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RESEARCH ARTICLE

Investigation of combining ability in maize for enhancing grain yield and related agronomic traits

Abdullah[1], M. Aslam[1], F. Gul[2], M. S. Akram[1], A. Khadim[2], A. Sattar[2], M. Z. Ul Din Haider[1], Abdurrehman[3]

1 Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad 38000 Pakistan

2 Department of Botany, University of Agriculture, Faisalabad 38000 Pakistan

3 Bahauddin Zakariya University, Multan, 60000 Pakistan

Corresponding author's email: ahelkarabdullah@gmail.com

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Abstract

Maize (*Zea mays* L.) is a staple cereal crop of strategic importance owing to its wide adaptability, short growth cycle and high genetic potential. However, maize productivity in Pakistan remains suboptimal, necessitating the identification of genetically superior hybrids to improve yield. This study was conducted to evaluate the combining ability of maize genotypes for yield and associated traits through Line × Tester analysis. Five inbred lines and five testers were crossed to generate 25 F_1 hybrids, which were evaluated for plant height, ear height, cob length, stem diameter, number of seed rows, 100-grain weight, internodal length and other morphological traits during the 2024 spring season at the University of Agriculture, Faisalabad. Highly significant differences were observed among crosses, lines, testers and their interactions for most traits, indicating substantial genetic variability. Line GB-5 and tester SB-10 exhibited strong general combining ability for key yield traits, whereas crosses such as GB-3 × SB-8 and GB-2 × SB-10 showed high specific combining ability, suggesting non-additive gene action plays a major role in trait expression. The significance of replication effects for traits such as plant height and seed row number confirmed environmental consistency in trait performance. Traits such as cob diameter and number of seed rows were strongly linked with plant and ear height, implying that vegetative vigor contributes to yield potential. Internodal length was positively associated with stem diameter and number of seed rows, highlighting its contribution to reproductive efficiency. These findings emphasize the potential of identified parents and crosses for hybrid development. The genetic diversity and significant GCA and SCA effects reported can guide breeders in selecting promising combinations to enhance maize yield in Pakistan's agro-climatic conditions.

Keywords: Line × Tester analysis, correlation, yield, variability, heterosis

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops worldwide and plays a significant role in economic development and human nutrition (Zahn, 2018).

Native to the Americas, it has been spread into various agroclimatic zones and is a staple food in many areas. As a "queen of cereals", maize ranks behind wheat and rice in global production as a food crop because of its high photosynthetic efficiency, adaptability and short growing season (Rojas *et al.*, 2020). It is an important food crop in poorer countries and a vital component of livestock feed, industrial food processing and bio-based applications in more modern economies (Lone *et al.*, 2021). Maize production has been rapidly increasing in Pakistan because of its adaptability to rabi and kharif seasons and increased demand for poultry, starch and wet milling industries. The full yield potential of maize in Pakistan has not yet been realized, as the country still relies on old open-pollinated varieties and lacks the modern technology-driven plant breeding (Rajpal et al., 2023). Significant developments at the global level have improved maize productivity through the utilization of its genetic resources. Advancements include molecular marker-assisted selection, genome editing (such as CRISPR/Cas9) and precision phenotyping technologies, which have led to the development of new and more resistant hybrids to environmental stresses (Lopes *et al.*, 2023). Classical plant breeding techniques are the basis for assessing general and specific combining ability (GCA and SCA) that are essential in selecting high-yielding hybrids, in particular to the Line × Tester and Diallel analyses (Aly *et al.*, 2023). In addition, agronomic characters like days to maturity, ear position and kernel type are frequently evaluated to determine yield stability and adaptability (Makumbi *et al.*, 2011). In the last few years, the use of correlation and path studies has been increasingly used to identify important traits that contribute directly or indirectly to grain yield and provide more efficient genotype selection (Yahaya *et al.*, 2021). Despite progress, improvement in maize yield has been slow in Pakistan. Information regarding the inheritance of yield traits is limited in local ecosystems. Genotype and environment interaction significantly affects breeding decisions because the performance of a given genotype is not always stable across the different ecological zones (Owusu *et al.*, 2018). Furthermore, the majority of the earlier studies have not been conducted for combining ability on region-specific adapted inbred lines for particular agro-climatic conditions of Pakistan (Hussain *et al.*, 2023). The lack of information of local research limits the progress being made in the development of maize hybrids tailored to the national agricultural requirements. Through the delineation of the most promising parents and hybrid combinations, we aim to contribute in the development of high-yielding, climate-resilient hybrids adaptable for diverse farming practices of Pakistan to achieve national food and nutritional security (Khalid *et al.*, 2020). In maize breeding, correlation analysis is essential for understanding trait associations that support indirect selection for yield enhancement. Higher genotypic than phenotypic correlations indicate reduced environmental impact on trait expression (Mohammed *et al.*, 2024). Positive associations among key traits allow simultaneous improvement, particularly when traits exhibit high heritability. Such insights enable breeders to efficiently combine desirable characteristics in hybrid development (Thomas *et al.*, 1971). The present study was conducted to estimate the general and specific combining ability of selected maize genotypes, with a focus on assessing genetic diversity and the nature of gene action controlling key quantitative traits such as plant height and kernel characteristics. The research aimed to evaluate genetic variability, identify superior parental lines and hybrid combinations for yield-related traits, and determine whether additive or non-additive effects predominate in their inheritance. The outcomes are intended to support the development of high-yielding, stress-resilient maize hybrids, thereby contributing to sustainable production and enhanced food security of Pakistan.

