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Estimates magnitude of heterosis, nature of gene action and combining ability in maize using Line ×Tester method for yield and attributing traits

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Abstract

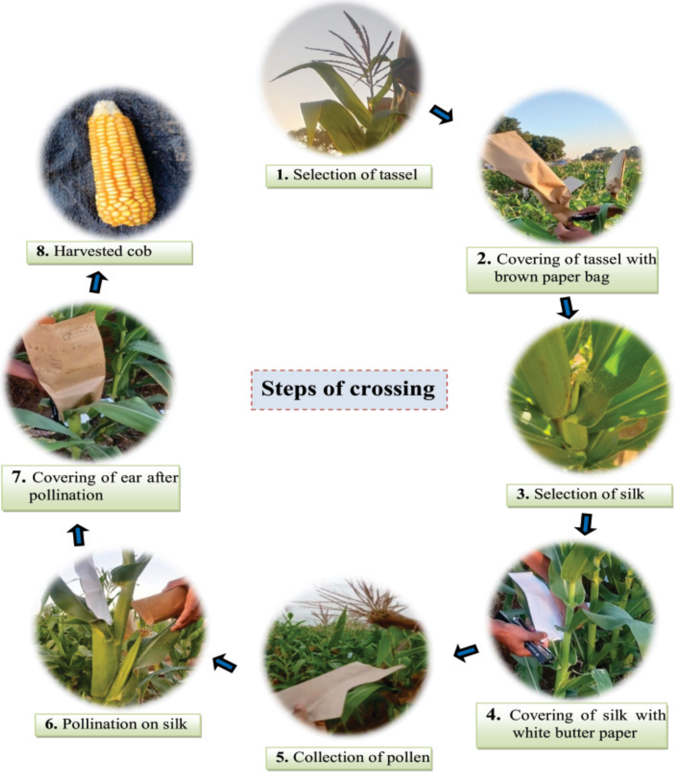
Aim: This study aimed to evaluate genetic variability and heterotic potential among maize genotypes *Zea mays* (L.) for key agronomic traits, with a focus on kernel yield and related characteristics, to enhance hybrid development strategies.

Methodology: Maize genotypes were assessed for growth, yield and quality traits. Analysis of variance (ANOVA) was conducted to identify significant differences, heterosis, and the combining ability was analyzed to determine the genetic potential of parent lines and hybrids.

Results: Significant genetic variability was observed for all traits. The inbred line BLD 203, tester WNC 40108, and their hybrid BLD 203 × WNC 40108 performed best for kernel yield. The crosses BLD 176 × WNC 40108, BLD 226 × WNC 40108, and BLD 246 × WNC 40223 demonstrated the highest heterotic effects for kernel yield and improvements in several agronomic traits. The ratio of general combining ability (GCA) to specific combining ability (SCA) was less than one for all traits, indicating dominance of non-additive gene action.

Interpretation: The study reveals substantial genetic diversity and hybrid potential in maize. WNC 40108 was identified as an excellent parent for kernel yield improvement, and the maize F1 hybrids BLD 176 × WNC 40108, BLD 226 × WNC 40108, and BLD 246 × WNC 40223 were found promising for yield related traits. These hybrids should be further evaluated across diverse environments for commercialization and their use in further maize improvement programs.

Key words: Combining ability, Gene action, Heterosis, Kernel yield, Maize F_1 hybrids



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Introduction

Maize (*Zea mays* L.), a crop native to Central America, is the world's leading cereal grain, recognized for its remarkable versatility and widespread adaptability to diverse agro-climatic conditions. Globally, it holds the title of the "queen of cereals," not only due to its substantial genetic yield capacity owing to its wide range of uses. In India, maize ranks as the third most important food crop after rice and wheat, serving both as a staple food and a vital component of livestock feed (Verma *et al.,* 2023). Beyond its direct consumption, maize is processed into numerous value-added products such as cornmeal, starch, oil, biofuels, thereby contributing significantly to the economy. Maize's utility across various sectors underpins its vital role in enhancing food security, rural livelihoods, and industrial growth worldwide (Abdel-Moneam *et al.,* 2024). Globally it is cultivated over an area of 201 million ha level, with annual production over 1162 million tonnes. However, In India, maize is cultivated on approximately 9.89m ha area, yielding 31.51 million tonnes, with an average productivity of 3200 kg ha^{-1} (Mishra *et al.,* 2024).

Heterosis is the phenomenon where hybrid offspring outperform their parents (East, 1908; Shull, 1908) in terms of traits such as yield, size and disease resistance (Yu *et al.,* 2020).In maize, heterosis is a critical factor driving the development of high-yielding hybrids exhibiting superior agronomic performance compared to the inbred parent lines (Lal *et al*., 2023). Whereas combining ability refers to the genetic potential of inbred lines to contribute desirable traits to their progeny in hybrid combinations. It is typically categorized into GCA and SCA (Sprague and Tatum, 1942). GCA indicates the additive genetic effects of a parent across various hybrid combinations, while SCA reflects non-additive effects specific to particular parent pairings. Assessing both GCA and SCA is fundamental for identifying superior parent lines and optimizing hybrid combinations for increased yield and other desirable traits. The inheritance of traits in maize is governed by both additive and non-additive gene actions (Kamal *et al.,* 2023). The relative contributions of additive and non-additive gene actions determine the selection strategies and breeding methodologies employed.

Unfortunately, domestication and selective breeding methods have resulted in an overall decrease in genetic diversity due to the continued cultivation of older maize varieties. Serious threats result from this loss of genetic variation, including an increased vulnerability to pests and disease (Yu *et al.,* 2020). Maintaining genetic variety in breeding materials is crucial for the long-term viability of maize production. However, with limited variability, hybridization programs are necessary to generate or maintain diversity (Kamal *et al.,* 2023). Therefore, selecting the appropriate parental lines is crucial for the success of new breeding initiatives. The genetic architecture of important agronomic traits in maize is examined in this study by assessing gene action, heterotic patterns, and general and specific combining abilities. This information is used to guide breeding strategies that improve hybrid performance and aid in the development of high-yielding, genetically robust maize cultivars.

Materials and Methods

Location and climatic condition: The experiment was conducted in two seasons during *rabi* 2021-22 and *kharif* 2022 at Maize Research Station, S.D. Agricultural University, Bhiloda (Aravalli). The research station is located at 23° 76' North latitude and 73° 24' East longitude, 259 m above the mean sea level. The soil of the experimental site was sandy loam. The climate of this region is sub-tropical monsoon type with semi-arid condition and average temperature of 35 °C.

