0.38*	0.87	2.02**	-6.05**
IGI-22-15 × ZL135440		-14.42**	-9.23**	-0.14	-1.22*	-18.57**	-1.03**	-2.09	0.40	-7.16**
IGI-22-15 × ZL153494		4.76	-2.29	-1.15**	1.64**	-4.93	0.05	-0.34	-1.7**	8.76**
IGI-22-17 × CML-451		1.59	2.19	-0.12	1.05	11.13**	0.18	2.24	2.28**	-0.59
IGI-22-17 × VL1055		-29.15**	-10.23**	-1.35**	-0.85	-11.91**	-1.32**	-2.68*	-2.17**	-1.65**
IGI-22-17 × ZL135437		-13.7**	-0.44	-1.15**	-0.71	-34.15**	0.52**	-0.80	1.25*	-1.39**
IGI-22-17 × ZL135440		29.75**	8.04**	-0.54*	3.22**	8.88**	0.43*	1.24	-0.41	2.22**
IGI-22-17 × ZL153494		11.51**	0.43	3.16**	-2.71**	26.04**	0.18	-0.01	-0.95	1.41**
IGI-22-18 × CML-451		-17.9**	-8.45**	-0.27	-2.81**	-14.9**	0.18	-0.09	0.42	-5.42**
IGI-22-18 × VL1055		22.67**	12.75**	0.20	1.91**	22.72**	0.68**	0.66	0.63	4.15**
IGI-22-18 × ZL135437		8.28*	-10.2**	0.69**	0.52	14.00**	-1.48**	-3.47**	0.13	3.76**
IGI-22-18 × ZL135440		-18.38**	-7.65**	-0.20	-1.05	-1.83	0.43*	1.58	-0.96	-4.12**
IGI-22-18 × ZL153494		5.33	13.55**	-0.42	1.43**	-19.99**	0.18	1.33	-0.22	1.63**
IGI-22-48 × CML-451		-7.02	-16.97**	0.33	-0.73	-12.9**	-0.22	-63**	-1.53*	1.69**
IGI-22-48 × VL1055		-10.78**	13.09**	-0.56*	-0.77	1.00**	0.28	-0.21	-0.55	-4.42**
IGI-22-48 × ZL135437		8.93*	-12.83**	1.02**	-1.00	2.53	0.12	2.33*	0.72	3.42**
IGI-22-48 × ZL135440		-18.12**	0.55	-0.98**	-0.08	-14.76**	0.03	-2.29*	-0.55	1.18*
IGI-22-48 × ZL153494		26.98**	16.16**	0.20	2.57**	44.94**	-0.22	6.79**	1.91**	-1.86**
IGI-22-57 × CML-451		35.1**	15.6**	0.45	2.03**	15.00**	-0.22	2.84*	0.93	5.85**
IGI-22-57 × VL1055		-19.17**	-2.66	-0.03	-1.16*	-6.77**	0.28	-2.08	1.27*	-6.71**
IGI-22-57 × ZL135437		0.95	-4.09	-0.33	1.82**	6.81**	0.12	4.13**	-0.81	4.35**
IGI-22-57 × ZL135440		4.95	7.95**	0.74**	-1.17*	0.62	0.03	-0.49	-2.47**	0.63
IGI-22-57 × ZL153494		-21.83**	-16.81**	-0.83**	-1.53**	-36.81**	-0.22	-4.41**	1.08	-4.12**
IGI-22-58 × CML-451		-23.34**	-12.73**	-0.71**	-1.56**	-24.34**	0.05	-2.03	0.61	0.23
IGI-22-58 × VL1055		34.09**	3.04**	0.73**	0.77	24.35**	0.55**	2.06	1.86**	2.33**
IGI-22-58 × ZL135437		13.34**	16.66**	0.46	0.81	0.63**	-0.28	1.93	-0.10	-0.30
IGI-22-58 × ZL135440		13.01**	3.99	0.27	1.24*	10.93**	-0.37*	2.31*	0.05	1.25*
IGI-22-58 × ZL153494		-37.1**	-10.95**	-0.76**	-1.25*	-28.57**	0.05	-4.28**	-2.41**	-3.52**
Range	Minimum	-39.65	-16.97	-1.35	-2.81	-36.81	-1.48	-6.63	-2.47	-7.16
	Maximum	35.1	16.66	3.16	3.22	44.94	0.68	6.79	3.34	8.76
S.E. (Sij) ±		3.61	2.41	0.24	0.54	2.52	0.18	1.13	0.59	0.49
No. of significant crosses		29	22	18	20	32	14	17	17	35
Positive significant crosses		15	11	8	10	16	9	9	8	21
Negative significant crosses		14	11	10	10	16	5	8	9	14

*, ** Significant at 5% and 1% levels of probability, respectively, PH- Plant height (cm), CG- Cob girth (cm), CL- Cob length (cm), CW- Cob weight (g), NR- Number of rows per cob, NK- Number of kernels per row, SP- Shelling percentage, HKW- Hundred kernel Weight (g), KYP- kernel yield per plant (g)

Conclusion

This study highlights the dominance of specific combining ability over general combining ability in maize, indicating that non-additive gene action, particularly over-dominance, plays a key role in trait inheritance. This suggests that heterosis breeding is likely the most effective strategy for improving maize yield and related traits. The ratio of GCA to SCA variance was consistently less than one, further emphasizing the importance of non-additive genetic effects. This finding is consistent with the patterns observed in other crops, where non-additive gene action plays a critical role in trait expression under various environmental conditions. The analysis of GCA effects identified several lines, such as IGI-22-18 and IGI-22-06, as strong general combiners for key traits like plant height, cob girth, and kernel yield. These lines exhibit significant potential for contributing to hybrid combinations aimed at improving yield stability and resilience. In contrast, SCA analysis highlighted specific hybrid combinations that showed superior performance, such as IGI-22-17 × ZL135440 and IGI-22-48 × ZL 153494, which demonstrated significant positive SCA effects for kernel yield. Overall, the results underscore the importance of selecting parental lines with desirable GCA effects and focusing on specific hybrid combinations with strong SCA effects to maximize breeding outcomes in maize. The predominant non-additive gene action suggests that breeding programs should prioritize strategies that exploit heterosis to achieve significant genetic gains in yield and related traits. This study delivers actionable insights for maize breeding by identifying high yielding parental lines and guiding hybrid development. Future research should validate the stability of these results across varied agro climatic zones and environmental conditions

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