Materials and methods

The study was carried out in the research field of the Department of Plant Breeding and Genetics at the University of Agriculture, Faisalabad. The experiment was sown on February 10, 2024, during the spring cropping season. The experimental material comprised 10 inbred maize genotypes including 5 lines and 5 testers. These genotypes were obtained from the Maize Breeding and Genetics Resource Laboratory, Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan. The lines were crossed with the testers in a Line × Tester mating design to generate 25 F_1 hybrids. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each replication included all 10 parental lines and 25 F_1 crosses. Individual plots were established with a plant-to-plant spacing of 22.5 cm and a row-to-row spacing of 75 cm. Uniform agronomic practices were applied across the field, including the application of recommended fertilizers, timely irrigation and integrated pest management to ensure optimal crop development and minimize environmental variation.

Table 1: Genetic material used in research

Lines	**GB-1**	**GB-2**	**GB-3**	**GB-4**	**GB-5**
	245	337	449	575	563
Testers	**SB-6**	**SB-7**	**SB-8**	**SB-9**	**SB-10**
	218	K23	356	162	268
Crosses	GB-1 × SB-6	GB-2 × SB-6	GB-3× SB-6	GB-4 × SB-6	GB-5 × SB-6
	GB-1 × SB-7	GB-2 × SB-7	GB-3× SB-7	GB-4 × SB-7	GB-5 × SB-7
	GB-1 × SB-8	GB-2 × SB-8	GB-3× SB-8	GB-4 × SB-8	GB-5 × SB-8
	GB-1 × SB-10	GB-2 × SB-10	GB-3× SB-10	GB-4 × SB-10	GB-5 × SB-10
	GB-1 × SB-9	GB-2 × SB-9	GB-3× SB-9	GB-4 × SB-9	GB-5 × SB-9

At the physiological maturity stage, data were collected for eleven morphological and yield-related traits in maize. Plant height was measured from the ground to the top of the tassel, while ear height was recorded from the base of the plant to the uppermost point of the ear. Cob length was assessed by measuring sun-dried, de-husked cobs from base to tip. Stem diameter was determined using a Vernier caliper, with the range taken from both the base and top of the stem to calculate an average. Seed count per row was manually recorded by sectioning the cob and counting the number of rows and seeds in each row. For grain yield components, 100 seeds were randomly selected, dried and weighed using an electronic balance. The number of rows per cob was counted manually and internodal length was measured as the distance between two nodes on the stem using a measuring tape. Cob diameter was determined by taking circumference measurements at the midpoint of the cob, again using a Vernier caliper. Similarly, pith diameter was taken at the center of the cob after removing the seeds. Lastly, the number of leaves per plant was recorded by manually counting all fully developed leaves from the base to the top. The collected data were analyzed using analysis of variance (ANOVA) to determine significant differences among genotypes (Steel *et al.*, 1997).

Combining ability analysis was conducted using the Line × Tester method to estimate general combining ability (GCA) and specific combining ability (SCA) effects. The analysis was carried out using DOS-based statistical tools operated through DOSBox version 0.74-3 to support legacy software. Correlation (Kwon and Torrie, 1964) among yield and yield-related traits was assessed using Statistix 8.1 software to evaluate the direction and strength of trait associations. Superior test crosses were identified using a combined comparison approach based on mean performance of F_1 hybrids, specific combining ability (SCA) effects and the general combining ability (GCA) status of parental lines. Hybrids showing significant and positive SCA effects in the desirable direction, along with mean values exceeding the overall mean of all hybrids and their respective parental means, were considered superior. In addition, crosses involving at least one good general combiner were prioritized. As no commercial check hybrid was included, parental means and overall hybrid means were used as checks for identifying promising test crosses, a method commonly adopted in Line × Tester–based maize breeding studies.