Experimental material: This study was conducted in two season first crossing season parent and evaluation season of thirty-two crosses were made through Line × Tester mating design by using 8 lines (BLD 170, BLD 175, BLD 176, BLD 201, BLD 203, BLD 226, BLD 227, BLD 246) and 4 testers (WNC-31702, WNC-40108, WNC-40104, WNC-40223). Thus, 45 maige genotypes including 32 crosses, 12 parents and one Standard check (GDYMH 101) were selected as experimental materials for the study. The maize plants were raised in a row measuring 4 m with a spacing of 60 cm × 20 cm. All the cultural practices were carried out as per the standard recommendation of ICAR-IIMR, Ludhiana (Bamboriya *et al*., 2020).

Experimental design and observations recorded: The experiment was laid out in Randomized Block Design with three replications of each genotype. The observation on plant growth, yield and quality related traits were taken using standard procedures (Kaur *et al*., 2024). Protein content of maize seeds of genotypes was estimated by the Microkjeldahl method of protein estimation (Hawk, 1951). Total nitrogen percentage was multiplied by 6.25 to obtain the protein content. Heterosis was estimated as per cent increase or decrease in the mean value of F_1 crosses over mid parent. Relative heterosis was measured as the proportion of deviation of F_1 value from the mid parent value, expressed in percentage (Turner, 1953). Heterobeltiosis was measured as the proportion of deviation of F_1 value from the better parent value, expressed in percentage (Fonseca and Patterson, 1968). Standard heterosis was measured as the proportion of deviation of F_1 value from the value of standard check, expressed in percentage (Meredith and Bridge, 1972). The variation among the crosses was partitioned further into sources attributable to GCA and SC Acomponents in accordance with the procedures recommend by Kempthorne (1957).

Statistical analyses: ANOVA was carried out to test the differences between the genotypes for all the characters under study (Panse and Sukhatme, 1978).

Results and Discussion

The ANOVA for the traits under study revealed significant differences among the genotypes for all the characters evaluated

Table 1: Analysis of variance for different characters in maize

Source of variation	d.f.	Mean sum of square													
		DT	DS	ASI	PH	EH	DM	CL	CG	KRC	KR	KYP	SP	KW	PC
Replications	2	6.98	2.87	1.189**	4.03	132.20	155.65**	4.90**	2.14**	1.15	32.79**	24.79	13.94	28.73**	7.08**
Genotypes (G)	43	15.61**	14.43**	0.391**	8.80**	271.15**	61.01**	2.10**	1.37**	2.72**	37.03**	222.85**	21.36**	22.57**	3.06**
Parents (P)	11	29.52**	26.45**	0.331	11.32*	59.41	12.52	2.11**	0.22	0.46	2.91	5.90	1.57	18.80**	1.56
Lines (L)	7	16.47**	17.12**	0.232	8.57	47.21	13.76	1.70**	0.33	0.46	3.98	5.67	2.20	17.05**	1.94
Testers (T)	3	34.75**	27.42**	0.444	17.89*	24.56	0.63	2.09**	0.03	0.30	1.36	3.93	0.17	20.97*	0.30
L vs. T	1	105.13**	88.89**	0.681	10.89	249.39	39.61	5.02**	0.05	0.93	0.02	13.36	1.36	24.50*	2.73
Crosses	31	10.30**	9.59*	0.418**	7.10	207.30*	35.51**	1.82**	0.38	0.79	13.46**	177.99**	11.10	18.06**	1.95*
P vs. C	1	27.28*	32.32*	0.213	33.96**	4579.70**	1384.90**	10.66**	44.43**	87.53**	1143.36**	3999.85**	557.09**	204.05**	53.82**
Error	86	5.12	5.14	0.205	4.70	125.72	18.45	0.51	0.43	1.09	6.74	63.73	9.79	5.38	1.10

DT = Days to tasseling, DS = Days to silking, ASI = Anthesis silking interval, PH = Plant height, EH = Ear height, DM – Days to maturity, CL = Cob length, CG = Cob girth, KRC = Kernel row per cob, KR = Kernel per row, KYP = Kernel yield per plant, SP =Shelling percentage, 100-KW = 100-kernel weight, PC = Protein content. *and ** indicate significance at 5% and 1%.

(Table 1), indicating a substantial degree of genetic variability present in the experimental material. The variance due to parents was significant for several traits including days to tasseling and silking, days to maturity, cob length, kernel yield per plant and 100-kernel weight, highlighted that the parental lines exhibited considerable variability in their genetic contribution. This indicates that significant variability exists among the parents utilised in crossing for kernel yield per plant and its contributing traits. Furthermore, the parent versus cross comparison was significant for all characters, except ASI, indicating that heterosis was evident in the crosses for most of the traits studied, which suggested the existence of differences between the parents and crosses for these characters leading to manifestation of heterosis. The interaction between line and tester showed significant differences for kernel yield. Testers used in the hybrid combinations were better differentiated for productivity, therefore, contribution towards variance due to hybrids could be better accounted for kernel yield. The results of the ANOVA are consistent with the earlier findings of Mukri *et al.* (2022) and Sharma *et al.* (2019), who similarly reported significant genetic variation in maize populations for these traits.

The evaluation of relative heterosis, heterobeltiosis, and standard heterosis for various traits is summarized in Table 2a,b. For days to tasseling and silking, negative heterosis is desirable as it indicates earliness. Among the 32 crosses, significant and negative relative heterosis was observed in 9 crosses, with values ranging from -9.34% to 7.29%. Similarly, the heterobeltiosis ranged from -6.74% to 10.00%. The magnitude of standard heterosis ranged from -0.61% to 12.88%, respectively. This confirms the existence of significant heterosis for earliness in maize. Dwarfism is generally preferred over tallness in maize for easier harvesting and better stalk strength. The magnitude of heterobeltiosis for plant height ranged from -3.74% to 24.51%. The standard heterosis for plant height ranged from -13.25% to 7.23%, with BLD 170 × WNC 31702 showing the most significant negative standard heterosis which can be beneficial for breeding dwarf varieties (Al-Jubouri *et al.,* 2024). For ear height, the cross BLD 175 × WNC 40223 showed the most significant negative standard heterosis at -11.52%, followed by BLD 170 × WNC 31702 (-10.60%). Negative heterosis for ear height is generally considered desirable, as it contributes to better ear placement for harvesting and reduced lodging risk. The magnitude of heterosis for cob length ranged from -10.09% to 14.51% over the mid parent, with six crosses exhibiting significant and positive heterobeltiosis. The standard heterosis for cob length ranged from -15.58% to 5.72%, with ten crosses exhibiting positive standard heterosis. For cob girth, the heterobeltiosis for cob girth ranged from 2.20% to 19.11%. The standard heterosis for cob girth ranged from -2.19% to 10.43%, with the cross BLD 176 × WNC 40108 showing positive standard heterosis (10.43%). For kernel rows per cob the BLD 176 × WNC 40108 cross had the high standard heterosis (20.99%), which varied from -2.47% to 20.99%. Thus, the majority of the crosses under evaluation had estimates of all three heterosis in the desired direction which suggests likelihood of increasing the number of kernel rows per cob through heterosis breeding (Tabu *et al.,* 2023).