Results and discussion

The analysis of variance (ANOVA) using the Line × Tester mating design revealed significant genetic variability among maize genotypes for a range of agronomic and yield-related traits (Table 2). Significant differences among lines, testers, and line × tester interactions confirm the presence of exploitable genetic diversity, which forms the basis for hybrid development and selection. Plant height (PH) showed highly significant mean squares for lines (4241.0), testers (564.4), and interactions (765.1), suggesting that additive genetic effects primarily contributed by the lines govern this trait, while the significant interaction highlights the importance of non-additive gene action, supporting hybrid breeding strategies (Fayyad and Hammadi, 2021). Similarly, ear height (EH) followed a comparable pattern, with lines contributing strongly but notable line × tester interactions indicating that specific combinations can further enhance expression, thereby offering opportunities to exploit heterosis (Talukder *et al.*, 2016). Cob length (CL) was significantly influenced by lines, testers, and their interactions, reflecting the combined effects of additive and non-additive gene action (Gazar *et al.*, 2024). Cob diameter (CD) was primarily controlled by line × tester interactions, indicating dominance or epistatic effects, which makes this trait particularly responsive to hybrid vigor (Abebe *et al.*, 2020). Stem diameter (SD) and internodal length (IL) also exhibited significant contributions from lines, testers, and their interactions, demonstrating complex genetic control and highlighting the importance of selecting both superior parental lines and optimal crosses (Moneam *et al.*, 2020). Number of seeds per row displayed the highest mean square for line × tester interactions, suggesting a predominance of non-additive effects and the potential for identifying superior hybrid combinations (Mohammed *et al.*, 2024). Seed rows per cob and 100-grain weight were significantly affected by both parental and interaction effects, reflecting polygenic inheritance and the involvement of both additive and dominance gene action (Owusu *et al.*, 2018). Pith diameter was mainly under non-additive control (Fayyad and Hammadi, 2021), while number of leaves was governed by a combination of additive and non-additive effects (Talukder *et al.*, 2016), confirming the need to consider all sources of variation in selection programs. These patterns indicate that the Line × Tester mating design is an effective tool for dissecting the genetic architecture of maize yield and its components (Amzeri *et al.*, 2025).

The combining ability analysis further highlighted the importance of both general combining ability (GCA) and specific combining ability (SCA) in determining hybrid performance (Table 3). Lines exhibiting high GCA effects can serve as superior donors of favorable alleles for multiple traits (Aly *et al.,* 2023), while testers with positive GCA can contribute specific improvements, particularly in grain-related and vegetative traits (Barzgari *et al.,* 2022). Significant SCA effects for traits such as plant height, cob length, stem diameter, 100-grain weight, and internodal length indicate that non-additive gene action, including dominance and epistasis, plays a crucial role in hybrid performance (Moneam *et al.,* 2020). These results suggest that both parental selection and the evaluation of specific hybrid combinations are essential for exploiting heterosis in maize breeding programs (Abebe *et al.,* 2020). The overall findings confirm that additive gene action contributes significantly to trait inheritance, particularly for plant height, ear height, and 100-grain weight (Fayyad and Hammadi, 2021), whereas non-additive effects dominate traits such as cob diameter, number of seeds per row, and pith diameter (Gazar *et al.,* 2024). These insights align with earlier reports demonstrating the efficacy of the Line × Tester mating design for identifying superior parental lines and hybrid combinations under diverse environmental conditions (Amzeri *et al.,* 2025). By integrating both ANOVA and combining ability analyses, the study identifies key parental lines and hybrid combinations that can serve as valuable resources for breeding programs aimed at improving maize productivity and stability (Aly *et al.,* 2023).

The GCA analysis of maize inbred lines and testers (Table 4) revealed significant variation for plant height, ear height, cob length, stem diameter, number of seeds per row (NSR), 100-grain weight , and other important agronomic traits. Among the lines, GB-5 exhibited the highest positive GCA effects for plant height (26.4**) and ear height (11.2**), indicating its potential as a donor for taller maize genotypes (Ahmed *et al.,* 2017). In contrast, GB-2 recorded highly negative GCA effects for plant height (–19.5**) and ear height (–5.7**), suggesting suitability for compact plant architecture (Ismail *et al.,* 2024). GB-3 showed a positive GCA effect for cob length (2.9**), reflecting its capacity to enhance ear size (Azeem *et al.,* 2021). For stem diameter, GB-5 recorded a positive effect (0.2*), while GB-1 had a negative effect (–0.2**), indicating differential additive contributions toward stalk robustness (Ahmed et al., 2017). GB-3 and GB-1 were favorable combiners for 100-grain weight (1.8** and 0.9*, respectively), whereas GB-2 and GB-5 were less favorable, highlighting the trait-specific nature of additive gene action (Ismail *et al.,* 2024). GB-2 and GB-4 showed positive effects for number of seed rows per cob (1.7** and 1.0**), whereas GB-3 and GB-5 contributed negatively. Internodal length was positively influenced by GB-5 (0.8*), suggesting potential for improved plant structure (Nadeem *et al.,* 2023).

Among testers, SB-10 exhibited high positive GCA for 100-grain weight (2.4**) and number of leaves (0.7*), but negative effects for plant height (–10.4**) and ear height (–5.7*) (Hussain *et al.,* 2022). SB-6 contributed positively to plant height (4.7**) and ear height (3.6*), while SB-7 was favorable for cob length (1.6**) and internodal length (0.7*) (Elmyhun *et al.,* 2020). SB-8 and SB-9 showed mixed effects, with SB-8 negatively affecting 100-grain weight (–1.8**) and SB-9 positively contributing to stem diameter (0.3**).Lines GB-3 and GB-5 consistently transmitted favorable alleles for multiple traits including grain yield, plant height, and 100-grain weight, making them suitable candidates for hybrid development (Ahmed *et al.,* 2017).

Table 2: Genetic variance assessment for yield and yield-contributing traits in maize through mean square analysis

Source of variation	Plant height	Ear height	Cob length	Stem diameter	Number of seed/ row	**100** grains weight	Number of rows	Internodal length	Pith diameter	Cob diameter	Number of leaves
Replications	1364.9**	176.4*	4.1	0.3*	13.9	15.5	4.9	11.9**	0.1	0.6*	3.8*
Genotypes	1277.7**	589.2**	28.6**	0.2**	42.2**	62.4**	7.9**	7.9**	0.2**	0.5**	3**
Crosses	1310.9**	524.1**	32.3**	0.2**	35.0**	37.5**	5.6**	5.4**	0.2**	0.3**	3.6**
Lines (c)	4241.1**	869.3**	58.9**	0.2**	8.0	25.3	12.3**	7.0**	0.3**	0.2	3.7**
Tester (c)	564.4**	373.7**	15.8**	0.3**	5.8	38.3	1.2	3.3	0.1	0.2	4.2**
LXT	765.1**	475.5**	29.8**	0.1**	49.1**	40.3**	5.0*	5.6**	0.2**	0.4**	3.4**
Parents	1312.7**	587.8**	7.4**	0.2**	40.1**	128.4**	15.1**	13.3**	0.3**	0.9**	1.2
Lines (p)	2691.2**	1106.8**	3.3	0.2**	78.2**	117.0**	16.9**	23.3**	0.3**	0.9**	1.4
Tester (p)	121.5**	146.7*	5.4**	0.2**	11.4	158.2	16.8**	5.9**	0.2**	1.0**	1.1
Lines (P) vs Testers (P)	563.3**	276.1**	32.1**	0.3**	2.7	54.9	1.2	1.9	0.4**	0.8**	0.5
Cross vs Parents	166.4**	2162.9**	128.9**	1.5**	233.4**	65.7**	0.5	18.0**	0.3**	0.4	4.7
Error	26.1	32.4	2.1	0.1	6.2	2.8	2.3	2.5	0.0	0.1	1.3

** = Highly Significant,* = Significant

Table 3: Analysis of variance for combining ability for grain yield, yield related characters and quality traits