However, the heterobeltiosis for kernels per row ranged from 15.42% to 70.75%, Furthermore, fifteen crosses showed significant positive standard heterosis for this trait, with BLD 203 × WNC 40108 (53.73%). For kernel yield per plant, the magnitude of heterobeltiosis ranged from -2.64% to 23.82%, with thirteen crosses showing significant positive heterobeltiosis, and the standard heterosis ranged from -11.97% to 13.36%, with BLD 176 × WNC 40108 showing the highest standard heterosis. Kernel

Table 2a: Magnitude of heterosis for different characters in maize

Crosses	DT			DS			ASI			DM			PH			EH			CL		
	MP	HB	SH	MP	HB	SH	MP	HB	SH	MP	HB	SH	MP	HB	SH	MP	HB	SH	MP	HB	SH
BLD 170 × WNC 40104	3.01	6.88*	4.91	2.26	5.85	4.62	-9.09	-9.09	0.00	3.25	4.38*	1.78	0.79	7.28	-7.71	1.03	5.35	-9.22	14.92**	14.21**	4.04
BLD 170 × WNC 40223	6.99*	10.00**	7.98*	5.41	8.19*	6.94*	-18.18*	-18.18	-10.00	3.76*	3.94*	3.20	0.66	6.67	-7.47	1.29	5.91	-9.22	10.71**	4.24	-5.04
BLD 170 × WNC 40108	-2.02	6.25	4.29	-1.91	5.26	4.05	0.00	11.11	0.00	1.58	3.57	3.20	1.06	7.89	-7.71	3.09	8.11	-7.83	10.44**	9.97*	0.18
BLD 170 × WNC 31702	-4.87	3.75	1.84	-4.07	3.51	2.31	10.00	22.22	10.00	1.08	1.44	0.36	-7.34	-3.74	-13.25*	0.31	5.55	-10.60*	4.64	3.20	-3.32
BLD 175 × WNC 40104	-1.19	1.22	1.84	-1.39	0.57	2.31	-4.35	0.00	10.00	2.17	2.92	0.36	5.09	7.00	-7.95	8.95	10.70	-4.61	5.64	4.04	-6.40
BLD 175 × WNC 40223	2.70	4.27	4.91	1.12	2.27	4.05	-21.74*	-18.18	-10.00	0.90	1.08	0.00	1.92	3.33	-10.36	1.32	3.23	-11.52*	16.61**	12.08**	-2.23
BLD 175 × WNC 40108	-4.84	1.83	2.45	-5.38*	0.00	1.73	-14.29	0.00	-10.00	-1.23	1.08	0.00	0.41	2.54	-12.29	3.70	5.95	-9.68*	13.91**	11.97**	1.14
BLD 175 × WNC 31702	-3.68	3.66	4.29	-3.74	2.27	4.05	-4.76	11.11	0.00	2.52	2.52	1.42	-1.34	-0.81	-11.57	4.56	7.18	-9.22	-2.31	-5.67	-11.63**
BLD 176 × WNC 40104	-2.94	-1.79	1.23	-3.60	-2.25	0.58	-14.29	-10.00	-10.00	-0.36	1.82	-0.71	11.29	13.17	-2.65	14.67**	16.57**	-2.76	8.03*	6.08	-1.00
BLD 176 × WNC 40223	-2.67	-2.38	0.61	-3.35	-2.81	0.00	-14.29	-10.00	-10.00	-0.18	1.08	0.36	22.09**	23.61**	7.23	12.81*	14.36*	-4.61	3.80	-3.36	-9.81
BLD 176 × WNC 40108	-5.92*	-0.6	2.45	-4.28	0.56	3.47	26.32*	33.33*	20.00	1.56	2.45	4.27*	14.36*	16.62*	-0.24	16.94**	18.23**	-1.38	9.10*	7.35	0.18
BLD 176 × WNC 31702	-5.88*	0.00	3.07	-4.79	0.56	3.47	15.79	22.22	10.00	0.71	2.16	1.07	17.09**	17.89*	4.82	18.42**	19.34**	-0.46	-8.74*	-8.92*	-14.67**
BLD 201 × WNC 40104	-2.11	1.89	-0.61	-1.14	2.96	0.58	14.29	20.00	20.00	2.72	3.28	0.71	13.51*	17.65*	1.20	13.76**	14.97**	-0.92	7.75*	6.12	-1.54
BLD 201 × WNC 40223	2.44	5.66	3.07	1.43	4.73	2.31	-14.29	-10.00	-10.00	1.44	1.81	0.36	11.17	14.72	-0.48	11.41*	12.90*	-3.23	-2.53	-9.01*	-15.58**
BLD 201 × WNC 40108	-2.31	6.29	3.68	-1.37	6.51*	4.05	15.79	22.22	10.00	0.35	2.89	1.42	17.07**	21.69**	4.10	16.49**	18.38**	0.92	1.98	0.64	-6.63