Source of variation	Plant height	Ear height	Cob length	Stem diameter	Number of seed/ row	**100** grains weight	Number of rows	Internodal length	Pith diameter	Cob diameter	Number of leaves
Replications	938.9**	107.3	5.9	0.1	16.9*	19.3**	10.3*	1.1	0.1	0.1	2.1
Crosses	1310.9**	524.1**	32.3**	0.2**	35.0*	37.5**	5.6	5.4**	0.2**	0.3**	3.6**
Lines (c)	4241.0**	869.3**	58.9**	0.3**	8.0	25.3**	12.4*	7.0**	0.3**	0.2	3.7**
Tester (c)	564.4**	373.7**	15.8**	0.3**	5.8	38.3**	1.2	3.3	0.1	0.2	4.2**
LXT	765.0**	475.5**	29.8**	0.2**	49.2*	40.3**	5.0	5.6**	0.2**	0.4**	3.4**
Error	28.5	40.2	2.2	0.1	8.3	3.0	2.9	1.9	0.	0.1	1.3

** = Highly Significant,* = Significant

GB-3 also contributed positively to cob diameter and seed weight, while GB-5 enhanced ear height and number of seeds per row (Ismail *et al.*, 2024). These results align with previous findings that high-GCA lines are essential for trait-specific maize breeding programs (Azeem *et al.*, 2021). The SCA analysis (Table 5) demonstrated significant non-additive genetic effects for several hybrids, indicating the importance of dominance and epistasis in trait expression. The hybrid GB-3 × SB-8 showed the highest SCA effect for cob length (5.2**) and also favorable values for stem diameter and 100-grain weight, highlighting its potential for improving ear characteristics (Azeem *et al.*, 2021). GB-2 × SB-10 exhibited significant SCA for cob length (3.4**), number of seeds per row (3.0), and 100-grain weight (3.6**), emphasizing its role in enhancing both yield and kernel quality (Nadeem *et al.*, 2023). GB-5 × SB-9 also showed positive SCA effects for cob length (3.2**) and number of seed rows per cob (2.3**), reflecting its contribution to improved cob structure (Hussain *et al.*, 2022). Vegetative traits were influenced by specific hybrid combinations. GB-4 × SB-7 and GB-3 × SB-10 recorded highly positive SCA effects for plant height (23.6** and 20.2**) and ear height (13.2** and 14.5**), indicating their potential for increasing plant vigor (Elmyhun *et al.*, 2020). Conversely, GB-1 × SB-8 and GB-5 × SB-10 exhibited significantly negative SCA effects for plant height (–18.7** and –10.8**), suggesting their suitability for shorter plants with better lodging resistance (Ahmed *et al.*, 2017).Reproductive traits were also influenced by cross-specific effects. GB-2 × SB-8 significantly increased the number of seeds per row (6.5**), while GB-1 × SB-9 positively affected the number of seed rows per cob (3.1**), supporting their use in improving yield components (Ismail et al., 2024). GB-4 × SB-6 and GB-3 × SB-6 contributed positively to 100-grain weight, demonstrating the importance of non-additive effects in kernel mass enhancement (Azeem *et al.*, 2021). Internodal length (IL) was highest in GB-5 × SB-7 (2.8**), with other crosses such as GB-1 × SB-6 and GB-2 × SB-10 showing favorable SCA effects, highlighting the role of non-additive interactions in determining plant structural traits (Nadeem *et al.*, 2023; Hussain *et al.*, 2022). Overall, the results indicate that parental lines GB-3 and GB-5, together with hybrids GB-3 × SB-8, GB-2 × SB-10, and GB-4 × SB-7, are promising for hybrid development due to their significant additive and non-additive effects. These genotypes may be prioritized for breeding programs aimed at improving yield, kernel quality, and plant architecture.

The 2nd study was to study the correlation among the traits. The correlation analysis (Table 6) revealed significant relationships among grain yield and its contributing traits at both genotypic and phenotypic levels. Plant height displayed a strong positive phenotypic correlation (0.7**) and genotypic correlation (0.7) with ear height, indicating that taller plants generally bear ears at higher positions. Similarly, plant height showed moderate correlations with cob length at the phenotypic (0.4**) and genotypic (0.4**) levels, suggesting that taller genotypes may contribute to larger cob development. A positive association was observed between plant height and stem diameter (phenotypic = 0.2*, genotypic = 0.2*), implying limited influence of plant stature on stalk thickness. These findings are consistent with earlier studies reporting that plant height and ear height are strongly associated and can serve as indirect selection criteria for yield improvement (Mohammed *et al.*, 2024; Yahaya *et al.*, 2021; Lone *et al.*, 2021). Ear height was positively correlated with stem diameter (phenotypic = 0.3**, genotypic = 0.3**) and internodal length, (phenotypic = 0.2*, genotypic = 0.2*), suggesting that higher ears are supported by stronger stems and longer internodes in our study. Cob length showed a significant negative correlation with number of seeds per row at both phenotypic (–0.4**) and genotypic (–0.4**) levels, indicating a potential trade-off between cob elongation and seed row formation. Stem diameter was positively associated with cob diameter (phenotypic = 0.3**, genotypic = 0.3**) and internodal length (phenotypic = 0.2*, genotypic = 0.2*), reflecting that robust stems may contribute to better reproductive architecture. Stem dameter also showed a moderate negative correlation with 100-grain weight (phenotypic = 0.3*, genotypic = –0.4), suggesting a trade-off between vegetative growth and grain mass (Hussain *et al.,* 2022; Talukder *et al.,* 2016). Number of seed rows exhibited significant positive associations with IL (phenotypic = 0.4**, genotypic = 0.5**) and cob diameter (phenotypic = 0.4**, genotypic = 0.2), highlighting the role of internode development and cob architecture in kernel arrangement. Similarly, number of rows per cob was positively correlated with cob diameter (phenotypic = 0.2*, genotypic = 0.3*) and pith diameter (phenotypic = 0.2, genotypic = 0.4**), indicating that broader and structurally strong cobs can accommodate more rows, consistent with prior observations (Mohammed *et al.,* 2024; Owusu *et al.,* 2018). Internodal length significantly correlated with NSR (phenotypic = 0.4**, genotypic = 0.5**) and stem diameter (phenotypic = 0.2*, genotypic = 0.2*), emphasizing the contribution of vegetative growth patterns to reproductive success. Cob diameter also correlated positively with plant height (phenotypic = 0.3**, genotypic = 0.4**) and NR (phenotypic = 0.2*, genotypic = 0.3*), supporting the role of taller plants in producing larger cobs. Interestingly, 100-grain weight (GW) exhibited negative correlations with plant height, ear head and stem diameter (phenotypic = –0.4**, –0.3**, 0.3*, genotypic = –0.4, –0.5, –0.4**), suggesting that increased vegetative growth may limit individual grain mass, consistent with findings by Hussain *et al.,* (2022) and Talukder *et al.,* (2016). Traits like number of leaves generally showed weak associations with other traits (phenotypic = 0.1–0.1, genotypic = 0.2), indicating a limited yet potential indirect role in yield determination. Overall, the correlation analysis indicates that plant height, ear height, internodal length, and cob architecture are key determinants of maize yield and can serve as effective traits for indirect selection in breeding programs (Mohammed *et al.,* 2024; Yahaya *et al.,* 2021; Lone *et al.,* 2021; Shivani, and Prasad, 2020). Conversely, trade-offs between vegetative biomass and grain weight must be carefully considered to optimize yield performance (Hussain *et al.,* 2022; Talukder *et al.,* 2016).

The results of this study provide clear guidance for selecting parent lines and hybrid combinations in maize breeding programs. Lines GB-3 and GB-5, which demonstrated consistently positive GCA effects for traits such as plant height, 100-grain weight, cob length, and ear height, are ideal candidates for parental selection in hybrid development. Their ability to transmit favorable alleles suggests that they can be effectively used in recurrent selection schemes or pedigree breeding programs to accumulate additive gene effects for yield and yield-related traits. This is particularly important for improving plant architecture and kernel traits simultaneously. The SCA analysis highlights superior hybrid combinations such as GB-3 × SB-8, GB-2 × SB-10, and GB-5 × SB-9, which exhibited significant positive effects for cob length, number of seeds per row, grain weight, and vegetative vigor. These crosses demonstrate the importance of non-additive genetic effects in determining hybrid performance. Therefore, selection of hybrids should not rely solely on parental GCA but should also consider cross-specific SCA values to maximize heterosis and yield potential. Hybrids like GB-4 × SB-7 and GB-3 × SB-10 that enhanced plant height and ear height could be utilized for improving crop standability and photosynthetic efficiency, which indirectly contributes to grain yie

Table. 4: General combining ability analysis of yield and yield-related characters in maize using Line × Tester design