BLD 201 × WNC 31702	-5.75*	3.14	0.61	-5.18	2.96	0.58	5.26	11.11	0.00	1.62	1.81	0.36	13.87*	15.24*	3.86	9.39	11.53*	-5.53	7.31	6.79	0.05
BLD 203 × WNC 40104	-3.81	-2.96	0.61	-3.03	-2.22	1.73	9.09	9.09	20.00	0.89	2.92	0.36	14.17*	17.37*	0.96	14.97**	14.97**	-0.92	-2.68	-9.61*	-5.18
BLD 203 × WNC 40223	0.00	0.00	3.68	0.00	0.00	4.05	0.00	0.00	10.00	1.77	2.87	2.14	12.35	15.00	-0.24	12.06*	12.37*	-3.69	1.78	-10.09**	-5.68
BLD 203 × WNC 40108	-8.99*	-4.14	-0.61	-8.51**	-4.44	-0.58	0.00	11.11	0.00	-1.39	-0.35	1.07	14.48*	18.03*	0.96	15.59**	16.22**	-0.92	1.19	-5.84	-1.23
BLD 203 × WNC 31702	-1.68	4.14	7.98*	-1.06	3.89	8.09*	10.00	22.22	10.00	4.09*	5.40**	4.27*	13.72*	14.17	2.89	20.82**	21.87**	3.23	3.18	-2.34	2.45
BLD 226 × WNC 40104	4.05	4.65	10.43**	2.44	3.28	9.25**	-21.74*	-18.18	-10.00	4.07*	7.30**	4.63*	14.25*	15.69*	-0.48	9.76*	11.23*	-4.15	6.03	3.82	-2.54
BLD 226 × WNC 40223	7.29*	8.88**	12.88**	5.46*	7.22*	11.56**	-21.74*	-18.18	-10.00	1.75	3.94*	3.20	14.05*	15.00	-0.24	13.23**	15.05**	-1.38	12.18**	4.16	-2.23
BLD 226 × WNC 40108	0.28	4.02	11.04**	0.52	3.23	10.98**	4.76	22.22	10.00	0.69	0.69	4.27*	18.45**	20.28*	2.89	17.24**	19.46**	1.84	9.22*	7.16	0.59
BLD 226 × WNC 31702	-3.58	0.57	7.36*	-3.13	0.00	7.51*	4.76	22.22	10.00	1.23	3.60	2.49	20.27**	21.58**	7.23	17.62**	20.24**	1.84	-1.02	-1.11	-7.18
BLD 227 × WNC 40104	-6.86*	-5.23	0.00	-6.45*	-4.92	0.58	0.00	0.00	10.00	0.18	2.55	0.00	14.91*	17.65*	1.20	18.54**	21.39**	4.61	5.99	2.40	-1.18
BLD 227 × WNC 40223	-0.86	1.78	5.52	-1.90	0.56	4.62	-18.18*	-18.18	-10.00	2.12	3.58	2.85	18.80**	21.11**	5.06	10.99*	13.98*	-2.30	8.61*	-0.42	-3.91
BLD 227 × WNC 40108	-9.04**	-6.74*	1.84	-8.05**	-6.35*	2.31	10.00	22.22	10.00	-1.04	-0.35	1.78	21.26**	24.51**	6.51	18.64**	22.16**	4.15	-2.19	-5.32	-8.63*
BLD 227 × WNC 31702	-8.99**	-6.18*	2.45	-9.04**	-6.88*	1.73	-10.00	0.00	-10.00	2.65	4.32*	3.20	17.38**	17.38*	5.78	17.43**	21.33**	2.76	5.92	4.38	0.73
BLD 246 × WNC 40104	-3.17	-2.33	3.07	-2.17	-1.64	4.05	14.29	20.00	20.00	3.91*	6.57**	3.91*	18.49**	22.97**	5.78	20.73**	22.99**	5.99	15.65**	14.17**	5.40
BLD 246 × WNC 40223	-4.07	-2.33	1.23	-4.66	-3.33	0.58	-14.29	-10.00	-10.00	3.70*	5.38**	4.63*	12.90*	16.67*	1.20	14.21**	16.67**	0.00	22.38**	14.51**	5.72
BLD 246 × WNC 40108	-8.84**	-5.71	1.23	-7.09**	-4.32	2.31	26.32*	33.33**	20.00	-2.94	-2.43	0.00	13.67*	18.31*	1.20	16.09**	18.92**	1.38	4.23	3.10	-4.81
BLD 246 × WNC 31702	-9.34**	-5.71	1.23	-8.09**	-4.86	1.73	15.79	22.22	10.00	2.12	3.96*	2.85	8.71	10.16	-0.72	14.35**	17.52**	-0.46	-3.66	-4.36	-10.40*
S.Em.±	1.60	1.85	1.85	1.60	1.85	1.85	0.32	0.37	0.37	1.53	1.77	1.77	7.93	9.15	9.15	3.04	3.51	3.51	0.51	0.59	0.59
Range Min	-9.34	-6.74	-0.61	-9.04	-6.88	-0.58	-21.74	-18.18	-10.00	-2.94	-2.43	-0.71	-7.34	-3.74	-13.25	0.31	3.23	-11.52	-8.74	-10.09	-15.58
Range Max.	7.29	10.00	12.88	5.46	8.19	11.56	26.32	33.33	20.00	4.09	7.30	4.63	22.09	24.51	7.23	20.82	22.99	5.99	22.38	14.51	5.72

*and ** indicate significance at 5% and 1 %.

Table 2b: Magnitude of heterosis for different characters in maize

Crosses	CG			KRC			KR			KYP			SP			100-KW			PC		
	MP	HB	SH	MP	HB	SH	MP	HB	SH	MP	HB	SH	MP	HB	SH	MP	HB	SH	MP	HB	SH
BLD 170 × WNC 40104	13.94**	12.89*	3.08	22.63**	20.00*	3.70	56.31**	51.89**	26.27*	14.71*	12.72	1.50	8.79**	8.01*	3.82	45.31**	43.08**	14.81*	21.44	18.71	-20.36*
BLD 170 × WNC 40223	13.58**	12.36*	2.91	12.86	12.86	-2.47	29.27*	26.19	3.92	3.48	2.02	-8.75	10.15**	9.01*	5.47	8.97	-1.25	-2.47	16.93	16.93	-21.56*
BLD 170 × WNC 40108	15.34**	13.42**	5.16	18.31*	16.67	3.70	22.72	15.42	2.75	24.89**	21.73**	11.50	5.41	4.47	0.79	31.78**	30.77**	4.94	23.12*	20.51	-15.57
BLD 170 × WNC 31702	16.5**	14.49**	6.28	25.35**	23.61**	9.88	35.98**	34.98*	7.45	4.79	2.20	-6.54	7.64*	6.88*	2.72	24.09**	18.06*	4.94	42.83**	38.35**	-7.19
BLD 175 × WNC 40104	13.22**	11.97*	2.24	20.00*	15.07	3.70	38.13**	35.85*	12.94	8.65	7.92	-2.82	12.74**	12.65**	8.27*	5.04	-3.95	-9.88	35.26**	32.73*	-14.97
BLD 175 × WNC 40223	17.69**	16.22**	6.45	30.07**	27.40**	14.81	46.99**	45.24**	19.61	14.99*	14.61*	2.50	6.37*	5.94	2.49	12.82*	10.00	8.64	17.22	12.49	-24.55**
BLD 175 × WNC 40108	8.22	6.23	-1.51	18.62*	17.81*	6.17	48.61**	41.41**	25.88*	9.64	8.01	-1.11	7.45*	7.16*	3.39	14.29*	5.26	-1.23	28.17*	20.51	-15.57
BLD 175 × WNC 31702	7.42	5.37	-2.19	8.97	8.22	-2.47	33.82*	33.17*	7.06	-1.23	-2.64	-10.96	1.06	0.98	-2.94	16.22*	13.16	6.17	29.80*	28.56*	-19.16*
BLD 176 × WNC 40104	8.93*	8.90	-0.50	20.43**	15.86	3.70	45.91**	40.79**	25.88*	16.10**	15.51*	4.01	2.62	2.50	-1.48	28.79**	23.19**	4.94	25.43*	18.18	-14.37
BLD 176 × WNC 40223	14.4**	14.26**	4.65	24.91**	22.76*	9.88	42.01**	36.40*	21.96	11.65*	11.46	-0.31	9.02**	8.54*	5.01	14.09*	6.25	4.94	5.57	1.65	-26.35**
BLD 176 × WNC 40108	19.98**	19.11**	10.43*	35.64**	35.17**	20.99**	69.23**	68.86**	50.98**	25.47**	23.82**	13.36*	5.15	4.84	1.15	45.86**	40.58**	19.75**	20.16	18.18	-14.37
BLD 176 × WNC 31702	15.03**	14.13**	5.94	24.57**	24.14**	11.11	56.38**	47.81**	32.16*	14.86*	13.41*	3.71	6.44*	6.32	2.18	24.82**	22.22**	8.64	39.84**	30.59*	-5.39
BLD 201 × WNC 40104	10.38*	10.15*	1.01	20.86*	16.67	3.70	48.61**	45.91**	25.88*	17.61**	17.41**	5.72	7.42*	6.70	2.55	26.15**	22.39**	1.23	17.59	16.51	-23.95**
BLD 201 × WNC 40223	11.56**	11.49*	2.24	16.90*	15.28	2.47	52.56**	49.09**	28.63*	9.37	9.18	-2.02	9.05**	7.96*	4.45	7.48	-1.25	-2.47	28.51*	26.77*	-14.96
BLD 201 × WNC 40108	13.68**	13.06**	4.82	12.50	12.50	0.00	48.10**	45.81**	29.80*	19.96**	18.77**	8.73	9.43**	8.48*	4.66	28.24**	25.37**	3.70	-1.77	-5.13	-33.53**
BLD 201 × WNC 31702	12.64**	11.96*	3.92	16.67*	16.67	3.70	44.21**	38.64**	19.61	6.05	5.05	-3.93	4.67	3.96	-0.08	19.42**	15.28	2.47	34.60**	32.13*	-13.77
BLD 203 × WNC 40104	12.77**	10.93*	4.71	15.86*	7.69	3.70	39.46**	32.91*	21.96	12.45*	12.39	1.20	4.31	4.27	0.22	25.71**	14.29	8.64	3.13	-10.92	-21.56*
BLD 203 × WNC 40223	14.77**	13.06**	6.73	17.57*	11.54	7.41	49.10**	41.45**	29.80*	10.70	10.39	-0.72	4.64	4.26	0.86	28.66*	26.25**	24.69**	11.18	-2.06	-13.77
BLD 203 × WNC 40108	14.08**	13.06**	6.73	20.00**	15.38	11.11	70.07**	67.52**	53.73**	15.84**	14.82*	5.12	7.00*	6.76	3.00	4.96	-3.90	-8.64	19.69*	7.46	-5.39
BLD 203 × WNC 31702	13.53**	12.59**	6.28	13.33	8.97	4.94	48.28**	38.46**	27.06*	6.26	5.38	-3.63	6.76*	6.71	2.56	-4.70	-7.79	-12.35	-1.59	-15.66	-25.75**
BLD 226 × WNC 40104	8.74*	7.85	0.11	17.48*	10.53	3.70	26.74*	21.03	10.59	0.39	0.33	-9.66	6.75*	6.23	2.10	13.70*	0.00	2.47	29.49*	22.47	-11.98
BLD 226 × WNC 40223	12.22**	11.47*	3.48	15.75*	11.18	4.32	38.15**	31.33*	20.00	13.05*	12.74	1.40	7.71*	6.84*	3.36	-16.56**	-18.07**	-16.05*	26.74*	22.51	-11.98
BLD 226 × WNC 40108	8.34*	8.27	0.50	21.62**	18.42*	11.11	44.35**	42.49**	30.20*	24.70**	23.60**	13.16*	7.78*	7.05*	3.29	8.84	-3.61	-1.23	42.59**	40.79**	1.20
BLD 226 × WNC 31702	10.27*	10.27*	2.35	17.57*	14.47	7.41	42.20**	33.05*	21.57	21.66**	20.66**	10.34	4.66	4.16	0.11	7.10	0.00	2.47	8.45	1.67	-26.95**
BLD 227 × WNC 40104	7.72	4.76	1.23	20.86*	16.67	3.70	61.84**	58.02**	31.37*	16.00**	15.74*	4.21	3.03	1.90	0.15	2.74	-9.64	-7.41	50.4**	42.82**	1.80
BLD 227 × WNC 40223	11.14**	8.24	4.60	21.13**	19.44*	6.17	33.01*	30.48*	7.45	-1.68	-1.79	-11.97*	5.11	4.29	2.50	-7.98	-9.64	-7.41	21.22	17.67	-16.17
BLD 227 × WNC 40108	4.32	2.20	-1.23	13.89	13.89	1.23	35.66**	28.19*	14.12	5.60	4.50	-4.33	7.72*	6.73*	4.90	-0.68	-12.05	-9.88	12.71	11.76	-20.36*
BLD 227 × WNC 31702	7.99	5.86	2.30	18.06*	18.06*	4.94	66.42**	66.01**	32.16*	7.99	6.92	-2.22	2.34	1.20	-0.53	7.10	0.00	2.47	35.73**	27.75*	-8.98
BLD 246 × WNC 40104	11.09**	8.28	4.15	25.00**	23.19*	4.94	81.00**	70.75**	41.96**	20.11**	19.25**	8.93	6.53*	6.29	2.16	10.49	-1.25	-2.47	28.53**	16.74	-8.38
BLD 246 × WNC 40223	14.39**	11.66*	7.40	26.62**	25.71**	8.64	56.28**	48.10**	21.96	24.74**	23.43**	12.75*	6.30*	5.71	2.27	-5.00	-5.00	-6.17	11.92	3.79	-18.56*
BLD 246 × WNC 40108	6.35	4.43	0.45	21.99**	19.44*	6.17	33.49*	22.03	8.63	6.59	6.48	-2.52	0.12	-0.30	-3.81	8.33	-2.50	-3.70	31.41**	24.37*	-2.40
BLD 246 × WNC 31702	13.29**	11.31*	7.06	17.73*	15.28	2.47	43.22**	37.93*	9.80	8.74	8.68	-0.61	3.52	3.29	-0.73	-3.95	-8.75	-9.88	22.02*	9.90	-13.77
S.Em.±	0.46	0.54	0.54	0.74	0.85	0.85	1.84	2.12	2.12	5.64	6.52	6.52	2.21	2.55	2.55	1.64	1.89	1.89	0.74	0.86	0.86
Range Min	4.32	2.20	8.97	8.97	7.69	-2.47	22.72	15.42	2.75	-1.68	-2.64	-11.97	0.12	-0.30	-3.81	-16.56	-18.07	-16.05	-1.77	-15.66	-33.53
Max.	19.98	19.11	35.64	35.64	35.17	20.99	81.00	70.75	53.73	25.47	23.82	13.36	12.74	12.65	8.27	45.86	43.08	24.69	50.40	42.82	1.80