Parents	Plant height	Ear height	Cob length	Stem diameter	Number of seed/ row	100 grains weight	Number of rows	Internodal length	Pith diameter	Cob diameter	Number of leaves
Lines											
GB-1	-7.5**	-6.3**	-1.0*	-0.2**	-0.8	0.9*	-0.1	-0.8*	0.2**	-0.0	-0.3
GB-2	-19.5**	-5.7**	-1.9**	0.1	0.6	-1.3**	1.7**	-0.5	0	0.1	0
GB-3	0.4	-3.7*	2.9**	-0.1	0.5	1.8**	-0.9**	0.1	-0.1	-0.0	0
GB-4	0.2	4.5**	-1.1**	0.1	0.5	-0.8	1.0**	0.5	-0.0	-0.2	-0.5
GB-5	26.4**	11.2**	1.3**	0.2*	-0.8	-0.7	-1.7**	0.8*	-0.1*	0.1	0.8**
Testers											
SB-6	4.7**	3.6*	0.1	-0.1	-0.9	0.5	0.4	-0.5	-0.0	-0.0	-0.7*
SB-7	-0.6	-5.2**	1.5**	-0.1	0.7	-0.1	-0.2	0.7*	-0.0	0	-0.1
SB-8	3.7*	4.1*	0.1	-0.1	0.2	-1.8**	0.1	-0.2	0.0	-0.2*	-0.1
SB-9	2.6	3.2	-0.3	0.3**	-0.4	-1.0*	-0.6*	-0.2	-0.0	0.1	0.3
SB-10	-10.4**	-5.7*	-1.4**	-0.0	0.4	2.4**	0.2	0.2	0.1	0.1	0.7*

** = Highly Significant, * = Significant

The correlation analysis (Table 6) further informs breeding strategies by identifying traits with strong positive associations that can be used as indirect selection criteria. For example, strong positive correlations between plant height and ear height (phenotypic = 0.7**, genotypic = 0.7) and between internodal length and number of seeds per row (phenotypic = 0.4*, genotypic = 0.5**) suggest that improving plant stature and internode elongation can indirectly enhance cob filling and kernel development. Conversely, negative correlations between 100-grain weight and traits like plant height and ear height indicate a trade-off between vegetative growth and grain mass, guiding breeders to select genotypes that balance biomass and kernel weight for optimum yield. By integrating the information from GCA, SCA, and trait correlations, maize breeders can prioritize lines and hybrids that combine both additive and non-additive effects, ensuring maximum genetic gain. Lines GB-3 and GB-5, along with superior crosses like GB-2 × SB-10, represent promising candidates for developing high-yielding, well-structured maize hybrids. This approach also supports targeted breeding for traits such as grain weight, cob structure, internodal length, and standability, which are crucial for improving productivity and climate resilience. Overall, these findings provide a strategic framework for hybrid maize improvement, emphasizing the importance of selecting both parents and specific crosses based on combining ability and trait interrelationships to enhance yield potential and crop stability.

In conclusion, the study assessed the study assessed the combining ability of maize genotypes using a Line × Tester design, revealing substantial genetic variability influenced by both additive (GCA) and non-additive (SCA) effects. Among the parental lines, GB-3 and GB-5 consistently exhibited superior general combining ability for multiple agronomic and yield-related traits, making them valuable candidates for hybrid breeding. In contrast, GB-2 showed limited potential as a parent.

Table 5 Specific combining ability analysis of yield and yield-related traits in maize