*and ** indicate significance at 5% and 1 %.

Table 3: Analysis of variance for combining ability and estimates of component of variance for different characters in Maize

Source of variation	d.f.	Mean sum of square													
		DT	DS	ASI	PH	EH	DM	CL	CG	KRC	KR	KYP	SP	KW	PC
Replications	2	7.16	9.38	0.59	2.26	307.54	153.26**	3.96**	2.79**	0.99	29.98*	77.76	13.02	20.57*	3.69*
Crosses	31	10.30**	9.59*	0.42*	7.10	207.30	35.51*	1.82**	0.38	0.79	13.46*	177.99**	11.10	18.06**	1.95*
Lines	7	30.47**	28.26**	0.30	11.98	758.74**	119.44**	1.09	0.58	1.04	21.32**	165.08	7.33	25.10**	1.63
Testers	3	6.71	2.28	1.38**	2.28*	9.09	25.62	2.24*	0.49	0.70	10.22	301.32*	20.19	0.47	1.18
Lines× Testers	21	4.09	4.41	0.32	6.16	51.81	8.95	2.00**	0.30	0.72	11.30	164.67*	11.07	18.23**	2.17*
Error	62	4.86	5.06	0.22	5.08	127.20	20.87	0.55	0.45	1.03	7.10	83.86	12.03	4.98	1.11
Estimates of variance component															
σ^2 Lines		2.20**	1.99**	0.002	0.49	58.91**	0.001**	0.08	0.02	0.03	0.84	0.03	0.31	0.57	0.05
σ^2 Testers		0.11	0.09	0.05*	0.16	1.78	0.70	0.01	0.01	0.00	0.05	7.59	0.38	0.74	0.04
σ^2gca		0.81**	0.60**	0.03*	0.05	18.45**	3.53**	0.02	0.01	0.01	0.25	4.57	0.15	0.30	0.04
σ^2sca		0.26	0.22	0.03	0.36	25.13	3.97	0.48**	0.05	0.10	1.40	26.94	0.32	4.42**	0.35*
σ^2gca/σ^2sca		3.14	2.79	0.87	0.15	0.73	0.89	0.04	0.26	0.08	0.18	0.17	0.47	0.07	0.12

*and ** indicate significance at 5 % and 1 %.

Table 4: Estimates of *gca* effects of parents for different characters in maize

	Parents	DT	DS	ASI	PH	EH	DM	CL	CG	KRC	KR	KYP	SP	KW	PC
Lines	BLD 170	0.60	0.50	-0.10	0.25	-11.61**	-4.91**	0.35	0.10	-0.22	-2.13	-1.87	0.90	1.29	-0.09
	BLD 175	-0.15	-0.33	-0.19	-1.33*	-13.7**	-4.57**	-0.20	-0.27	-0.02	-1.06	-4.62	0.59	0.04	-0.32
	BLD 176	-0.98	-1.00	-0.02	-0.58	4.05	0.09	-0.42	0.19	0.61	1.72	4.45	-0.24	2.38	0.01
	BLD 201	-1.06	-1.00	0.06	-1.08	3.89	0.18	-0.36	-0.06	-0.36	0.58	1.10	0.67	0.13	-0.61
	BLD 203	-0.40	-0.17	0.23	0.08	2.47	1.34	0.15	0.31	0.11	1.79	-0.69	-0.28	0.63	-0.13
	BLD 226	3.69**	3.58**	-0.10	1.67*	4.14	1.43	0.09	-0.22	0.09	-0.34	2.94	0.14	-1.04	0.28
	BLD 227	-0.65	-0.75	-0.10	0.08	7.30*	3.43*	0.03	-0.21	-0.19	-0.22	-5.15	-0.21	-1.71	0.42
	BLD 246	-1.06	-0.83	0.23	0.92	3.47	3.01*	0.36	0.15	-0.02	-0.34	3.85	-1.57	-1.71	0.44
	S.Em.±	0.64	0.65	0.13	0.65	3.26	1.32	0.21	0.19	0.29	0.77	2.64	1.00	0.64	0.30
Testers	WNC 40104	-0.52	-0.38	0.15	-0.46	-0.78	0.68	0.35*	-0.18	-0.21	0.34	0.56	0.15	0.21	0.10
	WNC 40223	0.73	0.38	-0.35**	0.21	-0.03	-1.49	-0.20	0.16	0.07	-0.58	-2.20	0.98	-0.08	-0.31
	WNC 40108	-0.19	-0.04	0.15	0.13	0.09	0.72	0.15	-0.04	0.19	0.75	4.77	0.11	-0.08	0.20
	WNC 31702	-0.02	0.04	0.06	0.13	0.72	0.09	-0.30*	0.06	-0.06	-0.51	-3.12	-1.24	-0.04	0.02
	S.Em.±	0.45	0.46	0.10	0.46	2.30	0.93	0.15	0.14	0.21	0.54	1.87	0.71	0.46	0.21
Range	Min.	-1.06	-1.00	-0.35	-1.33	-13.70	-4.91	-0.42	-0.27	-0.36	-2.13	-4.62	-1.57	-1.71	-0.61
	Max.	3.69	3.58	0.23	1.67	7.30	3.43	0.35	0.31	0.61	1.79	4.77	0.98	2.38	0.44

*and ** indicate significance at 5 % and 1 %.

yield is a dependent complex trait in maize. Improvement of kernel yield is the combinational effect of different direct as well as indirect yield attributing traits. In the present study, the estimates of heterosis were found in desired direction for most of the crosses under study. These crosses were also found desirable for any of the yield attributing traits. Thus, improvement of kernel yield in maize through heterosis breeding is rewarding (Abdel-Moneam *et al.,* 2024).

The results for 100-kernel weight exhibited a wide range of heterosis, with relative heterosis ranging from -16.56% to 45.86% and standard heterosis -16.05% to 24.69%. For protein content, the heterobeltiosis ranged from -15.66% to 42.82% and standard heterosis ranged from -33.53% to 1.80%, with the crosses BLD 227 × WNC 40104 and BLD 226 × WNC 40108 exhibited positive standard heterosis. Similar to our findings, Scaria *et al.*, (2020) demonstrated a positive standard heterosis for 100-kernel weight and protein content. The ANOVA for combining ability, which partitioned the total genetic variance into components attributable to GCA and SCA (Table 3). Significant mean squares for lines were observed for days to tasseling and silking, plant and ear height, kernels per row, and 100-kernel weight, indicating a notable role of additive gene action in the inheritance of these traits. Conversely, the mean squares for testers were significant for ASI, days to maturity, cob length, and kernel yield per plant, suggesting these traits were more

Table 5: Estimates of *sca* effects of crosses for different characters in maize

Crosses	DT	DS	ASI	PH	EH	DM	CL	CG	KRC	KR	KYP	SP	KW	PC
BLD 170 × WNC 40104	0.60	0.46	-0.15	0.13	2.61	-0.68	0.39	0.03	0.21	2.41	1.72	0.32	2.29	-0.51
BLD 170 × WNC 40223	1.02	1.04	0.02	0.79	2.20	1.49	-0.38	-0.33	-0.74	-0.47	-6.73	0.76	-2.08	-0.21
BLD 170 × WNC 40108	-0.06	-0.21	-0.15	0.88	1.74	0.28	0.02	0.13	-0.19	-2.00	8.40	-1.96	-0.08	-0.14
BLD 170 × WNC 31702	-1.56	-1.29	0.27	-1.79	-6.55	-1.09	-0.03	0.17	0.72	0.06	-3.39	0.87	-0.12	0.86
BLD 175 × WNC 40104	-0.31	-0.04	0.27	0.38	4.36	2.32	-0.59	0.30	0.01	-0.92	-0.26	4.04	-3.13*	0.25
BLD 175 × WNC 40223	0.10	0.21	0.10	-0.62	0.28	-0.51	0.58	0.46	0.93	1.13	8.34	-1.21	2.17	-0.27
BLD 175 × WNC 40108	-0.31	-0.71	-0.40	-0.54	-2.51	-1.39	0.71	-0.29	-0.13	0.87	-2.60	0.34	-0.50	0.09
BLD 175 × WNC 31702	0.52	0.54	0.02	0.79	-2.14	-0.43	-0.70	-0.47	-0.81	-1.07	-5.48	-3.16	1.46	-0.07
BLD 176 × WNC 40104	0.19	-0.38	-0.56*	-1.38	-6.05	-1.01	0.43	-0.49	-0.63	-1.51	-1.85	-2.60	-1.46	-0.03
BLD 176 × WNC 40223	-1.40	-1.46	-0.06	-1.04	6.86	-0.18	-0.31	-0.21	-0.24	-1.25	-3.82	1.55	-1.17	-0.78
BLD 176 × WNC 40108	0.52	0.96	0.44	2.71*	-3.59	-0.05	0.80	0.67	0.84	2.35	4.17	-0.55	2.83*	-0.12
BLD 176 × WNC 31702	0.69	0.88	0.19	-0.29	2.78	1.24	-0.92*	0.04	0.02	0.41	1.50	1.60	-0.21	0.93
BLD 201 × WNC 40104	-0.73	-0.38	0.35	0.46	-0.55	0.24	0.29	-0.06	0.34	-0.36	3.37	-0.42	-0.21	-0.34
BLD 201 × WNC 40223	0.02	-0.13	-0.15	-0.54	-3.64	0.74	-1.21**	-0.25	-0.07	1.03	-2.33	0.21	-0.92	0.96
BLD 201 × WNC 40108	1.27	1.29	0.02	0.54	2.57	1.53	-0.26	0.26	-0.46	-0.10	2.46	1.24	0.75	-1.36
BLD 201 × WNC 31702	-0.56	-0.79	-0.23	-0.46	1.61	-2.51	1.18**	0.05	0.19	-0.58	-3.50	-1.04	0.38	0.74
BLD 203 × WNC 40104	-0.73	-0.54	0.19	-1.04	0.53	-0.93	-0.76	0.01	-0.13	-2.24	0.21	-1.26	1.29	-0.58
BLD 203 × WNC 40223	-0.31	0.04	0.35	-0.04	-1.89	-0.76	-0.28	-0.08	0.00	0.02	0.88	-1.59	5.92	0.59
BLD 203 × WNC 40108	-1.73	-2.21	-0.48	-0.96	-0.34	-0.97	0.02	0.11	0.27	2.75	0.29	0.91	-3.08	0.90
BLD 203 × WNC 31702	2.77	2.71	-0.06	2.04	1.70	2.66	1.01	-0.04	-0.14	-0.52	-1.39	1.93	-4.13	-0.90
BLD 226 × WNC 40104	0.52	0.04	-0.48	1.38	-3.14	-3.34	-0.31	0.00	-0.11	-2.04	-15.3	-0.24	1.29	-0.06
BLD 226 × WNC 40223	0.60	0.63	0.02	-0.62	-3.55	0.82	0.29	0.07	-0.32	0.48	-0.44	-0.1	-3.42	0.36
BLD 226 × WNC 40108	0.52	0.71	0.19	0.46	0.66	0.95	0.35	-0.09	0.29	0.88	5.46	0.71	0.58	1.13
BLD 226 × WNC 31702	-1.65	-1.37	0.27	-1.21	6.03	1.57	-0.34	0.03	0.14	0.68	10.27	-0.38	1.54	-1.43
BLD 227 × WNC 40104	-0.81	-0.63	0.19	-1.38	-3.97	0.99	-0.05	0.12	0.17	1.38	7.96	-1.38	-0.71	1.14
BLD 227 × WNC 40223	0.94	0.96	0.02	0.63	0.61	-1.84	0.11	0.19	0.16	-1.77	-6.98	-0.41	-0.42	-0.20
BLD 227 × WNC 40108	-0.15	0.04	0.19	-0.29	2.49	0.61	-0.94	-0.31	-0.49	-1.97	-5.59	2.30	-1.08	-1.12
BLD 227 × WNC 31702	0.02	-0.38	-0.40	1.04	0.86	0.24	0.88	0.01	0.16	2.36	4.61	-0.51	2.21	0.18
BLD 246 × WNC 40104	1.27	1.46	0.19	1.46	6.20	2.41	0.59	0.10	0.14	3.29	4.14	1.52	0.63	0.13
BLD 246 × WNC 40223	-0.98	-1.29	-0.31	1.46	-0.89	0.24	1.19	0.16	0.26	0.82	11.09	0.78	-0.08	-0.44
BLD 246 × WNC 40108	-0.06	0.12	0.19	-2.79	-1.01	-0.97	-0.71	-0.47	-0.13	-2.78	-12.61	-3.01	0.58	0.62
BLD 246 × WNC 31702	-0.23	-0.29	-0.06	-0.13	-4.30	-1.68	-1.08	0.21	-0.28	-1.33	-2.62	0.70	-1.13	-0.31
S.Em.±	1.27	1.30	0.27	1.30	6.51	2.64	0.43	0.39	0.59	1.54	5.29	2.00	1.29	1.29
Range Min.	-1.73	-2.21	-0.56	-2.79	-6.55	-3.34	-1.21	-0.47	-0.81	-2.78	-15.30	-3.16	-4.13	-1.43
Max.	2.77	2.71	0.44	2.71	6.86	2.66	1.19	0.67	0.93	3.29	11.09	4.04	5.92	1.14