Crosses	Plant height	Ear height	Cob length	Stem diameter	Number of seed/ row	100 grains weight	Number of rows	Internodal length	Pith diameter	Cob diameter	Number of leaves
GB-1 × SB-6	5.9	-3.2	1.0	-0.2	-0.7	-0.4	-0.3	0.9	-0.2	-0.1	-0.5
GB-1 × SB-7	16.3**	16.3**	-0.4	0.2	-1.5	-3.7**	-1.7**	-2.2**	-0.2	-0.1	-1.1
GB-1 × SB-8	-18.7**	-8.6*	-3.6**	0.2	0.3	1.1	0.1	1.4	0.6**	0.0	-0.1
GB-1 × SB-9	4.4	6.6	0.8	-0.1	1.9	2.9**	3.1**	0.0	0.0	0.1	1.5*
GB-1 × SB-10	-7.9*	-11.2**	2.2*	-0.1	0.1	0.1	-1.2	-0.2	-0.3*	0.0	0.1
GB-2 × SB-6	6.0	6.9	-1.2	-0.2	1.3	-7.6**	-0.1	-0.3	-0.2	-0.2	1.9**
GB-2 × SB-7	-0.7	-8.3	0.2	0	-5.9**	-0.5	0.2	-0.5	-0.0	0.0	-0.7
GB-2 × SB-8	10.3**	9.1*	-3.4**	-0.2	6.5**	4.1**	1.9**	-0.3	-0.2	-0.4	0
GB-2 × SB-9	-4.2	10.0**	0.9	0.1	-4.9**	0.4	-2.4**	0.1	-0.0	0.2	-0.8
GB-2 × SB-10	9.1**	2.3	3.4**	0.4*	3	3.6**	0.4	1.0	0.4**	0.3	-0.5
GB-3 × SB-6	-2.2	-2.2	0.5	-0.1	-3.6*	3.5**	0.5	-0.9	0.1	-0.4*	0.6
GB-3 × SB-7	-15.6**	-10.4**	-0.3	-0.1	2.9	3.0**	1.4*	1.2	-0.1	-0.0	-0.3
GB-3 × SB-8	2.5	5.7	5.2**	0.3*	-3	-3.9**	-1.5*	-1.5	-0.1	0.1	-0.3
GB-3 × SB-9	-4.8	-7.8*	-5.8**	0	6.6**	0.7	-0.8	0.8	0.1	0.1	-0.8
GB-3 × SB-10	20.2**	14.5**	0.3	-0.2	-2.9	-3.3**	0.6	0.4	0.0	0.2	0.8
GB-4 × SB-6	-6.0	-13.3**	-0.8	0.4**	3	2.7*	0.9	-0.0	0.0	0.5**	-0.5
GB-4 × SB-7	23.6**	13.2**	2.8**	0	1.5	-0.0	0.2	-1.2	0.0	0.5*	1.2
GB-4 × SB-8	-4.4	-14.1**	-1.1	-0.2	-0.4	2.4*	0.3	1.4	-0.2	-0.1	-0.5
GB-5 × SB-9	7.2*	7.3*	3.1**	-0.00	-2.8	-1.8	2.3**	-0.9	-0.2	0.0	0.7
GB-5 × SB-10	-10.7**	-16.0**	-4.1**	0.0	3.0	2.5*	-0.5	-1.3	-0.1	-0.1	-0.9

**** = Highly significant, *= Significant**

Table 6: Genotypic and phenotypic correlation coefficients among yield and yield related traits

Source of variation	Plant height	Ear height	Cob length	Stem diameter	Number of seed/ row	**100** grains weight	Number of rows	Internodal length	Pith diameter	Cob diameter	Number of leaves
Plant height	1.0	0.7**	0.4**	0.2	-0.0	-0.4**	0.1	0.2	0.3**	-0.2	0.1
Ear height	0.7**	1.0	0.1	0.3**	0.2	-0.5**	0.2	0.2*	0.3**	0.1	0.1
Cob length	0.4**	0.1	1.0	-0.0	-0.4**	-0.1	0.0	-0.1	0.0	-0.2	0.2
Stem diameter	0.2*	0.3**	-0.0	1.0	0.2	0.3**	0.0	0.2*	0.3**	0.2	-0.1
Number of seed	-0.0	0.2	-0.4**	0.2*	1.0	0.0	0.1	0.4**	0.1	0.0	-0.1
100 grains weight	-0.4**	-0.5**	-0.0	-0.4**	-0.0	1.0	-0.0	-0.1	-0.0	-0.1	-0.0
Number of rows	0.1	0.1	0.0	0.0	-0.0	-0.2	1.0	-0.0	0.2*	0.2*	0.1
Internodal length	0.2	0.2*	-0.1	0.2*	0.5**	-0.2	0.0	1.0	-0.2	0.0	0.1
Pith diameter	0.4**	0.3**	0.0	0.3**	0.2*	-0.1	0.3*	0.1	1.0	-0.0	0.1
Cob diameter	-0.2	-0.0	-0.2*	0.3**	0.0	-0.1	0.4**	0.1	0.1	1.0	-0.1
Number of leaves	0.1	0.0	0.2	-0.2	-0.1	-0.0	0.2*	0.0	0.0	-0.2	1.0

**** = Highly significant, *= Significant**

Two parent testers, SB-10 and SB-6 emerged as favorable general combiners, contributing positively to key traits such as grain yield and plant architecture. Analysis of specific combining ability identified high-performing hybrids, including GB-3 × SB-8 and GB-2 × SB-10, which demonstrated strong hybrid vigor and overall performance. Conversely, certain crosses, such as GB-1 × SB-8 and GB-5 × SB-10, were less promising. These findings underscore the importance of selecting parents with high GCA and exploiting favorable SCA combinations to develop superior maize hybrids. The results provide a reliable basis for breeding programs aimed at improving maize productivity and yield stability.

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