*and ** indicate significance at 5 % and 1 %.

influenced by the testers' genetic effects, which indicate that lines and testers have unique ability from each other for different traits.Furthermore, significant mean squares for crosses were recorded for days to tasseling and silking, ASI, days to maturity, cob length, kernels per row, kernel yield per plant, 100-kernel weight and protein content. Previously, Abd El-Latif *et al*. (2023) reported significant mean squares in different crosses for number of days to 50% silking and kernel yield per plant. This proved that these traits are heritable from the both line and testers. The significant line × tester interactions observed for cob length, kernel yield per plant, 100-kernel weight, and protein content suggest the presence of specific combining ability, with further potential for improvement of these traits through heterosis breeding. To enhance the accuracy of genetic parameter estimates, further research should include multi-location trials to address genotype-by-environment interactions. The ratio of GCA variance to SCA variance was found to be less than unity for most of the traits, except days to tasseling and silking, indicating the predominance of non-additive gene action in the expression. Conversely, the traits days to tasseling and silking exhibited significant GCA variance, highlighting the role of additive gene action in their expression. Similarly, El Sayed *et al*., (2022) also reported an additive gene action in traits like days to tasseling and silking. The GCA effects of 12 parents and SCA effects of 32 crosses were studied in the present study (Table 4,5). The tester WNC 40223 exhibited a significant negative GCA effect for ASI, indicating its potential as a good general combiner for reducing this interval of days to tasseling and silking. The cross BLD 176 × WNC 40104 also demonstrated significant negative SCA effects, contributing to a reduced ASI. The line BLD 175 exhibited a significant negative GCA effect, making it a good general combiner as well as cross BLD 246 × WNC 40108 exhibited significant negative SCA effects, suggesting it as a good specific combiner for earlier maturity. Lines BLD 175 and BLD 170 displayed significant negative GCA effects for both plant and ear height, indicating their potential as good general combiners for dwarfness. The cross BLD 246 × WNC 40223 exhibited the highest positive SCA effects for cob length, suggesting it as a potential hybrid for improvement. Among the lines, BLD 176 exhibited the highest positive GCA effects, making it a good general combiner, cross BLD 175 × WNC 40223 demonstrated the highest positive SCA effects, indicating the potential for improving kernel rows per cob through heterosis.

The number of desired alleles increased in crosses formed from pairing parents with the best GCA and SCA values. Due to additive and additive dominant gene activities, crosses including strong general combiners as well as good weak combiner typically result in significant SCA effects. The cross BLD 246 × WNC 40223 (both parents are average general combiner) showed the highest levels of SCA in kernel yield per plant (Rahmani *et al.,* 2023). For 100-kernel weight, the lines BLD 176 and BLD 170 exhibited positive GCA effects and crosses BLD 203 × WNC 40223 and BLD 176 × WNC 40108 exhibited significant positive SCA effects, suggesting they are good specific combiners. The lines BLD 246, BLD 227, BLD 226, and BLD 176 demonstrated positive GCA effects, while the cross BLD 227 × WNC 40104 exhibited the highest positive SCA effects, suggesting it as a potential specific combiner for improving protein content (Abdulazeez *et al.,* 2021). The crosses BLD 176 × WNC 40108, BLD 226 × WNC 40108, andBLD 246 × WNC 40223 emerged as the most promising for kernel yield per plant and its component traits, demonstrating high mean performance, significant heterosis and SCA effects. These crosses are expected to offer valuable genetic combinations that can be further explored in diverse climatic conditions and breeding programs for the development of high-yielding hybrids and inbred lines (Mishra *et al.,* 2024). Additionally, the cross BLD 227 × WNC 40104 recorded the high mean performance, significant heterosis and SCA effects for protein content.

Thus, the findings of this study reveals noteworthy genetic variability and heterosis among the maize genotypes, emphasising strong potential for yield improvement through targeted hybrid breeding. Promising crosses, notably BLD 176 × WNC 40108, BLD 226 × WNC 40108 and BLD 246 × WNC 40223 proved to be outstanding crosses for kernel yield per plant on the basis of per se performance, heterosis, SCA effects and higher frequency of transgressive segregants compared to other crosses. The study supports targeted hybrid breeding strategies aimed at maximizing yield potential, improving food security, and promoting sustainable agricultural practices.

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